BLAST Basic Local Alignment Search Tool

Job Title: 3 sequences (BorrProbe)

- Your search parameters were adjusted to search for a short input sequence.

BLASTN 2.2.17 (Aug-26-2007)

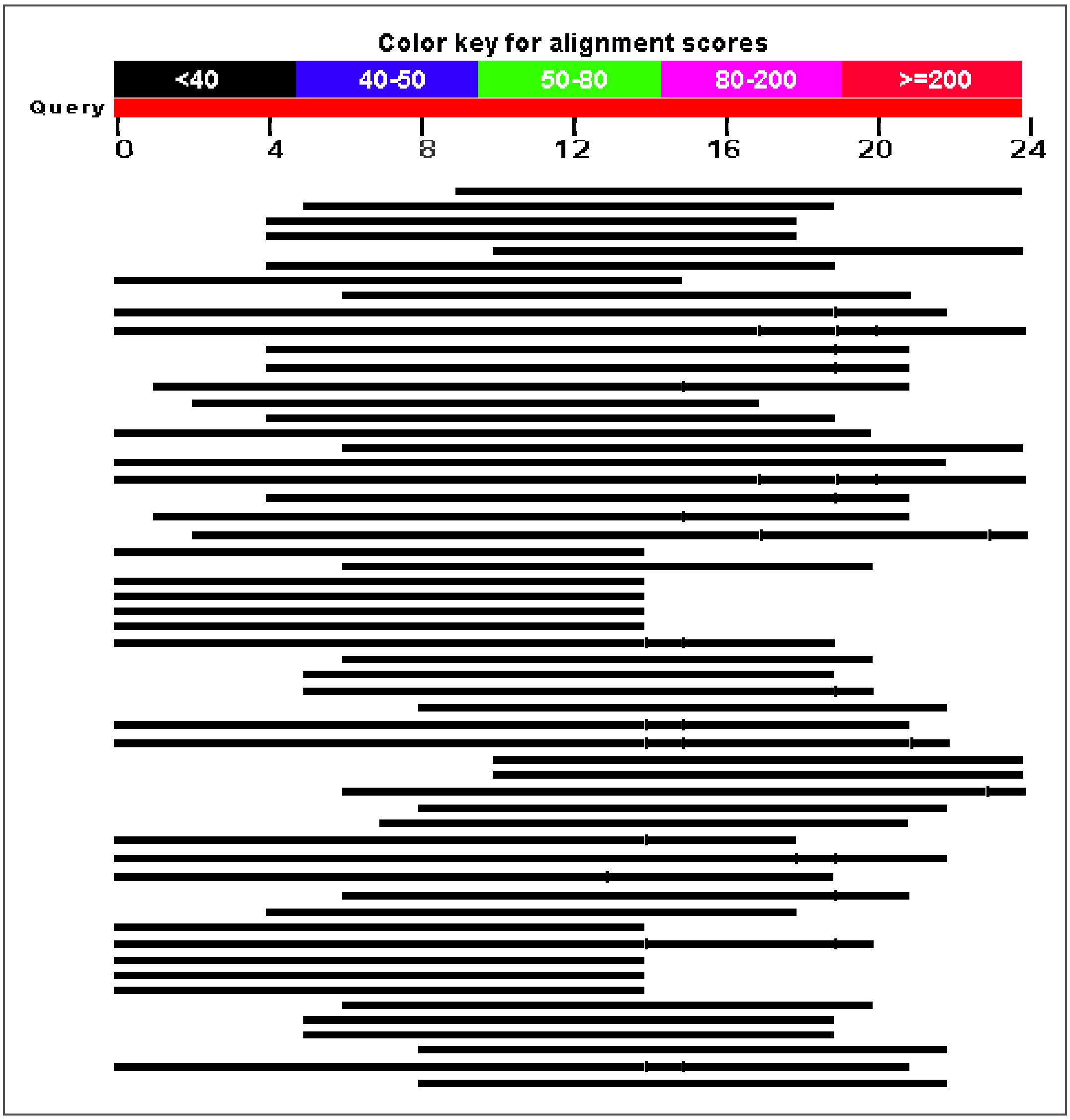
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. RID: PMMSN8R0013 **Database:** human build 36 RNA, reference and alternate assemblies 46,285 sequences; 5,957,977,502 total letters

Genome View

Show positions of the BLAST hits in the human genome using the Entrez Genomes MapViewer

Query= BorrProbe Length=24

Distribution of 175 Blast Hits on the Query Sequence



Distance tree of results NEW

Legend for links to other resources: U UniGene E GEO G Gene S Structure M M

Sequences producing significant alignments:
(Click headers to sort columns)

Transcripts

NM_014306.2	Homo sapiens chromosome 22 open reading frame 28 (C22orf28), mRNA	30.2	30.2	62%	28	100%	U E G M
NM_005413.1	Homo sapiens sine oculis homeobox homolog 3 (Drosophila) (SIX3), mRNA	28.2	28.2	58%	112	100%	
XM_001126326.1	PREDICTED: Homo sapiens agrin (AGRIN), mRNA	28.2	28.2	58%	112	100%	G M
NM_198576.2	Homo sapiens agrin (AGRIN), mRNA	28.2	28.2	58%	112	100%	U E G M
NM_006370.1	Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1B (yeast) (VTI1B), mRNA	28.2	28.2	58%	112	100%	U E G M

Genomic sequences [show first]

NW_924320.1	Homo sapiens genomic contig, alternate assembly (based on Celera assembly)	30.2	30.2	62%	28	100%
NW_927173.1	Homo sapiens chromosome 19 genomic contig, alternate assembly (based on Celera assembly)	30.2	30.2	62%	28	100%
NW_927129.1	Homo sapiens chromosome 18 genomic contig, alternate assembly (based on Celera assembly)	30.2	30.2	62%	28	100%
NW_926018.1	Homo sapiens chromosome 16 genomic contig, alternate assembly (based on Celera assembly)	30.2	135	91%	28	100%
NW_925561.1	Homo sapiens chromosome 14 genomic contig, alternate assembly (based on Celera assembly)	30.2	111	100%	28	100%
NW_923206.1	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on Celera assembly)	30.2	58.5	70%	28	100%
NT_079592.2	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on CRA_TCAGchr7v2)	30.2	84.7	70%	28	100%
NW_923184.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on Celera assembly)	30.2	111	83%	28	100%
NW_922984.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on Celera assembly)	30.2	30.2	62%	28	100%
NW_921562.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on Celera assembly)	30.2	60.5	62%	28	100%
NT_011255.14	Homo sapiens chromosome 19 genomic contig, reference assembly	30.2	58.5	83%	28	100%
NT_025028.13	Homo sapiens chromosome 18 genomic contig, reference assembly	30.2	82.8	75%	28	100%
NT_037887.4	Homo sapiens chromosome 16 genomic contig, reference assembly	30.2	82.8	91%	28	100%
NT_026437.11	Homo sapiens chromosome 14 genomic contig, reference assembly	30.2	111	100%	28	100%

NT_007819.16	Homo sapiens chromosome 7 genomic contig, reference assembly	30.2	84.7	70%	28	100%
NT_025741.14	Homo sapiens chromosome 6 genomic contig, reference assembly	30.2	84.7	83%	28	100%
NT_007592.14	Homo sapiens chromosome 6 genomic contig, reference assembly	30.2	84.7	91%	28	100%
NW_927628.1	Homo sapiens chromosome 22 genomic contig, alternate assembly (based on Celera assembly)	28.2	28.2	58%	112	100%
NW_927140.1	Homo sapiens chromosome 19 genomic contig, alternate assembly (based on Celera assembly)	28.2	28.2	58%	112	100%
NW_927206.1	Homo sapiens chromosome 19 genomic contig, alternate assembly (based on Celera assembly)	28.2	28.2	58%	112	100%
NW_926772.1	Homo sapiens chromosome 17 genomic contig, alternate assembly (based on Celera assembly)	28.2	28.2	58%	112	100%
NW_925484.1	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on Celera assembly)	28.2	28.2	58%	112	100%
NW_925473.1	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on Celera assembly)	28.2	28.2	58%	112	100%
NW_925517.1	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on Celera assembly)	28.2	82.8	79%	112	100%
NW_925173.1	Homo sapiens chromosome 11 genomic contig, alternate assembly (based on Celera assembly)	28.2	28.2	58%	112	100%
NW_924884.1	Homo sapiens chromosome 10 genomic contig, alternate assembly (based on Celera assembly)	28.2	28.2	58%	112	100%
NW_923907.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on Celera assembly)	28.2	54.5	62%	112	100%
NW_923707.1	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on Celera assembly)	28.2	54.5	58%	112	100%
NW_923640.1	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on Celera assembly)	28.2	82.8	87%	112	100%
NT_079596.2	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on CRA_TCAGchr7v2)	28.2	137	91%	112	100%
NT_113893.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (derived from QBL cell line)	28.2	28.2	58%	112	100%
NT_113891.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (derived from COX cell line)	28.2	28.2	58%	112	100%
NW_923073.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on Celera assembly)	28.2	54.5	75%	112	100%
NW_922751.1	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on Celera assembly)	28.2	28.2	58%	112	100%
NW_922729.1	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on Celera assembly)	28.2	28.2	58%	112	100%
NW_922073.1	Homo sapiens chromosome 4 genomic contig, alternate assembly (based on Celera assembly)	28.2	54.5	75%	112	100%
NW_921807.1	Homo sapiens chromosome 3 genomic contig, alternate assembly (based on Celera assembly)	28.2	187	91%	112	100%

NW_927719.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on Celera assembly)	28.2	54.5	79%	112	100%
NW_921618.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on Celera assembly)	28.2	80.8	62%	112	100%
NW_921350.1	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on Celera assembly)	28.2	28.2	58%	112	100%
NT_011520.11	Homo sapiens chromosome 22 genomic contig, reference assembly	28.2	28.2	58%	112	100%
NT_011109.15	Homo sapiens chromosome 19 genomic contig, reference assembly	28.2	80.8	83%	112	100%
NT_010799.14	Homo sapiens chromosome 17 genomic contig, reference assembly	28.2	28.2	58%	112	100%
NT_009952.14	Homo sapiens chromosome 13 genomic contig, reference assembly	28.2	28.2	58%	112	100%
NT_024524.13	Homo sapiens chromosome 13 genomic contig, reference assembly	28.2	56.5	58%	112	100%
NT_033899.7	Homo sapiens chromosome 11 genomic contig, reference assembly	28.2	28.2	58%	112	100%
NT_008818.15	Homo sapiens chromosome 10 genomic contig, reference assembly	28.2	28.2	58%	112	100%
NT_007995.14	Homo sapiens chromosome 8 genomic contig, reference assembly	28.2	28.2	58%	112	100%
NT_007914.14	Homo sapiens chromosome 7 genomic contig, reference assembly	28.2	54.5	58%	112	100%
NT_007933.14	Homo sapiens chromosome 7 genomic contig, reference assembly	28.2	82.8	87%	112	100%
NT_034772.5	Homo sapiens chromosome 5 genomic contig, reference assembly	28.2	28.2	58%	112	100%
NT_023148.12	Homo sapiens chromosome 5 genomic contig, reference assembly	28.2	28.2	58%	112	100%
NT_016297.15	Homo sapiens chromosome 4 genomic contig, reference assembly	28.2	54.5	75%	112	100%
NT_022517.17	Homo sapiens chromosome 3 genomic contig, reference assembly	28.2	54.5	62%	112	100%
NT_005612.15	Homo sapiens chromosome 3 genomic contig, reference assembly	28.2	187	91%	112	100%
NT_005120.15	Homo sapiens chromosome 2 genomic contig, reference assembly	28.2	28.2	58%	112	100%
NT_022184.14	Homo sapiens chromosome 2 genomic contig, reference assembly	28.2	28.2	58%	112	100%
NT_004350.18	Homo sapiens chromosome 1 genomic contig, reference assembly	28.2	28.2	58%	112	100%
NW_926918.1	Homo sapiens chromosome 17 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%
NW_926584.1	Homo sapiens chromosome 17 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	70%	444	94%
NW_926528.1	Homo sapiens chromosome 16 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%
NW_925907.1	Homo sapiens chromosome 15 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%
NW_925884.1	Homo sapiens chromosome 15 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%
NW_925940.1	Homo sapiens chromosome 15 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%

NW_925295.1	Homo sapiens chromosome 12 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%
NW_925395.1	Homo sapiens chromosome 12 genomic contig, alternate assembly (based on Celera assembly)	26.3	78.8	54%	444	100%
NW_924962.1	Homo sapiens chromosome 11 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%
NW_925106.1	Homo sapiens chromosome 11 genomic contig, alternate assembly (based on Celera assembly)	26.3	52.5	83%	444	100%
NW_924584.1	Homo sapiens chromosome 10 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%
NW_924062.1	Homo sapiens chromosome 9 genomic contig, alternate assembly (based on Celera assembly)	26.3	52.5	66%	444	100%
NW_924573.1	Homo sapiens chromosome 9 genomic contig, alternate assembly (based on Celera assembly)	26.3	52.5	62%	444	100%
NW_924018.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%
NW_923984.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on Celera assembly)	26.3	131	70%	444	100%
NW_923273.1	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%
NW_922784.1	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%
NW_922217.1	Homo sapiens chromosome 4 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%
NW_922162.1	Homo sapiens chromosome 4 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%
NW_921651.1	Homo sapiens chromosome 3 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%
NW_928052.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on Celera assembly)	26.3	52.5	79%	444	100%
NW_921351.1	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on Celera assembly)	26.3	78.8	62%	444	100%
NW_927128.1	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%
NW_926128.1	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on Celera assembly)	26.3	26.3	54%	444	100%
NT_035113.6	Homo sapiens chromosome 11 genomic contig, reference assembly	26.3	26.3	54%	444	100%
NT_007422.13	Homo sapiens chromosome 6 genomic contig, reference assembly	26.3	26.3	54%	444	100%
NT_005535.16	Homo sapiens chromosome 3 genomic contig, reference assembly	26.3	26.3	54%	444	100%
NT_005403.16	Homo sapiens chromosome 2 genomic contig, reference assembly	26.3	26.3	54%	444	100%
NT_022221.12	Homo sapiens chromosome 2 genomic contig, reference assembly	26.3	26.3	54%	444	100%

NT_022171.14	Homo sapiens chromosome 2 genomic contig, reference assembly	26.3	52.5	79%	444	100%
NT_005416.12	Homo sapiens chromosome 2 genomic contig, reference assembly	26.3	26.3	54%	444	100%
NT_004487.18	Homo sapiens chromosome 1 genomic contig, reference assembly	26.3	26.3	54%	444	100%
NT_032977.8	Homo sapiens chromosome 1 genomic contig, reference assembly	26.3	52.5	62%	444	100%
NT_004559.13	Homo sapiens chromosome 1 genomic contig, reference assembly	26.3	26.3	54%	444	100%
NT_004610.18	Homo sapiens chromosome 1 genomic contig, reference assembly	26.3	26.3	54%	444	100%

Alignments

```
>ref|NM_014306.2| UEGM Homo sapiens chromosome 22 open reading frame 28 (C22orf2
mRNA
Length=2056


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  10    CCGTCAGGCTTTCGC  24
             |||||||||||||||
Sbjct  1080  CCGTCAGGCTTTCGC  1094


>ref|NM_005413.1|  Homo sapiens sine oculis homeobox homolog 3 (Drosophila) (SIX3),
mRNA
Length=1926


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6     CGCTCCGTCAGGCT  19
             ||||||||||||||
Sbjct  1320  CGCTCCGTCAGGCT  1307


>ref|XM_001126326.1| GM PREDICTED: Homo sapiens agrin (AGRIN), mRNA
Length=6611

 GENE ID: 375790 AGRN | agrin [Homo sapiens] (Over 10 PubMed links)


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  5     TCGCTCCGTCAGGC  18
             ||||||||||||||
Sbjct  5782  TCGCTCCGTCAGGC  5795


>ref|NM_198576.2| UEGM Homo sapiens agrin (AGRIN), mRNA
Length=7319

 GENE ID: 375790 AGRN | agrin [Homo sapiens] (Over 10 PubMed links)


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  5     TCGCTCCGTCAGGC  18
             ||||||||||||||
Sbjct  6500  TCGCTCCGTCAGGC  6513


>ref|NM_006370.1| UEGM Homo sapiens vesicle transport through interaction with t
homolog 1B (yeast) (VTI1B), mRNA
Length=1287

 GENE ID: 10490 VTI1B | vesicle transport through interaction with t-SNAREs
homolog 1B (yeast) [Homo sapiens] (Over 10 PubMed links)


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  11   CGTCAGGCTTTCGC  24
            ||||||||||||||
Sbjct  124  CGTCAGGCTTTCGC  137
```

```
>ref|NW_924320.1|HsCraAADB02_3672  Homo sapiens genomic contig, alternate assembly
assembly)
Length=4459


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  5     TCGCTCCGTCAGGCT  19
             |||||||||||||||
Sbjct  4089  TCGCTCCGTCAGGCT  4075


>ref|NW_927173.1|HsCraAADB02_624 D Homo sapiens chromosome 19 genomic contig, alte
(based on Celera assembly)
Length=7929300

 Features flanking this part of subject sequence:
   30552 bp at 5' side: thrombospondin, type I, domain containing 6
   14647 bp at 3' side: ring finger and KH domain containing 1


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  1       AGTGTCGCTCCGTCA  15
               |||||||||||||||
Sbjct  734245  AGTGTCGCTCCGTCA  734259


>ref|NW_927129.1|HsCraAADB02_620 D Homo sapiens chromosome 18 genomic contig, alte
(based on Celera assembly)
Length=12826439

 Features flanking this part of subject sequence:
   6099 bp at 3' side: hypothetical protein LOC92126


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  7      GCTCCGTCAGGCTTT  21
              |||||||||||||||
Sbjct  55661  GCTCCGTCAGGCTTT  55647


>ref|NW_926018.1|HsCraAADB02_520 D Homo sapiens chromosome 16 genomic contig, alte
(based on Celera assembly)
Length=14690834

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   199382 bp at 5' side: hypothetical protein LOC196483 isoform 2
   1081772 bp at 3' side: hypothetical protein LOC440337


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  1        AGTGTCGCTCCGTCA  15
                |||||||||||||||
Sbjct  5272170  AGTGTCGCTCCGTCA  5272184


 Features in this part of subject sequence:
   hypothetical protein LOC115939


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCGTCAGGCTTTC  22
                |||||||||||||
Sbjct  1330007  CCGTCAGGCTTTC  1329995
```

```
 Features in this part of subject sequence:
   ataxin 2-binding protein 1 isoform 4
   ataxin 2-binding protein 1 isoform 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCGTCAGGCTTTC  22
                |||||||||||||
Sbjct  7587850  CCGTCAGGCTTTC  7587862


 Features in this part of subject sequence:
   RUN domain containing 2A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         AGTGTCGCTCCGT  13
                 |||||||||||||
Sbjct  12027536  AGTGTCGCTCCGT  12027524


 Features in this part of subject sequence:
   hypothetical protein LOC55313


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         GCTCCGTCAGGCT  19
                 |||||||||||||
Sbjct  12720409  GCTCCGTCAGGCT  12720397


>ref|NW_925561.1|HsCraAADB02_479 D Homo sapiens chromosome 14 genomic contig, alte
(based on Celera assembly)
Length=53999513

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features in this part of subject sequence:
   hypothetical protein LOC9895


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  5         TCGCTCCGTCAGGCT  19
                 |||||||||||||||
Sbjct  49683228  TCGCTCCGTCAGGCT  49683214


 Features flanking this part of subject sequence:
   206 bp at 5' side: vesicle transport through interaction with t-SNAREs 1B
   3613 bp at 3' side: androgen-regulated short-chain dehydrogenase/reductase 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  11        CGTCAGGCTTTCGC  24
                 ||||||||||||||
Sbjct  14954998  CGTCAGGCTTTCGC  14954985


 Features flanking this part of subject sequence:
   3437 bp at 5' side: DDHD domain containing 1
   793484 bp at 3' side: bone morphogenetic protein 4 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  8       CTCCGTCAGGCTT  20
               |||||||||||||
Sbjct  427538  CTCCGTCAGGCTT  427526


 Features in this part of subject sequence:
   putative protein O-mannosyltransferase


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  1         AGTGTCGCTCCGTCAGG  17
                 ||||||||||| |||||
Sbjct  24574716  AGTGTCGCTCCCTCAGG  24574700


>ref|NW_923206.1|HsCraAADB02_267 D Homo sapiens chromosome 7 genomic contig, alter
(based on Celera assembly)
Length=5843728

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Sul

 Features in this part of subject sequence:
   eukaryotic translation initiation factor 3, subunit 9 eta...
   eukaryotic translation initiation factor 3, subunit 9 eta...


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  5        TCGCTCCGTCAGGCT  19
                |||||||||||||||
Sbjct  2318989  TCGCTCCGTCAGGCT  2319003


 Features in this part of subject sequence:
   TRIAD3 protein isoform a
   TRIAD3 protein isoform b


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8        CTCCGTCAGGCTTT  21
                ||||||||||||||
Sbjct  5582463  CTCCGTCAGGCTTT  5582476


>ref|NT_079592.2|Hs7_79657 D Homo sapiens chromosome 7 genomic contig, alternate a
(based on CRA_TCAGchr7v2)
Length=58008433

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Sul

 Features in this part of subject sequence:
   eukaryotic translation initiation factor 3, subunit 9 eta...
   eukaryotic translation initiation factor 3, subunit 9 eta...


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  5        TCGCTCCGTCAGGCT  19
                |||||||||||||||
Sbjct  2405214  TCGCTCCGTCAGGCT  2405228


 Features in this part of subject sequence:
   TRIAD3 protein isoform a
   TRIAD3 protein isoform b


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus
```

```
Query  8        CTCCGTCAGGCTTT  21
                ||||||||||||||
Sbjct  5676794  CTCCGTCAGGCTTT  5676807


 Features flanking this part of subject sequence:
   46175 bp at 5' side: insulin-like growth factor binding protein 3 isoform a pr..
   722357 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         CTCCGTCAGGCTT  20
                 |||||||||||||
Sbjct  45996241  CTCCGTCAGGCTT  45996253


>ref|NW_923184.1|HsCraAADB02_265 D Homo sapiens chromosome 6 genomic contig, alter
(based on Celera assembly)
Length=103786604

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   299 bp at 5' side: hypothetical protein
   34188 bp at 3' side: D-aspartate oxidase isoform a


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  7         GCTCCGTCAGGCTTT  21
                 |||||||||||||||
Sbjct  43495013  GCTCCGTCAGGCTTT  43494999


 Features flanking this part of subject sequence:
   24118 bp at 5' side: serum/glucocorticoid regulated kinase
   194249 bp at 3' side: similar to Coiled-coil-helix-coiled-coil-helix domain-con.


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  2         GTGTCGCTCCGTCA  15
                 ||||||||||||||
Sbjct  67329650  GTGTCGCTCCGTCA  67329663


 Features flanking this part of subject sequence:
   1550086 bp at 5' side: hypothetical protein LOC253714
   2192 bp at 3' side: POU domain, class 3, transcription factor 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         GTGTCGCTCCGTC  14
                 |||||||||||||
Sbjct  31993349  GTGTCGCTCCGTC  31993337


 Features flanking this part of subject sequence:
   20602 bp at 5' side: hypothetical protein
   1789 bp at 3' side: brain protein 44-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         GCTCCGTCAGGCT  19
                 |||||||||||||
Sbjct  99585097  GCTCCGTCAGGCT  99585085
```

```
>ref|NW_922984.1|HsCraAADB02_247 D Homo sapiens chromosome 6 genomic contig, alter
(based on Celera assembly)
Length=26292868

 Features flanking this part of subject sequence:
   450908 bp at 5' side: hypothetical protein
   965316 bp at 3' side: vesicular membrane protein p24


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  3         TGTCGCTCCGTCAGG  17
                 |||||||||||||||
Sbjct  22797781  TGTCGCTCCGTCAGG  22797795


>ref|NW_921562.1|HsCraAADB02_119 D Homo sapiens chromosome 2 genomic contig, alter
(based on Celera assembly)
Length=510436

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   17102 bp at 5' side: hypothetical protein
   2317 bp at 3' side: similar to Cell division cycle protein 27 homolog (CDC27H...


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  5       TCGCTCCGTCAGGCT  19
               |||||||||||||||
Sbjct  193588  TCGCTCCGTCAGGCT  193574


 Features flanking this part of subject sequence:
   236299 bp at 5' side: hypothetical protein
   46526 bp at 3' side: similar to zinc finger protein 285


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  5       TCGCTCCGTCAGGCT  19
               |||||||||||||||
Sbjct  436924  TCGCTCCGTCAGGCT  436938


>ref|NT_011255.14|Hs19_11412 D Homo sapiens chromosome 19 genomic contig, referenc
Length=7286004

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   30656 bp at 5' side: thrombospondin, type I, domain containing 6
   13718 bp at 3' side: ring finger and KH domain containing 1


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  1        AGTGTCGCTCCGTCA  15
                |||||||||||||||
Sbjct  1481598  AGTGTCGCTCCGTCA  1481612


 Features flanking this part of subject sequence:
   2163 bp at 5' side: mucosal vascular addressin cell adhesion molecule 1 isofo...
   366 bp at 3' side: gene trap ROSA b-geo 22


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus
```

```
Query  7       GCTCCGTCAGGCTT  20
               ||||||||||||||
Sbjct  447128  GCTCCGTCAGGCTT  447141


>ref|NT_025028.13|Hs18_25184 D Homo sapiens chromosome 18 genomic contig, referenc
Length=20074199

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   932642 bp at 5' side: cadherin 19, type 2 preproprotein
   6110 bp at 3' side: hypothetical protein LOC92126


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  7         GCTCCGTCAGGCTTT  21
                 |||||||||||||||
Sbjct  12962943  GCTCCGTCAGGCTTT  12962929


 Features in this part of subject sequence:
   one cut domain, family member 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7        GCTCCGTCAGGCT  19
                |||||||||||||
Sbjct  2901581  GCTCCGTCAGGCT  2901593


 Features flanking this part of subject sequence:
   110711 bp at 5' side: mucosa associated lymphoid tissue lymphoma translocation .
   59723 bp at 3' side: zinc finger protein 532


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12       GTCAGGCTTTCGC  24
                |||||||||||||
Sbjct  4316643  GTCAGGCTTTCGC  4316631


>ref|NT_037887.4|Hs16_37891 D Homo sapiens chromosome 16 genomic contig, reference
Length=8576922

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   198965 bp at 5' side: hypothetical protein LOC196483 isoform 2
   1081231 bp at 3' side: hypothetical protein LOC440337


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  1        AGTGTCGCTCCGTCA  15
                |||||||||||||||
Sbjct  5286706  AGTGTCGCTCCGTCA  5286720


 Features in this part of subject sequence:
   hypothetical protein LOC115939


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCGTCAGGCTTTC  22
                |||||||||||||
```

```
Sbjct  1340243  CCGTCAGGCTTTC  1340231


 Features in this part of subject sequence:
   ataxin 2-binding protein 1 isoform 4
   ataxin 2-binding protein 1 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCGTCAGGCTTTC  22
                |||||||||||||
Sbjct  7598534  CCGTCAGGCTTTC  7598546


>ref|NT_026437.11|Hs14_26604 D Homo sapiens chromosome 14 genomic contig, referenc
Length=88290585

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features in this part of subject sequence:
   hypothetical protein LOC9895


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  5         TCGCTCCGTCAGGCT  19
                 |||||||||||||||
Sbjct  83874248  TCGCTCCGTCAGGCT  83874234


 Features flanking this part of subject sequence:
   206 bp at 5' side: vesicle transport through interaction with t-SNAREs 1B
   3613 bp at 3' side: androgen-regulated short-chain dehydrogenase/reductase 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  11        CGTCAGGCTTTCGC  24
                 ||||||||||||||
Sbjct  49141178  CGTCAGGCTTTCGC  49141165


 Features flanking this part of subject sequence:
   3437 bp at 5' side: DDHD domain containing 1
   793485 bp at 3' side: bone morphogenetic protein 4 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         CTCCGTCAGGCTT  20
                 |||||||||||||
Sbjct  34623015  CTCCGTCAGGCTT  34623003


 Features in this part of subject sequence:
   putative protein O-mannosyltransferase


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  1         AGTGTCGCTCCGTCAGG  17
                 ||||||||||| |||||
Sbjct  58781363  AGTGTCGCTCCCTCAGG  58781347


>ref|NT_007819.16|Hs7_7976 D Homo sapiens chromosome 7 genomic contig, reference a
Length=47690382

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su
```

```
 Features in this part of subject sequence:
   eukaryotic translation initiation factor 3, subunit 9 eta...
   eukaryotic translation initiation factor 3, subunit 9 eta...


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  5        TCGCTCCGTCAGGCT  19
                |||||||||||||||
Sbjct  1896097  TCGCTCCGTCAGGCT  1896111


 Features in this part of subject sequence:
   TRIAD3 protein isoform a
   TRIAD3 protein isoform b


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8        CTCCGTCAGGCTTT  21
                ||||||||||||||
Sbjct  5169408  CTCCGTCAGGCTTT  5169421


 Features flanking this part of subject sequence:
   46175 bp at 5' side: insulin-like growth factor binding protein 3 isoform a pr..
   1074956 bp at 3' side: similar to Splicing factor, arginine/serine-rich, 46kD


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         CTCCGTCAGGCTT  20
                 |||||||||||||
Sbjct  45495872  CTCCGTCAGGCTT  45495884


>ref|NT_025741.14|Hs6_25897 D Homo sapiens chromosome 6 genomic contig, reference a
Length=61645385

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent i
                                                                    Query start position  Sul

 Features flanking this part of subject sequence:
   33374 bp at 5' side: hypothetical protein
   34190 bp at 3' side: D-aspartate oxidase isoform a


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  7         GCTCCGTCAGGCTTT  21
                 |||||||||||||||
Sbjct  14849217  GCTCCGTCAGGCTTT  14849203


 Features flanking this part of subject sequence:
   24105 bp at 5' side: serum/glucocorticoid regulated kinase
   194276 bp at 3' side: similar to Coiled-coil-helix-coiled-coil-helix domain-con.


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  2         GTGTCGCTCCGTCA  15
                 ||||||||||||||
Sbjct  38624479  GTGTCGCTCCGTCA  38624492


 Features flanking this part of subject sequence:
   1550193 bp at 5' side: hypothetical protein LOC253714
   2192 bp at 3' side: POU domain, class 3, transcription factor 2


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2        GTGTCGCTCCGTC  14
                |||||||||||||
Sbjct  3450015  GTGTCGCTCCGTC  3450003


>ref|NT_007592.14|Hs6_7749 D Homo sapiens chromosome 6 genomic contig, reference as
Length=48945890

                                                              Sort alignments for this s
                                                                E value  Score  Percent i
                                                                Query start position  Sul

 Features flanking this part of subject sequence:
   450884 bp at 5' side: hypothetical protein
   965663 bp at 3' side: vesicular membrane protein p24


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  3         TGTCGCTCCGTCAGG  17
                 |||||||||||||||
Sbjct  14027130  TGTCGCTCCGTCAGG  14027144


 Features flanking this part of subject sequence:
   85828 bp at 5' side: PERB11 family member in MHC class I region
   299 bp at 3' side: zinc ribbon domain containing 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  11        CGTCAGGCTTTCGC  24
                 ||||||||||||||
Sbjct  20887254  CGTCAGGCTTTCGC  20887241


 Features flanking this part of subject sequence:
   20093 bp at 5' side: hypothetical protein
   11061 bp at 3' side: guanylate cyclase activator 1A (retina)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  7         GCTCCGTCAGGCTTTCG  23
                 |||||||||||| ||||
Sbjct  32988541  GCTCCGTCAGGCCTTCG  32988525


>ref|NW_927628.1|HsCraAADB02_665 D Homo sapiens chromosome 22 genomic contig, alte
(based on Celera assembly)
Length=20974061

 Features flanking this part of subject sequence:
   67456 bp at 5' side: RNA binding motif protein 9 isoform 1
   233484 bp at 3' side: apolipoprotein L3 isoform 3


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1         AGTGTCGCTCCGTC  14
                 ||||||||||||||
Sbjct  14372517  AGTGTCGCTCCGTC  14372530


>ref|NW_927140.1|HsCraAADB02_621 D Homo sapiens chromosome 19 genomic contig, alte
(based on Celera assembly)
Length=567504

 Features flanking this part of subject sequence:
   366 bp at 5' side: gene trap ROSA b-geo 22
   2163 bp at 3' side: mucosal vascular addressin cell adhesion molecule 1 isofo...
```

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7       GCTCCGTCAGGCTT  20
               ||||||||||||||
Sbjct  310490  GCTCCGTCAGGCTT  310477


>ref|NW_927206.1|HsCraAADB02_627 D Homo sapiens chromosome 19 genomic contig, alte
(based on Celera assembly)
Length=10109119

 Features in this part of subject sequence:
   RPB5-mediating protein isoform a
   RPB5-mediating protein isoform b


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  1        AGTGTCGCTCCGTC  14
                ||||||||||||||
Sbjct  2741277  AGTGTCGCTCCGTC  2741264


>ref|NW_926772.1|HsCraAADB02_588 D Homo sapiens chromosome 17 genomic contig, alte
(based on Celera assembly)
Length=5475862

 Features in this part of subject sequence:
   ras homolog gene family, member T1 isoform 2
   ras homolog gene family, member T1 isoform 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1        AGTGTCGCTCCGTC  14
                ||||||||||||||
Sbjct  1480731  AGTGTCGCTCCGTC  1480744


>ref|NW_925484.1|HsCraAADB02_472 D Homo sapiens chromosome 13 genomic contig, alte
(based on Celera assembly)
Length=183880


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1      AGTGTCGCTCCGTC  14
              ||||||||||||||
Sbjct  92336  AGTGTCGCTCCGTC  92349


>ref|NW_925473.1|HsCraAADB02_471 D Homo sapiens chromosome 13 genomic contig, alte
(based on Celera assembly)
Length=33583425

 Features in this part of subject sequence:
   DHHC-containing protein 20


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1        AGTGTCGCTCCGTC  14
                ||||||||||||||
Sbjct  2774625  AGTGTCGCTCCGTC  2774638


>ref|NW_925517.1|HsCraAADB02_475 D Homo sapiens chromosome 13 genomic contig, alte
(based on Celera assembly)
Length=28042733

                                                              Sort alignments for this s
                                                                E value  Score  Percent
                                                                Query start position  Su
```

```
 Features in this part of subject sequence:
   glypican 5


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1        AGTGTCGCTCCGTC  14
                ||||||||||||||
Sbjct  5912337  AGTGTCGCTCCGTC  5912350


 Features flanking this part of subject sequence:
   681721 bp at 5' side: D-amino acid oxidase activator
   205041 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  2         GTGTCGCTCCGTCA  15
                 ||||||||||||||
Sbjct  19921730  GTGTCGCTCCGTCA  19921717


 Features in this part of subject sequence:
   growth hormone regulated TBC protein 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         GCTCCGTCAGGCT  19
                 |||||||||||||
Sbjct  27077432  GCTCCGTCAGGCT  27077444


>ref|NW_925173.1|HsCraAADB02_444 D Homo sapiens chromosome 11 genomic contig, alte
(based on Celera assembly)
Length=44976370

 Features flanking this part of subject sequence:
   666827 bp at 5' side: hypothetical protein
   141520 bp at 3' side: BUD13 homolog


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  7         GCTCCGTCAGGCTT  20
                 ||||||||||||||
Sbjct  26501973  GCTCCGTCAGGCTT  26501986


>ref|NW_924884.1|HsCraAADB02_418 D Homo sapiens chromosome 10 genomic contig, alte
(based on Celera assembly)
Length=44859570

 Features flanking this part of subject sequence:
   164238 bp at 5' side: transcription elongation regulator 1-like
   270773 bp at 3' side: similar to DNA-directed RNA polymerase II largest subunit


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6         CGCTCCGTCAGGCT  19
                 ||||||||||||||
Sbjct  43945238  CGCTCCGTCAGGCT  43945225


>ref|NW_923907.1|HsCraAADB02_330 D Homo sapiens chromosome 8 genomic contig, alter
(based on Celera assembly)
Length=31321926

                                                         Sort alignments for this s
                                                           E value  Score  Percent 
                                                           Query start position  Su
```

```
 Features flanking this part of subject sequence:
   912139 bp at 5' side: similar to ribosomal protein L10a
   308889 bp at 3' side: netrin receptor Unc5h4


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6         CGCTCCGTCAGGCT  19
                 ||||||||||||||
Sbjct  22611006  CGCTCCGTCAGGCT  22610993


 Features flanking this part of subject sequence:
   459 bp at 5' side: sarcoglycan zeta
   302252 bp at 3' side: tumor suppressor candidate 3 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        CTCCGTCAGGCTT  20
                |||||||||||||
Sbjct  2627519  CTCCGTCAGGCTT  2627531


>ref|NW_923707.1|HsCraAADB02_312 D Homo sapiens chromosome 7 genomic contig, alter
(based on Celera assembly)
Length=5539637

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features in this part of subject sequence:
   cell recognition molecule Caspr2 precursor


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9        TCCGTCAGGCTTTC  22
                ||||||||||||||
Sbjct  2144382  TCCGTCAGGCTTTC  2144395


 Features in this part of subject sequence:
   rho guanine nucleotide exchange factor 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10     CCGTCAGGCTTTC  22
              |||||||||||||
Sbjct  14843  CCGTCAGGCTTTC  14831


>ref|NW_923640.1|HsCraAADB02_306 D Homo sapiens chromosome 7 genomic contig, alter
(based on Celera assembly)
Length=39238468

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   15605 bp at 5' side: Kruppel-like factor 14
   136133 bp at 3' side: hypothetical protein isoform 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1         AGTGTCGCTCCGTC  14
                 ||||||||||||||
Sbjct  27941057  AGTGTCGCTCCGTC  27941070
```

```
 Features flanking this part of subject sequence:
   640628 bp at 5' side: similar to ribosomal protein S14
   181111 bp at 3' side: plexin A4, B


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  2         GTGTCGCTCCGTCA  15
                 ||||||||||||||
Sbjct  29499478  GTGTCGCTCCGTCA  29499465


 Features in this part of subject sequence:
   similar to K06A9.1b isoform 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  5         TCGCTCCGTCAGGCTTT  21
                 |||| ||||||||||||
Sbjct  36061959  TCGCACCGTCAGGCTTT  36061943


>ref|NT_079596.2|Hs7_79661 D Homo sapiens chromosome 7 genomic contig, alternate a
(based on CRA_TCAGchr7v2)
Length=58365407

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   15604 bp at 5' side: Kruppel-like factor 14
   136126 bp at 3' side: hypothetical protein isoform 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1         AGTGTCGCTCCGTC  14
                 ||||||||||||||
Sbjct  29806508  AGTGTCGCTCCGTC  29806521


 Features flanking this part of subject sequence:
   637823 bp at 5' side: similar to ribosomal protein S14
   181112 bp at 3' side: plexin A4, B


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  2         GTGTCGCTCCGTCA  15
                 ||||||||||||||
Sbjct  31363529  GTGTCGCTCCGTCA  31363516


 Features in this part of subject sequence:
   cell recognition molecule Caspr2 precursor


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9         TCCGTCAGGCTTTC  22
                 ||||||||||||||
Sbjct  45578750  TCCGTCAGGCTTTC  45578763


 Features in this part of subject sequence:
   similar to K06A9.1b isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus
```

```
Query  5         TCGCTCCGTCAGGCTTT  21
                 |||| ||||||||||||
Sbjct  37945178  TCGCACCGTCAGGCTTT  37945162


 Features in this part of subject sequence:
   rho guanine nucleotide exchange factor 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCGTCAGGCTTTC  22
                 |||||||||||||
Sbjct  43448449  CCGTCAGGCTTTC  43448437


>ref|NT_113893.1|Hs6_111612 D Homo sapiens chromosome 6 genomic contig, alternate a
(derived from QBL cell line)
Length=1999704

 Features flanking this part of subject sequence:
   2605 bp at 5' side: HTEX4 protein
   300 bp at 3' side: zinc ribbon domain containing 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  11      CGTCAGGCTTTCGC  24
               ||||||||||||||
Sbjct  640794  CGTCAGGCTTTCGC  640781


>ref|NT_113891.1|Hs6_111610 D Homo sapiens chromosome 6 genomic contig, alternate a
(derived from COX cell line)
Length=4731698

 Features flanking this part of subject sequence:
   67997 bp at 5' side: similar to HLA-B-associated transcript 1A
   299 bp at 3' side: zinc ribbon domain containing 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  11       CGTCAGGCTTTCGC  24
                ||||||||||||||
Sbjct  1477616  CGTCAGGCTTTCGC  1477603


>ref|NW_923073.1|HsCraAADB02_255 D Homo sapiens chromosome 6 genomic contig, alter
(based on Celera assembly)
Length=30372612

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent i
                                                                   Query start position  Sul

 Features flanking this part of subject sequence:
   85896 bp at 5' side: hypothetical protein LOC10255
   299 bp at 3' side: zinc ribbon domain containing 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  11       CGTCAGGCTTTCGC  24
                ||||||||||||||
Sbjct  3091582  CGTCAGGCTTTCGC  3091569


 Features flanking this part of subject sequence:
   20096 bp at 5' side: hypothetical protein
   11058 bp at 3' side: guanylate cyclase activator 1A (retina)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
```

```
 Strand=Plus/Minus

Query  7         GCTCCGTCAGGCTTTCG  23
                 |||||||||||| ||||
Sbjct  15147075  GCTCCGTCAGGCCTTCG  15147059


>ref|NW_922751.1|HsCraAADB02_226 D Homo sapiens chromosome 5 genomic contig, alter
(based on Celera assembly)
Length=26804078

 Features flanking this part of subject sequence:
   857821 bp at 5' side: ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferas
   476275 bp at 3' side: solute carrier organic anion transporter family, member 4C


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9        TCCGTCAGGCTTTC  22
                ||||||||||||||
Sbjct  1665267  TCCGTCAGGCTTTC  1665280


>ref|NW_922729.1|HsCraAADB02_224 D Homo sapiens chromosome 5 genomic contig, alter
(based on Celera assembly)
Length=28665942

 Features flanking this part of subject sequence:
   575156 bp at 5' side: hypothetical protein LOC134187
   203541 bp at 3' side: hypothetical protein LOC285600


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         CTCCGTCAGGCTTT  21
                 ||||||||||||||
Sbjct  22912446  CTCCGTCAGGCTTT  22912459


>ref|NW_922073.1|HsCraAADB02_165 D Homo sapiens chromosome 4 genomic contig, alter
(based on Celera assembly)
Length=39674885

                                                               Sort alignments for this s
                                                                 E value  Score  Percent
                                                                 Query start position  Su

 Features flanking this part of subject sequence:
   284168 bp at 5' side: pituitary tumor-transforming 2
   368988 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1         AGTGTCGCTCCGTC  14
                 ||||||||||||||
Sbjct  28813838  AGTGTCGCTCCGTC  28813851


 Features flanking this part of subject sequence:
   12590 bp at 5' side: hypothetical protein LOC80008
   17591 bp at 3' side: kelch-like 5 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CGCTCCGTCAGGC  18
                 |||||||||||||
Sbjct  29611094  CGCTCCGTCAGGC  29611082


>ref|NW_921807.1|HsCraAADB02_141 D Homo sapiens chromosome 3 genomic contig, alter
(based on Celera assembly)
Length=101945515
```

Sort alignments for this s
E value **Score** **Percent**
Query start position **Su**

Features flanking this part of subject sequence:
260216 bp at 5' side: zona pellucida-like domain containing 1
803411 bp at 3' side: similar to synovial sarcoma, X breakpoint 2 interacting p.

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9        TCCGTCAGGCTTTC  22
                ||||||||||||||
Sbjct  9037620  TCCGTCAGGCTTTC  9037607
```

Features in this part of subject sequence:
SWI/SNF-related matrix-associated actin-dependent regulat...
SWI/SNF-related matrix-associated actin-dependent regulat...

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Minus

Query  1         AGTGTCGCTCCGTCAGGC  18
                 |||||||||| |||||||
Sbjct  55375135  AGTGTCGCTCTGTCAGGC  55375118
```

Features flanking this part of subject sequence:
73518 bp at 5' side: similar to CG17293-PA
1803860 bp at 3' side: similar to Ephrin type-A receptor 6 precursor (Tyrosine-p

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        TCCGTCAGGCTTT  21
                |||||||||||||
Sbjct  1303496  TCCGTCAGGCTTT  1303508
```

Features flanking this part of subject sequence:
282227 bp at 5' side: purinergic receptor P2Y1
9253 bp at 3' side: hypothetical protein

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         GCTCCGTCAGGCT  19
                 |||||||||||||
Sbjct  59441290  GCTCCGTCAGGCT  59441278
```

Features in this part of subject sequence:
ephrin receptor EphB3 precursor

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CGCTCCGTCAGGC  18
                 |||||||||||||
Sbjct  90928548  CGCTCCGTCAGGC  90928536
```

Features flanking this part of subject sequence:
138546 bp at 5' side: hypothetical protein LOC151963
188528 bp at 3' side: HRAS-like suppressor

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         AGTGTCGCTCCGT  13
                 |||||||||||||
Sbjct  99385852  AGTGTCGCTCCGT  99385840
```

```
 Features flanking this part of subject sequence:
   160499 bp at 5' side: hypothetical protein LOC131583
   143198 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7          GCTCCGTCAGGCT  19
                  |||||||||||||
Sbjct  101168819  GCTCCGTCAGGCT  101168807


>ref|NW_927719.1|HsCraAADB02_69 D Homo sapiens chromosome 2 genomic contig, altern
(based on Celera assembly)
Length=86821413

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent 
                                                                   Query start position  Su

 Features in this part of subject sequence:
   sine oculis homeobox homolog 3


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6         CGCTCCGTCAGGCT  19
                 ||||||||||||||
Sbjct  44942445  CGCTCCGTCAGGCT  44942432


 Features in this part of subject sequence:
   tumor suppressing subtransferable candidate 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        AGTGTCGCTCCGT  13
                |||||||||||||
Sbjct  3311829  AGTGTCGCTCCGT  3311841


>ref|NW_921618.1|HsCraAADB02_124 D Homo sapiens chromosome 2 genomic contig, alter
(based on Celera assembly)
Length=47628048

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent 
                                                                   Query start position  Su

 Features in this part of subject sequence:
   transient receptor potential cation channel, subfamily M,...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         CTCCGTCAGGCTTT  21
                 ||||||||||||||
Sbjct  39474648  CTCCGTCAGGCTTT  39474661


 Features flanking this part of subject sequence:
   20748 bp at 5' side: hypothetical protein LOC129563
   27338 bp at 3' side: placental alkaline phosphatase preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         GCTCCGTCAGGCT  19
                 |||||||||||||
Sbjct  37894863  GCTCCGTCAGGCT  37894851
```

```
 Features in this part of subject sequence:
   axonal transport of synaptic vesicles


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         CTCCGTCAGGCTT  20
                 |||||||||||||
Sbjct  46322417  CTCCGTCAGGCTT  46322429


>ref|NW_921350.1|HsCraAADB02_1 D Homo sapiens chromosome 1 genomic contig, alterna
(based on Celera assembly)
Length=1820082

 Features flanking this part of subject sequence:
   20888 bp at 5' side: similar to ring finger protein 183
   312 bp at 3' side: similar to agrin


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  5        TCGCTCCGTCAGGC  18
                ||||||||||||||
Sbjct  1597955  TCGCTCCGTCAGGC  1597942


>ref|NT_011520.11|Hs22_11677 D Homo sapiens chromosome 22 genomic contig, referenc
Length=23276302

 Features flanking this part of subject sequence:
   67456 bp at 5' side: RNA binding motif protein 9 isoform 1
   233514 bp at 3' side: apolipoprotein L3 isoform 3


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1         AGTGTCGCTCCGTC  14
                 ||||||||||||||
Sbjct  15694236  AGTGTCGCTCCGTC  15694249


>ref|NT_011109.15|Hs19_11266 D Homo sapiens chromosome 19 genomic contig, referenc
Length=31383029

                                                             Sort alignments for this s
                                                               E value  Score  Percent 
                                                               Query start position  Su

 Features in this part of subject sequence:
   RPB5-mediating protein isoform a
   RPB5-mediating protein isoform b


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  1        AGTGTCGCTCCGTC  14
                ||||||||||||||
Sbjct  2744237  AGTGTCGCTCCGTC  2744224


 Features in this part of subject sequence:
   RuvB (E coli homolog)-like 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         CTCCGTCAGGCTT  20
                 |||||||||||||
Sbjct  21784954  CTCCGTCAGGCTT  21784942


 Features flanking this part of subject sequence:
```

```
   16610 bp at 5' side: leukocyte immunoglobulin-like receptor subfamily A member..
   3932 bp at 3' side: leukocyte immunoglobulin-like receptor subfamily A member 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         GCTCCGTCAGGCT  19
                 |||||||||||||
Sbjct  27109101  GCTCCGTCAGGCT  27109089


>ref|NT_010799.14|Hs17_10956 D Homo sapiens chromosome 17 genomic contig, referenc
Length=9412828

 Features in this part of subject sequence:
   ras homolog gene family, member T1 isoform 4
   ras homolog gene family, member T1 isoform 3


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1        AGTGTCGCTCCGTC  14
                ||||||||||||||
Sbjct  5228259  AGTGTCGCTCCGTC  5228272


>ref|NT_009952.14|Hs13_10109 D Homo sapiens chromosome 13 genomic contig, referenc
Length=25443670

 Features in this part of subject sequence:
   glypican 5


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1        AGTGTCGCTCCGTC  14
                ||||||||||||||
Sbjct  5901557  AGTGTCGCTCCGTC  5901570


>ref|NT_024524.13|Hs13_24680 D Homo sapiens chromosome 13 genomic contig, referenc
Length=67740325
                                                         Sort alignments for this s
                                                           E value  Score  Percent :
                                                           Query start position  Sul

 Features in this part of subject sequence:
   DHHC-containing protein 20


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1        AGTGTCGCTCCGTC  14
                ||||||||||||||
Sbjct  2957852  AGTGTCGCTCCGTC  2957865


 Features in this part of subject sequence:
   vacuolar protein sorting 36


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  1         AGTGTCGCTCCGTC  14
                 ||||||||||||||
Sbjct  33980983  AGTGTCGCTCCGTC  33980970


>ref|NT_033899.7|Hs11_34054 D Homo sapiens chromosome 11 genomic contig, reference
Length=38509590

 Features flanking this part of subject sequence:
```

```
    666751 bp at 5' side: hypothetical protein
    141537 bp at 3' side: BUD13 homolog


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

Query  7         GCTCCGTCAGGCTT  20
                 ||||||||||||||
Sbjct  20040064  GCTCCGTCAGGCTT  20040077


>ref|NT_008818.15|Hs10_8975 D Homo sapiens chromosome 10 genomic contig, reference
Length=4615335

  Features flanking this part of subject sequence:
    164397 bp at 5' side: transcription elongation regulator 1-like


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

Query  6        CGCTCCGTCAGGCT  19
                ||||||||||||||
Sbjct  4508116  CGCTCCGTCAGGCT  4508103


>ref|NT_007995.14|Hs8_8152 D Homo sapiens chromosome 8 genomic contig, reference a
Length=14159284

  Features flanking this part of subject sequence:
    912295 bp at 5' side: similar to ribosomal protein L10a
    308498 bp at 3' side: netrin receptor Unc5h4


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

Query  6        CGCTCCGTCAGGCT  19
                ||||||||||||||
Sbjct  5414242  CGCTCCGTCAGGCT  5414229


>ref|NT_007914.14|Hs7_8071 D Homo sapiens chromosome 7 genomic contig, reference a
Length=14846650
                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

  Features in this part of subject sequence:
    cell recognition molecule Caspr2 precursor


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

Query  9        TCCGTCAGGCTTTC  22
                ||||||||||||||
Sbjct  6781191  TCCGTCAGGCTTTC  6781204


  Features in this part of subject sequence:
    rho guanine nucleotide exchange factor 5


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10       CCGTCAGGCTTTC  22
                |||||||||||||
Sbjct  4650638  CCGTCAGGCTTTC  4650626


>ref|NT_007933.14|Hs7_8090 D Homo sapiens chromosome 7 genomic contig, reference a
Length=64426257

                                                         Sort alignments for this s
```

```
                                                                  E value  Score  Percent :
                                                                  Query start position  Sul

  Features flanking this part of subject sequence:
    15599 bp at 5' side: Kruppel-like factor 14
    132898 bp at 3' side: hypothetical protein isoform 2


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

 Query  1         AGTGTCGCTCCGTC  14
                  ||||||||||||||
 Sbjct  55481339  AGTGTCGCTCCGTC  55481352


  Features flanking this part of subject sequence:
    637902 bp at 5' side: similar to ribosomal protein S14
    181115 bp at 3' side: plexin A4, B


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

 Query  2         GTGTCGCTCCGTCA  15
                  ||||||||||||||
 Sbjct  57035340  GTGTCGCTCCGTCA  57035327


  Features in this part of subject sequence:
    similar to K06A9.1b isoform 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 16/17 (94%), Gaps = 0/17 (0%)
  Strand=Plus/Minus

 Query  5         TCGCTCCGTCAGGCTTT  21
                  |||| ||||||||||||
 Sbjct  63612286  TCGCACCGTCAGGCTTT  63612270


 >ref|NT_034772.5|Hs5_34934 D Homo sapiens chromosome 5 genomic contig, reference as
 Length=41199371

  Features flanking this part of subject sequence:
    857451 bp at 5' side: ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferas.
    476439 bp at 3' side: solute carrier organic anion transporter family, member 4C


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

 Query  9        TCCGTCAGGCTTTC  22
                 ||||||||||||||
 Sbjct  3511123  TCCGTCAGGCTTTC  3511136


 >ref|NT_023148.12|Hs5_23304 D Homo sapiens chromosome 5 genomic contig, reference a
 Length=5878002

  Features flanking this part of subject sequence:
    575125 bp at 5' side: hypothetical protein LOC134187
    203541 bp at 3' side: hypothetical protein LOC285600


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

 Query  8        CTCCGTCAGGCTTT  21
                 ||||||||||||||
 Sbjct  1966266  CTCCGTCAGGCTTT  1966279


 >ref|NT_016297.15|Hs4_16453 D Homo sapiens chromosome 4 genomic contig, reference a
 Length=7445039

                                                                Sort alignments for this s
                                                                  E value  Score  Percent :
                                                                  Query start position  Sul
```

```
 Features flanking this part of subject sequence:
   283282 bp at 5' side: pituitary tumor-transforming 2
   368933 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1        AGTGTCGCTCCGTC  14
                ||||||||||||||
Sbjct  5394556  AGTGTCGCTCCGTC  5394569


 Features flanking this part of subject sequence:
   12591 bp at 5' side: hypothetical protein LOC80008
   17599 bp at 3' side: kelch-like 5 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6        CGCTCCGTCAGGC  18
                |||||||||||||
Sbjct  6195179  CGCTCCGTCAGGC  6195167


>ref|NT_022517.17|Hs3_22673 D Homo sapiens chromosome 3 genomic contig, reference a
Length=66080833

                                                         Sort alignments for this s
                                                           E value  Score  Percent i
                                                           Query start position  Sul

 Features in this part of subject sequence:
   similar to serine/threonine kinase 36 (fused homolog, Dro...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  8         CTCCGTCAGGCTTT  21
                 ||||||||||||||
Sbjct  41910525  CTCCGTCAGGCTTT  41910512


 Features flanking this part of subject sequence:
   25113 bp at 5' side: leucine rich repeat containing 2
   1254 bp at 3' side: teratocarcinoma-derived growth factor 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCGTCAGGCTTTC  22
                 |||||||||||||
Sbjct  46558198  CCGTCAGGCTTTC  46558210


>ref|NT_005612.15|Hs3_5769 D Homo sapiens chromosome 3 genomic contig, reference as
Length=100530253

                                                         Sort alignments for this s
                                                           E value  Score  Percent i
                                                           Query start position  Sul

 Features flanking this part of subject sequence:
   260567 bp at 5' side: zona pellucida-like domain containing 1
   801192 bp at 3' side: similar to synovial sarcoma, X breakpoint 2 interacting p.


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9        TCCGTCAGGCTTTC  22
                ||||||||||||||
Sbjct  8952188  TCCGTCAGGCTTTC  8952175
```

```
 Features in this part of subject sequence:
   SWI/SNF-related matrix-associated actin-dependent regulat...
   SWI/SNF-related matrix-associated actin-dependent regulat...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Minus

Query  1         AGTGTCGCTCCGTCAGGC  18
                 |||||||||| |||||||
Sbjct  55274336  AGTGTCGCTCTGTCAGGC  55274319


 Features flanking this part of subject sequence:
   73513 bp at 5' side: similar to CG17293-PA
   1803357 bp at 3' side: similar to Ephrin type-A receptor 6 precursor (Tyrosine-p


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        TCCGTCAGGCTTT  21
                |||||||||||||
Sbjct  1225527  TCCGTCAGGCTTT  1225539


 Features flanking this part of subject sequence:
   439 bp at 5' side: hypothetical protein LOC57461
   9027 bp at 3' side: zinc finger protein 9


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CGCTCCGTCAGGC  18
                 |||||||||||||
Sbjct  35375403  CGCTCCGTCAGGC  35375415


 Features flanking this part of subject sequence:
   282883 bp at 5' side: purinergic receptor P2Y1
   9251 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         GCTCCGTCAGGCT  19
                 |||||||||||||
Sbjct  59332734  GCTCCGTCAGGCT  59332722


 Features in this part of subject sequence:
   ephrin receptor EphB3 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CGCTCCGTCAGGC  18
                 |||||||||||||
Sbjct  90789990  CGCTCCGTCAGGC  90789978


 Features flanking this part of subject sequence:
   139183 bp at 5' side: hypothetical protein LOC151963
   198622 bp at 3' side: HRAS-like suppressor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         AGTGTCGCTCCGT  13
                 |||||||||||||
Sbjct  99269968  AGTGTCGCTCCGT  99269956


>ref|NT_005120.15|Hs2_5277 D Homo sapiens chromosome 2 genomic contig, reference as
```

```
Length=5688986

 Features in this part of subject sequence:
   transient receptor potential cation channel, subfamily M,...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8       CTCCGTCAGGCTTT  21
               ||||||||||||||
Sbjct  772504  CTCCGTCAGGCTTT  772517


>ref|NT_022184.14|Hs2_22340 D Homo sapiens chromosome 2 genomic contig, reference
Length=68373980

 Features in this part of subject sequence:
   sine oculis homeobox homolog 3


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6         CGCTCCGTCAGGCT  19
                 ||||||||||||||
Sbjct  23987771  CGCTCCGTCAGGCT  23987758


>ref|NT_004350.18|Hs1_4507 D Homo sapiens chromosome 1 genomic contig, reference a
Length=2112849

 Features flanking this part of subject sequence:
   312 bp at 5' side: agrin
   27587 bp at 3' side: hypothetical protein LOC54991


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  5       TCGCTCCGTCAGGC  18
               ||||||||||||||
Sbjct  469305  TCGCTCCGTCAGGC  469318


>ref|NW_926918.1|HsCraAADB02_601 D Homo sapiens chromosome 17 genomic contig, alte
(based on Celera assembly)
Length=18267748

 Features in this part of subject sequence:
   hypothetical protein LOC54868


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        CTCCGTCAGGCTT  20
                |||||||||||||
Sbjct  9902653  CTCCGTCAGGCTT  9902665


>ref|NW_926584.1|HsCraAADB02_571 D Homo sapiens chromosome 17 genomic contig, alte
(based on Celera assembly)
Length=15369037

 Features flanking this part of subject sequence:
   437030 bp at 5' side: death effector filament-forming Ced-4-like apoptosis prot.
   59512 bp at 3' side: hypothetical protein LOC23302


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  6        CGCTCCGTCAGGCTTTC  22
                |||||| ||||||||||
Sbjct  5857828  CGCTCCTTCAGGCTTTC  5857812
```

```
>ref|NW_926528.1|HsCraAADB02_566 D Homo sapiens chromosome 16 genomic contig, alte
(based on Celera assembly)
Length=13777636

 Features flanking this part of subject sequence:
   31555 bp at 5' side: cytochrome c oxidase subunit IV isoform 1 precursor
   64492 bp at 3' side: interferon regulatory factor 8


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CGTCAGGCTTTCG  23
                 |||||||||||||
Sbjct  11415027  CGTCAGGCTTTCG  11415039


>ref|NW_925907.1|HsCraAADB02_510 D Homo sapiens chromosome 15 genomic contig, alte
(based on Celera assembly)
Length=8306772

 Features flanking this part of subject sequence:
   60481 bp at 5' side: ADAM metallopeptidase with thrombospondin type 1 motif, 7..
   934 bp at 3' side: MORF-related gene 15 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1        AGTGTCGCTCCGT  13
                |||||||||||||
Sbjct  4757350  AGTGTCGCTCCGT  4757338


>ref|NW_925884.1|HsCraAADB02_508 D Homo sapiens chromosome 15 genomic contig, alte
(based on Celera assembly)
Length=30328800

 Features flanking this part of subject sequence:
   31088 bp at 5' side: D-PCa-2 protein isoform b
   365 bp at 3' side: pallidin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCGTCAGGCTTTC  22
                |||||||||||||
Sbjct  1868241  CCGTCAGGCTTTC  1868229


>ref|NW_925940.1|HsCraAADB02_513 D Homo sapiens chromosome 15 genomic contig, alte
(based on Celera assembly)
Length=17317633

 Features flanking this part of subject sequence:
   20798 bp at 5' side: leucine rich repeat containing 28
   158966 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCGTCAGGCTTTC  22
                 |||||||||||||
Sbjct  14858890  CCGTCAGGCTTTC  14858902


>ref|NW_925295.1|HsCraAADB02_455 D Homo sapiens chromosome 12 genomic contig, alte
(based on Celera assembly)
Length=12881912

 Features flanking this part of subject sequence:
   35562 bp at 5' side: decapping enzyme Dcp1b
   13551 bp at 3' side: calcium channel, voltage-dependent, L type, alpha 1C subuni


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
```

```
 Strand=Plus/Minus

Query  10       CCGTCAGGCTTTC  22
                |||||||||||||
Sbjct  1960446  CCGTCAGGCTTTC  1960434


>ref|NW_925395.1|HsCraAADB02_464 D Homo sapiens chromosome 12 genomic contig, alte
(based on Celera assembly)
Length=79994791

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   55628 bp at 5' side: TANK-binding kinase 1
   54089 bp at 3' side: Ras association (RalGDS/AF-6) domain family 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         GCTCCGTCAGGCT  19
                 |||||||||||||
Sbjct  12238909  GCTCCGTCAGGCT  12238921


 Features flanking this part of subject sequence:
   516638 bp at 5' side: transmembrane and tetratricopeptide repeat containing 2
   1208823 bp at 3' side: solute carrier family 6, member 15 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         GCTCCGTCAGGCT  19
                 |||||||||||||
Sbjct  31333991  GCTCCGTCAGGCT  31334003


 Features in this part of subject sequence:
   hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         GCTCCGTCAGGCT  19
                 |||||||||||||
Sbjct  40797372  GCTCCGTCAGGCT  40797360


>ref|NW_924962.1|HsCraAADB02_425 D Homo sapiens chromosome 11 genomic contig, alte
(based on Celera assembly)
Length=3852046

 Features flanking this part of subject sequence:
   653 bp at 5' side: similar to tumor protein p53 inducible protein 5
   11102 bp at 3' side: phosphatidylserine synthase 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4      GTCGCTCCGTCAG  16
              |||||||||||||
Sbjct  78874  GTCGCTCCGTCAG  78862


>ref|NW_925106.1|HsCraAADB02_438 D Homo sapiens chromosome 11 genomic contig, alte
(based on Celera assembly)
Length=33348968

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features in this part of subject sequence:
   solute carrier family 22 member 8
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        CTCCGTCAGGCTT  20
                |||||||||||||
Sbjct  8441157  CTCCGTCAGGCTT  8441169


 Features flanking this part of subject sequence:
   174305 bp at 5' side: SH3 and multiple ankyrin repeat domains 2 isoform 2
   27241 bp at 3' side: hypothetical protein LOC220070


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         AGTGTCGCTCCGT  13
                 |||||||||||||
Sbjct  16292149  AGTGTCGCTCCGT  16292161


>ref|NW_924584.1|HsCraAADB02_391 D Homo sapiens chromosome 10 genomic contig, alte
(based on Celera assembly)
Length=38429485

 Features flanking this part of subject sequence:
   45041 bp at 5' side: hypothetical protein
   233258 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7        GCTCCGTCAGGCT  19
                |||||||||||||
Sbjct  2253795  GCTCCGTCAGGCT  2253783


>ref|NW_924062.1|HsCraAADB02_344 D Homo sapiens chromosome 9 genomic contig, alter
(based on Celera assembly)
Length=38596040

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

 Features flanking this part of subject sequence:
   735237 bp at 5' side: hypothetical protein
   1345241 bp at 3' side: tyrosinase-related protein 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CGCTCCGTCAGGC  18
                 |||||||||||||
Sbjct  11165872  CGCTCCGTCAGGC  11165860


 Features in this part of subject sequence:
   tumor suppressor candidate 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         TCCGTCAGGCTTT  21
                 |||||||||||||
Sbjct  25489549  TCCGTCAGGCTTT  25489537


>ref|NW_924573.1|HsCraAADB02_390 D Homo sapiens chromosome 9 genomic contig, alter
(based on Celera assembly)
Length=25070985

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
```

```
                                                                   Query start position  Su

  Features flanking this part of subject sequence:
    281729 bp at 5' side: hypothetical protein LOC414318
    7958 bp at 3' side: hypothetical protein LOC375759


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         GCTCCGTCAGGCT  19
                 |||||||||||||
Sbjct  16505294  GCTCCGTCAGGCT  16505306


 Features flanking this part of subject sequence:
   27837 bp at 5' side: hypothetical protein
   160033 bp at 3' side: retinoid X receptor, alpha


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         TCCGTCAGGCTTT  21
                 |||||||||||||
Sbjct  21062076  TCCGTCAGGCTTT  21062088


>ref|NW_924018.1|HsCraAADB02_340 D Homo sapiens chromosome 8 genomic contig, alter
(based on Celera assembly)
Length=3385519

 Features in this part of subject sequence:
   similar to Brain-specific angiogenesis inhibitor 1 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7       GCTCCGTCAGGCT  19
               |||||||||||||
Sbjct  773846  GCTCCGTCAGGCT  773858


>ref|NW_923984.1|HsCraAADB02_337 D Homo sapiens chromosome 8 genomic contig, alter
(based on Celera assembly)
Length=55887796

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

 Features flanking this part of subject sequence:
   57552 bp at 5' side: pyruvate dehydrogenase phosphatase precursor
   147067 bp at 3' side: cadherin 17 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7        GCTCCGTCAGGCT  19
                |||||||||||||
Sbjct  8144844  GCTCCGTCAGGCT  8144832


 Features flanking this part of subject sequence:
   112835 bp at 5' side: thyrotropin-releasing hormone receptor
   10739 bp at 3' side: NudC domain containing 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCGTCAGGCTTTC  22
                 |||||||||||||
Sbjct  23397520  CCGTCAGGCTTTC  23397508


 Features in this part of subject sequence:
```

```
    metastasis suppressor 1

  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  9         TCCGTCAGGCTTT  21
                 |||||||||||||
Sbjct  38742448  TCCGTCAGGCTTT  38742460


  Features flanking this part of subject sequence:
    329258 bp at 5' side: collagen, type XXII, alpha 1
    406857 bp at 3' side: potassium channel, subfamily K, member 9


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  6         CGCTCCGTCAGGC  18
                 |||||||||||||
Sbjct  53357175  CGCTCCGTCAGGC  53357163


  Features flanking this part of subject sequence:
    203441 bp at 5' side: PTK2 protein tyrosine kinase 2 isoform a
    42577 bp at 3' side: hypothetical protein LOC22898


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  7         GCTCCGTCAGGCT  19
                 |||||||||||||
Sbjct  55237680  GCTCCGTCAGGCT  55237668


>ref|NW_923273.1|HsCraAADB02_273 D Homo sapiens chromosome 7 genomic contig, alter
(based on Celera assembly)
Length=10184856

  Features flanking this part of subject sequence:
    46165 bp at 5' side: insulin-like growth factor binding protein 3 isoform b pr..
    723311 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  8        CTCCGTCAGGCTT  20
                |||||||||||||
Sbjct  1930468  CTCCGTCAGGCTT  1930480


>ref|NW_922784.1|HsCraAADB02_229 D Homo sapiens chromosome 5 genomic contig, alter
(based on Celera assembly)
Length=48999907

  Features in this part of subject sequence:
    beta isoform of regulatory subunit B55, protein phosphata...
    beta isoform of regulatory subunit B55, protein phosphata...


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  10        CCGTCAGGCTTTC  22
                 |||||||||||||
Sbjct  19898481  CCGTCAGGCTTTC  19898493


>ref|NW_922217.1|HsCraAADB02_178 D Homo sapiens chromosome 4 genomic contig, alter
(based on Celera assembly)
Length=70496567

  Features in this part of subject sequence:
    mastermind-like 3
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         TCCGTCAGGCTTT  21
                 |||||||||||||
Sbjct  20383452  TCCGTCAGGCTTT  20383440


>ref|NW_922162.1|HsCraAADB02_173 D Homo sapiens chromosome 4 genomic contig, alter
(based on Celera assembly)
Length=66459542

 Features in this part of subject sequence:
   PDZ and LIM domain 5 isoform b
   PDZ and LIM domain 5 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         AGTGTCGCTCCGT  13
                 |||||||||||||
Sbjct  42568766  AGTGTCGCTCCGT  42568754


>ref|NW_921651.1|HsCraAADB02_127 D Homo sapiens chromosome 3 genomic contig, alter
(based on Celera assembly)
Length=75540080

 Features flanking this part of subject sequence:
   25127 bp at 5' side: leucine rich repeat containing 2
   1250 bp at 3' side: teratocarcinoma-derived growth factor 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCGTCAGGCTTTC  22
                 |||||||||||||
Sbjct  46555929  CCGTCAGGCTTTC  46555941


>ref|NW_928052.1|HsCraAADB02_99 D Homo sapiens chromosome 2 genomic contig, altern
(based on Celera assembly)
Length=10207486

                                                                Sort alignments for this s
                                                                  E value  Score  Percent
                                                                  Query start position  Su

 Features in this part of subject sequence:
   hypothetical protein LOC200403


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8       CTCCGTCAGGCTT  20
               |||||||||||||
Sbjct  597389  CTCCGTCAGGCTT  597377


 Features flanking this part of subject sequence:
   332503 bp at 5' side: UDP-glucuronate decarboxylase 1
   288835 bp at 3' side: beta-galactoside alpha-2,6-sialyltransferase II


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2        GTGTCGCTCCGTC  14
                |||||||||||||
Sbjct  8897988  GTGTCGCTCCGTC  8898000


>ref|NW_921351.1|HsCraAADB02_10 D Homo sapiens chromosome 1 genomic contig, altern
(based on Celera assembly)
Length=57745789
```

```
                                                                 Sort alignments for this s
                                                                   E value  Score  Percent i
                                                                   Query start position  Sul
  Features flanking this part of subject sequence:
    82844 bp at 5' side: mediator of RNA polymerase II transcription, subunit 18 h..
    41051 bp at 3' side: phosphatase and actin regulator 4


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  12       GTCAGGCTTTCGC  24
                 |||||||||||||
 Sbjct  3000949  GTCAGGCTTTCGC  3000937


  Features flanking this part of subject sequence:
    198907 bp at 5' side: colony stimulating factor 3 receptor isoform b precursor
    124461 bp at 3' side: glutamate receptor 7 precursor


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10        CCGTCAGGCTTTC  22
                  |||||||||||||
 Sbjct  11280658  CCGTCAGGCTTTC  11280646


  Features flanking this part of subject sequence:
    81738 bp at 5' side: hypothetical protein LOC400754
    393737 bp at 3' side: similar to laminin receptor 1 (ribosomal protein SA)


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  12        GTCAGGCTTTCGC  24
                  |||||||||||||
 Sbjct  30429662  GTCAGGCTTTCGC  30429674


 >ref|NW_927128.1|HsCraAADB02_62 D Homo sapiens chromosome 1 genomic contig, altern
 (based on Celera assembly)
 Length=18989345

  Features flanking this part of subject sequence:
    282616 bp at 5' side: hypothetical protein
    174505 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  8         CTCCGTCAGGCTT  20
                  |||||||||||||
 Sbjct  10880774  CTCCGTCAGGCTT  10880786


 >ref|NW_926128.1|HsCraAADB02_53 D Homo sapiens chromosome 1 genomic contig, altern
 (based on Celera assembly)
 Length=44521323

  Features flanking this part of subject sequence:
    302812 bp at 5' side: hypothetical protein
    370896 bp at 3' side: pogo transposable element with KRAB domain


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  9        TCCGTCAGGCTTT  21
                 |||||||||||||
 Sbjct  4799190  TCCGTCAGGCTTT  4799178


 >ref|NT_035113.6|Hs11_35275 D Homo sapiens chromosome 11 genomic contig, reference
```

```
Length=1102759

 Features in this part of subject sequence:
   tumor protein p53 inducible protein 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4       GTCGCTCCGTCAG  16
               |||||||||||||
Sbjct  379914  GTCGCTCCGTCAG  379902


>ref|NT_007422.13|Hs6_7579 D Homo sapiens chromosome 6 genomic contig, reference a
Length=10134273

 Features flanking this part of subject sequence:
   20602 bp at 5' side: hypothetical protein
   1789 bp at 3' side: brain protein 44-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7        GCTCCGTCAGGCT  19
                |||||||||||||
Sbjct  9064469  GCTCCGTCAGGCT  9064457


>ref|NT_005535.16|Hs3_5692 D Homo sapiens chromosome 3 genomic contig, reference a
Length=1299866

 Features flanking this part of subject sequence:
   160471 bp at 5' side: hypothetical protein LOC131583
   221134 bp at 3' side: hypothetical protein LOC152002


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7       GCTCCGTCAGGCT  19
               |||||||||||||
Sbjct  512802  GCTCCGTCAGGCT  512790


>ref|NT_005403.16|Hs2_5560 D Homo sapiens chromosome 2 genomic contig, reference a
Length=84213157

 Features flanking this part of subject sequence:
   20747 bp at 5' side: hypothetical protein LOC129563
   27345 bp at 3' side: placental alkaline phosphatase preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         GCTCCGTCAGGCT  19
                 |||||||||||||
Sbjct  83425584  GCTCCGTCAGGCT  83425572


>ref|NT_022221.12|Hs2_22377 D Homo sapiens chromosome 2 genomic contig, reference
Length=2252116

 Features in this part of subject sequence:
   tumor suppressing subtransferable candidate 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        AGTGTCGCTCCGT  13
                |||||||||||||
Sbjct  2052114  AGTGTCGCTCCGT  2052126


>ref|NT_022171.14|Hs2_22327 D Homo sapiens chromosome 2 genomic contig, reference
```

```
Length=12173457

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features in this part of subject sequence:
   hypothetical protein LOC200403


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8       CTCCGTCAGGCTT  20
               |||||||||||||
Sbjct  908725  CTCCGTCAGGCTT  908713


 Features flanking this part of subject sequence:
   49451 bp at 5' side: similar to RAN binding protein 2 isoform 7
   288927 bp at 3' side: beta-galactoside alpha-2,6-sialyltransferase II


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2        GTGTCGCTCCGTC  14
                |||||||||||||
Sbjct  9203780  GTGTCGCTCCGTC  9203792


>ref|NT_005416.12|Hs2_5573 D Homo sapiens chromosome 2 genomic contig, reference a
Length=2277080

 Features in this part of subject sequence:
   axonal transport of synaptic vesicles


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8       CTCCGTCAGGCTT  20
               |||||||||||||
Sbjct  908185  CTCCGTCAGGCTT  908197


>ref|NT_004487.18|Hs1_4644 D Homo sapiens chromosome 1 genomic contig, reference a
Length=56413061

 Features flanking this part of subject sequence:
   302851 bp at 5' side: hypothetical protein
   371091 bp at 3' side: pogo transposable element with KRAB domain


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         TCCGTCAGGCTTT  21
                 |||||||||||||
Sbjct  16929458  TCCGTCAGGCTTT  16929446


>ref|NT_032977.8|Hs1_33153 D Homo sapiens chromosome 1 genomic contig, reference a
Length=73835825

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   199013 bp at 5' side: colony stimulating factor 3 receptor isoform b precursor
   123330 bp at 3' side: glutamate receptor 7 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCGTCAGGCTTTC  22
                |||||||||||||
```

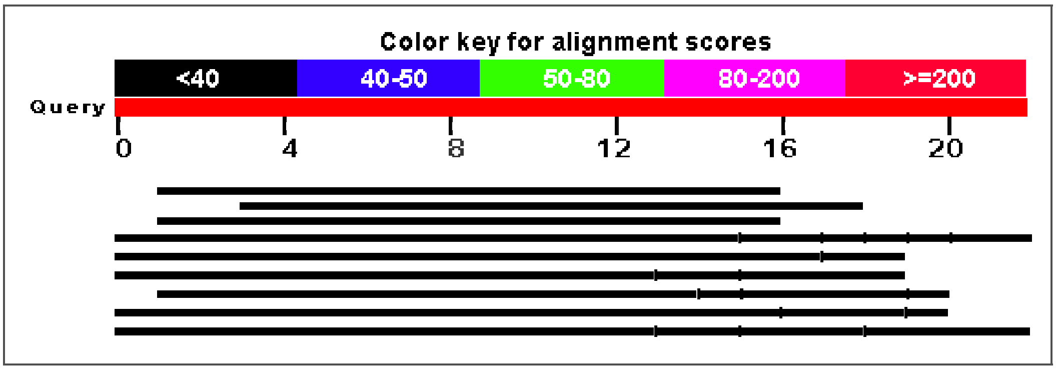
```
Sbjct  7116040  CCGTCAGGCTTTC  7116028


 Features flanking this part of subject sequence:
   81741 bp at 5' side: hypothetical protein LOC400754
   394062 bp at 3' side: similar to laminin receptor 1 (ribosomal protein SA)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12        GTCAGGCTTTCGC  24
                 |||||||||||||
Sbjct  26251452  GTCAGGCTTTCGC  26251464


>ref|NT_004559.13|Hs1_4716 D Homo sapiens chromosome 1 genomic contig, reference a
Length=11394365

 Features flanking this part of subject sequence:
   282596 bp at 5' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         CTCCGTCAGGCTT  20
                 |||||||||||||
Sbjct  11231507  CTCCGTCAGGCTT  11231519


>ref|NT_004610.18|Hs1_4767 D Homo sapiens chromosome 1 genomic contig, reference a
Length=12702424

 Features flanking this part of subject sequence:
   83312 bp at 5' side: mediator of RNA polymerase II transcription, subunit 18 h..
   40823 bp at 3' side: phosphatase and actin regulator 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12        GTCAGGCTTTCGC  24
                 |||||||||||||
Sbjct  11569147  GTCAGGCTTTCGC  11569135
```

Genome View

Show positions of the BLAST hits in the human genome using the Entrez Genomes MapViewer

```
Query= BorrPrimerS Length=22
```

Distribution of 1086 Blast Hits on the Query Sequence



Distance tree of results NEW

Legend for links to other resources: U UniGene E GEO G Gene S Structure M M

Sequences producing significant alignments:
(Click headers to sort columns)

Transcripts

XM_001127571.1	PREDICTED: Homo sapiens poly (ADP-ribose) polymerase family, member 10 (PARP10), mRNA	30.2	30.2	68%	28	100%	G M
NM_001005501.1	Homo sapiens olfactory receptor, family 4, subfamily K, member 2 (OR4K2), mRNA	30.2	30.2	68%	28	100%	U E G M
NM_032789.1	Homo sapiens poly (ADP-ribose) polymerase family, member 10 (PARP10), mRNA	30.2	30.2	68%	28	100%	U E G M

Genomic sequences [show first]

NW_925395.1	Homo sapiens chromosome 12 genomic contig, alternate assembly (based on Celera assembly)	34.2	359	100%	1.8	100%
NT_009775.16	Homo sapiens chromosome 12 genomic contig, reference assembly	34.2	86.7	86%	1.8	100%
NW_927700.1	Homo sapiens chromosome X genomic contig, alternate assembly (based on Celera assembly)	32.2	379	86%	7.2	100%
NW_927317.1	Homo sapiens chromosome 20 genomic contig, alternate assembly (based on Celera assembly)	32.2	139	86%	7.2	100%
NW_925884.1	Homo sapiens chromosome 15 genomic contig, alternate assembly (based on Celera assembly)	32.2	375	90%	7.2	100%
NW_925561.1	Homo sapiens chromosome 14 genomic contig, alternate assembly (based on Celera assembly)	32.2	537	100%	7.2	100%
NW_924884.1	Homo sapiens chromosome 10 genomic contig, alternate assembly (based on Celera assembly)	32.2	411	100%	7.2	100%
NW_922217.1	Homo sapiens chromosome 4 genomic contig, alternate assembly (based on Celera assembly)	32.2	694	100%	7.2	100%
NW_922073.1	Homo sapiens chromosome 4 genomic contig, alternate assembly (based on Celera assembly)	32.2	351	90%	7.2	100%
NT_011757.15	Homo sapiens chromosome X genomic contig, reference assembly	32.2	353	86%	7.2	100%
NT_011387.8	Homo sapiens chromosome 20 genomic contig, reference assembly	32.2	139	86%	7.2	100%
NT_010194.16	Homo sapiens chromosome 15 genomic contig, reference assembly	32.2	537	90%	7.2	100%
NT_026437.11	Homo sapiens chromosome 14 genomic contig, reference assembly	32.2	830	100%	7.2	100%
NT_030059.12	Homo sapiens chromosome 10 genomic contig, reference assembly	32.2	274	100%	7.2	100%
NT_006316.15	Homo sapiens chromosome 4 genomic contig, reference assembly	32.2	244	86%	7.2	100%
NT_016354.18	Homo sapiens chromosome 4 genomic contig, reference assembly	32.2	805	100%	7.2	100%

NW_927717.1	Homo sapiens chromosome X genomic contig, alternate assembly (based on Celera assembly)	30.2	214	90%	28	100%
NW_927715.1	Homo sapiens chromosome X genomic contig, alternate assembly (based on Celera assembly)	30.2	111	77%	28	100%
NW_927711.1	Homo sapiens chromosome X genomic contig, alternate assembly (based on Celera assembly)	30.2	82.8	77%	28	100%
NW_927339.1	Homo sapiens chromosome 20 genomic contig, alternate assembly (based on Celera assembly)	30.2	298	90%	28	100%
NW_927217.1	Homo sapiens chromosome 19 genomic contig, alternate assembly (based on Celera assembly)	30.2	56.5	68%	28	100%
NW_927129.1	Homo sapiens chromosome 18 genomic contig, alternate assembly (based on Celera assembly)	30.2	82.8	72%	28	100%
NW_926918.1	Homo sapiens chromosome 17 genomic contig, alternate assembly (based on Celera assembly)	30.2	165	81%	28	100%
NW_925818.1	Homo sapiens chromosome 15 genomic contig, alternate assembly (based on Celera assembly)	30.2	30.2	68%	28	100%
NW_925539.1	Homo sapiens chromosome 14 genomic contig, alternate assembly (based on Celera assembly)	30.2	292	81%	28	100%
NW_925473.1	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on Celera assembly)	30.2	244	86%	28	100%
NW_925106.1	Homo sapiens chromosome 11 genomic contig, alternate assembly (based on Celera assembly)	30.2	296	81%	28	100%
NW_925173.1	Homo sapiens chromosome 11 genomic contig, alternate assembly (based on Celera assembly)	30.2	541	100%	28	100%
NW_924796.1	Homo sapiens chromosome 10 genomic contig, alternate assembly (based on Celera assembly)	30.2	242	86%	28	100%
NW_924062.1	Homo sapiens chromosome 9 genomic contig, alternate assembly (based on Celera assembly)	30.2	294	90%	28	100%
NW_924573.1	Homo sapiens chromosome 9 genomic contig, alternate assembly (based on Celera assembly)	30.2	294	81%	28	100%
NW_923929.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on Celera assembly)	30.2	187	72%	28	100%
NW_923907.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on Celera assembly)	30.2	462	95%	28	100%
NW_924018.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on Celera assembly)	30.2	30.2	68%	28	100%
NW_923984.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on Celera assembly)	30.2	492	100%	28	100%
NW_923796.1	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on Celera assembly)	30.2	56.5	68%	28	100%
NW_923640.1	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on Celera assembly)	30.2	456	100%	28	100%
NT_079596.2	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on CRA_TCAGchr7v2)	30.2	567	100%	28	100%

NW_923184.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on Celera assembly)	30.2	1120	100%	28	100%
NW_922984.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on Celera assembly)	30.2	355	90%	28	100%
NW_923073.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on Celera assembly)	30.2	347	86%	28	100%
NW_922784.1	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on Celera assembly)	30.2	397	90%	28	100%
NW_922751.1	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on Celera assembly)	30.2	216	86%	28	100%
NW_922162.1	Homo sapiens chromosome 4 genomic contig, alternate assembly (based on Celera assembly)	30.2	430	90%	28	100%
NW_921807.1	Homo sapiens chromosome 3 genomic contig, alternate assembly (based on Celera assembly)	30.2	890	95%	28	100%
NW_927997.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on Celera assembly)	30.2	30.2	68%	28	100%
NW_925683.1	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on Celera assembly)	30.2	218	86%	28	100%
NW_926794.1	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on Celera assembly)	30.2	193	81%	28	100%
NW_926128.1	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on Celera assembly)	30.2	272	90%	28	100%
NT_011896.9	Homo sapiens chromosome Y genomic contig, reference assembly	30.2	137	86%	28	100%
NT_011669.16	Homo sapiens chromosome X genomic contig, reference assembly	30.2	135	77%	28	100%
NT_011651.16	Homo sapiens chromosome X genomic contig, reference assembly	30.2	379	90%	28	100%
NT_011362.9	Homo sapiens chromosome 20 genomic contig, reference assembly	30.2	272	90%	28	100%
NT_011109.15	Homo sapiens chromosome 19 genomic contig, reference assembly	30.2	216	100%	28	100%
NT_025028.13	Homo sapiens chromosome 18 genomic contig, reference assembly	30.2	135	90%	28	100%
NT_024871.11	Homo sapiens chromosome 17 genomic contig, reference assembly	30.2	30.2	68%	28	100%
NT_024524.13	Homo sapiens chromosome 13 genomic contig, reference assembly	30.2	510	95%	28	100%
NT_019546.15	Homo sapiens chromosome 12 genomic contig, reference assembly	30.2	137	100%	28	100%
NT_033899.7	Homo sapiens chromosome 11 genomic contig, reference assembly	30.2	432	100%	28	100%
NT_008984.17	Homo sapiens chromosome 11 genomic contig, reference assembly	30.2	109	90%	28	100%
NT_033903.7	Homo sapiens chromosome 11 genomic contig, reference assembly	30.2	84.7	77%	28	100%
NT_008583.16	Homo sapiens chromosome 10 genomic contig, reference assembly	30.2	242	86%	28	100%
NT_008413.17	Homo sapiens chromosome 9 genomic contig, reference assembly	30.2	294	90%	28	100%
NT_008470.18	Homo sapiens chromosome 9 genomic contig, reference assembly	30.2	347	86%	28	100%

NT_008183.18	Homo sapiens chromosome 8 genomic contig, reference assembly	30.2	187	72%	28	100%
NT_007995.14	Homo sapiens chromosome 8 genomic contig, reference assembly	30.2	248	90%	28	100%
NT_023684.17	Homo sapiens chromosome 8 genomic contig, reference assembly	30.2	30.2	68%	28	100%
NT_008046.15	Homo sapiens chromosome 8 genomic contig, reference assembly	30.2	492	100%	28	100%
NT_034885.3	Homo sapiens chromosome 7 genomic contig, reference assembly	30.2	56.5	68%	28	100%
NT_007933.14	Homo sapiens chromosome 7 genomic contig, reference assembly	30.2	613	100%	28	100%
NT_025741.14	Homo sapiens chromosome 6 genomic contig, reference assembly	30.2	692	100%	28	100%
NT_034880.3	Homo sapiens chromosome 6 genomic contig, reference assembly	30.2	191	90%	28	100%
NT_007592.14	Homo sapiens chromosome 6 genomic contig, reference assembly	30.2	563	90%	28	100%
NT_007422.13	Homo sapiens chromosome 6 genomic contig, reference assembly	30.2	84.7	95%	28	100%
NT_034772.5	Homo sapiens chromosome 5 genomic contig, reference assembly	30.2	268	86%	28	100%
NT_029289.10	Homo sapiens chromosome 5 genomic contig, reference assembly	30.2	214	81%	28	100%
NT_022853.14	Homo sapiens chromosome 4 genomic contig, reference assembly	30.2	56.5	68%	28	100%
NT_005612.15	Homo sapiens chromosome 3 genomic contig, reference assembly	30.2	973	95%	28	100%
NT_026970.9	Homo sapiens chromosome 2 genomic contig, reference assembly	30.2	56.5	77%	28	100%
NT_004487.18	Homo sapiens chromosome 1 genomic contig, reference assembly	30.2	490	90%	28	100%
NT_021877.18	Homo sapiens chromosome 1 genomic contig, reference assembly	30.2	193	81%	28	100%
NW_926584.1	Homo sapiens chromosome 17 genomic contig, alternate assembly (based on Celera assembly)	28.2	133	86%	112	100%
NW_926462.1	Homo sapiens chromosome 16 genomic contig, alternate assembly (based on Celera assembly)	28.2	373	90%	112	100%
NW_926528.1	Homo sapiens chromosome 16 genomic contig, alternate assembly (based on Celera assembly)	28.2	80.8	77%	112	100%
NW_925940.1	Homo sapiens chromosome 15 genomic contig, alternate assembly (based on Celera assembly)	28.2	242	100%	112	100%
NW_925506.1	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on Celera assembly)	28.2	161	86%	112	100%
NW_925495.1	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on Celera assembly)	28.2	133	95%	112	100%
NT_079592.2	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on CRA_TCAGchr7v2)	28.2	500	100%	112	100%
NW_923095.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on Celera assembly)	28.2	56.5	86%	112	100%
NW_921351.1	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on Celera assembly)	28.2	452	100%	112	100%
NT_010641.15	Homo sapiens chromosome 17 genomic contig, reference assembly	28.2	109	77%	112	100%

NT_010498.15	Homo sapiens chromosome 16 genomic contig, reference assembly	28.2	533	90%	112	100%
NT_010274.16	Homo sapiens chromosome 15 genomic contig, reference assembly	28.2	189	100%	112	100%
NT_009952.14	Homo sapiens chromosome 13 genomic contig, reference assembly	28.2	240	86%	112	100%
NT_029419.11	Homo sapiens chromosome 12 genomic contig, reference assembly	28.2	268	100%	112	100%
NT_007299.12	Homo sapiens chromosome 6 genomic contig, reference assembly	28.2	373	90%	112	100%
NT_022517.17	Homo sapiens chromosome 3 genomic contig, reference assembly	28.2	745	100%	112	100%

Alignments

```
>ref|XM_001127571.1| GM PREDICTED: Homo sapiens poly (ADP-ribose) polymerase famil
member 10 (PARP10), mRNA
Length=3360

 GENE ID: 84875 PARP10 | poly (ADP-ribose) polymerase family, member 10
[Homo sapiens] (10 or fewer PubMed links)


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  2     CACACTGGAACTGAG  16
             |||||||||||||||
Sbjct  1705  CACACTGGAACTGAG  1691


>ref|NM_001005501.1| UEGM Homo sapiens olfactory receptor, family 4, subfamily K
2 (OR4K2), mRNA
Length=945

 GENE ID: 390431 OR4K2 | olfactory receptor, family 4, subfamily K, member 2
[Homo sapiens] (10 or fewer PubMed links)


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  4    CACTGGAACTGAGAT  18
            |||||||||||||||
Sbjct  321  CACTGGAACTGAGAT  335


>ref|NM_032789.1| UEGM Homo sapiens poly (ADP-ribose) polymerase family, member
mRNA
Length=3471


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  2     CACACTGGAACTGAG  16
             |||||||||||||||
Sbjct  1696  CACACTGGAACTGAG  1682


>ref|NW_925395.1|HsCraAADB02_464 D Homo sapiens chromosome 12 genomic contig, alte
(based on Celera assembly)
Length=79994791

                                                              Sort alignments for this s
                                                                E value  Score  Percent
                                                                Query start position  Su

 Features in this part of subject sequence:
   kinase suppressor of ras 2


 Score = 34.2 bits (17),  Expect = 1.8
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGAGATA  19
                 |||||||||||||||||
Sbjct  65533536  ACACTGGAACTGAGATA  65533520


 Features flanking this part of subject sequence:
   625340 bp at 5' side: decorin isoform e precursor
   340299 bp at 3' side: B-cell translocation protein 1


 Score = 30.2 bits (15),  Expect =    28
```

```
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACTGA  15
                 |||||||||||||||
Sbjct  39492654  TCACACTGGAACTGA  39492668


 Features flanking this part of subject sequence:
   259772 bp at 5' side: transmembrane 4 superfamily member 3
   22052 bp at 3' side: leucine-rich repeat-containing G protein-coupled receptor 5


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  19098395  TGGAACTGAGATAC  19098382


 Features flanking this part of subject sequence:
   51432 bp at 5' side: lin-7 homolog A
   89017 bp at 3' side: hypothetical protein LOC79611


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9         GAACTGAGATACGG  22
                 ||||||||||||||
Sbjct  28672922  GAACTGAGATACGG  28672935


 Features flanking this part of subject sequence:
   28738 bp at 5' side: similar to CG32774-PA
   455418 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  73429202  CACTGGAACTGAGA  73429215


 Features in this part of subject sequence:
   SLIT-ROBO Rho GTPase-activating protein 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  11628577  CTGGAACTGAGAT  11628589


 Features in this part of subject sequence:
   leucine-rich repeat-containing G protein-coupled receptor 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  19232410  CACTGGAACTGAG  19232398


 Features flanking this part of subject sequence:
   570277 bp at 5' side: thyrotropin-releasing hormone degrading enzyme
   1811704 bp at 3' side: Shaw-related voltage-gated potassium channel protein 2 is


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  20915646  ACACTGGAACTGA  20915658


 Features in this part of subject sequence:
   methionyl aminopeptidase 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTGAGAT  18
                 |||||||||| ||||||
Sbjct  43197006  CACACTGGAAATGAGAT  43196990


 Features flanking this part of subject sequence:
   1923 bp at 5' side: hypothetical protein LOC55332
   89914 bp at 3' side: coiled-coil domain containing 53


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  49604810  ACACTGGAACTGA  49604822


 Features in this part of subject sequence:
   hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACTGAGA  17
                 |||||||||| ||||||
Sbjct  50799197  TCACACTGGATCTGAGA  50799181


 Features in this part of subject sequence:
   ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 ...
   ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 ...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACTGAGA  17
                 ||||||||||| |||||
Sbjct  58024066  TCACACTGGAATTGAGA  58024082


 Features flanking this part of subject sequence:
   152322 bp at 5' side: T-box 3 protein isoform 2
   1127851 bp at 3' side: thyroid hormone receptor associated protein 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  62524653  ACACTGGAACTGA  62524641


>ref|NT_009775.16|Hs12_9932 D Homo sapiens chromosome 12 genomic contig, reference
Length=13091146

                                                         Sort alignments for this s
                                                           E value  Score  Percent :
                                                           Query start position  Su

 Features in this part of subject sequence:
   kinase suppressor of ras 2
```

```
 Score = 34.2 bits (17),  Expect = 1.8
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGAGATA  19
                |||||||||||||||||
Sbjct  8848902  ACACTGGAACTGAGATA  8848886


 Features in this part of subject sequence:
   ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 ...
   ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 ...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACTGAGA  17
                ||||||||||| |||||
Sbjct  1344002  TCACACTGGAATTGAGA  1344018


 Features flanking this part of subject sequence:
   150455 bp at 5' side: T-box 3 protein isoform 2
   1127599 bp at 3' side: thyroid hormone receptor associated protein 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  5840981  ACACTGGAACTGA  5840969


>ref|NW_927700.1|HsCraAADB02_672 D Homo sapiens chromosome X genomic contig, alter
(based on Celera assembly)
Length=35626972

                                                               Sort alignments for this s
                                                                 E value  Score  Percent
                                                                 Query start position  Su

 Features flanking this part of subject sequence:
   315437 bp at 5' side: similar to Melanoma-associated antigen B3 (MAGE-B3 antigen
   1214355 bp at 3' side: similar to WD repeat domain 42B


 Score = 32.2 bits (16),  Expect = 7.2
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGATA  19
                 ||||||||||||||||
Sbjct  25077414  CACTGGAACTGAGATA  25077399


 Features flanking this part of subject sequence:
   260234 bp at 5' side: aristaless related homeobox
   368044 bp at 3' side: similar to Ran-specific GTPase-activating protein (Ran-bi.


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  23816316  CACTGGAACTGAGA  23816303


 Features flanking this part of subject sequence:
   363067 bp at 5' side: WD repeat domain 42B
   444233 bp at 3' side: interleukin 1 receptor accessory protein-like 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
```

```
Sbjct  26889068  ACTGGAACTGAGAT  26889081


 Features flanking this part of subject sequence:
   2053 bp at 5' side: melanoma antigen family B, 1
   50921 bp at 3' side: nuclear receptor subfamily 0, group B, member 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTGA  15
                 ||||||||||||||
Sbjct  28791609  CACACTGGAACTGA  28791622


 Features flanking this part of subject sequence:
   77611 bp at 5' side: acetylserotonin O-methyltransferase
   95216 bp at 3' side: similar to CG15040-PA


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1       TCACACTGGAACT  13
               |||||||||||||
Sbjct  511824  TCACACTGGAACT  511812


 Features flanking this part of subject sequence:
   150231 bp at 5' side: adlican
   117788 bp at 3' side: protein kinase, X-linked


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  2091607  TCACACTGGAACT  2091619


 Features flanking this part of subject sequence:
   150275 bp at 5' side: adlican
   117744 bp at 3' side: protein kinase, X-linked


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  2091651  TCACACTGGAACT  2091663


 Features in this part of subject sequence:
   midline 1 isoform alpha
   midline 1 isoform alpha


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  9017863  CACTGGAACTGAG  9017875


 Features flanking this part of subject sequence:
   48420 bp at 5' side: PDZ domain containing 10
   22573 bp at 3' side: phosphoribosyl pyrophosphate synthetase 2 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  11299332  TCACACTGGAACT  11299320
```

```
  Features in this part of subject sequence:
    connector enhancer of kinase suppressor of Ras 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  20173707  ACTGGAACTGAGA  20173719


  Features flanking this part of subject sequence:
    8238 bp at 5' side: similar to 40S ribosomal protein S26
    27286 bp at 3' side: pyruvate dehydrogenase kinase, isoenzyme 3


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  22977447  ACTGGAACTGAGA  22977459


  Features flanking this part of subject sequence:
    1338523 bp at 5' side: similar to Melanoma-associated antigen B3 (MAGE-B3 antige
    191272 bp at 3' side: similar to WD repeat domain 42B


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  26100497  CTGGAACTGAGAT  26100485


  Features flanking this part of subject sequence:
    55593 bp at 5' side: hypothetical protein LOC170062
    711276 bp at 3' side: similar to melanoma antigen family B, 18


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  33544023  TGGAACTGAGATA  33544011


  Features flanking this part of subject sequence:
    471864 bp at 5' side: hypothetical protein LOC170062
    295005 bp at 3' side: similar to melanoma antigen family B, 18


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  33960282  CACTGGAACTGAG  33960294


>ref|NW_927317.1|HsCraAADB02_637 D Homo sapiens chromosome 20 genomic contig, alte
(based on Celera assembly)
Length=26235423

                                                             Sort alignments for this s
                                                               E value  Score  Percent :
                                                               Query start position  Sul

  Features flanking this part of subject sequence:
    77692 bp at 5' side: gamma-glutamyltransferase-like activity 4
    479763 bp at 3' side: hypothetical protein LOC79953
```

```
 Score = 32.2 bits (16),  Expect = 7.2
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAGATA  19
                 ||||||||||||||||
Sbjct  23975457  CACTGGAACTGAGATA  23975472


 Features flanking this part of subject sequence:
   704210 bp at 5' side: hypothetical protein
   109071 bp at 3' side: phospholipase C beta 4 isoform a


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATA  19
                ||||||||||||||
Sbjct  9106578  CTGGAACTGAGATA  9106565


 Features flanking this part of subject sequence:
   32709 bp at 5' side: jagged 1 precursor
   321684 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  10614019  ACACTGGAACTGA  10614031


 Features in this part of subject sequence:
   proprotein convertase subtilisin/kexin type 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  17281853  CACACTGGAACTG  17281865


 Features in this part of subject sequence:
   Ras and Rab interactor 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  19859838  GGAACTGAGATAC  19859850


>ref|NW_925884.1|HsCraAADB02_508 D Homo sapiens chromosome 15 genomic contig, alte
(based on Celera assembly)
Length=30328800

                                                              Sort alignments for this s
                                                                E value  Score  Percent 
                                                                Query start position  Su

 Features in this part of subject sequence:
   COP9 constitutive photomorphogenic homolog subunit 2


 Score = 32.2 bits (16),  Expect = 7.2
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query  1        TCACACTGGAACTGAG  16
                ||||||||||||||||
Sbjct  5438719  TCACACTGGAACTGAG  5438704


 Features flanking this part of subject sequence:
```

```
   17870 bp at 5' side: carbonic anhydrase XII isoform 2 precursor
   106027 bp at 3' side: ubiquitin specific protease 3


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
Sbjct  19668262  ACTGGAACTGAGAT  19668249


 Features flanking this part of subject sequence:
   31036 bp at 5' side: ring finger protein 36 isoform a
   11360 bp at 3' side: similar to Sorbitol dehydrogenase (L-iditol 2-dehydrogenase


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  1078569  CACACTGGAACTG  1078581


 Features flanking this part of subject sequence:
   551896 bp at 5' side: sulfide dehydrogenase like
   1518141 bp at 3' side: semaphorin 6D isoform 6 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  2524117  GGAACTGAGATAC  2524129


 Features in this part of subject sequence:
   ATPase class I type 8B member 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGAGATA  19
                ||||||||| |||||||
Sbjct  6306879  ACACTGGAATTGAGATA  6306863


 Features flanking this part of subject sequence:
   272099 bp at 5' side: similar to 40S ribosomal protein SA (p40) (34/67 kDa lami.
   358960 bp at 3' side: WD repeat domain 72


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  9443686  TGGAACTGAGATA  9443698


 Features flanking this part of subject sequence:
   86855 bp at 5' side: hypothetical protein
   43529 bp at 3' side: cingulin-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  13674785  GGAACTGAGATAC  13674797


 Features flanking this part of subject sequence:
   22565 bp at 5' side: hypothetical protein LOC145773
   74667 bp at 3' side: glucosaminyl (N-acetyl) transferase 3, mucin type
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  15821536  ACTGGAACTGAGA  15821548


 Features flanking this part of subject sequence:
   141209 bp at 5' side: MAD, mothers against decapentaplegic homolog 6
   9107 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  23201193  TGGAACTGAGATA  23201181


 Features flanking this part of subject sequence:
   107043 bp at 5' side: hypothetical protein
   17147 bp at 3' side: mothers against decapentaplegic homolog 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  23327590  TCACACTGGAACT  23327602


 Features flanking this part of subject sequence:
   108663 bp at 5' side: hypothetical protein
   15527 bp at 3' side: mothers against decapentaplegic homolog 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  23329222  ACTGGAACTGAGA  23329210


 Features in this part of subject sequence:
   membrane progestin receptor gamma


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  25678187  TCACACTGGAACT  25678175


 Features in this part of subject sequence:
   thrombospondin, type I, domain containing 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  27629552  CTGGAACTGAGAT  27629540


 Features flanking this part of subject sequence:
   11828 bp at 5' side: hypothetical protein LOC80072
   9502 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  28665138  CACACTGGAACTG  28665150


>ref|NW_925561.1|HsCraAADB02_479 D Homo sapiens chromosome 14 genomic contig, alte
(based on Celera assembly)
Length=53999513

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features in this part of subject sequence:
   chromosome 14 open reading frame 145


 Score = 32.2 bits (16),  Expect = 7.2
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGAGAT  18
                 ||||||||||||||||
Sbjct  27879528  ACACTGGAACTGAGAT  27879543


 Features flanking this part of subject sequence:
   88176 bp at 5' side: spectrin beta isoform b
   59 bp at 3' side: churchill domain containing 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         GAACTGAGATACGG  22
                 ||||||||||||||
Sbjct  12190270  GAACTGAGATACGG  12190257


 Features flanking this part of subject sequence:
   116439 bp at 5' side: deiodinase, iodothyronine, type II isoform a
   171429 bp at 3' side: chromosome 14 open reading frame 145


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
Sbjct  27586855  ACTGGAACTGAGAT  27586868


 Features flanking this part of subject sequence:
   106739 bp at 5' side: hypothetical protein
   745727 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTGA  15
                 ||||||||||||||
Sbjct  33434495  CACACTGGAACTGA  33434482


 Features in this part of subject sequence:
   DDHD domain containing 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7       TGGAACTGAGATA  19
               |||||||||||||
Sbjct  393484  TGGAACTGAGATA  393472


 Features flanking this part of subject sequence:
```

```
    232882 bp at 5' side: pellino 2
    49564 bp at 3' side: hypothetical protein LOC54916


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  9        GAACTGAGATACG  21
                |||||||||||||
Sbjct  3800936  GAACTGAGATACG  3800924


  Features flanking this part of subject sequence:
    99447 bp at 5' side: dehydrogenase/reductase (SDR family) member 7
    18233 bp at 3' side: protein phosphatase 1A isoform 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  7535851  CACTGGAACTGAG  7535839


  Features flanking this part of subject sequence:
    21707 bp at 5' side: hypothetical protein LOC317761
    2605 bp at 3' side: sine oculis homeobox homolog 6


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  7778198  ACTGGAACTGAGA  7778186


  Features in this part of subject sequence:
    gephyrin isoform 2
    gephyrin isoform 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  14185560  TGGAACTGAGATA  14185548


  Features in this part of subject sequence:
    RAD51-like 1 isoform 3
    RAD51-like 1 isoform 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  15644899  TCACACTGGAACT  15644887


  Features in this part of subject sequence:
    hypothetical protein LOC91750


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  21396634  TGGAACTGAGATA  21396646


  Features flanking this part of subject sequence:
    9496 bp at 5' side: hypothetical protein LOC55668 isoform 2
    227668 bp at 3' side: estrogen-related receptor beta
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  23470350  CTGGAACTGAGAT  23470362


 Features flanking this part of subject sequence:
   129292 bp at 5' side: hypothetical protein LOC55668 isoform 2
   107872 bp at 3' side: estrogen-related receptor beta


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  23590146  TCACACTGGAACT  23590158


 Features flanking this part of subject sequence:
   144076 bp at 5' side: hypothetical protein
   525290 bp at 3' side: neurexin 3 isoform alpha precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  25384552  CTGGAACTGAGAT  25384540


 Features flanking this part of subject sequence:
   314562 bp at 5' side: hypothetical protein
   2417936 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  30375961  CTGGAACTGAGAT  30375973


 Features flanking this part of subject sequence:
   2361446 bp at 5' side: hypothetical protein
   371052 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  32422857  ACTGGAACTGAGA  32422845


 Features flanking this part of subject sequence:
   180179 bp at 5' side: hypothetical protein
   99217 bp at 3' side: galactosylceramidase isoform a precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGATACGG  22
                 |||||||||| ||||||
Sbjct  35102057  CTGGAACTGACATACGG  35102041


 Features in this part of subject sequence:
   hypothetical protein LOC84193 isoform a
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  46680054  ACACTGGAACTGA  46680066


 Features flanking this part of subject sequence:
   62281 bp at 5' side: hypothetical protein
   375345 bp at 3' side: deiodinase, iodothyronine, type III


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  48462186  CACACTGGAACTG  48462174


 Features flanking this part of subject sequence:
   52962 bp at 5' side: similar to zinc finger protein 36-like 3
   104486 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  48901657  TCACACTGGAACT  48901645


>ref|NW_924884.1|HsCraAADB02_418 D Homo sapiens chromosome 10 genomic contig, alte
(based on Celera assembly)
Length=44859570

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent :
                                                                    Query start position  Sul

 Features flanking this part of subject sequence:
   9588 bp at 5' side: arsenic (+3 oxidation state) methyltransferase
   18180 bp at 3' side: cyclin M2 isoform 1


 Score = 32.2 bits (16),  Expect = 7.2
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATACGG  22
                 ||||||||||||||||
Sbjct  15403090  TGGAACTGAGATACGG  15403075


 Features in this part of subject sequence:
   hypothetical protein LOC55328 isoform 2
   hypothetical protein LOC55328 isoform 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAGA  17
                ||||||||||||||
Sbjct  1008751  CACTGGAACTGAGA  1008738


 Features in this part of subject sequence:
   MAX interactor 1 isoform b
   MAX interactor 1 isoform a


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
```

```
Sbjct  22727407  TGGAACTGAGATAC  22727394


 Features flanking this part of subject sequence:
   522751 bp at 5' side: alpha-2A-adrenergic receptor
   547355 bp at 3' side: mitochondrial glycerol 3-phosphate acyltransferase


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACTG  14
                 ||||||||||||||
Sbjct  24096318  TCACACTGGAACTG  24096331


 Features flanking this part of subject sequence:
   407538 bp at 5' side: antigen identified by monoclonal antibody Ki-67
   381375 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  41005771  TGGAACTGAGATAC  41005784


 Features flanking this part of subject sequence:
   541472 bp at 5' side: antigen identified by monoclonal antibody Ki-67
   247441 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  41139705  TGGAACTGAGATAC  41139718


 Features flanking this part of subject sequence:
   675294 bp at 5' side: antigen identified by monoclonal antibody Ki-67
   113619 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACTG  14
                 ||||||||||||||
Sbjct  41273540  TCACACTGGAACTG  41273527


 Features in this part of subject sequence:
   BTAF1 RNA polymerase II, B-TFIID transcription factor-ass...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  4529396  TGGAACTGAGATA  4529408


 Features in this part of subject sequence:
   heparanase 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  11382285  GGAACTGAGATAC  11382297
```

```
  Features flanking this part of subject sequence:
    908 bp at 5' side: hypothetical protein LOC119395
    14438 bp at 3' side: neuralized-like


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  15982461  ACTGGAACTGAGA  15982449


  Features in this part of subject sequence:
    SORCS receptor 1 isoform b
    SORCS receptor 1 isoform a


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  19124782  CTGGAACTGAGAT  19124770


  Features flanking this part of subject sequence:
    2064942 bp at 5' side: SORCS receptor 1 isoform a
    628306 bp at 3' side: X-prolyl aminopeptidase (aminopeptidase P) 1, soluble


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  21731137  TGGAACTGAGATA  21731125


  Features in this part of subject sequence:
    fibronectin type III and ankyrin repeat domains 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  38466550  AACTGAGATACGG  38466538


  Features flanking this part of subject sequence:
    15864 bp at 5' side: hypothetical protein
    66798 bp at 3' side: dedicator of cytokinesis 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  39375176  TGGAACTGAGATA  39375188


  Features in this part of subject sequence:
    transcription elongation regulator 1-like


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  43661476  CACACTGGAACTG  43661488


>ref|NW_922217.1|HsCraAADB02_178 D Homo sapiens chromosome 4 genomic contig, alter
(based on Celera assembly)
Length=70496567
```

```
                                                          Sort alignments for this s
                                                            E value  Score  Percent 
                                                            Query start position  Su

  Features flanking this part of subject sequence:
    134223 bp at 5' side: hypothetical protein
    190408 bp at 3' side: protocadherin 18 precursor


  Score = 32.2 bits (16),  Expect = 7.2
  Identities = 19/20 (95%), Gaps = 0/20 (0%)
  Strand=Plus/Plus

 Query  1         TCACACTGGAACTGAGATAC  20
                  |||||||||||||| |||||
 Sbjct  17844929  TCACACTGGAACTGGGATAC  17844948


  Features in this part of subject sequence:
    hypothetical protein


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Minus

 Query  6         CTGGAACTGAGATAC  20
                  |||||||||||||||
 Sbjct  30018738  CTGGAACTGAGATAC  30018724


  Features flanking this part of subject sequence:
    1754677 bp at 5' side: FAT tumor suppressor homolog 4
    374253 bp at 3' side: hypothetical protein


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

 Query  7        TGGAACTGAGATAC  20
                 ||||||||||||||
 Sbjct  7805377  TGGAACTGAGATAC  7805364


  Features in this part of subject sequence:
    phosphodiesterase 5A isoform 1
    phosphodiesterase 5A isoform 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 16/17 (94%), Gaps = 0/17 (0%)
  Strand=Plus/Plus

 Query  4      CACTGGAACTGAGATAC  20
               ||||||||||| |||||
 Sbjct  86039  CACTGGAACTGTGATAC  86055


  Features flanking this part of subject sequence:
    46267 bp at 5' side: transient receptor potential cation channel, subfamily C,..
    189109 bp at 3' side: similar to CG15133-PA isoform 10


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  6        CTGGAACTGAGAT  18
                 |||||||||||||
 Sbjct  2543768  CTGGAACTGAGAT  2543756


  Features flanking this part of subject sequence:
    105989 bp at 5' side: interleukin 2 precursor
    49913 bp at 3' side: interleukin 21


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  6        CTGGAACTGAGAT  18
                 |||||||||||||
```

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Sbjct  3124468  CTGGAACTGAGAT  3124480


 Features flanking this part of subject sequence:
   119298 bp at 5' side: interleukin 21
   1540 bp at 3' side: hypothetical protein LOC166379


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  3301993  ACACTGGAACTGA  3302005


 Features flanking this part of subject sequence:
   169156 bp at 5' side: E74-like factor 2 (ets domain transcription factor) isofo.
   13193 bp at 3' side: ovary-specific acidic protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  19764124  TGGAACTGAGATA  19764112


 Features flanking this part of subject sequence:
   25768 bp at 5' side: uncoupling protein 1
   27683 bp at 3' side: TBC1 domain family, member 9 (with GRAM domain)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  21103130  ACTGGAACTGAGA  21103118


 Features in this part of subject sequence:
   anaphase promoting complex subunit 10


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  25543114  GGAACTGAGATAC  25543126


 Features flanking this part of subject sequence:
   759386 bp at 5' side: nuclear receptor subfamily 3, group C, member 2
   315473 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  29696205  AACTGAGATACGG  29696217


 Features flanking this part of subject sequence:
   837450 bp at 5' side: nuclear receptor subfamily 3, group C, member 2
   237409 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  29774269  CTGGAACTGAGAT  29774281
```

```
 Features flanking this part of subject sequence:
   298284 bp at 5' side: hypothetical protein
   93661 bp at 3' side: doublecortin and CaM kinase-like 2 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  30481714  ACTGGAACTGAGA  30481702


 Features in this part of subject sequence:
   glycine receptor, beta


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  37604741  GGAACTGAGATAC  37604753


 Features flanking this part of subject sequence:
   217273 bp at 5' side: hypothetical protein
   265702 bp at 3' side: hypothetical protein LOC51313 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  38382775  CACACTGGAACTG  38382787


 Features flanking this part of subject sequence:
   247760 bp at 5' side: hypothetical protein
   235215 bp at 3' side: hypothetical protein LOC51313 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  38413262  TGGAACTGAGATA  38413274


 Features flanking this part of subject sequence:
   922942 bp at 5' side: hypothetical protein
   129332 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  43490683  ACTGGAACTGAGA  43490695


 Features in this part of subject sequence:
   hypothetical protein LOC55601


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  48798673  GGAACTGAGATAC  48798661


 Features in this part of subject sequence:
   polypeptide N-acetylgalactosaminyltransferase 17
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  52341457  TCACACTGGAACT  52341469


 Features flanking this part of subject sequence:
   799191 bp at 5' side: hypothetical protein
   1786886 bp at 3' side: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomp


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  59295485  ACACTGGAACTGA  59295497


 Features flanking this part of subject sequence:
   1017276 bp at 5' side: hypothetical protein
   1568801 bp at 3' side: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomp


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  59513582  ACACTGGAACTGA  59513570


 Features flanking this part of subject sequence:
   315800 bp at 5' side: hypothetical protein
   349022 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  61981898  CTGGAACTGAGAT  61981886


 Features flanking this part of subject sequence:
   352924 bp at 5' side: hypothetical protein
   311898 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  62019010  TCACACTGGAACT  62019022


 Features flanking this part of subject sequence:
   121268 bp at 5' side: hypothetical protein
   334785 bp at 3' side: similar to odd Oz/ten-m homolog 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  62499380  GGAACTGAGATAC  62499392


 Features in this part of subject sequence:
   coiled-coil domain containing 111
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  65189684  TCACACTGGAACT  65189672


 Features flanking this part of subject sequence:
   355723 bp at 5' side: similar to Papilin CG33103-PA, isoform A
   110723 bp at 3' side: similar to gamma-aminobutyric acid  A receptor, epsilon


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTGAGAT  18
                 |||||||||||| ||||
Sbjct  69852571  CACACTGGAACTCAGAT  69852587


>ref|NW_922073.1|HsCraAADB02_165 D Homo sapiens chromosome 4 genomic contig, alter
(based on Celera assembly)
Length=39674885

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent 
                                                                   Query start position  Su

 Features flanking this part of subject sequence:
   1294042 bp at 5' side: hypothetical protein
   267211 bp at 3' side: heat shock protein HSP 90-beta


 Score = 32.2 bits (16),  Expect = 7.2
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGATAC  20
                ||||||||||||||||
Sbjct  3660768  ACTGGAACTGAGATAC  3660783


 Features flanking this part of subject sequence:
   591384 bp at 5' side: Kv channel interacting protein 4 isoform 3
   939762 bp at 3' side: similar to Probable G-protein coupled receptor 125 precurs


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  12026886  CACTGGAACTGAGA  12026899


 Features in this part of subject sequence:
   ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiole...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  31830045  TGGAACTGAGATAC  31830032


 Features flanking this part of subject sequence:
   1294213 bp at 5' side: hypothetical protein
   267039 bp at 3' side: heat shock protein HSP 90-beta


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  2        CACACTGGAACTGAGAT  18
                |||| ||||||||||||
Sbjct  3660939  CACAGTGGAACTGAGAT  3660955
```

```
  Features flanking this part of subject sequence:
    539550 bp at 5' side: hypothetical protein
    322418 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  5272631  ACTGGAACTGAGA  5272619


  Features in this part of subject sequence:
    bone marrow stromal cell antigen 1 precursor


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  6298149  CACACTGGAACTG  6298161


  Features in this part of subject sequence:
    Kv channel interacting protein 4 isoform 4
    Kv channel interacting protein 4 isoform 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  11414969  GGAACTGAGATAC  11414981


  Features flanking this part of subject sequence:
    225356 bp at 5' side: similar to cell division cycle 42 isoform 3
    841385 bp at 3' side: peroxisome proliferative activated receptor gamma coactiv.


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  13532602  CACACTGGAACTG  13532614


  Features flanking this part of subject sequence:
    60520 bp at 5' side: peroxisome proliferative activated receptor gamma coactiv..
    521501 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  14528581  ACACTGGAACTGA  14528593


  Features flanking this part of subject sequence:
    137508 bp at 5' side: stromal interaction molecule 2
    47280 bp at 3' side: hypothetical protein LOC401123


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  17738097  CTGGAACTGAGAT  17738085
```

```
 Features flanking this part of subject sequence:
   347751 bp at 5' side: hypothetical protein
   21152 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  25585104  ACACTGGAACTGA  25585116


 Features flanking this part of subject sequence:
   212835 bp at 5' side: similar to glutaredoxin cysteine-rich 1 protein
   655012 bp at 3' side: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomp.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  33819992  TCACACTGGAACT  33819980


 Features flanking this part of subject sequence:
   836438 bp at 5' side: glucosamine-6-phosphate deaminase 2
   484535 bp at 3' side: gamma-aminobutyric acid A receptor, gamma 1 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  36135427  CTGGAACTGAGAT  36135439


>ref|NT_011757.15|HsX_11914 D Homo sapiens chromosome X genomic contig, reference a
Length=34879939

                                                             Sort alignments for this s
                                                               E value  Score  Percent i
                                                               Query start position  Sul

 Features flanking this part of subject sequence:
   315417 bp at 5' side: similar to Melanoma-associated antigen B3 (MAGE-B3 antigen
   1213328 bp at 3' side: similar to WD repeat domain 42B


 Score = 32.2 bits (16),  Expect = 7.2
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGATA  19
                 ||||||||||||||||
Sbjct  24333368  CACTGGAACTGAGATA  24333353


 Features flanking this part of subject sequence:
   260618 bp at 5' side: aristaless related homeobox
   369354 bp at 3' side: similar to Ran-specific GTPase-activating protein (Ran-bi.


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  23076168  CACTGGAACTGAGA  23076155

 Features flanking this part of subject sequence:
   364545 bp at 5' side: WD repeat domain 42B
   443452 bp at 3' side: interleukin 1 receptor accessory protein-like 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
```

```
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
Sbjct  26145679  ACTGGAACTGAGAT  26145692


 Features flanking this part of subject sequence:
   2054 bp at 5' side: melanoma antigen family B, 1
   50975 bp at 3' side: nuclear receptor subfamily 0, group B, member 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTGA  15
                 ||||||||||||||
Sbjct  28053391  CACACTGGAACTGA  28053404


 Features flanking this part of subject sequence:
   150161 bp at 5' side: adlican
   118194 bp at 3' side: protein kinase, X-linked


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  1293797  TCACACTGGAACT  1293809


 Features flanking this part of subject sequence:
   150205 bp at 5' side: adlican
   118150 bp at 3' side: protein kinase, X-linked


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  1293841  TCACACTGGAACT  1293853


 Features in this part of subject sequence:
   midline 1 isoform alpha
   midline 1 isoform alpha


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  8280083  CACTGGAACTGAG  8280095


 Features flanking this part of subject sequence:
   48399 bp at 5' side: PDZ domain containing 10
   22554 bp at 3' side: phosphoribosyl pyrophosphate synthetase 2 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  10568746  TCACACTGGAACT  10568734


 Features in this part of subject sequence:
   connector enhancer of kinase suppressor of Ras 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  19436211  ACTGGAACTGAGA  19436223


 Features flanking this part of subject sequence:
   8238 bp at 5' side: similar to 40S ribosomal protein S26
   27286 bp at 3' side: pyruvate dehydrogenase kinase, isoenzyme 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  22237958  ACTGGAACTGAGA  22237970


 Features flanking this part of subject sequence:
   1337454 bp at 5' side: similar to Melanoma-associated antigen B3 (MAGE-B3 antige
   191294 bp at 3' side: similar to WD repeat domain 42B


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  25355402  CTGGAACTGAGAT  25355390


 Features flanking this part of subject sequence:
   55391 bp at 5' side: hypothetical protein LOC170062
   711106 bp at 3' side: similar to melanoma antigen family B, 18


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  32799972  TGGAACTGAGATA  32799960


 Features flanking this part of subject sequence:
   471646 bp at 5' side: hypothetical protein LOC170062
   294851 bp at 3' side: similar to melanoma antigen family B, 18


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  33216215  CACTGGAACTGAG  33216227


>ref|NT_011387.8|Hs20_11544 D Homo sapiens chromosome 20 genomic contig, reference
Length=26259569
                                                                Sort alignments for this s
                                                                  E value  Score  Percent :
                                                                  Query start position  Sul

 Features flanking this part of subject sequence:
   76366 bp at 5' side: gamma-glutamyltransferase-like activity 4
   480105 bp at 3' side: hypothetical protein LOC79953


 Score = 32.2 bits (16),  Expect = 7.2
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAGATA  19
                 ||||||||||||||||
Sbjct  23983614  CACTGGAACTGAGATA  23983629


 Features flanking this part of subject sequence:
   703821 bp at 5' side: hypothetical protein
```

```
   109062 bp at 3' side: phospholipase C beta 4 isoform a


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATA  19
                ||||||||||||||
Sbjct  9119400  CTGGAACTGAGATA  9119387


 Features flanking this part of subject sequence:
   32710 bp at 5' side: jagged 1 precursor
   321641 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  10626888  ACACTGGAACTGA  10626900


 Features in this part of subject sequence:
   proprotein convertase subtilisin/kexin type 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  17290205  CACACTGGAACTG  17290217


 Features in this part of subject sequence:
   Ras and Rab interactor 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  19868615  GGAACTGAGATAC  19868627


>ref|NT_010194.16|Hs15_10351 D Homo sapiens chromosome 15 genomic contig, referenc
Length=53619965

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

 Features in this part of subject sequence:
   COP9 constitutive photomorphogenic homolog subunit 2


 Score = 32.2 bits (16),  Expect = 7.2
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACTGAG  16
                 ||||||||||||||||
Sbjct  20237883  TCACACTGGAACTGAG  20237868


 Features flanking this part of subject sequence:
   372936 bp at 5' side: OTU domain containing 7A
   2399 bp at 3' side: cholinergic receptor, nicotinic, alpha 7 precursor


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGATA  19
                |||||||||||||||
Sbjct  3110956  ACTGGAACTGAGATA  3110942
```

```
 Features flanking this part of subject sequence:
   17886 bp at 5' side: carbonic anhydrase XII isoform 2 precursor
   105121 bp at 3' side: ubiquitin specific protease 3


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
Sbjct  34482136  ACTGGAACTGAGAT  34482123


 Features flanking this part of subject sequence:
   121244 bp at 5' side: homeobox protein Meis2 isoform e
   715602 bp at 3' side: transmembrane and coiled-coil domains 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  8303480  GGAACTGAGATAC  8303468


 Features flanking this part of subject sequence:
   6481 bp at 5' side: similar to CG6405-PA
   13064 bp at 3' side: exonuclease 3'-5' domain-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  12253622  CTGGAACTGAGAT  12253610


 Features in this part of subject sequence:
   spectrin, beta, non-erythrocytic 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  12955651  CACACTGGAACTG  12955663


 Features flanking this part of subject sequence:
   31039 bp at 5' side: ring finger protein 36 isoform a
   157896 bp at 3' side: hypothetical protein LOC145645


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  15881566  CACACTGGAACTG  15881578


 Features flanking this part of subject sequence:
   549706 bp at 5' side: sulfide dehydrogenase like
   1519050 bp at 3' side: semaphorin 6D isoform 6 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  17323491  GGAACTGAGATAC  17323503


 Features in this part of subject sequence:
```

```
    ATPase class I type 8B member 4

  Score = 26.3 bits (13),  Expect =   444
  Identities = 16/17 (94%), Gaps = 0/17 (0%)
  Strand=Plus/Minus

Query  3         ACACTGGAACTGAGATA  19
                 ||||||||| |||||||
Sbjct  21106335  ACACTGGAATTGAGATA  21106319


  Features flanking this part of subject sequence:
    272193 bp at 5' side: similar to 40S ribosomal protein SA (p40) (34/67 kDa lami.
    359021 bp at 3' side: WD repeat domain 72


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  24241420  TGGAACTGAGATA  24241432


  Features flanking this part of subject sequence:
    86825 bp at 5' side: hypothetical protein
    43520 bp at 3' side: cingulin-like 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  28477223  GGAACTGAGATAC  28477235


  Features flanking this part of subject sequence:
    22722 bp at 5' side: hypothetical protein LOC145773
    74127 bp at 3' side: glucosaminyl (N-acetyl) transferase 3, mucin type


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  30626856  ACTGGAACTGAGA  30626868


  Features flanking this part of subject sequence:
    141054 bp at 5' side: MAD, mothers against decapentaplegic homolog 6
    9091 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  38005258  TGGAACTGAGATA  38005246


  Features flanking this part of subject sequence:
    107057 bp at 5' side: hypothetical protein
    17149 bp at 3' side: mothers against decapentaplegic homolog 3


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  38131651  TCACACTGGAACT  38131663


  Features flanking this part of subject sequence:
    108677 bp at 5' side: hypothetical protein
    15529 bp at 3' side: mothers against decapentaplegic homolog 3
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  38133283  ACTGGAACTGAGA  38133271


 Features in this part of subject sequence:
   membrane progestin receptor gamma


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  40481900  TCACACTGGAACT  40481888


 Features in this part of subject sequence:
   thrombospondin, type I, domain containing 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  42430835  CTGGAACTGAGAT  42430823


 Features flanking this part of subject sequence:
   11829 bp at 5' side: hypothetical protein LOC80072
   9502 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  43471473  CACACTGGAACTG  43471485


 Features in this part of subject sequence:
   hypothetical protein LOC79834 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  48253971  ACTGGAACTGAGA  48253983


 Features flanking this part of subject sequence:
   27834 bp at 5' side: high-mobility group 20A
   106883 bp at 3' side: leucine-rich repeat neuronal 6A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  48589811  TCACACTGGAACT  48589823


>ref|NT_026437.11|Hs14_26604 D Homo sapiens chromosome 14 genomic contig, referenc
Length=88290585

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su
```

```
 Features in this part of subject sequence:
   chromosome 14 open reading frame 145


 Score = 32.2 bits (16),  Expect = 7.2
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGAGAT  18
                 ||||||||||||||||
Sbjct  62084805  ACACTGGAACTGAGAT  62084820


 Features in this part of subject sequence:
   olfactory receptor, family 4, subfamily K, member 2


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAGAT  18
                |||||||||||||||
Sbjct  1344587  CACTGGAACTGAGAT  1344601


 Features flanking this part of subject sequence:
   91330 bp at 5' side: spectrin beta isoform b
   59 bp at 3' side: churchill domain containing 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         GAACTGAGATACGG  22
                 ||||||||||||||
Sbjct  46380908  GAACTGAGATACGG  46380895


 Features flanking this part of subject sequence:
   40789 bp at 5' side: hypothetical protein
   169544 bp at 3' side: chromosome 14 open reading frame 145


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
Sbjct  61794018  ACTGGAACTGAGAT  61794031


 Features flanking this part of subject sequence:
   106774 bp at 5' side: hypothetical protein
   745199 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTGA  15
                 ||||||||||||||
Sbjct  67634421  CACACTGGAACTGA  67634408


 Features flanking this part of subject sequence:
   45521 bp at 5' side: dehydrogenase/reductase (SDR family) member 2 isoform 2
   133758 bp at 3' side: similar to dehydrogenase/reductase (SDR family) member 2 .


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  5159835  CACTGGAACTGAG  5159823


 Features flanking this part of subject sequence:
   115503 bp at 5' side: granzyme B precursor
   63034 bp at 3' side: amisyn
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  6218709  ACTGGAACTGAGA  6218721


 Features flanking this part of subject sequence:
   414053 bp at 5' side: similar to Nonhistone chromosomal protein HMG-17 (High-mo.
   766558 bp at 3' side: neuro-oncological ventral antigen 1 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  7150447  CACACTGGAACTG  7150435


 Features flanking this part of subject sequence:
   186671 bp at 5' side: neuro-oncological ventral antigen 1 isoform 3
   537909 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  8253153  CACTGGAACTGAG  8253165


 Features in this part of subject sequence:
   nucleotide binding protein-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  13075348  CTGGAACTGAGAT  13075360


 Features flanking this part of subject sequence:
   10206 bp at 5' side: bromodomain adjacent to zinc finger domain, 1A isoform b
   111888 bp at 3' side: signal recognition particle 54kDa


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  16353779  ACACTGGAACTGA  16353767


 Features flanking this part of subject sequence:
   280082 bp at 5' side: C-type lectin domain family 14, member A
   302650 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  20005072  ACTGGAACTGAGA  20005060


 Features flanking this part of subject sequence:
   405972 bp at 5' side: MAM domain containing 1
   137129 bp at 3' side: hypothetical protein
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  29006669  ACACTGGAACTGA  29006681


 Features flanking this part of subject sequence:
   755641 bp at 5' side: hypothetical protein
   1138405 bp at 3' side: ribosomal protein S29 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  29905863  TGGAACTGAGATA  29905875


 Features in this part of subject sequence:
   cyclin-dependent kinase-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  31833264  CACACTGGAACTG  31833276


 Features in this part of subject sequence:
   DDHD domain containing 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  34588964  TGGAACTGAGATA  34588952


 Features flanking this part of subject sequence:
   232818 bp at 5' side: pellino 2
   49919 bp at 3' side: hypothetical protein LOC54916


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         GAACTGAGATACG  21
                 |||||||||||||
Sbjct  37996467  GAACTGAGATACG  37996455


 Features flanking this part of subject sequence:
   99478 bp at 5' side: dehydrogenase/reductase (SDR family) member 7
   17905 bp at 3' side: protein phosphatase 1A isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  41731270  CACTGGAACTGAG  41731258


 Features flanking this part of subject sequence:
   21704 bp at 5' side: hypothetical protein LOC317761
   2605 bp at 3' side: sine oculis homeobox homolog 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  41973265  ACTGGAACTGAGA  41973253


 Features in this part of subject sequence:
   gephyrin isoform 2
   gephyrin isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  48371728  TGGAACTGAGATA  48371716


 Features in this part of subject sequence:
   RAD51-like 1 isoform 3
   RAD51-like 1 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  49831238  TCACACTGGAACT  49831226


 Features in this part of subject sequence:
   hypothetical protein LOC91750


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  55604904  TGGAACTGAGATA  55604916


 Features flanking this part of subject sequence:
   9494 bp at 5' side: hypothetical protein LOC55668 isoform 2
   227997 bp at 3' side: estrogen-related receptor beta


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  57677441  CTGGAACTGAGAT  57677453


 Features flanking this part of subject sequence:
   129188 bp at 5' side: hypothetical protein LOC55668 isoform 2
   108303 bp at 3' side: estrogen-related receptor beta


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  57797135  TCACACTGGAACT  57797147


 Features flanking this part of subject sequence:
   192097 bp at 5' side: aarF domain containing kinase 1
   525725 bp at 3' side: neurexin 3 isoform alpha precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
```

```
                  |||||||||||||
Sbjct  59591596  CTGGAACTGAGAT  59591584


 Features flanking this part of subject sequence:
   314578 bp at 5' side: hypothetical protein
   2416250 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  64578518  CTGGAACTGAGAT  64578530


 Features flanking this part of subject sequence:
   2359720 bp at 5' side: hypothetical protein
   371108 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  66623672  ACTGGAACTGAGA  66623660


 Features flanking this part of subject sequence:
   180167 bp at 5' side: hypothetical protein
   99280 bp at 3' side: galactosylceramidase isoform a precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGATACGG  22
                 |||||||||| ||||||
Sbjct  69301549  CTGGAACTGACATACGG  69301533


 Features in this part of subject sequence:
   hypothetical protein LOC84193 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  80870392  ACACTGGAACTGA  80870404


 Features flanking this part of subject sequence:
   145256 bp at 5' side: hypothetical protein
   372513 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  82651338  CACACTGGAACTG  82651326


 Features flanking this part of subject sequence:
   53313 bp at 5' side: similar to zinc finger protein 36-like 3
   104403 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  83092142  TCACACTGGAACT  83092130
```

```
>ref|NT_030059.12|Hs10_30314 D Homo sapiens chromosome 10 genomic contig, referenc
Length=44617998

                                                              Sort alignments for this s
                                                                E value  Score  Percent
                                                                Query start position  Su

 Features flanking this part of subject sequence:
   9588 bp at 5' side: arsenic (+3 oxidation state) methyltransferase
   18202 bp at 3' side: cyclin M2 isoform 1


 Score = 32.2 bits (16),  Expect = 7.2
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATACGG  22
                 ||||||||||||||||
Sbjct  23408562  TGGAACTGAGATACGG  23408547


 Features in this part of subject sequence:
   hypothetical protein LOC55328 isoform 2
   hypothetical protein LOC55328 isoform 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAGA  17
                ||||||||||||||
Sbjct  9007631  CACTGGAACTGAGA  9007618


 Features in this part of subject sequence:
   MAX interactor 1 isoform b
   MAX interactor 1 isoform a


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  30741455  TGGAACTGAGATAC  30741442


 Features flanking this part of subject sequence:
   526742 bp at 5' side: alpha-2A-adrenergic receptor
   547401 bp at 3' side: mitochondrial glycerol 3-phosphate acyltransferase


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACTG  14
                 ||||||||||||||
Sbjct  32114420  TCACACTGGAACTG  32114433


 Features flanking this part of subject sequence:
   309816 bp at 5' side: hypothetical protein
   62274 bp at 3' side: neuregulin 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  2321327  CACTGGAACTGAG  2321339


 Features in this part of subject sequence:
   BTAF1 RNA polymerase II, B-TFIID transcription factor-ass...


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  12530594  TGGAACTGAGATA  12530606


 Features in this part of subject sequence:
   heparanase 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  19391157  GGAACTGAGATAC  19391169


 Features flanking this part of subject sequence:
   908 bp at 5' side: hypothetical protein LOC119395
   14436 bp at 3' side: neuralized-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  23988235  ACTGGAACTGAGA  23988223


 Features in this part of subject sequence:
   SORCS receptor 1 isoform b
   SORCS receptor 1 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  27131388  CTGGAACTGAGAT  27131376


 Features flanking this part of subject sequence:
   2065874 bp at 5' side: SORCS receptor 1 isoform a
   634772 bp at 3' side: X-prolyl aminopeptidase (aminopeptidase P) 1, soluble


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  29738696  TGGAACTGAGATA  29738684


>ref|NT_006316.15|Hs4_6473 D Homo sapiens chromosome 4 genomic contig, reference as
Length=22487426
                                                                  Sort alignments for this s
                                                                    E value  Score  Percent i
                                                                    Query start position  Sul

 Features flanking this part of subject sequence:
   1294056 bp at 5' side: hypothetical protein
   267486 bp at 3' side: heat shock protein HSP 90-beta


 Score = 32.2 bits (16),  Expect = 7.2
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGATAC  20
                ||||||||||||||||
Sbjct  3742895  ACTGGAACTGAGATAC  3742910
```

```
 Features flanking this part of subject sequence:
   144094 bp at 5' side: Kv channel interacting protein 4 isoform 4
   939692 bp at 3' side: G protein-coupled receptor 125


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  12124981  CACTGGAACTGAGA  12124994


 Features flanking this part of subject sequence:
   1294227 bp at 5' side: hypothetical protein
   267314 bp at 3' side: heat shock protein HSP 90-beta


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  2        CACACTGGAACTGAGAT  18
                |||| ||||||||||||
Sbjct  3743066  CACAGTGGAACTGAGAT  3743082


 Features flanking this part of subject sequence:
   539693 bp at 5' side: hypothetical protein
   323579 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  5355222  ACTGGAACTGAGA  5355210


 Features in this part of subject sequence:
   bone marrow stromal cell antigen 1 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  6382132  CACACTGGAACTG  6382144


 Features in this part of subject sequence:
   Kv channel interacting protein 4 isoform 3
   Kv channel interacting protein 4 isoform 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  11507096  GGAACTGAGATAC  11507108


 Features flanking this part of subject sequence:
   225405 bp at 5' side: similar to cell division cycle 42 isoform 3
   842455 bp at 3' side: peroxisome proliferative activated receptor gamma coactiv.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  13630336  CACACTGGAACTG  13630348


 Features flanking this part of subject sequence:
   60576 bp at 5' side: peroxisome proliferative activated receptor gamma coactiv..
```

```
    521338 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  14627514  ACACTGGAACTGA  14627526


  Features flanking this part of subject sequence:
    137504 bp at 5' side: stromal interaction molecule 2
    47081 bp at 3' side: hypothetical protein LOC401123


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  17837492  CTGGAACTGAGAT  17837480


>ref|NT_016354.18|Hs4_16510 D Homo sapiens chromosome 4 genomic contig, reference
Length=92123751

                                                                  Sort alignments for this
                                                                    E value  Score  Percent
                                                                    Query start position  Su

  Features flanking this part of subject sequence:
    134171 bp at 5' side: hypothetical protein
    189557 bp at 3' side: protocadherin 18 precursor


  Score = 32.2 bits (16),  Expect = 7.2
  Identities = 19/20 (95%), Gaps = 0/20 (0%)
  Strand=Plus/Plus

Query  1         TCACACTGGAACTGAGATAC  20
                 |||||||||||||| |||||
Sbjct  62800754  TCACACTGGAACTGGGATAC  62800773


  Features in this part of subject sequence:
    hypothetical protein


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Minus

Query  6         CTGGAACTGAGATAC  20
                 |||||||||||||||
Sbjct  74991035  CTGGAACTGAGATAC  74991021


  Features flanking this part of subject sequence:
    194803 bp at 5' side: pyruvate dehydrogenase (lipoamide) alpha 2
    1522925 bp at 3' side: hypothetical protein LOC285555


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

Query  6         CTGGAACTGAGATA  19
                 ||||||||||||||
Sbjct  21505004  CTGGAACTGAGATA  21504991


  Features in this part of subject sequence:
    inorganic pyrophosphatase 2 isoform 1 precursor
    inorganic pyrophosphatase 2 isoform 4 precursor


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

Query  1         TCACACTGGAACTG  14
```

```
                 ||||||||||||||
Sbjct  30841994  TCACACTGGAACTG  30842007


 Features flanking this part of subject sequence:
   365146 bp at 5' side: N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4
   1642088 bp at 3' side: translocation associated membrane protein 1-like 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  40911497  CACTGGAACTGAGA  40911484


 Features flanking this part of subject sequence:
   1755920 bp at 5' side: FAT tumor suppressor homolog 4
   374286 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  52717003  TGGAACTGAGATAC  52716990


 Features flanking this part of subject sequence:
   4731 bp at 5' side: Fraser syndrome 1 isoform 1
   8607 bp at 3' side: annexin A3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  4014742  TGGAACTGAGATA  4014730


 Features flanking this part of subject sequence:
   171813 bp at 5' side: glycerol kinase 2
   327404 bp at 3' side: anthrax toxin receptor 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  5048900  ACTGGAACTGAGA  5048888


 Features flanking this part of subject sequence:
   435950 bp at 5' side: hypothetical protein LOC84803
   452560 bp at 3' side: NK6 transcription factor related, locus 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  9509603  TGGAACTGAGATA  9509591


 Features flanking this part of subject sequence:
   268732 bp at 5' side: mitogen-activated protein kinase 10 isoform 4
   264487 bp at 3' side: protein tyrosine phosphatase, non-receptor type 13 isoform


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACTGAGA  17
                 ||||| |||||||||||
```

```
Sbjct  11839644  TCACAGTGGAACTGAGA  11839628


 Features flanking this part of subject sequence:
   16189 bp at 5' side: hypothetical protein
   26925 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  12377752  TCACACTGGAACT  12377740


 Features flanking this part of subject sequence:
   86818 bp at 5' side: dentin matrix acidic phosphoprotein
   52212 bp at 3' side: integrin-binding sialoprotein precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  13219023  CACACTGGAACTG  13219011


 Features flanking this part of subject sequence:
   1103805 bp at 5' side: pyruvate dehydrogenase (lipoamide) alpha 2
   613924 bp at 3' side: hypothetical protein LOC285555


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  22414005  CACTGGAACTGAG  22413993


 Features flanking this part of subject sequence:
   50294 bp at 5' side: centromere protein E
   341057 bp at 3' side: tachykinin receptor 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  28717916  TCACACTGGAACT  28717928


 Features flanking this part of subject sequence:
   89413 bp at 5' side: hypothetical protein isoform 2
   24566 bp at 3' side: hypothetical protein LOC54790


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  30678680  ACACTGGAACTGA  30678668


 Features flanking this part of subject sequence:
   64908 bp at 5' side: small inducible cytokine subfamily E, member 1
   511342 bp at 3' side: dickkopf homolog 2 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  31881903  CTGGAACTGAGAT  31881915
```

```
 Features in this part of subject sequence:
   phosphodiesterase 5A isoform 1
   phosphodiesterase 5A isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAGATAC  20
                 ||||||||||| |||||
Sbjct  44997180  CACTGGAACTGTGATAC  44997196


 Features flanking this part of subject sequence:
   46288 bp at 5' side: transient receptor potential cation channel, subfamily C,..
   191310 bp at 3' side: similar to CG15133-PA isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  47448640  CTGGAACTGAGAT  47448628


 Features flanking this part of subject sequence:
   106269 bp at 5' side: interleukin 2 precursor
   49989 bp at 3' side: interleukin 21


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  48032011  CTGGAACTGAGAT  48032023


 Features flanking this part of subject sequence:
   119330 bp at 5' side: interleukin 21
   1540 bp at 3' side: hypothetical protein LOC166379


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  48209643  ACACTGGAACTGA  48209655


 Features flanking this part of subject sequence:
   169115 bp at 5' side: E74-like factor 2 (ets domain transcription factor) isofo.
   13200 bp at 3' side: ovary-specific acidic protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  64722618  TGGAACTGAGATA  64722606


 Features flanking this part of subject sequence:
   25772 bp at 5' side: uncoupling protein 1
   27682 bp at 3' side: TBC1 domain family, member 9 (with GRAM domain)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  66063814  ACTGGAACTGAGA  66063802
```

```
 Features in this part of subject sequence:
   anaphase promoting complex subunit 10


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  70506247  GGAACTGAGATAC  70506259


 Features flanking this part of subject sequence:
   761814 bp at 5' side: nuclear receptor subfamily 3, group C, member 2
   316010 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  74667973  AACTGAGATACGG  74667985


 Features flanking this part of subject sequence:
   840195 bp at 5' side: nuclear receptor subfamily 3, group C, member 2
   237629 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  74746354  CTGGAACTGAGAT  74746366


 Features flanking this part of subject sequence:
   298749 bp at 5' side: hypothetical protein
   93822 bp at 3' side: doublecortin and CaM kinase-like 2 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  75454505  ACTGGAACTGAGA  75454493


 Features in this part of subject sequence:
   glycine receptor, beta


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  82552548  GGAACTGAGATAC  82552560


 Features flanking this part of subject sequence:
   217306 bp at 5' side: hypothetical protein
   265642 bp at 3' side: hypothetical protein LOC51313 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  83331052  CACACTGGAACTG  83331064


 Features flanking this part of subject sequence:
   247816 bp at 5' side: hypothetical protein
```

```
    235132 bp at 3' side: hypothetical protein LOC51313 isoform 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  7         TGGAACTGAGATA  19
                  |||||||||||||
 Sbjct  83361562  TGGAACTGAGATA  83361574


  Features flanking this part of subject sequence:
    922381 bp at 5' side: hypothetical protein
    129341 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  5         ACTGGAACTGAGA  17
                  |||||||||||||
 Sbjct  88448770  ACTGGAACTGAGA  88448782


 >ref|NW_927717.1|HsCraAADB02_688 D Homo sapiens chromosome X genomic contig, alter
 (based on Celera assembly)
 Length=11680561

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

  Features flanking this part of subject sequence:
    1097506 bp at 5' side: angiomotin
    419410 bp at 3' side: similar to Ssu72 RNA polymerase II CTD phosphatase homolog


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Minus

 Query  3        ACACTGGAACTGAGA  17
                 |||||||||||||||
 Sbjct  9925419  ACACTGGAACTGAGA  9925405


  Features flanking this part of subject sequence:
    2745 bp at 5' side: hypothetical protein LOC139231
    57658 bp at 3' side: extraembryonic, spermatogenesis, homeobox 1-like


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  8       GGAACTGAGATAC  20
                |||||||||||||
 Sbjct  196358  GGAACTGAGATAC  196346


  Features in this part of subject sequence:
    similar to PDZ domain containing 10


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  5        ACTGGAACTGAGA  17
                 |||||||||||||
 Sbjct  3534165  ACTGGAACTGAGA  3534153


  Features flanking this part of subject sequence:
    133434 bp at 5' side: insulin receptor substrate 4
    514295 bp at 3' side: guanylate cyclase 2F


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus
```

```
Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  4868945  CACACTGGAACTG  4868957


 Features flanking this part of subject sequence:
   427678 bp at 5' side: insulin receptor substrate 4
   220051 bp at 3' side: guanylate cyclase 2F


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  5163189  CACACTGGAACTG  5163201


 Features flanking this part of subject sequence:
   4075 bp at 5' side: potassium voltage-gated channel, Isk-related family, memb...
   14922 bp at 3' side: acyl-CoA synthetase long-chain family member 4 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  5636492  CTGGAACTGAGAT  5636480


 Features flanking this part of subject sequence:
   173791 bp at 5' side: acyl-CoA synthetase long-chain family member 4 isoform 1
   146607 bp at 3' side: hypothetical protein LOC84187


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  5864540  ACTGGAACTGAGA  5864552


 Features in this part of subject sequence:
   doublecortin isoform c
   doublecortin isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        GAACTGAGATACG  21
                |||||||||||||
Sbjct  7333048  GAACTGAGATACG  7333060


>ref|NW_927715.1|HsCraAADB02_686 D Homo sapiens chromosome X genomic contig, alter
(based on Celera assembly)
Length=13135424

                                                                Sort alignments for this s
                                                                  E value  Score  Percent 
                                                                  Query start position  Su

 Features flanking this part of subject sequence:
   246539 bp at 5' side: similar to poly(A) binding protein, cytoplasmic 5
   97520 bp at 3' side: hypothetical protein


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAGAT  18
                |||||||||||||||
Sbjct  2592775  CACTGGAACTGAGAT  2592761


 Features flanking this part of subject sequence:
```

```
    771299 bp at 5' side: protocadherin 11 X-linked isoform a precursor
    664063 bp at 3' side: similar to heat shock 70kD protein binding protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTGA  15
                ||||||||||||||
Sbjct  3565703  CACACTGGAACTGA  3565690


 Features flanking this part of subject sequence:
   136409 bp at 5' side: similar to testis-specific bromodomain protein
   211292 bp at 3' side: diaphanous 2 isoform 156


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  7408899  ACACTGGAACTGA  7408887


 Features in this part of subject sequence:
   diaphanous 2 isoform 156
   diaphanous 2 isoform 12C


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  8098575  CTGGAACTGAGAT  8098563


>ref|NW_927711.1|HsCraAADB02_682 D Homo sapiens chromosome X genomic contig, alter
(based on Celera assembly)
Length=8793495

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features in this part of subject sequence:
   zinc finger protein 261
   zinc finger protein 261


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGAGA  17
                |||||||||||||||
Sbjct  8313632  ACACTGGAACTGAGA  8313646


 Features flanking this part of subject sequence:
   239984 bp at 5' side: hepatocellular carcinoma-associated antigen 127
   140817 bp at 3' side: similar to UPF0308 protein C9orf21


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  2272234  TCACACTGGAACT  2272246


 Features flanking this part of subject sequence:
   183942 bp at 5' side: hephaestin isoform b
   148916 bp at 3' side: X-linked ectodysplasin receptor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
```

```
 Strand=Plus/Plus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  3507152  CACACTGGAACTG  3507164


>ref|NW_927339.1|HsCraAADB02_639 D Homo sapiens chromosome 20 genomic contig, alte
(based on Celera assembly)
Length=33108650

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   3019 bp at 5' side: zinc finger protein 313
   27880 bp at 3' side: snail 1 homolog


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGAGA  17
                 |||||||||||||||
Sbjct  18779373  ACACTGGAACTGAGA  18779387


 Features flanking this part of subject sequence:
   33930 bp at 5' side: cadherin 4, type 1 preproprotein
   3229 bp at 3' side: TBP-associated factor 4


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGAGA  17
                 |||||||||||||||
Sbjct  30787143  ACACTGGAACTGAGA  30787129


 Features flanking this part of subject sequence:
   352133 bp at 5' side: transcription factor AP-2 gamma
   166102 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  25808791  TGGAACTGAGATAC  25808778


 Features flanking this part of subject sequence:
   19061 bp at 5' side: cell division cycle 91-like 1 protein
   12570 bp at 3' side: tumor protein p53 inducible nuclear protein 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  3536171  TGGAACTGAGATA  3536159


 Features flanking this part of subject sequence:
   273293 bp at 5' side: transcription factor MAFB
   67003 bp at 3' side: DNA topoisomerase I


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  9804380  CACACTGGAACTG  9804368
```

```
 Features flanking this part of subject sequence:
   47760 bp at 5' side: arginine/serine-rich splicing factor 6
   5691 bp at 3' side: l(3)mbt-like isoform II


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  12348061  CTGGAACTGAGAT  12348073


 Features in this part of subject sequence:
   nuclear factor of activated T-cells, cytoplasmic, calcine...
   nuclear factor of activated T-cells, cytoplasmic, calcine...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  20331365  TCACACTGGAACT  20331377


 Features flanking this part of subject sequence:
   1829 bp at 5' side: hypothetical protein
   228696 bp at 3' side: hypothetical protein LOC284757


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  28909251  CACACTGGAACTG  28909239


 Features flanking this part of subject sequence:
   67932 bp at 5' side: hypothetical protein LOC284757
   828758 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  29206322  ACACTGGAACTGA  29206310


 Features flanking this part of subject sequence:
   520368 bp at 5' side: hypothetical protein LOC284757
   376322 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  29658746  TCACACTGGAACT  29658758


 Features flanking this part of subject sequence:
   10917 bp at 5' side: SRY-box 18
   2853 bp at 3' side: transcription elongation factor A protein 2 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  32881013  CACACTGGAACTG  32881001
```

```
>ref|NW_927217.1|HsCraAADB02_628 D Homo sapiens chromosome 19 genomic contig, alte
(based on Celera assembly)
Length=10620956

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   24560 bp at 5' side: carcinoembryonic antigen-related cell adhesion molecule
   8277 bp at 3' side: carcinoembryonic antigen-related cell adhesion molecule 4


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGATA  19
                |||||||||||||||
Sbjct  4324017  ACTGGAACTGAGATA  4324031


 Features flanking this part of subject sequence:
   17579 bp at 5' side: zinc finger protein 226 isoform b
   25166 bp at 3' side: zinc finger protein 227


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  6907629  TGGAACTGAGATA  6907641


>ref|NW_927129.1|HsCraAADB02_620 D Homo sapiens chromosome 18 genomic contig, alte
(based on Celera assembly)
Length=12826439

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   202755 bp at 5' side: suppressor of cytokine signaling 6
   107327 bp at 3' side: hypothetical protein LOC220158


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACTGA  15
                |||||||||||||||
Sbjct  3077166  TCACACTGGAACTGA  3077180


 Features flanking this part of subject sequence:
   49003 bp at 5' side: hypothetical protein LOC220158
   1828609 bp at 3' side: cerebellin 2 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  3262196  CACTGGAACTGAG  3262208


 Features flanking this part of subject sequence:
   945832 bp at 5' side: galanin receptor 1
   295064 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  10779602  CACTGGAACTGAG  10779590
```

```
>ref|NW_926918.1|HsCraAADB02_601 D Homo sapiens chromosome 17 genomic contig, alte
(based on Celera assembly)
Length=18267748

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent 
                                                                   Query start position  Su

 Features in this part of subject sequence:
   raptor


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGAGA  17
                 |||||||||||||||
Sbjct  15910030  ACACTGGAACTGAGA  15910044


 Features in this part of subject sequence:
   ATP-binding cassette, sub-family A, member 6


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGAG  16
                ||||||||||||||
Sbjct  4194873  ACACTGGAACTGAG  4194886


 Features flanking this part of subject sequence:
   937593 bp at 5' side: potassium inwardly-rectifying channel J2
   506705 bp at 3' side: similar to Myosin light polypeptide 6 (Smooth muscle and .


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGAT  18
                ||||||||||||||
Sbjct  6187351  ACTGGAACTGAGAT  6187338


 Features flanking this part of subject sequence:
   193596 bp at 5' side: nucleolar protein 11
   97600 bp at 3' side: karyopherin alpha 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  3011038  TCACACTGGAACT  3011050


 Features flanking this part of subject sequence:
   80854 bp at 5' side: similar to R102.4b
   19269 bp at 3' side: suppressor of cytokine signaling 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  13434661  CACACTGGAACTG  13434649


 Features in this part of subject sequence:
   pleckstrin homology, Sec7 and coiled/coil domains 1 isofo...
   pleckstrin homology, Sec7 and coiled/coil domains 1 isofo...


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  13876736  ACTGGAACTGAGA  13876748


>ref|NW_925818.1|HsCraAADB02_502 D Homo sapiens chromosome 15 genomic contig, alte
(based on Celera assembly)
Length=436686

 Features flanking this part of subject sequence:
   2399 bp at 5' side: similar to Neuronal acetylcholine receptor protein, alpha...


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  5       ACTGGAACTGAGATA  19
               |||||||||||||||
Sbjct  134836  ACTGGAACTGAGATA  134850


>ref|NW_925539.1|HsCraAADB02_477 D Homo sapiens chromosome 14 genomic contig, alte
(based on Celera assembly)
Length=33050393

                                                         Sort alignments for this s
                                                           E value  Score  Percent 
                                                           Query start position  Su

 Features in this part of subject sequence:
   olfactory receptor, family 4, subfamily K, member 2


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  4       CACTGGAACTGAGAT  18
               |||||||||||||||
Sbjct  152338  CACTGGAACTGAGAT  152352


 Features flanking this part of subject sequence:
   45493 bp at 5' side: dehydrogenase/reductase (SDR family) member 2 isoform 2
   133810 bp at 3' side: similar to dehydrogenase/reductase (SDR family) member 2 .


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  3964820  CACTGGAACTGAG  3964808


 Features flanking this part of subject sequence:
   115107 bp at 5' side: granzyme B precursor
   63062 bp at 3' side: amisyn


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  5025387  ACTGGAACTGAGA  5025399


 Features flanking this part of subject sequence:
   414018 bp at 5' side: similar to Nonhistone chromosomal protein HMG-17 (High-mo.
   766488 bp at 3' side: neuro-oncological ventral antigen 1 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTG  14
```

```
                    |||||||||||||
Sbjct  5957186  CACACTGGAACTG  5957174


 Features flanking this part of subject sequence:
   186680 bp at 5' side: neuro-oncological ventral antigen 1 isoform 3
   539053 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  7059844  CACTGGAACTGAG  7059856


 Features in this part of subject sequence:
   nucleotide binding protein-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  11883039  CTGGAACTGAGAT  11883051


 Features flanking this part of subject sequence:
   10221 bp at 5' side: bromodomain adjacent to zinc finger domain, 1A isoform b
   111542 bp at 3' side: similar to signal recognition particle 54 kDa


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  15160327  ACACTGGAACTGA  15160315


 Features flanking this part of subject sequence:
   280068 bp at 5' side: C-type lectin domain family 14, member A
   302609 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  18811950  ACTGGAACTGAGA  18811938


 Features flanking this part of subject sequence:
   405979 bp at 5' side: MAM domain containing 1
   137133 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  27809599  ACACTGGAACTGA  27809611


 Features flanking this part of subject sequence:
   755256 bp at 5' side: hypothetical protein
   1138055 bp at 3' side: ribosomal protein S29 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  28708412  TGGAACTGAGATA  28708424
```

```
 Features in this part of subject sequence:
   cyclin-dependent kinase-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  30642766  CACACTGGAACTG  30642778


>ref|NW_925473.1|HsCraAADB02_471 D Homo sapiens chromosome 13 genomic contig, alte
(based on Celera assembly)
Length=33583425

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent :
                                                                    Query start position  Sul

 Features flanking this part of subject sequence:
   10815 bp at 5' side: similar to FRAS1-related extracellular matrix protein 2 p..
   13747 bp at 3' side: hypothetical protein


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTGAG  16
                |||||||||||||||
Sbjct  2683357  CACACTGGAACTGAG  2683343


 Features in this part of subject sequence:
   hypothetical protein LOC23281 isoform a


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACTG  14
                 ||||||||||||||
Sbjct  10629506  TCACACTGGAACTG  10629493


 Features in this part of subject sequence:
   spermatogenesis and oogenesis specific basic helix-loop-h...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGAG  16
                 ||||||||||||||
Sbjct  17588571  ACACTGGAACTGAG  17588558


 Features flanking this part of subject sequence:
   59095 bp at 5' side: exportin 4
   47065 bp at 3' side: LATS, large tumor suppressor, homolog 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  2299091  ACTGGAACTGAGA  2299103


 Features flanking this part of subject sequence:
   24999 bp at 5' side: G protein-coupled receptor 12
   284385 bp at 3' side: ubiquitin-specific protease 12-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
```

```
 Strand=Plus/Plus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  8163147  CACTGGAACTGAG  8163159


 Features flanking this part of subject sequence:
   564178 bp at 5' side: replication factor C 3 isoform 2
   548259 bp at 3' side: neurobeachin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  15770907  TGGAACTGAGATA  15770919


 Features flanking this part of subject sequence:
   9092 bp at 5' side: hypothetical protein LOC55068
   12137 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  24787561  CTGGAACTGAGAT  24787549


 Features in this part of subject sequence:
   leucine-rich repeats and calponin homology (CH) domain co...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  28041936  CACACTGGAACTG  28041924


 Features in this part of subject sequence:
   retinoblastoma 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  29707784  ACTGGAACTGAGA  29707796


>ref|NW_925106.1|HsCraAADB02_438 D Homo sapiens chromosome 11 genomic contig, alte
(based on Celera assembly)
Length=33348968

                                                         Sort alignments for this s
                                                           E value  Score  Percent :
                                                           Query start position  Sul

 Features in this part of subject sequence:
   syntaxin 3A


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGAGA  17
                |||||||||||||||
Sbjct  5239600  ACACTGGAACTGAGA  5239586


 Features in this part of subject sequence:
   solute carrier family 22 member 8
```

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATA  19
                ||||||||||||||
Sbjct  8453763  CTGGAACTGAGATA  8453750


 Features flanking this part of subject sequence:
   328892 bp at 5' side: similar to odd Oz/ten-m homolog 4
   3291387 bp at 3' side: similar to 40S ribosomal protein S28 isoform 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGAG  16
                 ||||||||||||||
Sbjct  24767128  ACACTGGAACTGAG  24767141


 Features in this part of subject sequence:
   hypothetical protein LOC219990


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  5523585  TGGAACTGAGATA  5523597


 Features flanking this part of subject sequence:
   5613 bp at 5' side: RAB6A, member RAS oncogene family isoform b
   23010 bp at 3' side: mitochondrial ribosomal protein L48 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  19130990  CACACTGGAACTG  19131002


 Features flanking this part of subject sequence:
   9981 bp at 5' side: diacylglycerol O-acyltransferase homolog 2
   4908 bp at 3' side: UV radiation resistance associated


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  21177408  CACTGGAACTGAG  21177420


 Features flanking this part of subject sequence:
   21204 bp at 5' side: protein-kinase, interferon-inducible double stranded RNA ..
   43116 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  21768980  TGGAACTGAGATA  21768968


 Features flanking this part of subject sequence:
   45387 bp at 5' side: p21-activated kinase 1
   34520 bp at 3' side: hypothetical protein DKFZp434E1119


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  22804668  CACTGGAACTGAG  22804680


 Features in this part of subject sequence:
   chapsyn-110


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  30034831  ACTGGAACTGAGA  30034843


 Features in this part of subject sequence:
   synaptotagmin-like 2 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  31106072  CACACTGGAACTG  31106084


 Features flanking this part of subject sequence:
   3171 bp at 5' side: coiled-coil domain containing 81
   15381 bp at 3' side: malic enzyme 3, NADP(+)-dependent, mitochondrial


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  31795626  ACTGGAACTGAGA  31795614


>ref|NW_925173.1|HsCraAADB02_444 D Homo sapiens chromosome 11 genomic contig, alte
(based on Celera assembly)
Length=44976370

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent 
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   106859 bp at 5' side: FN5 protein
   150023 bp at 3' side: Josephin domain containing 3


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAGAT  18
                |||||||||||||||
Sbjct  3479642  CACTGGAACTGAGAT  3479656


 Features in this part of subject sequence:
   transient receptor potential cation channel, subfamily C,...


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGATAC  20
                 |||||||||||||||
Sbjct  11488707  CTGGAACTGAGATAC  11488693


 Features in this part of subject sequence:
   hypothetical protein LOC120406
```

```
 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGATA  19
                 |||||||||||||||
Sbjct  24587605  ACTGGAACTGAGATA  24587619


 Features flanking this part of subject sequence:
   19364 bp at 5' side: hypothetical protein
   788983 bp at 3' side: BUD13 homolog


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACTG  14
                 ||||||||||||||
Sbjct  25854523  TCACACTGGAACTG  25854510


 Features flanking this part of subject sequence:
   64910 bp at 5' side: olfactory receptor, family 10, subfamily G, member 7
   13547 bp at 3' side: BCSC-1 isoform 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  34002720  TGGAACTGAGATAC  34002707


 Features flanking this part of subject sequence:
   298036 bp at 5' side: cysteine and histidine-rich domain (CHORD)-containing, zi.
   1703775 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5       ACTGGAACTGAGA  17
               |||||||||||||
Sbjct  423582  ACTGGAACTGAGA  423594


 Features flanking this part of subject sequence:
   136333 bp at 5' side: hypothetical protein
   16644 bp at 3' side: similar to hephaestin isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  3893825  GGAACTGAGATAC  3893837


 Features flanking this part of subject sequence:
   104056 bp at 5' side: piwi-like 4
   43430 bp at 3' side: angiomotin like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  4614935  TCACACTGGAACT  4614923


 Features flanking this part of subject sequence:
   228097 bp at 5' side: jerky homolog-like
   2942590 bp at 3' side: contactin 5 isoform short
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  6522597  ACACTGGAACTGA  6522585


 Features flanking this part of subject sequence:
   2029740 bp at 5' side: jerky homolog-like
   1140947 bp at 3' side: contactin 5 isoform short


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  8324228  TCACACTGGAACT  8324240


 Features flanking this part of subject sequence:
   3095571 bp at 5' side: jerky homolog-like
   75116 bp at 3' side: contactin 5 isoform short


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  9390071  TGGAACTGAGATA  9390059


 Features in this part of subject sequence:
   contactin 5 isoform short
   contactin 5 isoform long


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  10114921  TGGAACTGAGATA  10114909


 Features in this part of subject sequence:
   glutamate receptor, ionotrophic


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  15883548  CACACTGGAACTG  15883560


 Features flanking this part of subject sequence:
   310102 bp at 5' side: DEAD (Asp-Glu-Ala-Asp) box polypeptide 10
   172446 bp at 3' side: hypothetical protein LOC399947


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  19145025  TGGAACTGAGATA  19145013


 Features flanking this part of subject sequence:
   172468 bp at 5' side: hypothetical protein LOC120406
   297873 bp at 3' side: immunoglobulin superfamily, member 4D


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  24772584  AACTGAGATACGG  24772596


 Features in this part of subject sequence:
   KIAA0999 protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  26862601  ACTGGAACTGAGA  26862589


 Features in this part of subject sequence:
   SID1 transmembrane family, member 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  27081553  TCACACTGGAACT  27081541


 Features in this part of subject sequence:
   Down syndrome cell adhesion molecule like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGAGATA  19
                 ||||| |||||||||||
Sbjct  27466891  ACACTTGAACTGAGATA  27466907


 Features flanking this part of subject sequence:
   10236 bp at 5' side: hypothetical protein isoform 11
   20030 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  35011734  CACTGGAACTGAG  35011746


 Features flanking this part of subject sequence:
   199732 bp at 5' side: hypothetical protein LOC399980
   20476 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  41767816  CTGGAACTGAGAT  41767804


>ref|NW_924796.1|HsCraAADB02_410 D Homo sapiens chromosome 10 genomic contig, alte
(based on Celera assembly)
Length=28940744

                                                              Sort alignments for this s
                                                                E value  Score  Percent 
                                                                Query start position  Su

 Features in this part of subject sequence:
   protein kinase, cGMP-dependent, type I
```

```
 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATAC  20
                |||||||||||||||
Sbjct  1176292  CTGGAACTGAGATAC  1176278


 Features in this part of subject sequence:
   protein kinase, cGMP-dependent, type I


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTGA  15
                ||||||||||||||
Sbjct  1001333  CACACTGGAACTGA  1001320


 Features flanking this part of subject sequence:
   312739 bp at 5' side: ankyrin 3 isoform 2
   55457 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  9672692  CTGGAACTGAGAT  9672680


 Features flanking this part of subject sequence:
   118659 bp at 5' side: Rho-related BTB domain containing 1
   380352 bp at 3' side: transmembrane protein 26


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  10250968  CTGGAACTGAGAT  10250956


 Features in this part of subject sequence:
   jumonji domain containing 1C


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  12432623  CTGGAACTGAGAT  12432635


 Features flanking this part of subject sequence:
   810026 bp at 5' side: similar to activator of S phase kinase
   944161 bp at 3' side: catenin, alpha 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  14203014  ACACTGGAACTGA  14203002


 Features flanking this part of subject sequence:
   1104851 bp at 5' side: similar to activator of S phase kinase
   649336 bp at 3' side: catenin, alpha 3


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  14497839  ACTGGAACTGAGA  14497827


 Features flanking this part of subject sequence:
   1233475 bp at 5' side: similar to activator of S phase kinase
   520712 bp at 3' side: catenin, alpha 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  14626451  TGGAACTGAGATA  14626463


 Features flanking this part of subject sequence:
   260113 bp at 5' side: zinc finger protein 503
   120800 bp at 3' side: chromosome 10 open reading frame 11


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  24905179  ACTGGAACTGAGA  24905167


>ref|NW_924062.1|HsCraAADB02_344 D Homo sapiens chromosome 9 genomic contig, alter
(based on Celera assembly)
Length=38596040

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   65551 bp at 5' side: insulin-like 4 precursor
   664 bp at 3' side: relaxin 2 isoform 1 preproprotein


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGAGA  17
                |||||||||||||||
Sbjct  5109566  ACACTGGAACTGAGA  5109580


 Features in this part of subject sequence:
   solute carrier family 24 (sodium/potassium/calcium exchan...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  19331180  TGGAACTGAGATAC  19331167


 Features in this part of subject sequence:
   jumonji domain containing 2C


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        GAACTGAGATACG  21
                |||||||||||||
Sbjct  6879207  GAACTGAGATACG  6879219


 Features in this part of subject sequence:
```

```
   jumonji domain containing 2C


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  6901554  ACTGGAACTGAGA  6901542


 Features flanking this part of subject sequence:
   928424 bp at 5' side: protein tyrosine phosphatase, receptor type, D isoform 1 .
   949141 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  9481177  ACTGGAACTGAGA  9481165


 Features flanking this part of subject sequence:
   35316 bp at 5' side: multiple PDZ domain protein
   123052 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  13102833  CTGGAACTGAGAT  13102821


 Features flanking this part of subject sequence:
   38588 bp at 5' side: SH3-domain GRB2-like 2
   637058 bp at 3' side: ADAMTS-like 1 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  17647396  CTGGAACTGAGAT  17647384


 Features in this part of subject sequence:
   solute carrier family 24 (sodium/potassium/calcium exchan...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  19426896  AACTGAGATACGG  19426908


 Features flanking this part of subject sequence:
   406027 bp at 5' side: DMRT-like family A1
   818914 bp at 3' side: ELAV (embryonic lethal, abnormal vision, Drosophila)-like.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  22680769  TGGAACTGAGATA  22680757


 Features flanking this part of subject sequence:
   839737 bp at 5' side: hypothetical protein
   1402162 bp at 3' side: hypothetical protein
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  28801483  ACACTGGAACTGA  28801471


 Features flanking this part of subject sequence:
   35062 bp at 5' side: hypothetical protein
   11396 bp at 3' side: olfactory receptor, family 2, subfamily S, member 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  35763812  CTGGAACTGAGAT  35763824


>ref|NW_924573.1|HsCraAADB02_390 D Homo sapiens chromosome 9 genomic contig, alter
(based on Celera assembly)
Length=25070985

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent 
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   345893 bp at 5' side: deleted in esophageal cancer 1
   156347 bp at 3' side: chromosome 9 open reading frame 27


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGAGA  17
                |||||||||||||||
Sbjct  2645745  ACACTGGAACTGAGA  2645759


 Features in this part of subject sequence:
   v-abl Abelson murine leukemia viral oncogene homolog 1 is...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGAG  16
                 ||||||||||||||
Sbjct  17639503  ACACTGGAACTGAG  17639490


 Features in this part of subject sequence:
   tumor necrosis factor (ligand) superfamily, member 8


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  1808107  ACACTGGAACTGA  1808119


 Features in this part of subject sequence:
   pregnancy-associated plasma protein A preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  3098366  CACACTGGAACTG  3098354
```

```
 Features in this part of subject sequence:
   pregnancy-associated plasma protein A preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  3283338  CACTGGAACTGAG  3283326


 Features in this part of subject sequence:
   astrotactin 2 isoform a
   astrotactin 2 isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  4003344  TGGAACTGAGATA  4003356


 Features in this part of subject sequence:
   astrotactin 2 isoform a
   astrotactin 2 isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  4258515  CACTGGAACTGAG  4258527


 Features in this part of subject sequence:
   astrotactin 2 isoform a
   astrotactin 2 isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  4282860  ACACTGGAACTGA  4282848


 Features in this part of subject sequence:
   complement component 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  7924879  CTGGAACTGAGAT  7924867


 Features flanking this part of subject sequence:
   34996 bp at 5' side: DAB2 interacting protein isoform 1
   170294 bp at 3' side: tubulin tyrosine ligase-like family, member 11


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  8717207  ACACTGGAACTGA  8717219


 Features flanking this part of subject sequence:
   89878 bp at 5' side: phosphatidic acid phosphatase type 2 domain containing 3
   107159 bp at 3' side: protein-O-mannosyltransferase 1
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  18300438  TGGAACTGAGATA  18300450


>ref|NW_923929.1|HsCraAADB02_332 D Homo sapiens chromosome 8 genomic contig, alter
(based on Celera assembly)
Length=39695605

                                                               Sort alignments for this s
                                                                 E value  Score  Percent 
                                                                 Query start position  Su

 Features flanking this part of subject sequence:
   6957 bp at 5' side: valosin containing protein (p97)/p47 complex interacting ...
   3778 bp at 3' side: hypothetical protein LOC56260


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGAT  18
                 |||||||||||||||
Sbjct  20712017  CACTGGAACTGAGAT  20712003


 Features in this part of subject sequence:
   hypothetical protein LOC23514


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  1555930  ACACTGGAACTGA  1555918


 Features flanking this part of subject sequence:
   17533 bp at 5' side: similar to pleiomorphic adenoma gene 1
   26977 bp at 3' side: coiled-coil-helix-coiled-coil-helix domain containing 7 i..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  10222179  ACTGGAACTGAGA  10222191


 Features flanking this part of subject sequence:
   440488 bp at 5' side: proenkephalin
   77278 bp at 3' side: myo-inositol monophosphatase A3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  10922873  ACTGGAACTGAGA  10922861


 Features flanking this part of subject sequence:
   125933 bp at 5' side: similar to Collagen alpha-1(VII) chain precursor (Long-ch.
   25164 bp at 3' side: hypothetical protein LOC90362


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
```

```
                 |||||||||||||
Sbjct  12159815  CACTGGAACTGAG  12159803

 Features flanking this part of subject sequence:
   823851 bp at 5' side: similar to ribosomal protein S15a
   218564 bp at 3' side: sulfatase 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  23388402  ACTGGAACTGAGA  23388414

 Features in this part of subject sequence:
   hypothetical protein LOC138046


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  38844195  CTGGAACTGAGAT  38844207


>ref|NW_923907.1|HsCraAADB02_330 D Homo sapiens chromosome 8 genomic contig, alter
(based on Celera assembly)
Length=31321926
                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features in this part of subject sequence:
   similar to indoleamine 2,3-dioxygenase


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACTGA  15
                 |||||||||||||||
Sbjct  27375742  TCACACTGGAACTGA  27375728

 Features flanking this part of subject sequence:
   429913 bp at 5' side: zinc finger, matrin type 4
   4347 bp at 3' side: secreted frizzled-related protein 1


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGATAC  20
                 |||||||||||||||
Sbjct  28635204  CTGGAACTGAGATAC  28635218

 Features flanking this part of subject sequence:
   16816 bp at 5' side: deleted in liver cancer 1 isoform 3
   572926 bp at 3' side: sarcoglycan zeta


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query  2       CACACTGGAACTGAGATA  19
               |||||||||||| |||||
Sbjct  907539  CACACTGGAACTCAGATA  907556

 Features in this part of subject sequence:
   ADP-ribosylation factor guanine nucleotide factor 6 isofo...
```

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATA  19
                ||||||||||||||
Sbjct  5942533  CTGGAACTGAGATA  5942520


 Features flanking this part of subject sequence:
   2133 bp at 5' side: steroidogenic acute regulator isoform 2
   10699 bp at 3' side: Lsm1 protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACTG  14
                 ||||||||||||||
Sbjct  25530850  TCACACTGGAACTG  25530863


 Features flanking this part of subject sequence:
   90607 bp at 5' side: protein expressed in prostate, ovary, testis, and placent..
   224969 bp at 3' side: similar to Ciliary dynein heavy chain 11 (Axonemal beta d.


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
Sbjct  30820264  ACTGGAACTGAGAT  30820251


 Features flanking this part of subject sequence:
   973362 bp at 5' side: leucine zipper, putative tumor suppressor 1
   82110 bp at 3' side: similar to filaggrin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  8616465  TGGAACTGAGATA  8616477


 Features flanking this part of subject sequence:
   999412 bp at 5' side: leucine zipper, putative tumor suppressor 1
   56060 bp at 3' side: similar to filaggrin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  8642527  ACACTGGAACTGA  8642515


 Features in this part of subject sequence:
   erythrocyte membrane protein band 4.9 (dematin)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  9463730  TGGAACTGAGATA  9463742


 Features flanking this part of subject sequence:
   242 bp at 5' side: paraneoplastic antigen MA2
   69264 bp at 3' side: dihydropyrimidinase-like 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
```

```
 Strand=Plus/Minus

Query  9         GAACTGAGATACG  21
                 |||||||||||||
Sbjct  13896785  GAACTGAGATACG  13896773


 Features flanking this part of subject sequence:
   63037 bp at 5' side: dihydropyrimidinase-like 2
   30364 bp at 3' side: alpha-1A-adrenergic receptor isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  14106521  TCACACTGGAACT  14106509


 Features flanking this part of subject sequence:
   5157 bp at 5' side: protein phosphatase 2, catalytic subunit, beta isoform
   15695 bp at 3' side: testis expressed sequence 15


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  18203031  ACACTGGAACTGA  18203019


 Features flanking this part of subject sequence:
   838467 bp at 5' side: similar to ribosomal protein L10a
   382562 bp at 3' side: netrin receptor Unc5h4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  22537321  CACTGGAACTGAG  22537333


 Features flanking this part of subject sequence:
   3177 bp at 5' side: HTPAP protein
   3511 bp at 3' side: WHSC1L1 protein isoform long


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  25650538  TGGAACTGAGATA  25650526


 Features flanking this part of subject sequence:
   165759 bp at 5' side: ankyrin 1 isoform 8
   101953 bp at 3' side: MYST histone acetyltransferase (monocytic leukemia) 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  29204667  GGAACTGAGATAC  29204679


 Features flanking this part of subject sequence:
   37346 bp at 5' side: plasminogen activator, tissue type isoform 2 precursor
   41583 bp at 3' side: inhibitor of kappa light polypeptide gene enhancer in B-c..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  29604840  ACTGGAACTGAGA  29604852


 Features flanking this part of subject sequence:
   34819 bp at 5' side: hypothetical protein
   10880 bp at 3' side: protein expressed in prostate, ovary, testis, and placent..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  30654364  CACACTGGAACTG  30654376


>ref|NW_924018.1|HsCraAADB02_340 D Homo sapiens chromosome 8 genomic contig, alter
(based on Celera assembly)
Length=3385519

 Features in this part of subject sequence:
   similar to poly (ADP-ribose) polymerase family, member 10


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  2        CACACTGGAACTGAG  16
                |||||||||||||||
Sbjct  2279832  CACACTGGAACTGAG  2279846


>ref|NW_923984.1|HsCraAADB02_337 D Homo sapiens chromosome 8 genomic contig, alter
(based on Celera assembly)
Length=55887796

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features in this part of subject sequence:
   cyclic nucleotide gated channel beta 3


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  6       CTGGAACTGAGATAC  20
               |||||||||||||||
Sbjct  774803  CTGGAACTGAGATAC  774789


 Features in this part of subject sequence:
   basic beta 1 syntrophin


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGAT  18
                 |||||||||||||||
Sbjct  34875166  CACTGGAACTGAGAT  34875152


 Features flanking this part of subject sequence:
   17794 bp at 5' side: hypothetical protein
   194883 bp at 3' side: ankyrin repeat domain 46


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGAG  16
                 ||||||||||||||
Sbjct  14490596  ACACTGGAACTGAG  14490583
```

```
 Features flanking this part of subject sequence:
   197335 bp at 5' side: hypothetical protein LOC9694
   100303 bp at 3' side: hypothetical protein LOC157753


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  22848654  TGGAACTGAGATAC  22848641


 Features flanking this part of subject sequence:
   744776 bp at 5' side: zinc finger transcription factor TRPS1
   275949 bp at 3' side: eukaryotic translation initiation factor 3, subunit 3 gam.


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  30532676  TGGAACTGAGATAC  30532689


 Features in this part of subject sequence:
   basic beta 1 syntrophin


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
Sbjct  34938812  ACTGGAACTGAGAT  34938825


 Features flanking this part of subject sequence:
   135234 bp at 5' side: zinc finger protein 406 isoform TR-ZFAT
   664508 bp at 3' side: KH domain containing, RNA binding, signal transduction as.


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGAG  16
                 ||||||||||||||
Sbjct  48943673  ACACTGGAACTGAG  48943686


 Features flanking this part of subject sequence:
   328071 bp at 5' side: KH domain containing, RNA binding, signal transduction as.
   1835429 bp at 3' side: hypothetical protein LOC401478


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         GAACTGAGATACGG  22
                 ||||||||||||||
Sbjct  50124770  GAACTGAGATACGG  50124757


 Features in this part of subject sequence:
   cyclic nucleotide binding domain containing 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  1285195  TCACACTGGAACT  1285183


 Features in this part of subject sequence:
   matrix metalloproteinase 16 isoform 1 preproprotein
```

```
    matrix metalloproteinase 16 isoform 2 preproprotein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  2415311  CTGGAACTGAGAT  2415299


  Features flanking this part of subject sequence:
    622019 bp at 5' side: matrix metalloproteinase 16 isoform 2 preproprotein
    809057 bp at 3' side: receptor-interacting serine-threonine kinase 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  3121406  GGAACTGAGATAC  3121394


  Features flanking this part of subject sequence:
    125621 bp at 5' side: solute carrier family 26, member 7 isoform b
    432482 bp at 3' side: acute myelogenous leukemia 1 translocation 1 protein isof.


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  5691656  ACTGGAACTGAGA  5691644


  Features in this part of subject sequence:
    RNA binding motif protein 35A isoform 1
    RNA binding motif protein 35A isoform 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  8837477  ACTGGAACTGAGA  8837489


  Features in this part of subject sequence:
    suppression of tumorigenicity


  Score = 26.3 bits (13),  Expect =   444
  Identities = 16/17 (94%), Gaps = 0/17 (0%)
  Strand=Plus/Minus

Query  1         TCACACTGGAACTGAGA  17
                 |||| ||||||||||||
Sbjct  18750977  TCACCCTGGAACTGAGA  18750961


  Features in this part of subject sequence:
    collagen, type XIV, alpha 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  9         GAACTGAGATACG  21
                 |||||||||||||
Sbjct  34423076  GAACTGAGATACG  34423088


  Features flanking this part of subject sequence:
    679685 bp at 5' side: hypothetical protein LOC641384
    588086 bp at 3' side: hypothetical protein
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  42786075  CACTGGAACTGAG  42786087


 Features flanking this part of subject sequence:
   550740 bp at 5' side: KH domain containing, RNA binding, signal transduction as.
   1612761 bp at 3' side: hypothetical protein LOC401478


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  50347438  ACTGGAACTGAGA  50347426


 Features flanking this part of subject sequence:
   150299 bp at 5' side: collagen, type XXII, alpha 1
   585816 bp at 3' side: potassium channel, subfamily K, member 9


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  53178216  ACACTGGAACTGA  53178204


>ref|NW_923796.1|HsCraAADB02_320 D Homo sapiens chromosome 7 genomic contig, alter
(based on Celera assembly)
Length=5180218

                                                              Sort alignments for this s
                                                                E value  Score  Percent 
                                                                Query start position  Sul

 Features in this part of subject sequence:
   dipeptidyl-peptidase 6 isoform 2
   dipeptidyl-peptidase 6 isoform 3


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  2       CACACTGGAACTGAG  16
               |||||||||||||||
Sbjct  708846  CACACTGGAACTGAG  708832


 Features in this part of subject sequence:
   dipeptidyl-peptidase 6 isoform 2
   dipeptidyl-peptidase 6 isoform 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4       CACTGGAACTGAG  16
               |||||||||||||
Sbjct  707737  CACTGGAACTGAG  707749


>ref|NW_923640.1|HsCraAADB02_306 D Homo sapiens chromosome 7 genomic contig, alter
(based on Celera assembly)
Length=39238468

                                                              Sort alignments for this s
                                                                E value  Score  Percent 
                                                                Query start position  Sul

 Features flanking this part of subject sequence:
   9066 bp at 5' side: NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5
   47630 bp at 3' side: ankyrin repeat and SOCS box-containing 15
```

```
 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAGAT  18
                 |||||||||||||||
Sbjct  20769420  CACTGGAACTGAGAT  20769434


 Features flanking this part of subject sequence:
   5269 bp at 5' side: similar to aldo-keto reductase family 1, member B10 isofo...
   76677 bp at 3' side: 2,3-bisphosphoglycerate mutase


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGATA  19
                 |||||||||||||||
Sbjct  31765740  ACTGGAACTGAGATA  31765754


 Features in this part of subject sequence:
   HMG-box transcription factor 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGAT  18
                ||||||||||||||
Sbjct  4393511  ACTGGAACTGAGAT  4393498


 Features in this part of subject sequence:
   component of oligomeric golgi complex 5 isoform 2
   component of oligomeric golgi complex 5 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  4711536  ACACTGGAACTGA  4711524


 Features flanking this part of subject sequence:
   18588 bp at 5' side: hypothetical protein LOC154907
   1760160 bp at 3' side: IMP2 inner mitochondrial membrane protease-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  6114881  ACTGGAACTGAGA  6114869


 Features in this part of subject sequence:
   interferon-related developmental regulator 1
   interferon-related developmental regulator 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  9662608  TCACACTGGAACT  9662620


 Features flanking this part of subject sequence:
   504309 bp at 5' side: protein phosphatase 1 glycogen-binding regulatory subunit
   3205 bp at 3' side: forkhead box P2 isoform II
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  11628608  ACACTGGAACTGA  11628596


 Features in this part of subject sequence:
   forkhead box P2 isoform II
   forkhead box P2 isoform I


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  11805025  ACTGGAACTGAGA  11805013


 Features in this part of subject sequence:
   transmembrane 4 superfamily member 12


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  18046794  ACTGGAACTGAGA  18046782


 Features flanking this part of subject sequence:
   85895 bp at 5' side: similar to Ssu72 RNA polymerase II CTD phosphatase homolog
   183612 bp at 3' side: G protein-coupled receptor 37


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  21766954  ACACTGGAACTGA  21766966


 Features in this part of subject sequence:
   coatomer protein complex, subunit gamma 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTGAGAT  18
                 ||||||||| |||||||
Sbjct  27710653  CACACTGGATCTGAGAT  27710637


 Features flanking this part of subject sequence:
   1052 bp at 5' side: hypothetical protein isoform 2
   413778 bp at 3' side: muskelin 1, intracellular mediator containing kelch motifs


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  28108599  GGAACTGAGATAC  28108611


 Features in this part of subject sequence:
   SEC8 protein isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  31054157  CACACTGGAACTG  31054169


 Features flanking this part of subject sequence:
   107311 bp at 5' side: ATP/GTP binding protein-like 3
   6078 bp at 3' side: hypothetical protein LOC55281


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  32339343  CTGGAACTGAGAT  32339331


 Features in this part of subject sequence:
   solute carrier family 13 (sodium/sulfate symporters), mem...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  32892509  AACTGAGATACGG  32892497


 Features flanking this part of subject sequence:
   272384 bp at 5' side: similar to transient receptor potential cation channel, s.
   337627 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  33716202  ACACTGGAACTGA  33716214


 Features flanking this part of subject sequence:
   48414 bp at 5' side: hypothetical protein LOC136242
   29440 bp at 3' side: olfactory receptor, family 9, subfamily A, member 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  39069475  GGAACTGAGATAC  39069463


>ref|NT_079596.2|Hs7_79661 D Homo sapiens chromosome 7 genomic contig, alternate a
(based on CRA_TCAGchr7v2)
Length=58365407

                                                                Sort alignments for this s
                                                                  E value  Score  Percent
                                                                  Query start position  Su

 Features flanking this part of subject sequence:
   9066 bp at 5' side: NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5
   47633 bp at 3' side: ankyrin repeat and SOCS box-containing 15


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAGAT  18
                 |||||||||||||||
Sbjct  22631113  CACTGGAACTGAGAT  22631127


 Features flanking this part of subject sequence:
   5269 bp at 5' side: similar to aldo-keto reductase family 1, member B10 isofo...
```

```
    76677 bp at 3' side: 2,3-bisphosphoglycerate mutase


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Plus

 Query  5         ACTGGAACTGAGATA  19
                  |||||||||||||||
 Sbjct  33649455  ACTGGAACTGAGATA  33649469


  Features in this part of subject sequence:
    dipeptidyl-peptidase 6 isoform 3
    dipeptidyl-peptidase 6 isoform 1


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Minus

 Query  2         CACACTGGAACTGAG  16
                  |||||||||||||||
 Sbjct  53936291  CACACTGGAACTGAG  53936277


  Features in this part of subject sequence:
    HMG-box transcription factor 1


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

 Query  5        ACTGGAACTGAGAT  18
                 ||||||||||||||
 Sbjct  6226118  ACTGGAACTGAGAT  6226105


  Features in this part of subject sequence:
    cell recognition molecule Caspr2 precursor


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

 Query  9         GAACTGAGATACGG  22
                  ||||||||||||||
 Sbjct  46666352  GAACTGAGATACGG  46666339


  Features in this part of subject sequence:
    component of oligomeric golgi complex 5 isoform 1
    component of oligomeric golgi complex 5 isoform 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  3        ACACTGGAACTGA  15
                 |||||||||||||
 Sbjct  6544167  ACACTGGAACTGA  6544155


  Features flanking this part of subject sequence:
    18587 bp at 5' side: hypothetical protein LOC154907
    1760314 bp at 3' side: IMP2 inner mitochondrial membrane protease-like


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  5        ACTGGAACTGAGA  17
                 |||||||||||||
 Sbjct  7946055  ACTGGAACTGAGA  7946043


  Features in this part of subject sequence:
    interferon-related developmental regulator 1
    interferon-related developmental regulator 1
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  11495699  TCACACTGGAACT  11495711


 Features flanking this part of subject sequence:
   504160 bp at 5' side: protein phosphatase 1 glycogen-binding regulatory subunit
   3205 bp at 3' side: forkhead box P2 isoform I


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  13494155  ACACTGGAACTGA  13494143


 Features in this part of subject sequence:
   forkhead box P2 isoform I
   forkhead box P2 isoform II


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  13670572  ACTGGAACTGAGA  13670560


 Features in this part of subject sequence:
   transmembrane 4 superfamily member 12


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  19909184  ACTGGAACTGAGA  19909172


 Features flanking this part of subject sequence:
   85921 bp at 5' side: similar to Ssu72 RNA polymerase II CTD phosphatase homolog
   183655 bp at 3' side: G protein-coupled receptor 37


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  23627871  ACACTGGAACTGA  23627883


 Features in this part of subject sequence:
   coatomer protein complex, subunit gamma 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTGAGAT  18
                 ||||||||| |||||||
Sbjct  29577101  CACACTGGATCTGAGAT  29577085


 Features flanking this part of subject sequence:
   1052 bp at 5' side: hypothetical protein isoform 2
   413841 bp at 3' side: muskelin 1, intracellular mediator containing kelch motifs


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  29974042  GGAACTGAGATAC  29974054


 Features in this part of subject sequence:
   SEC8 protein isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  32918925  CACACTGGAACTG  32918937


 Features flanking this part of subject sequence:
   107301 bp at 5' side: ATP/GTP binding protein-like 3
   6078 bp at 3' side: hypothetical protein LOC55281


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  34223042  CTGGAACTGAGAT  34223030


 Features in this part of subject sequence:
   solute carrier family 13 (sodium/sulfate symporters), mem...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  34776295  AACTGAGATACGG  34776283


 Features flanking this part of subject sequence:
   270913 bp at 5' side: similar to transient receptor potential cation channel, s.
   337211 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  35598571  ACACTGGAACTGA  35598583


 Features flanking this part of subject sequence:
   48861 bp at 5' side: hypothetical protein LOC136242
   29449 bp at 3' side: olfactory receptor, family 9, subfamily A, member 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  40963004  GGAACTGAGATAC  40962992


 Features in this part of subject sequence:
   Ras homolog enriched in brain


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  50557206  ACTGGAACTGAGA  50557194
```

```
 Features in this part of subject sequence:
   dipeptidyl-peptidase 6 isoform 3
   dipeptidyl-peptidase 6 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  53935182  CACTGGAACTGAG  53935194


>ref|NW_923184.1|HsCraAADB02_265 D Homo sapiens chromosome 6 genomic contig, alter
(based on Celera assembly)
Length=103786604
                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

 Features in this part of subject sequence:
   peptidylprolyl isomerase (cyclophilin)-like 6


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGAGA  17
                 |||||||||||||||
Sbjct  42573891  ACACTGGAACTGAGA  42573877


 Features flanking this part of subject sequence:
   205323 bp at 5' side: hypothetical protein
   17082 bp at 3' side: similar to quaking homolog, KH domain RNA binding isoform..


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTGAG  16
                 |||||||||||||||
Sbjct  96615780  CACACTGGAACTGAG  96615766


 Features flanking this part of subject sequence:
   113874 bp at 5' side: hypothetical protein
   119180 bp at 3' side: inhibitor of Bruton's tyrosine kinase


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  15253457  CACTGGAACTGAGA  15253444


 Features flanking this part of subject sequence:
   482241 bp at 5' side: mannosidase, alpha, class 1A, member 1
   1258791 bp at 3' side: hypothetical protein LOC221322


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGATA  19
                 ||||||||||||||
Sbjct  52965373  CTGGAACTGAGATA  52965360


 Features flanking this part of subject sequence:
   159863 bp at 5' side: A-kinase anchor protein 7 isoform beta
   131684 bp at 3' side: arginase, type I
```

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  64577968  CACTGGAACTGAGA  64577981


 Features in this part of subject sequence:
   eyes absent 4 isoform a
   eyes absent 4 isoform d


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGATA  19
                 ||||||||||||||
Sbjct  66522462  CTGGAACTGAGATA  66522449


 Features in this part of subject sequence:
   NEW1 domain containing protein isoform 1
   NEW1 domain containing protein isoform 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9         GAACTGAGATACGG  22
                 ||||||||||||||
Sbjct  90535967  GAACTGAGATACGG  90535980


 Features in this part of subject sequence:
   brain-specific angiogenesis inhibitor 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  2109609  TCACACTGGAACT  2109621


 Features flanking this part of subject sequence:
   571844 bp at 5' side: CD109
   689889 bp at 3' side: collagen, type XII, alpha 1 long isoform precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  7568741  ACTGGAACTGAGA  7568753


 Features flanking this part of subject sequence:
   847414 bp at 5' side: 5-hydroxytryptamine (serotonin) receptor 1B
   556386 bp at 3' side: interleukin-1 receptor-associated kinase 1 binding protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  11476795  CTGGAACTGAGAT  11476783


 Features in this part of subject sequence:
   SH3 domain binding glutamic acid-rich protein like 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  12838877  CACTGGAACTGAG  12838889


 Features flanking this part of subject sequence:
   50805 bp at 5' side: SH3 domain binding glutamic acid-rich protein like 2
   169129 bp at 3' side: elongation of very long chain fatty acids (FEN1/Elo2, SUR.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  12943775  ACACTGGAACTGA  12943763


 Features flanking this part of subject sequence:
   1169117 bp at 5' side: similar to citrate synthase precursor, isoform a
   24715 bp at 3' side: family with sequence similarity 46, member A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  14926197  GGAACTGAGATAC  14926185


 Features flanking this part of subject sequence:
   498090 bp at 5' side: 5T4 oncofetal trophoblast glycoprotein
   28854 bp at 3' side: hypothetical protein LOC90025


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  16075734  TGGAACTGAGATA  16075722


 Features flanking this part of subject sequence:
   250796 bp at 5' side: similar to T-box transcription factor TBX18 (T-box protei.
   242353 bp at 3' side: similar to ribosomal protein L31


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  18220528  CACACTGGAACTG  18220540


 Features flanking this part of subject sequence:
   41449 bp at 5' side: glycoprotein hormones, alpha polypeptide precursor
   25915 bp at 3' side: similar to Zinc finger protein 292 isoform 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  20326739  GGAACTGAGATAC  20326727


 Features in this part of subject sequence:
   RNA guanylyltransferase and 5'-phosphatase


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
```

```
                 |||||||||||||
Sbjct  21930423  GGAACTGAGATAC  21930435


 Features in this part of subject sequence:
   RNA guanylyltransferase and 5'-phosphatase


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  22104782  CACACTGGAACTG  22104770


 Features flanking this part of subject sequence:
   95651 bp at 5' side: similar to mannosidase, endo-alpha
   502167 bp at 3' side: fucosyltransferase 9 (alpha (1,3) fucosyltransferase)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  28859545  TCACACTGGAACT  28859533


 Features flanking this part of subject sequence:
   216339 bp at 5' side: fucosyltransferase 9 (alpha (1,3) fucosyltransferase)
   100978 bp at 3' side: hypothetical protein LOC23376


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  29579130  ACACTGGAACTGA  29579142


 Features in this part of subject sequence:
   APG5 autophagy 5-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  39384151  TGGAACTGAGATA  39384163


 Features flanking this part of subject sequence:
   142560 bp at 5' side: Sac domain-containing inositol phosphatase 3
   11300 bp at 3' side: G protein-coupled receptor 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTGAGAT  18
                 ||||| |||||||||||
Sbjct  43104306  CACACAGGAACTGAGAT  43104290


 Features flanking this part of subject sequence:
   564 bp at 5' side: REV3-like, catalytic subunit of DNA polymerase zeta
   66612 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  44553321  CACACTGGAACTG  44553309
```

```
 Features flanking this part of subject sequence:
   149093 bp at 5' side: phospholamban
   187474 bp at 3' side: ASF1 anti-silencing function 1 homolog A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  51841270  GGAACTGAGATAC  51841258


 Features flanking this part of subject sequence:
   1484989 bp at 5' side: mannosidase, alpha, class 1A, member 1
   256044 bp at 3' side: hypothetical protein LOC221322


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  53968108  TGGAACTGAGATA  53968120


 Features flanking this part of subject sequence:
   130975 bp at 5' side: connexin 43
   820611 bp at 3' side: heat shock transcription factor 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  54713163  GGAACTGAGATAC  54713151


 Features flanking this part of subject sequence:
   25063 bp at 5' side: hypothetical protein LOC134829
   129481 bp at 3' side: triadin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  56223037  TGGAACTGAGATA  56223025


 Features in this part of subject sequence:
   T-cell lymphoma breakpoint-associated target 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  56954659  CTGGAACTGAGAT  56954671


 Features in this part of subject sequence:
   T-cell lymphoma breakpoint-associated target 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  57019875  TCACACTGGAACT  57019863


 Features flanking this part of subject sequence:
   32743 bp at 5' side: KIAA1913
```

```
   352685 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  63610795  AACTGAGATACGG  63610807


 Features in this part of subject sequence:
   heme binding protein 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  71539513  CACACTGGAACTG  71539525


 Features flanking this part of subject sequence:
   224 bp at 5' side: similar to NHS-like 1 isoform 5
   71212 bp at 3' side: coiled-coil domain containing 28A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         GAACTGAGATACG  21
                 |||||||||||||
Sbjct  71832308  GAACTGAGATACG  71832296


 Features in this part of subject sequence:
   similar to ECT2 protein (Epithelial cell-transforming seq...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  71979365  TGGAACTGAGATA  71979353


 Features flanking this part of subject sequence:
   48257 bp at 5' side: muscle-derived protein 77
   35960 bp at 3' side: Cbp/p300-interacting transactivator, with Glu/Asp-rich ca..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTGAGAT  18
                 |||||| ||||||||||
Sbjct  72466960  CACACTTGAACTGAGAT  72466976


 Features flanking this part of subject sequence:
   111919 bp at 5' side: G protein-coupled receptor 126 beta 2
   197665 bp at 3' side: human immunodeficiency virus type I enhancer binding prot.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  75685691  TCACACTGGAACT  75685703


 Features in this part of subject sequence:
   androgen-induced 1


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  76422985  CACTGGAACTGAG  76422973


 Features flanking this part of subject sequence:
   42392 bp at 5' side: utrophin
   732351 bp at 3' side: laforin isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACTGAGA  17
                 |||||||||| ||||||
Sbjct  78023428  TCACACTGGAGCTGAGA  78023444


 Features flanking this part of subject sequence:
   268369 bp at 5' side: uronyl-2-sulfotransferase
   27550 bp at 3' side: mitogen-activated protein kinase kinase kinase 7 interact..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  82467277  CTGGAACTGAGAT  82467289


 Features in this part of subject sequence:
   chromosome 6 open reading frame 71


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  83515517  ACACTGGAACTGA  83515529


 Features in this part of subject sequence:
   opioid receptor, mu 1 isoform MOR-1O
   opioid receptor, mu 1 isoform MOR-1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  87226078  ACACTGGAACTGA  87226090


 Features flanking this part of subject sequence:
   76890 bp at 5' side: claudin 20
   43573 bp at 3' side: NADPH oxidase 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  88477313  ACTGGAACTGAGA  88477301


 Features in this part of subject sequence:
   ribosomal protein S6 kinase, 90kDa, polypeptide 2 isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  99898284  ACTGGAACTGAGA  99898296


>ref|NW_922984.1|HsCraAADB02_247 D Homo sapiens chromosome 6 genomic contig, alter
(based on Celera assembly)
Length=26292868

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   107686 bp at 5' side: phenylalanine-tRNA synthetase 2
   119396 bp at 3' side: neuritin precursor


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  2        CACACTGGAACTGAG  16
                |||||||||||||||
Sbjct  5501735  CACACTGGAACTGAG  5501749


 Features in this part of subject sequence:
   bone morphogenetic protein 6 precursor


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATAC  20
                |||||||||||||||
Sbjct  7426003  CTGGAACTGAGATAC  7425989


 Features in this part of subject sequence:
   CDK5 regulatory subunit associated protein 1-like 1


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGAGA  17
                 |||||||||||||||
Sbjct  20592624  ACACTGGAACTGAGA  20592610


 Features flanking this part of subject sequence:
   256893 bp at 5' side: CDK5 regulatory subunit associated protein 1-like 1
   106607 bp at 3' side: SRY (sex determining region Y)-box 4


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACTG  14
                 ||||||||||||||
Sbjct  21116734  TCACACTGGAACTG  21116747


 Features in this part of subject sequence:
   hypothetical protein LOC221749


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  3348779  CACACTGGAACTG  3348791


 Features in this part of subject sequence:
   phenylalanine-tRNA synthetase 2


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  5151415  CACACTGGAACTG  5151427


 Features in this part of subject sequence:
   coagulation factor XIII A1 subunit precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  5852805  TGGAACTGAGATA  5852817


 Features flanking this part of subject sequence:
   179553 bp at 5' side: MD-1, RP105-associated
   216991 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  6459460  CTGGAACTGAGAT  6459448


 Features flanking this part of subject sequence:
   381066 bp at 5' side: neural precursor cell expressed, developmentally down-reg.
   100405 bp at 3' side: hypothetical protein LOC84830


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  11237564  CACTGGAACTGAG  11237552


 Features flanking this part of subject sequence:
   95606 bp at 5' side: DEK oncogene (DNA binding)
   39879 bp at 3' side: IBR domain containing 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  17993028  ACTGGAACTGAGA  17993040


 Features flanking this part of subject sequence:
   219895 bp at 5' side: inhibitor of DNA binding 4, dominant negative helix-loop-.
   43592 bp at 3' side: similar to O-acyltransferase (membrane bound) domain cont..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  19687266  CACACTGGAACTG  19687254


 Features flanking this part of subject sequence:
   215335 bp at 5' side: CDK5 regulatory subunit associated protein 1-like 1
   148166 bp at 3' side: SRY (sex determining region Y)-box 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  21075176  CACACTGGAACTG  21075188


 Features flanking this part of subject sequence:
   31784 bp at 5' side: chromosome 6 open reading frame 62
   26777 bp at 3' side: geminin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  24379312  TCACACTGGAACT  24379324


>ref|NW_923073.1|HsCraAADB02_255 D Homo sapiens chromosome 6 genomic contig, alter
(based on Celera assembly)
Length=30372612

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Sul

 Features in this part of subject sequence:
   polyductin isoform 1
   polyductin isoform 2


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGAT  18
                 |||||||||||||||
Sbjct  24923576  CACTGGAACTGAGAT  24923562


 Features in this part of subject sequence:
   leucine rich repeat containing 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  26887818  CACTGGAACTGAGA  26887831


 Features flanking this part of subject sequence:
   139228 bp at 5' side: zinc finger protein 184 (Kruppel-like)
   195987 bp at 3' side: H2B histone family, member C


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7       TGGAACTGAGATA  19
               |||||||||||||
Sbjct  649664  TGGAACTGAGATA  649676


 Features flanking this part of subject sequence:
   4932 bp at 5' side: LEM domain containing 2
   766 bp at 3' side: motilin isoform 2 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  6780564  CACACTGGAACTG  6780552


 Features flanking this part of subject sequence:
```

```
   31917 bp at 5' side: tubby like protein 1
   31029 bp at 3' side: FK506 binding protein 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  8530867  ACACTGGAACTGA  8530855


 Features in this part of subject sequence:
   kinesin family member 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  12408496  CACACTGGAACTG  12408484


 Features flanking this part of subject sequence:
   31505 bp at 5' side: transcription factor EB
   14125 bp at 3' side: progastricsin (pepsinogen C)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  14708223  CTGGAACTGAGAT  14708211


 Features flanking this part of subject sequence:
   118555 bp at 5' side: runt-related transcription factor 2 isoform c
   237103 bp at 3' side: chloride intracellular channel 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  18650928  CACACTGGAACTG  18650916


 Features flanking this part of subject sequence:
   205023 bp at 5' side: transcription factor AP-2 beta (activating enhancer bindi.
   571590 bp at 3' side: polyductin isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  24036356  ACACTGGAACTGA  24036368


 Features flanking this part of subject sequence:
   253625 bp at 5' side: transcription factor AP-2 beta (activating enhancer bindi.
   522988 bp at 3' side: polyductin isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  24084970  ACTGGAACTGAGA  24084958


 Features in this part of subject sequence:
   homolog of yeast long chain polyunsaturated fatty acid el...
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  26271705  GGAACTGAGATAC  26271717


 Features flanking this part of subject sequence:
   146044 bp at 5' side: 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1
   30415 bp at 3' side: bone morphogenetic protein 5 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  28715433  ACTGGAACTGAGA  28715445


 Features in this part of subject sequence:
   bone morphogenetic protein 5 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  28846714  CTGGAACTGAGAT  28846726


>ref|NW_922784.1|HsCraAADB02_229 D Homo sapiens chromosome 5 genomic contig, alter
(based on Celera assembly)
Length=48999907

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent 
                                                                   Query start position  Sul

 Features flanking this part of subject sequence:
   953166 bp at 5' side: neuromedin U receptor 2
   132767 bp at 3' side: glutamate receptor, ionotropic, AMPA 1


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGATAC  20
                 |||||||||||||||
Sbjct  26441216  CTGGAACTGAGATAC  26441230


 Features flanking this part of subject sequence:
   26115 bp at 5' side: heat shock 70kDa protein 4 isoform b
   67812 bp at 3' side: follistatin-like 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  6223022  ACTGGAACTGAGA  6223010


 Features in this part of subject sequence:
   small inducible cytokine B14 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  8664873  CACTGGAACTGAG  8664861
```

```
 Features flanking this part of subject sequence:
   122481 bp at 5' side: similar to Pro-neuregulin-2, membrane-bound isoform precu.
   130386 bp at 3' side: purine-rich element binding protein A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  13067201  ACTGGAACTGAGA  13067213


 Features in this part of subject sequence:
   putative nuclear protein ORF1-FL49


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  13306868  ACACTGGAACTGA  13306856


 Features in this part of subject sequence:
   serine peptidase inhibitor, Kazal type 5 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  21178919  TGGAACTGAGATA  21178931


 Features flanking this part of subject sequence:
   19771 bp at 5' side: hypothetical protein
   12772 bp at 3' side: actin binding LIM protein family, member 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  22219010  CTGGAACTGAGAT  22218998


 Features in this part of subject sequence:
   FAT tumor suppressor 2 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  24609428  TGGAACTGAGATA  24609416


 Features in this part of subject sequence:
   FAT tumor suppressor 2 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  24649375  TGGAACTGAGATA  24649387


 Features flanking this part of subject sequence:
   807696 bp at 5' side: neuromedin U receptor 2
   278239 bp at 3' side: glutamate receptor, ionotropic, AMPA 1
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  26295758  ACTGGAACTGAGA  26295746


 Features in this part of subject sequence:
   gamma-aminobutyric acid (GABA) A receptor, beta 2 isoform 2
   gamma-aminobutyric acid (GABA) A receptor, beta 2 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  34465738  ACACTGGAACTGA  34465726


 Features in this part of subject sequence:
   gamma-aminobutyric acid (GABA) A receptor, beta 2 isoform 2
   gamma-aminobutyric acid (GABA) A receptor, beta 2 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  34513295  ACTGGAACTGAGA  34513307


 Features flanking this part of subject sequence:
   3524569 bp at 5' side: methionine adenosyltransferase II, beta isoform 1
   532927 bp at 3' side: similar to odd Oz/ten-m homolog 2 isoform 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  40132049  AACTGAGATACGG  40132061


 Features flanking this part of subject sequence:
   15677 bp at 5' side: cytoplasmic polyadenylation element binding protein 4
   1799 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  47059381  GGAACTGAGATAC  47059369


 Features flanking this part of subject sequence:
   31967 bp at 5' side: hypothetical protein
   14168 bp at 3' side: HMP19 protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  47120482  GGAACTGAGATAC  47120470


>ref|NW_922751.1|HsCraAADB02_226 D Homo sapiens chromosome 5 genomic contig, alter
(based on Celera assembly)
Length=26804078

                                                    Sort alignments for this s
```

```
                                                                E value  Score  Percent :
                                                               Query start position  Sul

 Features flanking this part of subject sequence:
   906244 bp at 5' side: nudix -type motif 12
   2906835 bp at 3' side: ephrin-A5


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGATA  19
                |||||||||||||||
Sbjct  4371200  ACTGGAACTGAGATA  4371214


 Features flanking this part of subject sequence:
   1128483 bp at 5' side: ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferas
   205613 bp at 3' side: solute carrier organic anion transporter family, member 4C


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  7        TGGAACTGAGATAC  20
                ||||||||||||||
Sbjct  1935929  TGGAACTGAGATAC  1935942


 Features flanking this part of subject sequence:
   1244521 bp at 5' side: ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferas
   89572 bp at 3' side: solute carrier organic anion transporter family, member 4C1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAGATAC  20
                |||||||||||| ||||
Sbjct  2051983  CACTGGAACTGACATAC  2051967


 Features flanking this part of subject sequence:
   1100627 bp at 5' side: nudix -type motif 12
   2712454 bp at 3' side: ephrin-A5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  4565595  CACTGGAACTGAG  4565583


 Features flanking this part of subject sequence:
   2826296 bp at 5' side: nudix -type motif 12
   986785 bp at 3' side: ephrin-A5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  6291264  ACTGGAACTGAGA  6291252


 Features flanking this part of subject sequence:
   3260761 bp at 5' side: nudix -type motif 12
   552320 bp at 3' side: ephrin-A5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  6725717  GGAACTGAGATAC  6725729
```

```
 Features flanking this part of subject sequence:
   1178173 bp at 5' side: hypothetical protein
   83111 bp at 3' side: DTW domain containing 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  18661585  TGGAACTGAGATA  18661573


 Features flanking this part of subject sequence:
   739473 bp at 5' side: casein kinase 1, gamma 3 isoform 2
   284379 bp at 3' side: zinc finger protein 608


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGATACGG  22
                 ||||| |||||||||||
Sbjct  24266122  CTGGAGCTGAGATACGG  24266138


>ref|NW_922162.1|HsCraAADB02_173 D Homo sapiens chromosome 4 genomic contig, alter
(based on Celera assembly)
Length=66459542

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   11952 bp at 5' side: platelet-derived growth factor receptor alpha precursor
   352161 bp at 3' side: v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene hom.


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATAC  20
                |||||||||||||||
Sbjct  2499140  CTGGAACTGAGATAC  2499126


 Features flanking this part of subject sequence:
   194749 bp at 5' side: pyruvate dehydrogenase (lipoamide) alpha 2
   1521198 bp at 3' side: hypothetical protein LOC285555


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGATA  19
                 ||||||||||||||
Sbjct  44078827  CTGGAACTGAGATA  44078814


 Features in this part of subject sequence:
   inorganic pyrophosphatase 2 isoform 1 precursor
   inorganic pyrophosphatase 2 isoform 4 precursor


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACTG  14
                 ||||||||||||||
Sbjct  53418042  TCACACTGGAACTG  53418055


 Features flanking this part of subject sequence:
   365019 bp at 5' side: N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4
   1641537 bp at 3' side: translocation associated membrane protein 1-like 1
```

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  63481074  CACTGGAACTGAGA  63481061


 Features flanking this part of subject sequence:
   326770 bp at 5' side: v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene hom.
   14372 bp at 3' side: kinase insert domain receptor (a type III receptor tyrosi..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  3258613  CTGGAACTGAGAT  3258625


 Features flanking this part of subject sequence:
   361082 bp at 5' side: hypothetical protein
   1027378 bp at 3' side: hypothetical protein LOC644484


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  8549534  CTGGAACTGAGAT  8549522


 Features flanking this part of subject sequence:
   4731 bp at 5' side: Fraser syndrome 1 isoform 1
   8606 bp at 3' side: annexin A3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  26588033  TGGAACTGAGATA  26588021


 Features flanking this part of subject sequence:
   171823 bp at 5' side: glycerol kinase 2
   331384 bp at 3' side: anthrax toxin receptor 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  27621841  ACTGGAACTGAGA  27621829


 Features flanking this part of subject sequence:
   435813 bp at 5' side: hypothetical protein LOC84803
   441865 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  32077151  TGGAACTGAGATA  32077139


 Features flanking this part of subject sequence:
   176346 bp at 5' side: mitogen-activated protein kinase 10 isoform 1
   264308 bp at 3' side: protein tyrosine phosphatase, non-receptor type 13 isoform
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACTGAGA  17
                 ||||| |||||||||||
Sbjct  34406151  TCACAGTGGAACTGAGA  34406135


 Features flanking this part of subject sequence:
   16191 bp at 5' side: hypothetical protein
   26922 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  34944441  TCACACTGGAACT  34944429


 Features flanking this part of subject sequence:
   86685 bp at 5' side: dentin matrix acidic phosphoprotein
   52221 bp at 3' side: integrin-binding sialoprotein precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  35784528  CACACTGGAACTG  35784516


 Features flanking this part of subject sequence:
   1102798 bp at 5' side: pyruvate dehydrogenase (lipoamide) alpha 2
   613150 bp at 3' side: hypothetical protein LOC285555


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  44986875  CACTGGAACTGAG  44986863


 Features flanking this part of subject sequence:
   50292 bp at 5' side: centromere protein E
   342392 bp at 3' side: tachykinin receptor 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  51291909  TCACACTGGAACT  51291921


 Features flanking this part of subject sequence:
   89375 bp at 5' side: hypothetical protein isoform 2
   24567 bp at 3' side: hypothetical protein LOC54790


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  53254793  ACACTGGAACTGA  53254781


 Features flanking this part of subject sequence:
   64968 bp at 5' side: small inducible cytokine subfamily E, member 1
   511105 bp at 3' side: dickkopf homolog 2 precursor


 Score = 26.3 bits (13),  Expect =   444
```

```
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  54458026  CTGGAACTGAGAT  54458038


>ref|NW_921807.1|HsCraAADB02_141 D Homo sapiens chromosome 3 genomic contig, alter
(based on Celera assembly)
Length=101945515

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent 
                                                                   Query start position  Su

  Features flanking this part of subject sequence:
    41475 bp at 5' side: profilin 2 isoform a
    252967 bp at 3' side: hypothetical protein


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Minus

Query  6         CTGGAACTGAGATAC  20
                 |||||||||||||||
Sbjct  56329162  CTGGAACTGAGATAC  56329148


  Features flanking this part of subject sequence:
    40404 bp at 5' side: hypothetical protein
    727216 bp at 3' side: similar to mesenchymal stem cell protein DSC92 isoform 2


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Minus

Query  6         CTGGAACTGAGATAC  20
                 |||||||||||||||
Sbjct  69577750  CTGGAACTGAGATAC  69577736


  Features flanking this part of subject sequence:
    222642 bp at 5' side: similar to CG17293-PA
    1654735 bp at 3' side: similar to Ephrin type-A receptor 6 precursor (Tyrosine-p


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

Query  6        CTGGAACTGAGATA  19
                ||||||||||||||
Sbjct  1452633  CTGGAACTGAGATA  1452620


  Features flanking this part of subject sequence:
    224244 bp at 5' side: similar to CG17293-PA
    1653133 bp at 3' side: similar to Ephrin type-A receptor 6 precursor (Tyrosine-p


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

Query  6        CTGGAACTGAGATA  19
                ||||||||||||||
Sbjct  1454235  CTGGAACTGAGATA  1454222


  Features in this part of subject sequence:
    zinc finger protein ZNF-U69274


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

Query  1        TCACACTGGAACTG  14
                ||||||||||||||
Sbjct  7953784  TCACACTGGAACTG  7953797
```

```
 Features flanking this part of subject sequence:
   107050 bp at 5' side: follistatin-like 1 precursor
   38513 bp at 3' side: NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGATA  19
                 ||||||||||||||
Sbjct  26871745  CTGGAACTGAGATA  26871758


 Features flanking this part of subject sequence:
   2770 bp at 5' side: RAB, member of RAS oncogene family-like 3
   5263 bp at 3' side: general transcription factor IIE, polypeptide 1 (alpha su...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
Sbjct  27059544  ACTGGAACTGAGAT  27059557


 Features flanking this part of subject sequence:
   3875 bp at 5' side: eukaryotic elongation factor, selenocysteine-tRNA-specific
   48967 bp at 3' side: DnaJ homolog, subfamily B, member 8


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGAG  16
                 ||||||||||||||
Sbjct  34746093  ACACTGGAACTGAG  34746080


 Features flanking this part of subject sequence:
   11164 bp at 5' side: phospholipase D1, phophatidylcholine-specific
   363079 bp at 3' side: fibronectin type III domain containing 3B


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTGA  15
                 ||||||||||||||
Sbjct  78052511  CACACTGGAACTGA  78052524


 Features flanking this part of subject sequence:
   120647 bp at 5' side: p53 target zinc finger protein isoform 2
   10232 bp at 3' side: phosphoinositide-3-kinase, catalytic, alpha polypeptide


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  85521268  CACTGGAACTGAGA  85521281


 Features in this part of subject sequence:
   similar to Ephrin type-A receptor 6 precursor (Tyrosine-p...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        GAACTGAGATACG  21
                |||||||||||||
Sbjct  3600531  GAACTGAGATACG  3600543


 Features in this part of subject sequence:
```

```
   Cas-Br-M (murine) ecotropic retroviral transforming seque...

 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  11967411  TGGAACTGAGATA  11967423


 Features flanking this part of subject sequence:
   17295 bp at 5' side: hypothetical protein
   167091 bp at 3' side: HMG-BOX transcription factor BBX


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  13844150  TGGAACTGAGATA  13844162


 Features flanking this part of subject sequence:
   1252335 bp at 5' side: developmental pluripotency associated 4
   303176 bp at 3' side: hypothetical protein LOC151760 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  16893044  ACACTGGAACTGA  16893056


 Features flanking this part of subject sequence:
   86282 bp at 5' side: hypothetical protein LOC151760 isoform 2
   92340 bp at 3' side: nectin 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  17283659  ACACTGGAACTGA  17283647


 Features flanking this part of subject sequence:
   440334 bp at 5' side: hypothetical protein
   48489 bp at 3' side: growth associated protein 43


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  21887608  TGGAACTGAGATA  21887596


 Features flanking this part of subject sequence:
   51738 bp at 5' side: limbic system-associated membrane protein
   148878 bp at 3' side: similar to basic leucine zipper and W2 domains 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  22809331  TCACACTGGAACT  22809343


 Features flanking this part of subject sequence:
   997755 bp at 5' side: similar to basic leucine zipper and W2 domains 1
   1247331 bp at 3' side: immunoglobulin superfamily, member 11 isoform a
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  23968198  CTGGAACTGAGAT  23968210


 Features flanking this part of subject sequence:
   2111525 bp at 5' side: similar to basic leucine zipper and W2 domains 1
   133557 bp at 3' side: immunoglobulin superfamily, member 11 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACTGAGA  17
                 ||||||||||| |||||
Sbjct  25081968  TCACACTGGAAGTGAGA  25081984


 Features in this part of subject sequence:
   sorting nexin 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  31794730  TGGAACTGAGATA  31794742


 Features in this part of subject sequence:
   5'-3' exoribonuclease 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  48693012  ACTGGAACTGAGA  48693024


 Features in this part of subject sequence:
   solute carrier family 9 (sodium/hydrogen exchanger), isof...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  49971515  TGGAACTGAGATA  49971527


 Features flanking this part of subject sequence:
   558498 bp at 5' side: hypothetical protein isoform 3
   758913 bp at 3' side: angiotensin II receptor, type 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  54295909  TCACACTGGAACT  54295921


 Features flanking this part of subject sequence:
   714231 bp at 5' side: hypothetical protein isoform 3
   603180 bp at 3' side: angiotensin II receptor, type 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
```

```
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  54451654  CTGGAACTGAGAT  54451642


 Features in this part of subject sequence:
   WW domain containing transcription regulator 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  55854946  ACTGGAACTGAGA  55854934


 Features flanking this part of subject sequence:
   265848 bp at 5' side: hypothetical protein
   353523 bp at 3' side: Src homology 3 domain-containing guanine nucleotide excha.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  60089440  CACTGGAACTGAG  60089452


 Features flanking this part of subject sequence:
   132098 bp at 5' side: slit and trk like 3 protein
   450339 bp at 3' side: butyrylcholinesterase precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  71625078  CACTGGAACTGAG  71625090


 Features flanking this part of subject sequence:
   209250 bp at 5' side: similar to EGF-like-domain, multiple 3 isoform 3
   65402 bp at 3' side: ecotropic viral integration site 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  75321489  CACACTGGAACTG  75321477


 Features flanking this part of subject sequence:
   186825 bp at 5' side: PXR2b protein
   379036 bp at 3' side: tetratricopeptide repeat domain 14


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  86558795  GGAACTGAGATAC  86558807


 Features flanking this part of subject sequence:
   579079 bp at 5' side: sex-determining region Y-box 2
   391240 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  88629536  CACTGGAACTGAG  88629548


 Features flanking this part of subject sequence:
   177862 bp at 5' side: UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransfera.
   44170 bp at 3' side: kelch-like 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  89787589  CACTGGAACTGAG  89787577


 Features in this part of subject sequence:
   TBCC domain containing 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         GAACTGAGATACG  21
                 |||||||||||||
Sbjct  92892303  GAACTGAGATACG  92892291


 Features flanking this part of subject sequence:
   258724 bp at 5' side: LIM domain containing preferred translocation partner in .
   74588 bp at 3' side: hypothetical protein LOC285386


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  95470921  ACACTGGAACTGA  95470909


>ref|NW_927997.1|HsCraAADB02_94 D Homo sapiens chromosome 2 genomic contig, alterna
(based on Celera assembly)
Length=240645

 Features flanking this part of subject sequence:
   49008 bp at 5' side: similar to ankyrin repeat domain 26


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  1      TCACACTGGAACTGA  15
              |||||||||||||||
Sbjct  91177  TCACACTGGAACTGA  91191


>ref|NW_925683.1|HsCraAADB02_49 D Homo sapiens chromosome 1 genomic contig, alterna
(based on Celera assembly)
Length=11514521

                                                         Sort alignments for this s
                                                           E value  Score  Percent 
                                                           Query start position  Sul

 Features flanking this part of subject sequence:
   5445 bp at 5' side: MADS box transcription enhancer factor 2, polypeptide D (...
   37744 bp at 3' side: IQ motif containing GTPase activating protein 3


 Score = 30.2 bits (15),  Expect =    28
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query  1        TCACACTGGAACTGAGATA  19
                |||||| ||||||||||||
Sbjct  6568385  TCACACAGGAACTGAGATA  6568367
```

```
 Features in this part of subject sequence:
   Fc receptor-like 5


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGAGA  17
                |||||||||||||||
Sbjct  7605714  ACACTGGAACTGAGA  7605728


 Features flanking this part of subject sequence:
   859 bp at 5' side: hypothetical protein LOC54964
   2919 bp at 3' side: CDC42 small effector 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  1175928  ACTGGAACTGAGA  1175940


 Features in this part of subject sequence:
   S100 calcium-binding protein A9


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  3439786  ACTGGAACTGAGA  3439774


 Features in this part of subject sequence:
   similar to S100 calcium binding protein A7-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  3518509  ACTGGAACTGAGA  3518497


 Features in this part of subject sequence:
   Fc receptor-like 2 isoform b
   Fc receptor-like 2 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  7845301  ACACTGGAACTGA  7845313


 Features in this part of subject sequence:
   hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  8003790  ACACTGGAACTGA  8003778


 Features flanking this part of subject sequence:
   67386 bp at 5' side: hypothetical protein
   83022 bp at 3' side: kin of IRRE like
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  8071234  CTGGAACTGAGAT  8071222


>ref|NW_926794.1|HsCraAADB02_59 D Homo sapiens chromosome 1 genomic contig, alterna
(based on Celera assembly)
Length=17411188

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent :
                                                                    Query start position  Sul

 Features flanking this part of subject sequence:
   661654 bp at 5' side: plexin A2
   352429 bp at 3' side: hypothetical protein


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAGAT  18
                |||||||||||||||
Sbjct  2449175  CACTGGAACTGAGAT  2449161


 Features flanking this part of subject sequence:
   50880 bp at 5' side: Fc alpha/mu receptor
   940 bp at 3' side: specifically androgen-regulated protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  4       CACTGGAACTGAGA  17
               ||||||||||||||
Sbjct  611614  CACTGGAACTGAGA  611627


 Features flanking this part of subject sequence:
   41639 bp at 5' side: plexin A2
   972445 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGAG  16
                ||||||||||||||
Sbjct  1829146  ACACTGGAACTGAG  1829159


 Features flanking this part of subject sequence:
   12522 bp at 5' side: SCIRP10-related protein
   156828 bp at 3' side: activating transcription factor 3 isoform 3


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGAT  18
                ||||||||||||||
Sbjct  6023359  ACTGGAACTGAGAT  6023346


 Features in this part of subject sequence:
   IKK-related kinase epsilon
   hypothetical protein LOC574431


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1      TCACACTGGAACTGAGA  17
```

```
              ||||||||||| |||||
Sbjct  83182  TCACACTGGAAATGAGA  83198


 Features flanking this part of subject sequence:
   75867 bp at 5' side: H2.0-like homeo box 1
   373258 bp at 3' side: hypothetical protein LOC400804


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  14519064  CACTGGAACTGAG  14519052


 Features flanking this part of subject sequence:
   39053 bp at 5' side: hypothetical protein LOC400823
   154592 bp at 3' side: dispatched A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  16346425  CACTGGAACTGAG  16346413


>ref|NW_926128.1|HsCraAADB02_53 D Homo sapiens chromosome 1 genomic contig, altern
(based on Celera assembly)
Length=44521323

                                                         Sort alignments for this s
                                                           E value  Score  Percent 
                                                           Query start position  Su


 Features flanking this part of subject sequence:
   262234 bp at 5' side: tenascin R (restrictin, janusin)
   276200 bp at 3' side: ring finger and WD repeat domain 2 isoform d24


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTGAG  16
                 |||||||||||||||
Sbjct  14003575  CACACTGGAACTGAG  14003561


 Features flanking this part of subject sequence:
   178771 bp at 5' side: similar to Y74C9A.3
   185433 bp at 3' side: NTKL-binding protein 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGAT  18
                ||||||||||||||
Sbjct  8680247  ACTGGAACTGAGAT  8680234


 Features in this part of subject sequence:
   ring finger and WD repeat domain 2 isoform d24
   ring finger and WD repeat domain 2 isoform a


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTGA  15
                 ||||||||||||||
Sbjct  14366585  CACACTGGAACTGA  14366572


 Features flanking this part of subject sequence:
   130871 bp at 5' side: hypothetical protein LOC116461
```

```
   273786 bp at 3' side: chromosome 1 open reading frame 21


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACTG  14
                 ||||||||||||||
Sbjct  22538559  TCACACTGGAACTG  22538546


 Features in this part of subject sequence:
   G protein-coupled receptor 161 isoform 2
   G protein-coupled receptor 161 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  6432650  TCACACTGGAACT  6432638


 Features in this part of subject sequence:
   coagulation factor V precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  7895275  GGAACTGAGATAC  7895287


 Features flanking this part of subject sequence:
   37053 bp at 5' side: influenza virus NS1A binding protein isoform b
   388229 bp at 3' side: hemicentin 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  23681144  ACTGGAACTGAGA  23681132


 Features flanking this part of subject sequence:
   494465 bp at 5' side: similar to solute carrier family 4 (anion exchanger), mem.
   1895652 bp at 3' side: family with sequence similarity 5, member C


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  26534884  ACACTGGAACTGA  26534896


 Features flanking this part of subject sequence:
   1807992 bp at 5' side: similar to solute carrier family 4 (anion exchanger), mem
   582125 bp at 3' side: family with sequence similarity 5, member C


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  27848411  TGGAACTGAGATA  27848423


 Features in this part of subject sequence:
   zinc finger and BTB domain containing 41
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  35543016  GGAACTGAGATAC  35543004


>ref|NT_011896.9|HsY_12053 D Homo sapiens chromosome Y genomic contig, reference as
Length=6265435

                                                                Sort alignments for this s
                                                                  E value  Score  Percent :
                                                                  Query start position  Sul

 Features flanking this part of subject sequence:
   1339005 bp at 5' side: TGFB-induced factor 2-like, Y-linked
   113876 bp at 3' side: protocadherin 11 Y-linked isoform a


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAGAT  18
                |||||||||||||||
Sbjct  2137342  CACTGGAACTGAGAT  2137328


 Features flanking this part of subject sequence:
   657708 bp at 5' side: protocadherin 11 Y-linked isoform b
   484187 bp at 3' side: testis specific protein, Y-linked 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTGA  15
                ||||||||||||||
Sbjct  2980603  CACACTGGAACTGA  2980590


 Features flanking this part of subject sequence:
   9679 bp at 5' side: similar to proline-rich protein MP5
   103514 bp at 3' side: transducin beta-like 1Y


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  4140080  CTGGAACTGAGAT  4140092


 Features flanking this part of subject sequence:
   38797 bp at 5' side: similar to proline-rich protein MP5
   74396 bp at 3' side: transducin beta-like 1Y


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  4169198  GGAACTGAGATAC  4169210


 Features flanking this part of subject sequence:
   75770 bp at 5' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  4985173  CACACTGGAACTG  4985161
```

```
>ref|NT_011669.16|HsX_11826 D Homo sapiens chromosome X genomic contig, reference a
Length=14971611

                                                     Sort alignments for this s
                                                       E value  Score  Percent
                                                       Query start position  Su

 Features in this part of subject sequence:
   zinc finger protein 261
   zinc finger protein 261


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGAGA  17
                |||||||||||||||
Sbjct  8788556  ACACTGGAACTGAGA  8788570


 Features flanking this part of subject sequence:
   239966 bp at 5' side: hepatocellular carcinoma-associated antigen 127
   272480 bp at 3' side: zinc finger CCCH-type containing 12B


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  2754211  TCACACTGGAACT  2754223


 Features flanking this part of subject sequence:
   183850 bp at 5' side: hephaestin isoform b
   148950 bp at 3' side: X-linked ectodysplasin receptor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  3988352  CACACTGGAACTG  3988364


 Features flanking this part of subject sequence:
   335064 bp at 5' side: cysteine-rich hydrophobic domain 1
   44460 bp at 3' side: similar to scotin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  11553892  ACTGGAACTGAGA  11553904


 Features flanking this part of subject sequence:
   74765 bp at 5' side: hypothetical protein LOC51260
   175805 bp at 3' side: melanoma antigen family E, 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  13790186  ACACTGGAACTGA  13790174


>ref|NT_011651.16|HsX_11808 D Homo sapiens chromosome X genomic contig, reference a
Length=36813576

                                                     Sort alignments for this s
                                                       E value  Score  Percent
                                                       Query start position  Su
```

```
 Features flanking this part of subject sequence:
   242887 bp at 5' side: poly(A) binding protein, cytoplasmic 5
   97874 bp at 3' side: hypothetical protein


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGAT  18
                 |||||||||||||||
Sbjct  14230934  CACTGGAACTGAGAT  14230920


 Features flanking this part of subject sequence:
   1098888 bp at 5' side: angiomotin


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGAGA  17
                 |||||||||||||||
Sbjct  36453960  ACACTGGAACTGAGA  36453946


 Features flanking this part of subject sequence:
   2607 bp at 5' side: bromo domain-containing protein disrupted in leukemia
   302558 bp at 3' side: nucleosomal binding protein 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  6        CTGGAACTGAGATA  19
                ||||||||||||||
Sbjct  3363885  CTGGAACTGAGATA  3363898


 Features flanking this part of subject sequence:
   766012 bp at 5' side: protocadherin 11 X-linked isoform a precursor
   642402 bp at 3' side: similar to heat shock 70kD protein binding protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTGA  15
                 ||||||||||||||
Sbjct  15196638  CACACTGGAACTGA  15196625


 Features flanking this part of subject sequence:
   947431 bp at 5' side: kelch-like 4 isoform 1
   139439 bp at 3' side: hypothetical protein LOC53336


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  11165273  TGGAACTGAGATA  11165285


 Features flanking this part of subject sequence:
   136373 bp at 5' side: similar to testis-specific bromodomain protein
   210923 bp at 3' side: diaphanous 2 isoform 12C


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  19025443  ACACTGGAACTGA  19025431


 Features in this part of subject sequence:
```

```
    diaphanous 2 isoform 12C
    diaphanous 2 isoform 156


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  6         CTGGAACTGAGAT  18
                  |||||||||||||
 Sbjct  19714986  CTGGAACTGAGAT  19714974


  Features flanking this part of subject sequence:
    2745 bp at 5' side: hypothetical protein LOC139231
    57693 bp at 3' side: extraembryonic, spermatogenesis, homeobox 1-like


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  8         GGAACTGAGATAC  20
                  |||||||||||||
 Sbjct  26733524  GGAACTGAGATAC  26733512


  Features in this part of subject sequence:
    similar to PDZ domain containing 10


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  5         ACTGGAACTGAGA  17
                  |||||||||||||
 Sbjct  30074452  ACTGGAACTGAGA  30074440


  Features flanking this part of subject sequence:
    124362 bp at 5' side: insulin receptor substrate 4
    515180 bp at 3' side: guanylate cyclase 2F


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  2         CACACTGGAACTG  14
                  |||||||||||||
 Sbjct  31400244  CACACTGGAACTG  31400256


  Features flanking this part of subject sequence:
    419488 bp at 5' side: insulin receptor substrate 4
    220054 bp at 3' side: guanylate cyclase 2F


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  2         CACACTGGAACTG  14
                  |||||||||||||
 Sbjct  31695370  CACACTGGAACTG  31695382


  Features flanking this part of subject sequence:
    4075 bp at 5' side: potassium voltage-gated channel, Isk-related family, memb...
    14922 bp at 3' side: acyl-CoA synthetase long-chain family member 4 isoform 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  6         CTGGAACTGAGAT  18
                  |||||||||||||
 Sbjct  32168644  CTGGAACTGAGAT  32168632


  Features flanking this part of subject sequence:
    173806 bp at 5' side: acyl-CoA synthetase long-chain family member 4 isoform 1
    146593 bp at 3' side: hypothetical protein LOC84187
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  32396706  ACTGGAACTGAGA  32396718


 Features in this part of subject sequence:
   doublecortin isoform a
   doublecortin isoform c


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         GAACTGAGATACG  21
                 |||||||||||||
Sbjct  33865222  GAACTGAGATACG  33865234


>ref|NT_011362.9|Hs20_11519 D Homo sapiens chromosome 20 genomic contig, reference
Length=26144333

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent :
                                                                   Query start position  Sul

 Features flanking this part of subject sequence:
   3018 bp at 5' side: zinc finger protein 313
   27887 bp at 3' side: snail 1 homolog


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGAGA  17
                 |||||||||||||||
Sbjct  13624604  ACACTGGAACTGAGA  13624618


 Features flanking this part of subject sequence:
   35980 bp at 5' side: cadherin 4, type 1 preproprotein
   3229 bp at 3' side: TBP-associated factor 4


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGAGA  17
                 |||||||||||||||
Sbjct  25600891  ACACTGGAACTGAGA  25600877


 Features flanking this part of subject sequence:
   352287 bp at 5' side: transcription factor AP-2 gamma
   166199 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  20618277  TGGAACTGAGATAC  20618264


 Features flanking this part of subject sequence:
   273285 bp at 5' side: transcription factor MAFB
   66921 bp at 3' side: DNA topoisomerase I


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTG  14
```

```
                |||||||||||||
Sbjct  4643702  CACACTGGAACTG  4643690


 Features flanking this part of subject sequence:
   47779 bp at 5' side: arginine/serine-rich splicing factor 6
   5691 bp at 3' side: l(3)mbt-like isoform I


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  7190397  CTGGAACTGAGAT  7190409


 Features flanking this part of subject sequence:
   716918 bp at 5' side: sulfatase 2 isoform b precursor
   139386 bp at 3' side: PREX1 protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  12155933  TCACACTGGAACT  12155945


 Features in this part of subject sequence:
   nuclear factor of activated T-cells, cytoplasmic, calcine...
   nuclear factor of activated T-cells, cytoplasmic, calcine...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  15176975  TCACACTGGAACT  15176987


 Features flanking this part of subject sequence:
   1830 bp at 5' side: hypothetical protein
   228687 bp at 3' side: hypothetical protein LOC284757


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  23718395  CACACTGGAACTG  23718383


 Features flanking this part of subject sequence:
   67933 bp at 5' side: hypothetical protein LOC284757
   830467 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  24015458  ACACTGGAACTGA  24015446


 Features flanking this part of subject sequence:
   521005 bp at 5' side: hypothetical protein LOC284757
   377395 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
```

```
Sbjct  24468518  TCACACTGGAACT  24468530


>ref|NT_011109.15|Hs19_11266 D Homo sapiens chromosome 19 genomic contig, referenc
Length=31383029

                                                               Sort alignments for this s
                                                                 E value  Score  Percent :
                                                                 Query start position  Sul

 Features flanking this part of subject sequence:
   24565 bp at 5' side: carcinoembryonic antigen-related cell adhesion molecule
   8308 bp at 3' side: carcinoembryonic antigen-related cell adhesion molecule 4


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  5          ACTGGAACTGAGATA  19
                  |||||||||||||||
Sbjct  14385599  ACTGGAACTGAGATA  14385613


 Features flanking this part of subject sequence:
   757586 bp at 5' side: hypothetical protein
   244848 bp at 3' side: zinc finger protein 507


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGAT  18
                ||||||||||||||
Sbjct  4867094  ACTGGAACTGAGAT  4867107


 Features in this part of subject sequence:
   similar to Nucleoside diphosphate-linked moiety X motif 1...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  5470666  TGGAACTGAGATA  5470654


 Features in this part of subject sequence:
   similar to Nucleoside diphosphate-linked moiety X motif 1...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  5470719  TGGAACTGAGATA  5470707


 Features flanking this part of subject sequence:
   49147 bp at 5' side: CCAAT/enhancer binding protein alpha
   27667 bp at 3' side: CCAAT/enhancer binding protein gamma


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       AACTGAGATACGG  22
                |||||||||||||
Sbjct  6110697  AACTGAGATACGG  6110685


 Features flanking this part of subject sequence:
   24418 bp at 5' side: LSM14 homolog A
   48656 bp at 3' side: hypothetical protein LOC9710


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  7010929  TCACACTGGAACT  7010941


 Features flanking this part of subject sequence:
   14936 bp at 5' side: zinc finger protein 226 isoform a
   25171 bp at 3' side: zinc finger protein 227


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  16964981  TGGAACTGAGATA  16964993


 Features in this part of subject sequence:
   killer cell immunoglobulin-like receptor, three domains, ...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGATACGG  22
                 |||||| ||||||||||
Sbjct  27504508  CTGGAATTGAGATACGG  27504524


>ref|NT_025028.13|Hs18_25184 D Homo sapiens chromosome 18 genomic contig, referenc
Length=20074199

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent 
                                                                   Query start position  Su

 Features flanking this part of subject sequence:
   196979 bp at 5' side: suppressor of cytokine signaling 6
   107291 bp at 3' side: hypothetical protein LOC220158


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACTGA  15
                 |||||||||||||||
Sbjct  15981337  TCACACTGGAACTGA  15981351


 Features in this part of subject sequence:
   PH domain and leucine rich repeat protein phosphatase


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  8412889  GGAACTGAGATAC  8412877


 Features in this part of subject sequence:
   B-cell lymphoma protein 2 alpha isoform


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  8626502  ACACTGGAACTGA  8626514


 Features flanking this part of subject sequence:
   1064532 bp at 5' side: hypothetical protein LOC221241
```

```
    599691 bp at 3' side: cadherin 7, type 2 preproprotein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  7         TGGAACTGAGATA  19
                  |||||||||||||
 Sbjct  10621222  TGGAACTGAGATA  10621234


  Features flanking this part of subject sequence:
    49032 bp at 5' side: hypothetical protein LOC220158
    1649850 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  4         CACTGGAACTGAG  16
                  |||||||||||||
 Sbjct  16166342  CACTGGAACTGAG  16166354


 >ref|NT_024871.11|Hs17_25027 D Homo sapiens chromosome 17 genomic contig, referenc
 Length=2103126

  Features in this part of subject sequence:
    raptor


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Plus

 Query  3        ACACTGGAACTGAGA  17
                 |||||||||||||||
 Sbjct  1181202  ACACTGGAACTGAGA  1181216


 >ref|NT_024524.13|Hs13_24680 D Homo sapiens chromosome 13 genomic contig, referenc
 Length=67740325
                                                              Sort alignments for this s
                                                                E value  Score  Percent i
                                                                Query start position  Sul

  Features flanking this part of subject sequence:
    10814 bp at 5' side: similar to FRAS1-related extracellular matrix protein 2 p..
    13747 bp at 3' side: hypothetical protein


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Minus

 Query  2        CACACTGGAACTGAG  16
                 |||||||||||||||
 Sbjct  2866446  CACACTGGAACTGAG  2866432


  Features in this part of subject sequence:
    hypothetical protein LOC23281 isoform a


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

 Query  1         TCACACTGGAACTG  14
                  ||||||||||||||
 Sbjct  10798393  TCACACTGGAACTG  10798380


  Features in this part of subject sequence:
    spermatogenesis and oogenesis specific basic helix-loop-h...


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus
```

```
Query  3         ACACTGGAACTGAG  16
                 ||||||||||||||
Sbjct  17766179  ACACTGGAACTGAG  17766166
```

 Features flanking this part of subject sequence:
   94143 bp at 5' side: protocadherin 20
   896821 bp at 3' side: similar to sequestosome 1 isoform 1

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACTGAGAT  18
                 |||||||||| |||||||
Sbjct  43063354  TCACACTGGATCTGAGAT  43063371
```

 Features flanking this part of subject sequence:
   2014973 bp at 5' side: hypothetical protein
   455327 bp at 3' side: kelch-like 1 protein

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGATA  19
                 ||||||||||||||
Sbjct  50800495  CTGGAACTGAGATA  50800508
```

 Features flanking this part of subject sequence:
   59090 bp at 5' side: exportin 4
   47079 bp at 3' side: LATS, large tumor suppressor, homolog 2

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  2481918  ACTGGAACTGAGA  2481930
```

 Features flanking this part of subject sequence:
   25002 bp at 5' side: G protein-coupled receptor 12
   284442 bp at 3' side: ubiquitin-specific protease 12-like 1

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  8338966  CACTGGAACTGAG  8338978
```

 Features flanking this part of subject sequence:
   558198 bp at 5' side: replication factor C 3 isoform 1
   548316 bp at 3' side: neurobeachin

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  15948630  TGGAACTGAGATA  15948642
```

 Features flanking this part of subject sequence:
   9090 bp at 5' side: hypothetical protein LOC55068
   12137 bp at 3' side: hypothetical protein

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
```

```
                   |||||||||||||
Sbjct  24976152  CTGGAACTGAGAT  24976140


 Features in this part of subject sequence:
   leucine-rich repeats and calponin homology (CH) domain co...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  28230847  CACACTGGAACTG  28230835


 Features in this part of subject sequence:
   retinoblastoma 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  29897833  ACTGGAACTGAGA  29897845


 Features flanking this part of subject sequence:
   1376409 bp at 5' side: olfactomedin 4 precursor
   2714112 bp at 3' side: hypothetical protein LOC122183


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  35981328  ACACTGGAACTGA  35981316


 Features flanking this part of subject sequence:
   1641907 bp at 5' side: olfactomedin 4 precursor
   2448614 bp at 3' side: hypothetical protein LOC122183


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  36246814  TCACACTGGAACT  36246826


 Features flanking this part of subject sequence:
   2928227 bp at 5' side: olfactomedin 4 precursor
   1162294 bp at 3' side: hypothetical protein LOC122183


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  37533146  CTGGAACTGAGAT  37533134


 Features flanking this part of subject sequence:
   3912825 bp at 5' side: olfactomedin 4 precursor
   177696 bp at 3' side: hypothetical protein LOC122183


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         GAACTGAGATACG  21
                 |||||||||||||
Sbjct  38517744  GAACTGAGATACG  38517732
```

```
 Features flanking this part of subject sequence:
   227972 bp at 5' side: dachshund homolog 1 isoform c
   615569 bp at 3' side: hypothetical protein isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  53648892  CACTGGAACTGAG  53648880


 Features flanking this part of subject sequence:
   715261 bp at 5' side: dachshund homolog 1 isoform c
   128280 bp at 3' side: hypothetical protein isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  54136169  TCACACTGGAACT  54136181


 Features flanking this part of subject sequence:
   89570 bp at 5' side: similar to Fatty acid-binding protein, epidermal (E-FABP)..
   217185 bp at 3' side: similar to MAP/microtubule affinity-regulating kinase 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  54744694  ACTGGAACTGAGA  54744706


 Features flanking this part of subject sequence:
   285580 bp at 5' side: slit and trk like 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  67636224  CACACTGGAACTG  67636236


>ref|NT_019546.15|Hs12_19702 D Homo sapiens chromosome 12 genomic contig, referenc
Length=32815934

                                                          Sort alignments for this s
                                                            E value  Score  Percent :
                                                            Query start position  Sul

 Features flanking this part of subject sequence:
   625389 bp at 5' side: decorin isoform e precursor
   340124 bp at 3' side: B-cell translocation protein 1


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACTGA  15
                 |||||||||||||||
Sbjct  15679909  TCACACTGGAACTGA  15679923


 Features flanking this part of subject sequence:
   51407 bp at 5' side: lin-7 homolog A
   88979 bp at 3' side: hypothetical protein LOC79611


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
```

```
 Strand=Plus/Plus

Query  9        GAACTGAGATACGG  22
                ||||||||||||||
Sbjct  4865099  GAACTGAGATACGG  4865112


 Features in this part of subject sequence:
   methionyl aminopeptidase 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTGAGAT  18
                 |||||||||| ||||||
Sbjct  19384245  CACACTGGAAATGAGAT  19384229


 Features flanking this part of subject sequence:
   1923 bp at 5' side: hypothetical protein LOC55332
   89913 bp at 3' side: coiled-coil domain containing 53


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  25799152  ACACTGGAACTGA  25799164


 Features in this part of subject sequence:
   hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACTGAGA  17
                 |||||||||| ||||||
Sbjct  26993421  TCACACTGGATCTGAGA  26993405


>ref|NT_033899.7|Hs11_34054 D Homo sapiens chromosome 11 genomic contig, reference
Length=38509590

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent 
                                                                   Query start position  Su

 Features in this part of subject sequence:
   transient receptor potential cation channel, subfamily C,...


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATAC  20
                |||||||||||||||
Sbjct  5012963  CTGGAACTGAGATAC  5012949


 Features in this part of subject sequence:
   hypothetical protein LOC120406


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGATA  19
                 |||||||||||||||
Sbjct  18128176  ACTGGAACTGAGATA  18128190


 Features flanking this part of subject sequence:
   19366 bp at 5' side: hypothetical protein
   788922 bp at 3' side: BUD13 homolog
```

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACTG  14
                 ||||||||||||||
Sbjct  19392692  TCACACTGGAACTG  19392679


 Features flanking this part of subject sequence:
   64951 bp at 5' side: olfactory receptor, family 10, subfamily G, member 7
   13547 bp at 3' side: BCSC-1 isoform 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  27537088  TGGAACTGAGATAC  27537075


 Features flanking this part of subject sequence:
   2940907 bp at 3' side: contactin 5 isoform long


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3      ACACTGGAACTGA  15
              |||||||||||||
Sbjct  48455  ACACTGGAACTGA  48443


 Features flanking this part of subject sequence:
   1141190 bp at 3' side: contactin 5 isoform long


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  1848160  TCACACTGGAACT  1848172


 Features flanking this part of subject sequence:
   75129 bp at 3' side: contactin 5 isoform long


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  2914233  TGGAACTGAGATA  2914221


 Features in this part of subject sequence:
   contactin 5 isoform long
   contactin 5 isoform short


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  3639071  TGGAACTGAGATA  3639059


 Features in this part of subject sequence:
   glutamate receptor, ionotrophic


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2        CACACTGGAACTG  14
```

```
                |||||||||||||
Sbjct  9412820  CACACTGGAACTG  9412832


 Features flanking this part of subject sequence:
   310772 bp at 5' side: DEAD (Asp-Glu-Ala-Asp) box polypeptide 10
   172426 bp at 3' side: hypothetical protein LOC399947


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  12684350  TGGAACTGAGATA  12684338


 Features flanking this part of subject sequence:
   170831 bp at 5' side: hypothetical protein LOC120406
   298066 bp at 3' side: immunoglobulin superfamily, member 4D


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  18311532  AACTGAGATACGG  18311544


 Features in this part of subject sequence:
   KIAA0999 protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  20398325  ACTGGAACTGAGA  20398313


 Features in this part of subject sequence:
   SID1 transmembrane family, member 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  20617454  TCACACTGGAACT  20617442


 Features in this part of subject sequence:
   Down syndrome cell adhesion molecule like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGAGATA  19
                 ||||| |||||||||||
Sbjct  21002766  ACACTTGAACTGAGATA  21002782


 Features flanking this part of subject sequence:
   10664 bp at 5' side: hypothetical protein isoform 10
   20016 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  28545217  CACTGGAACTGAG  28545229
```

```
 Features flanking this part of subject sequence:
   196732 bp at 5' side: hypothetical protein LOC399980
   20476 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  35289719  CTGGAACTGAGAT  35289707


>ref|NT_008984.17|Hs11_9141 D Homo sapiens chromosome 11 genomic contig, reference
Length=8549206

                                                                Sort alignments for this s
                                                                  E value  Score  Percent 
                                                                  Query start position  Sul

 Features flanking this part of subject sequence:
   106911 bp at 5' side: FN5 protein
   150047 bp at 3' side: Josephin domain containing 3


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAGAT  18
                |||||||||||||||
Sbjct  5580888  CACTGGAACTGAGAT  5580902


 Features flanking this part of subject sequence:
   297842 bp at 5' side: cysteine and histidine-rich domain (CHORD)-containing, zi.
   1704222 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  2515586  ACTGGAACTGAGA  2515598


 Features flanking this part of subject sequence:
   139956 bp at 5' side: hypothetical protein
   16651 bp at 3' side: similar to hephaestin isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  5998723  GGAACTGAGATAC  5998735


 Features flanking this part of subject sequence:
   104088 bp at 5' side: piwi-like 4
   43420 bp at 3' side: angiomotin like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  6719880  TCACACTGGAACT  6719868


>ref|NT_033903.7|Hs11_34058 D Homo sapiens chromosome 11 genomic contig, reference
Length=14395596

                                                                Sort alignments for this s
                                                                  E value  Score  Percent 
                                                                  Query start position  Sul
```

```
 Features in this part of subject sequence:
   syntaxin 3A


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGAGA  17
                |||||||||||||||
Sbjct  4834576  ACACTGGAACTGAGA  4834562


 Features in this part of subject sequence:
   solute carrier family 22 member 8


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATA  19
                ||||||||||||||
Sbjct  8087436  CTGGAACTGAGATA  8087423


 Features in this part of subject sequence:
   hypothetical protein LOC219990


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  5118563  TGGAACTGAGATA  5118575


>ref|NT_008583.16|Hs10_8740 D Homo sapiens chromosome 10 genomic contig, reference
Length=30112613

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features in this part of subject sequence:
   protein kinase, cGMP-dependent, type I


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATAC  20
                |||||||||||||||
Sbjct  2270436  CTGGAACTGAGATAC  2270422


 Features in this part of subject sequence:
   protein kinase, cGMP-dependent, type I


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTGA  15
                ||||||||||||||
Sbjct  2095486  CACACTGGAACTGA  2095473


 Features flanking this part of subject sequence:
   312763 bp at 5' side: ankyrin 3 isoform 2
   55480 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  10764055  CTGGAACTGAGAT  10764043
```

```
 Features flanking this part of subject sequence:
   118456 bp at 5' side: Rho-related BTB domain containing 1
   380312 bp at 3' side: transmembrane protein 26


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  11340923  CTGGAACTGAGAT  11340911


 Features in this part of subject sequence:
   jumonji domain containing 1C


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  13521863  CTGGAACTGAGAT  13521875


 Features flanking this part of subject sequence:
   810176 bp at 5' side: similar to activator of S phase kinase
   940448 bp at 3' side: catenin, alpha 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  15290795  ACACTGGAACTGA  15290783


 Features flanking this part of subject sequence:
   1105382 bp at 5' side: similar to activator of S phase kinase
   645242 bp at 3' side: catenin, alpha 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  15586001  ACTGGAACTGAGA  15585989


 Features flanking this part of subject sequence:
   1234037 bp at 5' side: similar to activator of S phase kinase
   516587 bp at 3' side: catenin, alpha 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  15714644  TGGAACTGAGATA  15714656


 Features flanking this part of subject sequence:
   260503 bp at 5' side: zinc finger protein 503
   121042 bp at 3' side: chromosome 10 open reading frame 11


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  25972847  ACTGGAACTGAGA  25972835
```

```
>ref|NT_008413.17|Hs9_8570 D Homo sapiens chromosome 9 genomic contig, reference a
Length=39653686

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

 Features flanking this part of subject sequence:
   65543 bp at 5' side: insulin-like 4 precursor
   664 bp at 3' side: relaxin 2 isoform 1 preproprotein


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGAGA  17
                |||||||||||||||
Sbjct  5289420  ACACTGGAACTGAGA  5289434


 Features in this part of subject sequence:
   solute carrier family 24 (sodium/potassium/calcium exchan...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  19510602  TGGAACTGAGATAC  19510589


 Features in this part of subject sequence:
   jumonji domain containing 2C


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        GAACTGAGATACG  21
                |||||||||||||
Sbjct  7054185  GAACTGAGATACG  7054197


 Features in this part of subject sequence:
   jumonji domain containing 2C


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  7076540  ACTGGAACTGAGA  7076528


 Features flanking this part of subject sequence:
   928343 bp at 5' side: protein tyrosine phosphatase, receptor type, D isoform 4 .
   950868 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  9652198  ACTGGAACTGAGA  9652186


 Features flanking this part of subject sequence:
   35317 bp at 5' side: multiple PDZ domain protein
   122701 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
```

```
                     |||||||||||||
Sbjct  13275643  CTGGAACTGAGAT  13275631


 Features flanking this part of subject sequence:
   38551 bp at 5' side: SH3-domain GRB2-like 2
   639927 bp at 3' side: ADAMTS-like 1 isoform 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  17824304  CTGGAACTGAGAT  17824292


 Features in this part of subject sequence:
   solute carrier family 24 (sodium/potassium/calcium exchan...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  19606372  AACTGAGATACGG  19606384


 Features flanking this part of subject sequence:
   406033 bp at 5' side: DMRT-like family A1
   834600 bp at 3' side: ELAV (embryonic lethal, abnormal vision, Drosophila)-like.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  22847955  TGGAACTGAGATA  22847943


 Features flanking this part of subject sequence:
   1037394 bp at 5' side: leucine rich repeat neuronal 6C
   1401992 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  28978075  ACACTGGAACTGA  28978063


 Features flanking this part of subject sequence:
   35030 bp at 5' side: hypothetical protein
   11406 bp at 3' side: olfactory receptor, family 2, subfamily S, member 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  35935718  CTGGAACTGAGAT  35935730


>ref|NT_008470.18|Hs9_8627 D Homo sapiens chromosome 9 genomic contig, reference a
Length=40394265

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

 Features flanking this part of subject sequence:
   345907 bp at 5' side: deleted in esophageal cancer 1
   156339 bp at 3' side: chromosome 9 open reading frame 27
```

```
 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGAGA  17
                 |||||||||||||||
Sbjct  25831516  ACACTGGAACTGAGA  25831530


 Features flanking this part of subject sequence:
   25514 bp at 5' side: hypothetical protein
   5197 bp at 3' side: hyaluronan binding protein 4


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAGA  17
                ||||||||||||||
Sbjct  6528570  CACTGGAACTGAGA  6528557


 Features flanking this part of subject sequence:
   46422 bp at 5' side: cathepsin L2 preproprotein
   113826 bp at 3' side: zinc finger protein 322B


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  7167964  TCACACTGGAACT  7167952


 Features flanking this part of subject sequence:
   33682 bp at 5' side: alpha 1 type XV collagen precursor
   1626 bp at 3' side: transforming growth factor, beta receptor I precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  9187055  ACTGGAACTGAGA  9187067


 Features flanking this part of subject sequence:
   510318 bp at 5' side: Kruppel-like factor 4 (gut)
   627474 bp at 3' side: similar to ribosomal protein L36


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  18082844  CTGGAACTGAGAT  18082832


 Features in this part of subject sequence:
   tumor necrosis factor (ligand) superfamily, member 8


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  24994054  ACACTGGAACTGA  24994066


 Features in this part of subject sequence:
   pregnancy-associated plasma protein A preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
```

```
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  26284065  CACACTGGAACTG  26284053
```

Features in this part of subject sequence:
  pregnancy-associated plasma protein A preproprotein

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  26469022  CACTGGAACTGAG  26469010
```

Features in this part of subject sequence:
  astrotactin 2 isoform a
  astrotactin 2 isoform b

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  27189004  TGGAACTGAGATA  27189016
```

Features in this part of subject sequence:
  astrotactin 2 isoform a
  astrotactin 2 isoform b

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  27444169  CACTGGAACTGAG  27444181
```

Features in this part of subject sequence:
  astrotactin 2 isoform a
  astrotactin 2 isoform b

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  27468505  ACACTGGAACTGA  27468493
```

Features in this part of subject sequence:
  complement component 5

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  31109812  CTGGAACTGAGAT  31109800
```

Features flanking this part of subject sequence:
  35102 bp at 5' side: DAB2 interacting protein isoform 1
  170458 bp at 3' side: tubulin tyrosine ligase-like family, member 11

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
```

```
                     |||||||||||||
Sbjct  31902131  ACACTGGAACTGA  31902143


>ref|NT_008183.18|Hs8_8340 D Homo sapiens chromosome 8 genomic contig, reference as
Length=38454502
                                                                  Sort alignments for this s
                                                                    E value  Score  Percent 
                                                                    Query start position  Sul

 Features flanking this part of subject sequence:
   6959 bp at 5' side: valosin containing protein (p97)/p47 complex interacting ...
   3778 bp at 3' side: hypothetical protein LOC56260


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGAT  18
                 |||||||||||||||
Sbjct  19439519  CACTGGAACTGAGAT  19439505


 Features in this part of subject sequence:
   hypothetical protein LOC23514


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3       ACACTGGAACTGA  15
               |||||||||||||
Sbjct  291006  ACACTGGAACTGA  290994


 Features flanking this part of subject sequence:
   17490 bp at 5' side: pleiomorphic adenoma gene 1
   27080 bp at 3' side: coiled-coil-helix-coiled-coil-helix domain containing 7 i..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  8951671  ACTGGAACTGAGA  8951683


 Features flanking this part of subject sequence:
   440541 bp at 5' side: proenkephalin
   77287 bp at 3' side: myo-inositol monophosphatase A3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  9652418  ACTGGAACTGAGA  9652406


 Features flanking this part of subject sequence:
   125944 bp at 5' side: similar to Collagen alpha-1(VII) chain precursor (Long-ch.
   25167 bp at 3' side: hypothetical protein LOC90362


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  10886976  CACTGGAACTGAG  10886964


 Features flanking this part of subject sequence:
   819497 bp at 5' side: similar to ribosomal protein S15a
   218561 bp at 3' side: sulfatase 1
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  22110991  ACTGGAACTGAGA  22111003


 Features in this part of subject sequence:
   hypothetical protein LOC138046


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  37560091  CTGGAACTGAGAT  37560103


>ref|NT_007995.14|Hs8_8152 D Homo sapiens chromosome 8 genomic contig, reference as
Length=14159284
                                                                 Sort alignments for this s
                                                                   E value  Score  Percent i
                                                                   Query start position  Sul

 Features in this part of subject sequence:
   similar to indoleamine 2,3-dioxygenase


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACTGA  15
                 |||||||||||||||
Sbjct  10176487  TCACACTGGAACTGA  10176473


 Features in this part of subject sequence:
   hypothetical protein


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGATAC  20
                 |||||||||||||||
Sbjct  11438714  CTGGAACTGAGATAC  11438728


 Features flanking this part of subject sequence:
   2138 bp at 5' side: steroidogenic acute regulator isoform 2
   10701 bp at 3' side: Lsm1 protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACTG  14
                ||||||||||||||
Sbjct  8330863  TCACACTGGAACTG  8330876


 Features flanking this part of subject sequence:
   90536 bp at 5' side: protein expressed in prostate, ovary, testis, and placent..
   225456 bp at 3' side: similar to Ciliary dynein heavy chain 11 (Axonemal beta d.


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
Sbjct  13622976  ACTGGAACTGAGAT  13622963


 Features flanking this part of subject sequence:
```

```
    5158 bp at 5' side: protein phosphatase 2, catalytic subunit, beta isoform
    15695 bp at 3' side: testis expressed sequence 15


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  3       ACACTGGAACTGA  15
                |||||||||||||
 Sbjct  995881  ACACTGGAACTGA  995869


  Features flanking this part of subject sequence:
    838598 bp at 5' side: similar to ribosomal protein L10a
    382196 bp at 3' side: netrin receptor Unc5h4


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  4        CACTGGAACTGAG  16
                 |||||||||||||
 Sbjct  5340532  CACTGGAACTGAG  5340544


  Features flanking this part of subject sequence:
    3177 bp at 5' side: HTPAP protein
    3511 bp at 3' side: WHSC1L1 protein isoform long


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  7        TGGAACTGAGATA  19
                 |||||||||||||
 Sbjct  8450037  TGGAACTGAGATA  8450025


  Features flanking this part of subject sequence:
    166040 bp at 5' side: ankyrin 1 isoform 8
    101130 bp at 3' side: MYST histone acetyltransferase (monocytic leukemia) 3


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  8         GGAACTGAGATAC  20
                  |||||||||||||
 Sbjct  12008970  GGAACTGAGATAC  12008982


  Features flanking this part of subject sequence:
    37346 bp at 5' side: plasminogen activator, tissue type isoform 2 precursor
    41558 bp at 3' side: inhibitor of kappa light polypeptide gene enhancer in B-c..


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  5         ACTGGAACTGAGA  17
                  |||||||||||||
 Sbjct  12408438  ACTGGAACTGAGA  12408450


 >ref|NT_023684.17|Hs8_23840 D Homo sapiens chromosome 8 genomic contig, reference a
 Length=1290020

  Features in this part of subject sequence:
    poly (ADP-ribose) polymerase family, member 10


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Plus

 Query  2        CACACTGGAACTGAG  16
                 |||||||||||||||
 Sbjct  1024143  CACACTGGAACTGAG  1024157
```

```
>ref|NT_008046.15|Hs8_8203 D Homo sapiens chromosome 8 genomic contig, reference as
Length=57155273

                                                           Sort alignments for this s
                                                             E value  Score  Percent 
                                                             Query start position  Su

 Features in this part of subject sequence:
   cyclic nucleotide gated channel beta 3


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  6       CTGGAACTGAGATAC  20
               |||||||||||||||
Sbjct  833034  CTGGAACTGAGATAC  833020


 Features in this part of subject sequence:
   basic beta 1 syntrophin


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGAT  18
                 |||||||||||||||
Sbjct  34939903  CACTGGAACTGAGAT  34939889


 Features flanking this part of subject sequence:
   17796 bp at 5' side: hypothetical protein
   194874 bp at 3' side: ankyrin repeat domain 46


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGAG  16
                 ||||||||||||||
Sbjct  14558082  ACACTGGAACTGAG  14558069


 Features flanking this part of subject sequence:
   197294 bp at 5' side: hypothetical protein LOC9694
   100276 bp at 3' side: hypothetical protein LOC157753


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  22914307  TGGAACTGAGATAC  22914294


 Features flanking this part of subject sequence:
   745044 bp at 5' side: zinc finger transcription factor TRPS1
   276330 bp at 3' side: eukaryotic translation initiation factor 3, subunit 3 gam.


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  30599080  TGGAACTGAGATAC  30599093


 Features in this part of subject sequence:
   basic beta 1 syntrophin


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus
```

```
Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
Sbjct  35003550  ACTGGAACTGAGAT  35003563


 Features flanking this part of subject sequence:
   135651 bp at 5' side: zinc finger protein 406 isoform TR-ZFAT
   664483 bp at 3' side: KH domain containing, RNA binding, signal transduction as.


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGAG  16
                 ||||||||||||||
Sbjct  49023793  ACACTGGAACTGAG  49023806


 Features flanking this part of subject sequence:
   328846 bp at 5' side: KH domain containing, RNA binding, signal transduction as.
   1836897 bp at 3' side: hypothetical protein LOC401478


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         GAACTGAGATACGG  22
                 ||||||||||||||
Sbjct  50206365  GAACTGAGATACGG  50206352


 Features in this part of subject sequence:
   cyclic nucleotide binding domain containing 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  1343550  TCACACTGGAACT  1343538


 Features in this part of subject sequence:
   matrix metalloproteinase 16 isoform 1 preproprotein
   matrix metalloproteinase 16 isoform 2 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  2473488  CTGGAACTGAGAT  2473476


 Features flanking this part of subject sequence:
   622405 bp at 5' side: matrix metalloproteinase 16 isoform 2 preproprotein
   808456 bp at 3' side: receptor-interacting serine-threonine kinase 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  3179965  GGAACTGAGATAC  3179953


 Features flanking this part of subject sequence:
   125607 bp at 5' side: solute carrier family 26, member 7 isoform b
   440349 bp at 3' side: acute myelogenous leukemia 1 translocation 1 protein isof.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
```

```
Sbjct  5750294  ACTGGAACTGAGA  5750282


 Features in this part of subject sequence:
   RNA binding motif protein 35A isoform 2
   RNA binding motif protein 35A isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  8904250  ACTGGAACTGAGA  8904262


 Features in this part of subject sequence:
   suppression of tumorigenicity


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACTGAGA  17
                 |||| ||||||||||||
Sbjct  18817178  TCACCCTGGAACTGAGA  18817162


 Features in this part of subject sequence:
   collagen, type XIV, alpha 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         GAACTGAGATACG  21
                 |||||||||||||
Sbjct  34486845  GAACTGAGATACG  34486857


 Features flanking this part of subject sequence:
   685322 bp at 5' side: hypothetical protein LOC641384
   583954 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  42863781  CACTGGAACTGAG  42863793


 Features flanking this part of subject sequence:
   553411 bp at 5' side: KH domain containing, RNA binding, signal transduction as.
   1612333 bp at 3' side: hypothetical protein LOC401478


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  50430929  ACTGGAACTGAGA  50430917


 Features flanking this part of subject sequence:
   150115 bp at 5' side: collagen, type XXII, alpha 1
   584959 bp at 3' side: potassium channel, subfamily K, member 9


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  53263721  ACACTGGAACTGA  53263709
```

```
>ref|NT_034885.3|Hs7_35047 D Homo sapiens chromosome 7 genomic contig, reference as
Length=736332

                                                                Sort alignments for this s
                                                                  E value  Score  Percent i
                                                                  Query start position  Sul

 Features in this part of subject sequence:
   dipeptidyl-peptidase 6 isoform 3


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  2       CACACTGGAACTGAG  16
               |||||||||||||||
Sbjct  302064  CACACTGGAACTGAG  302050


 Features in this part of subject sequence:
   dipeptidyl-peptidase 6 isoform 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4       CACTGGAACTGAG  16
               |||||||||||||
Sbjct  300955  CACTGGAACTGAG  300967


>ref|NT_007933.14|Hs7_8090 D Homo sapiens chromosome 7 genomic contig, reference as
Length=64426257

                                                                Sort alignments for this s
                                                                  E value  Score  Percent i
                                                                  Query start position  Sul

 Features flanking this part of subject sequence:
   9068 bp at 5' side: NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5
   47626 bp at 3' side: ankyrin repeat and SOCS box-containing 15


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAGAT  18
                 |||||||||||||||
Sbjct  48390493  CACTGGAACTGAGAT  48390507


 Features flanking this part of subject sequence:
   5269 bp at 5' side: similar to aldo-keto reductase family 1, member B10 isofo...
   76676 bp at 3' side: 2,3-bisphosphoglycerate mutase


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGATA  19
                 |||||||||||||||
Sbjct  59316450  ACTGGAACTGAGATA  59316464


 Features in this part of subject sequence:
   HMG-box transcription factor 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
Sbjct  32013039  ACTGGAACTGAGAT  32013026


 Features flanking this part of subject sequence:
   9867 bp at 5' side: similar to opposite strand transcription unit to Stag3
   33091 bp at 3' side: hypothetical protein
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4       CACTGGAACTGAG  16
               |||||||||||||
Sbjct  111484  CACTGGAACTGAG  111496


 Features flanking this part of subject sequence:
   50280 bp at 5' side: protein tyrosine phosphatase, non-receptor type 12
   6898 bp at 3' side: round spermatid basic protein 1-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  2553153  ACACTGGAACTGA  2553165


 Features flanking this part of subject sequence:
   48164 bp at 5' side: hypothetical protein
   735042 bp at 3' side: hepatocyte growth factor isoform 1 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  5831119  ACACTGGAACTGA  5831131


 Features flanking this part of subject sequence:
   249061 bp at 5' side: semaphorin 3E
   63752 bp at 3' side: semaphorin 3A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAGATAC  20
                |||| ||||||||||||
Sbjct  8761211  CACTTGAACTGAGATAC  8761195


 Features flanking this part of subject sequence:
   62398 bp at 5' side: semaphorin 3D
   1627 bp at 3' side: similar to dynein, cytoplasmic, light peptide


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         GAACTGAGATACG  21
                 |||||||||||||
Sbjct  10047893  GAACTGAGATACG  10047881


 Features flanking this part of subject sequence:
   602244 bp at 5' side: similar to dynein, cytoplasmic, light peptide
   592964 bp at 3' side: glutamate receptor, metabotropic 3 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  11035774  GGAACTGAGATAC  11035762


 Features flanking this part of subject sequence:
   3160 bp at 5' side: opposite strand transcription unit to STAG3
   32731 bp at 3' side: hypothetical protein LOC441272
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  25107042  CACTGGAACTGAG  25107054


 Features flanking this part of subject sequence:
   26 bp at 5' side: thyroid receptor-interacting protein 6
   2249 bp at 3' side: arsenate resistance protein ARS2 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  25705239  ACTGGAACTGAGA  25705227


 Features in this part of subject sequence:
   component of oligomeric golgi complex 5 isoform 1
   component of oligomeric golgi complex 5 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  32331086  ACACTGGAACTGA  32331074


 Features flanking this part of subject sequence:
   18578 bp at 5' side: hypothetical protein LOC154907
   1760479 bp at 3' side: IMP2 inner mitochondrial membrane protease-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  33726755  ACTGGAACTGAGA  33726743


 Features in this part of subject sequence:
   interferon-related developmental regulator 1
   interferon-related developmental regulator 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  37275442  TCACACTGGAACT  37275454


 Features flanking this part of subject sequence:
   504299 bp at 5' side: protein phosphatase 1 glycogen-binding regulatory subunit
   3205 bp at 3' side: forkhead box P2 isoform I


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  39246938  ACACTGGAACTGA  39246926


 Features in this part of subject sequence:
   forkhead box P2 isoform I
   forkhead box P2 isoform II
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  39423353  ACTGGAACTGAGA  39423341


 Features in this part of subject sequence:
   transmembrane 4 superfamily member 12


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  45662107  ACTGGAACTGAGA  45662095


 Features flanking this part of subject sequence:
   85923 bp at 5' side: similar to Ssu72 RNA polymerase II CTD phosphatase homolog
   183635 bp at 3' side: G protein-coupled receptor 37


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  49386508  ACACTGGAACTGA  49386520


 Features flanking this part of subject sequence:
   1052 bp at 5' side: hypothetical protein isoform 2
   413874 bp at 3' side: muskelin 1, intracellular mediator containing kelch motifs


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  55645653  GGAACTGAGATAC  55645665


 Features in this part of subject sequence:
   SEC8 protein isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  58591100  CACACTGGAACTG  58591112


 Features flanking this part of subject sequence:
   107308 bp at 5' side: ATP/GTP binding protein-like 3
   6077 bp at 3' side: hypothetical protein LOC55281


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  59889997  CTGGAACTGAGAT  59889985


 Features in this part of subject sequence:
   solute carrier family 13 (sodium/sulfate symporters), mem...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  60443168  AACTGAGATACGG  60443156


 Features flanking this part of subject sequence:
   271052 bp at 5' side: similar to transient receptor potential cation channel, s.
   337118 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  61265621  ACACTGGAACTGA  61265633


>ref|NT_025741.14|Hs6_25897 D Homo sapiens chromosome 6 genomic contig, reference a
Length=61645385

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent i
                                                                    Query start position  Sul

 Features in this part of subject sequence:
   peptidylprolyl isomerase (cyclophilin)-like 6


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGAGA  17
                 |||||||||||||||
Sbjct  13928132  ACACTGGAACTGAGA  13928118


 Features in this part of subject sequence:
   hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGATA  19
                 ||||||||||||||
Sbjct  24256869  CTGGAACTGAGATA  24256856


 Features flanking this part of subject sequence:
   159853 bp at 5' side: A-kinase anchor protein 7 isoform beta
   131691 bp at 3' side: arginase, type I


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  35867148  CACTGGAACTGAGA  35867161


 Features in this part of subject sequence:
   eyes absent 4 isoform a
   eyes absent 4 isoform d


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGATA  19
                 ||||||||||||||
Sbjct  37817227  CTGGAACTGAGATA  37817214


 Features flanking this part of subject sequence:
   95462 bp at 5' side: mannosidase, endo-alpha
   501277 bp at 3' side: fucosyltransferase 9 (alpha (1,3) fucosyltransferase)
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1       TCACACTGGAACT  13
               |||||||||||||
Sbjct  319212  TCACACTGGAACT  319200


 Features flanking this part of subject sequence:
   216662 bp at 5' side: fucosyltransferase 9 (alpha (1,3) fucosyltransferase)
   100965 bp at 3' side: hypothetical protein LOC23376


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  1038230  ACACTGGAACTGA  1038242


 Features in this part of subject sequence:
   APG5 autophagy 5-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  10863422  TGGAACTGAGATA  10863434


 Features flanking this part of subject sequence:
   142542 bp at 5' side: Sac domain-containing inositol phosphatase 3
   11290 bp at 3' side: G protein-coupled receptor 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTGAGAT  18
                 ||||| |||||||||||
Sbjct  14458455  CACACAGGAACTGAGAT  14458439


 Features flanking this part of subject sequence:
   564 bp at 5' side: REV3-like, catalytic subunit of DNA polymerase zeta
   66609 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  15907585  CACACTGGAACTG  15907573


 Features flanking this part of subject sequence:
   147893 bp at 5' side: phospholamban
   128789 bp at 3' side: ASF1 anti-silencing function 1 homolog A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  23197577  GGAACTGAGATAC  23197565


 Features flanking this part of subject sequence:
   988920 bp at 5' side: hypothetical protein
   256346 bp at 3' side: hypothetical protein LOC221322


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  25259229  TGGAACTGAGATA  25259241


 Features flanking this part of subject sequence:
   25067 bp at 5' side: hypothetical protein LOC134829
   129761 bp at 3' side: triadin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  27514420  TGGAACTGAGATA  27514408


 Features in this part of subject sequence:
   T-cell lymphoma breakpoint-associated target 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  28245602  CTGGAACTGAGAT  28245614


 Features in this part of subject sequence:
   T-cell lymphoma breakpoint-associated target 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  28310810  TCACACTGGAACT  28310798


 Features flanking this part of subject sequence:
   32740 bp at 5' side: KIAA1913
   326787 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  34900212  AACTGAGATACGG  34900224


 Features in this part of subject sequence:
   heme binding protein 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  42835203  CACACTGGAACTG  42835215


 Features flanking this part of subject sequence:
   224 bp at 5' side: similar to NHS-like 1 isoform 1
   71223 bp at 3' side: coiled-coil domain containing 28A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         GAACTGAGATACG  21
```

```
                 |||||||||||||
Sbjct  43128018  GAACTGAGATACG  43128006


 Features in this part of subject sequence:
   similar to ECT2 protein (Epithelial cell-transforming seq...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  43275092  TGGAACTGAGATA  43275080


 Features flanking this part of subject sequence:
   48252 bp at 5' side: muscle-derived protein 77
   35965 bp at 3' side: Cbp/p300-interacting transactivator, with Glu/Asp-rich ca..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTGAGAT  18
                 |||||| ||||||||||
Sbjct  43762717  CACACTTGAACTGAGAT  43762733


 Features flanking this part of subject sequence:
   111926 bp at 5' side: G protein-coupled receptor 126 beta 2
   197654 bp at 3' side: human immunodeficiency virus type I enhancer binding prot.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  46981007  TCACACTGGAACT  46981019


 Features in this part of subject sequence:
   androgen-induced 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  47718404  CACTGGAACTGAG  47718392


 Features flanking this part of subject sequence:
   42401 bp at 5' side: utrophin
   732281 bp at 3' side: laforin isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACTGAGA  17
                 |||||||||| ||||||
Sbjct  49318963  TCACACTGGAGCTGAGA  49318979


 Features flanking this part of subject sequence:
   268339 bp at 5' side: uronyl-2-sulfotransferase
   27531 bp at 3' side: mitogen-activated protein kinase kinase kinase 7 interact..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  53768020  CTGGAACTGAGAT  53768032
```

```
 Features in this part of subject sequence:
   chromosome 6 open reading frame 71


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  54816413  ACACTGGAACTGA  54816425


 Features in this part of subject sequence:
   opioid receptor, mu 1 isoform MOR-1O
   opioid receptor, mu 1 isoform MOR-1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  58527189  ACACTGGAACTGA  58527201


 Features flanking this part of subject sequence:
   76887 bp at 5' side: claudin 20
   43558 bp at 3' side: NADPH oxidase 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  59778840  ACTGGAACTGAGA  59778828


>ref|NT_034880.3|Hs6_35042 D Homo sapiens chromosome 6 genomic contig, reference as
Length=9194728

                                                         Sort alignments for this s
                                                           E value  Score  Percent i
                                                           Query start position  Sul

 Features flanking this part of subject sequence:
   108105 bp at 5' side: phenylalanine-tRNA synthetase 2
   119428 bp at 3' side: neuritin precursor


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  2        CACACTGGAACTGAG  16
                |||||||||||||||
Sbjct  5819766  CACACTGGAACTGAG  5819780


 Features in this part of subject sequence:
   bone morphogenetic protein 6 precursor


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATAC  20
                |||||||||||||||
Sbjct  7741307  CTGGAACTGAGATAC  7741293


 Features flanking this part of subject sequence:
   17000 bp at 5' side: hypothetical protein LOC642316
   65906 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus
```

```
Query  5       ACTGGAACTGAGATACG  21
               |||||||||||| ||||
Sbjct  160817  ACTGGAACTGAGCTACG  160801


 Features in this part of subject sequence:
   hypothetical protein LOC221749


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  3664641  CACACTGGAACTG  3664653


 Features in this part of subject sequence:
   phenylalanine-tRNA synthetase 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  5469035  CACACTGGAACTG  5469047


 Features in this part of subject sequence:
   coagulation factor XIII A1 subunit precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  6169125  TGGAACTGAGATA  6169137


 Features flanking this part of subject sequence:
   179585 bp at 5' side: MD-1, RP105-associated
   216991 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  6774456  CTGGAACTGAGAT  6774444


>ref|NT_007592.14|Hs6_7749 D Homo sapiens chromosome 6 genomic contig, reference a
Length=48945890

                                                                Sort alignments for this s
                                                                  E value  Score  Percent
                                                                  Query start position  Su

 Features in this part of subject sequence:
   CDK5 regulatory subunit associated protein 1-like 1


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGAGA  17
                 |||||||||||||||
Sbjct  11822303  ACACTGGAACTGAGA  11822289


 Features in this part of subject sequence:
   polyductin isoform 1
   polyductin isoform 2


 Score = 30.2 bits (15),  Expect =    28
```

```
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGAT  18
                 |||||||||||||||
Sbjct  42658007  CACTGGAACTGAGAT  42657993


 Features flanking this part of subject sequence:
   256240 bp at 5' side: CDK5 regulatory subunit associated protein 1-like 1
   107243 bp at 3' side: SRY (sex determining region Y)-box 4


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACTG  14
                 ||||||||||||||
Sbjct  12345761  TCACACTGGAACTG  12345774


 Features in this part of subject sequence:
   leucine rich repeat containing 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  44619544  CACTGGAACTGAGA  44619557


 Features flanking this part of subject sequence:
   381412 bp at 5' side: neural precursor cell expressed, developmentally down-reg.
   100539 bp at 3' side: hypothetical protein LOC84830


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  2472430  CACTGGAACTGAG  2472418


 Features flanking this part of subject sequence:
   448408 bp at 5' side: CD83 antigen isoform a
   393629 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  5442138  GGAACTGAGATAC  5442126


 Features flanking this part of subject sequence:
   95662 bp at 5' side: DEK oncogene (DNA binding)
   39874 bp at 3' side: IBR domain containing 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  9218131  ACTGGAACTGAGA  9218143


 Features flanking this part of subject sequence:
   220021 bp at 5' side: inhibitor of DNA binding 4, dominant negative helix-loop-.
   43625 bp at 3' side: similar to O-acyltransferase (membrane bound) domain cont..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  10917143  CACACTGGAACTG  10917131


 Features flanking this part of subject sequence:
   215268 bp at 5' side: CDK5 regulatory subunit associated protein 1-like 1
   148216 bp at 3' side: SRY (sex determining region Y)-box 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  12304789  CACACTGGAACTG  12304801


 Features flanking this part of subject sequence:
   31791 bp at 5' side: chromosome 6 open reading frame 62
   26776 bp at 3' side: geminin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  15608938  TCACACTGGAACT  15608950


 Features flanking this part of subject sequence:
   139233 bp at 5' side: zinc finger protein 184 (Kruppel-like)
   195986 bp at 3' side: H2B histone family, member C


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  18437557  TGGAACTGAGATA  18437569


 Features flanking this part of subject sequence:
   4931 bp at 5' side: LEM domain containing 2
   766 bp at 3' side: motilin isoform 1 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  24620086  CACACTGGAACTG  24620074


 Features flanking this part of subject sequence:
   31926 bp at 5' side: tubby like protein 1
   31039 bp at 3' side: FK506 binding protein 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  26370823  ACACTGGAACTGA  26370811


 Features in this part of subject sequence:
   kinesin family member 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
```

```
                 |||||||||||||
Sbjct  30249155  CACACTGGAACTG  30249143


 Features flanking this part of subject sequence:
   31503 bp at 5' side: transcription factor EB
   14124 bp at 3' side: progastricsin (pepsinogen C)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  32548716  CTGGAACTGAGAT  32548704


 Features flanking this part of subject sequence:
   118663 bp at 5' side: runt-related transcription factor 2 isoform c
   237108 bp at 3' side: chloride intracellular channel 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  36491967  CACACTGGAACTG  36491955


 Features flanking this part of subject sequence:
   204996 bp at 5' side: transcription factor AP-2 beta (activating enhancer bindi.
   467766 bp at 3' side: polyductin isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  41874332  ACACTGGAACTGA  41874344


 Features flanking this part of subject sequence:
   253581 bp at 5' side: transcription factor AP-2 beta (activating enhancer bindi.
   419181 bp at 3' side: polyductin isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  41922929  ACTGGAACTGAGA  41922917


 Features in this part of subject sequence:
   homolog of yeast long chain polyunsaturated fatty acid el...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  44003386  GGAACTGAGATAC  44003398


 Features flanking this part of subject sequence:
   146039 bp at 5' side: 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1
   30427 bp at 3' side: bone morphogenetic protein 5 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  46448123  ACTGGAACTGAGA  46448135
```

```
 Features in this part of subject sequence:
   bone morphogenetic protein 5 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  46579420  CTGGAACTGAGAT  46579432


>ref|NT_007422.13|Hs6_7579 D Homo sapiens chromosome 6 genomic contig, reference a
Length=10134273
                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   205172 bp at 5' side: hypothetical protein
   19081 bp at 3' side: quaking homolog, KH domain RNA binding isoform HQK-5


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTGAG  16
                |||||||||||||||
Sbjct  6104486  CACACTGGAACTGAG  6104472


 Features in this part of subject sequence:
   NEW1 domain containing protein isoform 1
   NEW1 domain containing protein isoform 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9       GAACTGAGATACGG  22
               ||||||||||||||
Sbjct  115559  GAACTGAGATACGG  115572


 Features in this part of subject sequence:
   ribosomal protein S6 kinase, 90kDa, polypeptide 2 isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  9377747  ACTGGAACTGAGA  9377759


>ref|NT_034772.5|Hs5_34934 D Homo sapiens chromosome 5 genomic contig, reference a
Length=41199371
                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   905429 bp at 5' side: nudix -type motif 12
   2915564 bp at 3' side: ephrin-A5


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGATA  19
                |||||||||||||||
Sbjct  6216391  ACTGGAACTGAGATA  6216405
```

```
 Features flanking this part of subject sequence:
   1128058 bp at 5' side: ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferas
   205832 bp at 3' side: solute carrier organic anion transporter family, member 4C


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  7        TGGAACTGAGATAC  20
                ||||||||||||||
Sbjct  3781730  TGGAACTGAGATAC  3781743


 Features flanking this part of subject sequence:
   1244313 bp at 5' side: ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferas
   89574 bp at 3' side: solute carrier organic anion transporter family, member 4C1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAGATAC  20
                |||||||||||| ||||
Sbjct  3898001  CACTGGAACTGACATAC  3897985


 Features flanking this part of subject sequence:
   1104658 bp at 5' side: nudix -type motif 12
   2716337 bp at 3' side: ephrin-A5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  6415632  CACTGGAACTGAG  6415620


 Features flanking this part of subject sequence:
   2833481 bp at 5' side: nudix -type motif 12
   987514 bp at 3' side: ephrin-A5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  8144455  ACTGGAACTGAGA  8144443


 Features flanking this part of subject sequence:
   3267560 bp at 5' side: nudix -type motif 12
   553435 bp at 3' side: ephrin-A5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  8578522  GGAACTGAGATAC  8578534


 Features flanking this part of subject sequence:
   1180524 bp at 5' side: hypothetical protein
   83130 bp at 3' side: DTW domain containing 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  20508495  TGGAACTGAGATA  20508483


 Features flanking this part of subject sequence:
```

```
    739480 bp at 5' side: casein kinase 1, gamma 3 isoform 2
    284007 bp at 3' side: zinc finger protein 608


  Score = 26.3 bits (13),  Expect =   444
  Identities = 16/17 (94%), Gaps = 0/17 (0%)
  Strand=Plus/Plus

Query  6         CTGGAACTGAGATACGG  22
                 ||||| |||||||||||
Sbjct  26104583  CTGGAGCTGAGATACGG  26104599


  Features flanking this part of subject sequence:
    26290 bp at 5' side: heat shock 70kDa protein 4 isoform b
    68357 bp at 3' side: follistatin-like 4


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  34881443  ACTGGAACTGAGA  34881431


  Features in this part of subject sequence:
    small inducible cytokine B14 precursor


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  37328137  CACTGGAACTGAG  37328125


>ref|NT_029289.10|Hs5_29448 D Homo sapiens chromosome 5 genomic contig, reference a
Length=16301663
                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

  Features flanking this part of subject sequence:
    952946 bp at 5' side: neuromedin U receptor 2
    132815 bp at 3' side: glutamate receptor, ionotropic, AMPA 1


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Plus

Query  6         CTGGAACTGAGATAC  20
                 |||||||||||||||
Sbjct  13900556  CTGGAACTGAGATAC  13900570


  Features in this part of subject sequence:
    neuregulin 2 isoform 4
    neuregulin 2 isoform 3


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  5       ACTGGAACTGAGA  17
               |||||||||||||
Sbjct  526286  ACTGGAACTGAGA  526298


  Features in this part of subject sequence:
    putative nuclear protein ORF1-FL49


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  3       ACACTGGAACTGA  15
```

```
                 |||||||||||||
Sbjct  765102  ACACTGGAACTGA  765090

 Features in this part of subject sequence:
   serine peptidase inhibitor, Kazal type 5 precursor

 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  8633059  TGGAACTGAGATA  8633071

 Features flanking this part of subject sequence:
   57971 bp at 5' side: hypothetical protein
   12751 bp at 3' side: actin binding LIM protein family, member 3

 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  9671844  CTGGAACTGAGAT  9671832

 Features in this part of subject sequence:
   FAT tumor suppressor 2 precursor

 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  12062927  TGGAACTGAGATA  12062915

 Features in this part of subject sequence:
   FAT tumor suppressor 2 precursor

 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  12102884  TGGAACTGAGATA  12102896

 Features flanking this part of subject sequence:
   806973 bp at 5' side: neuromedin U receptor 2
   278790 bp at 3' side: glutamate receptor, ionotropic, AMPA 1

 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  13754595  ACTGGAACTGAGA  13754583

>ref|NT_022853.14|Hs4_23009 D Homo sapiens chromosome 4 genomic contig, reference
Length=7074452

                                                             Sort alignments for this
                                                               E value  Score  Percent
                                                               Query start position  Su

 Features flanking this part of subject sequence:
   11954 bp at 5' side: platelet-derived growth factor receptor alpha precursor
   350775 bp at 3' side: v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene hom.

 Score = 30.2 bits (15),  Expect =    28
```

```
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATAC  20
                |||||||||||||||
Sbjct  2513290  CTGGAACTGAGATAC  2513276


 Features flanking this part of subject sequence:
   326688 bp at 5' side: v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene hom.
   14685 bp at 3' side: kinase insert domain receptor (a type III receptor tyrosi..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  3271294  CTGGAACTGAGAT  3271306


>ref|NT_005612.15|Hs3_5769 D Homo sapiens chromosome 3 genomic contig, reference a
Length=100530253
                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

 Features flanking this part of subject sequence:
   41474 bp at 5' side: profilin 2 isoform a
   253286 bp at 3' side: hypothetical protein


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGATAC  20
                 |||||||||||||||
Sbjct  56225277  CTGGAACTGAGATAC  56225263


 Features flanking this part of subject sequence:
   179948 bp at 5' side: similar to PQ loop repeat containing 2 isoform 1
   339732 bp at 3' side: short stature homeobox 2 isoform a


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGATAC  20
                 |||||||||||||||
Sbjct  63971220  CTGGAACTGAGATAC  63971234


 Features flanking this part of subject sequence:
   40504 bp at 5' side: hypothetical protein
   727728 bp at 3' side: similar to mesenchymal stem cell protein DSC92 isoform 2


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGATAC  20
                 |||||||||||||||
Sbjct  69486807  CTGGAACTGAGATAC  69486793


 Features flanking this part of subject sequence:
   222670 bp at 5' side: similar to CG17293-PA
   1654199 bp at 3' side: similar to Ephrin type-A receptor 6 precursor (Tyrosine-p


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATA  19
                ||||||||||||||
Sbjct  1374697  CTGGAACTGAGATA  1374684
```

```
 Features flanking this part of subject sequence:
   224272 bp at 5' side: similar to CG17293-PA
   1652597 bp at 3' side: similar to Ephrin type-A receptor 6 precursor (Tyrosine-p


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATA  19
                ||||||||||||||
Sbjct  1376299  CTGGAACTGAGATA  1376286


 Features in this part of subject sequence:
   zinc finger protein ZNF-U69274


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACTG  14
                ||||||||||||||
Sbjct  7870156  TCACACTGGAACTG  7870169


 Features flanking this part of subject sequence:
   107087 bp at 5' side: follistatin-like 1 precursor
   38514 bp at 3' side: NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGATA  19
                 ||||||||||||||
Sbjct  26771826  CTGGAACTGAGATA  26771839


 Features flanking this part of subject sequence:
   2770 bp at 5' side: RAB, member of RAS oncogene family-like 3
   5263 bp at 3' side: general transcription factor IIE, polypeptide 1 (alpha su...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
Sbjct  26959270  ACTGGAACTGAGAT  26959283


 Features flanking this part of subject sequence:
   3875 bp at 5' side: eukaryotic elongation factor, selenocysteine-tRNA-specific
   50400 bp at 3' side: DnaJ homolog, subfamily B, member 8


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGAG  16
                 ||||||||||||||
Sbjct  34626136  ACACTGGAACTGAG  34626123


 Features flanking this part of subject sequence:
   11164 bp at 5' side: phospholipase D1, phophatidylcholine-specific
   363252 bp at 3' side: fibronectin type III domain containing 3B


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTGA  15
                 ||||||||||||||
Sbjct  77962155  CACACTGGAACTGA  77962168


 Features flanking this part of subject sequence:
```

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    120830 bp at 5' side: p53 target zinc finger protein isoform 2
    10231 bp at 3' side: phosphoinositide-3-kinase, catalytic, alpha polypeptide


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  85401520  CACTGGAACTGAGA  85401533


  Features in this part of subject sequence:
    similar to Ephrin type-A receptor 6 precursor (Tyrosine-p...


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  9        GAACTGAGATACG  21
                |||||||||||||
Sbjct  3521527  GAACTGAGATACG  3521539


  Features in this part of subject sequence:
    Cas-Br-M (murine) ecotropic retroviral transforming seque...


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  11878399  TGGAACTGAGATA  11878411


  Features flanking this part of subject sequence:
    164711 bp at 5' side: testes development-related NYD-SP17
    167164 bp at 3' side: HMG-BOX transcription factor BBX


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  13757278  TGGAACTGAGATA  13757290


  Features flanking this part of subject sequence:
    1251558 bp at 5' side: developmental pluripotency associated 4
    303142 bp at 3' side: hypothetical protein LOC151760 isoform 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  16803068  ACACTGGAACTGA  16803080


  Features flanking this part of subject sequence:
    86329 bp at 5' side: hypothetical protein LOC151760 isoform 1
    92315 bp at 3' side: nectin 3


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  17193696  ACACTGGAACTGA  17193684


  Features flanking this part of subject sequence:
    153078 bp at 5' side: steroid-sensitive protein 1
    22968 bp at 3' side: CD200 cell surface glycoprotein receptor isoform 2
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  19006988  TCACACTGGAACT  19006976


 Features flanking this part of subject sequence:
   1223324 bp at 5' side: zinc finger and BTB domain containing 20
   48496 bp at 3' side: growth associated protein 43


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  21789187  TGGAACTGAGATA  21789175


 Features flanking this part of subject sequence:
   51637 bp at 5' side: limbic system-associated membrane protein
   149217 bp at 3' side: similar to basic leucine zipper and W2 domains 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  22710661  TCACACTGGAACT  22710673


 Features flanking this part of subject sequence:
   828277 bp at 5' side: similar to heat shock 70kD protein binding protein
   1246994 bp at 3' side: immunoglobulin superfamily, member 11 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  23869507  CTGGAACTGAGAT  23869519


 Features flanking this part of subject sequence:
   1941715 bp at 5' side: similar to heat shock 70kD protein binding protein
   133552 bp at 3' side: immunoglobulin superfamily, member 11 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACTGAGA  17
                 ||||||||||| |||||
Sbjct  24982945  TCACACTGGAAGTGAGA  24982961


 Features in this part of subject sequence:
   sorting nexin 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  31694535  TGGAACTGAGATA  31694547


 Features flanking this part of subject sequence:
   1880 bp at 5' side: hypothetical protein LOC57461
   7586 bp at 3' side: zinc finger protein 9


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  35376856  TGGAACTGAGATA  35376844


 Features in this part of subject sequence:
   5'-3' exoribonuclease 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  48579070  ACTGGAACTGAGA  48579082


 Features in this part of subject sequence:
   solute carrier family 9 (sodium/hydrogen exchanger), isof...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  49858259  TGGAACTGAGATA  49858271


 Features flanking this part of subject sequence:
   556775 bp at 5' side: hypothetical protein isoform 1
   762747 bp at 3' side: angiotensin II receptor, type 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  54191210  TCACACTGGAACT  54191222


 Features flanking this part of subject sequence:
   712523 bp at 5' side: hypothetical protein isoform 1
   606999 bp at 3' side: angiotensin II receptor, type 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  54346970  CTGGAACTGAGAT  54346958


 Features in this part of subject sequence:
   WW domain containing transcription regulator 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  55751690  ACTGGAACTGAGA  55751678


 Features flanking this part of subject sequence:
   265916 bp at 5' side: hypothetical protein
   353583 bp at 3' side: Src homology 3 domain-containing guanine nucleotide excha.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
```

```
                 |||||||||||||
Sbjct  59981333  CACTGGAACTGAG  59981345


 Features flanking this part of subject sequence:
   132096 bp at 5' side: slit and trk like 3 protein
   450444 bp at 3' side: butyrylcholinesterase precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  71535864  CACTGGAACTGAG  71535876


 Features flanking this part of subject sequence:
   209248 bp at 5' side: similar to EGF-like-domain, multiple 3 isoform 2
   65401 bp at 3' side: ecotropic viral integration site 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  75232446  CACACTGGAACTG  75232434


 Features flanking this part of subject sequence:
   186847 bp at 5' side: PXR2b protein
   378804 bp at 3' side: tetratricopeptide repeat domain 14


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  86436384  GGAACTGAGATAC  86436396


 Features flanking this part of subject sequence:
   578502 bp at 5' side: sex-determining region Y-box 2
   390873 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  88504754  CACTGGAACTGAG  88504766


 Features flanking this part of subject sequence:
   177553 bp at 5' side: UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransfera.
   43427 bp at 3' side: kelch-like 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  89661438  CACTGGAACTGAG  89661426


 Features in this part of subject sequence:
   TBCC domain containing 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         GAACTGAGATACG  21
                 |||||||||||||
Sbjct  92765406  GAACTGAGATACG  92765394
```

```
 Features flanking this part of subject sequence:
   258344 bp at 5' side: LIM domain containing preferred translocation partner in .
   74551 bp at 3' side: hypothetical protein LOC285386


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  95345773  ACACTGGAACTGA  95345761


>ref|NT_026970.9|Hs2_27130 D Homo sapiens chromosome 2 genomic contig, reference a
Length=2594449

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   175721 bp at 5' side: similar to Nucleolar transcription factor 1 (Upstream-bin.
   57891 bp at 3' side: protein immuno-reactive with anti-PTH polyclonal antibodies


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  1        TCACACTGGAACTGA  15
                |||||||||||||||
Sbjct  1141743  TCACACTGGAACTGA  1141729


 Features flanking this part of subject sequence:
   10970 bp at 5' side: similar to lung-inducible neuralized-related C3HC4 RING d..
   20559 bp at 3' side: AT rich interactive domain 5A isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  1855822  ACTGGAACTGAGA  1855834


>ref|NT_004487.18|Hs1_4644 D Homo sapiens chromosome 1 genomic contig, reference a
Length=56413061

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   5445 bp at 5' side: MADS box transcription enhancer factor 2, polypeptide D (...
   37731 bp at 3' side: IQ motif containing GTPase activating protein 3


 Score = 30.2 bits (15),  Expect =    28
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query  1        TCACACTGGAACTGAGATA  19
                |||||| ||||||||||||
Sbjct  6948902  TCACACAGGAACTGAGATA  6948884


 Features in this part of subject sequence:
   Fc receptor-like 5


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGAGA  17
                |||||||||||||||
Sbjct  7988032  ACACTGGAACTGAGA  7988046
```

```
 Features flanking this part of subject sequence:
   262235 bp at 5' side: tenascin R (restrictin, janusin)
   276190 bp at 3' side: ring finger and WD repeat domain 2 isoform d24


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTGAG  16
                 |||||||||||||||
Sbjct  26128453  CACACTGGAACTGAG  26128439


 Features flanking this part of subject sequence:
   178766 bp at 5' side: similar to Y74C9A.3
   185613 bp at 3' side: NTKL-binding protein 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
Sbjct  20806032  ACTGGAACTGAGAT  20806019


 Features in this part of subject sequence:
   ring finger and WD repeat domain 2 isoform d24
   ring finger and WD repeat domain 2 isoform a


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTGA  15
                 ||||||||||||||
Sbjct  26491465  CACACTGGAACTGA  26491452


 Features flanking this part of subject sequence:
   130847 bp at 5' side: hypothetical protein LOC116461
   273803 bp at 3' side: chromosome 1 open reading frame 21


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACTG  14
                 ||||||||||||||
Sbjct  34663195  TCACACTGGAACTG  34663182


 Features flanking this part of subject sequence:
   859 bp at 5' side: hypothetical protein LOC54964
   2918 bp at 3' side: CDC42 small effector 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  1514148  ACTGGAACTGAGA  1514160


 Features in this part of subject sequence:
   S100 calcium-binding protein A9


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  3822060  ACTGGAACTGAGA  3822048


 Features in this part of subject sequence:
```

```
    similar to S100 calcium binding protein A7-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  3900782  ACTGGAACTGAGA  3900770


 Features in this part of subject sequence:
    Fc receptor-like 2 isoform b
    Fc receptor-like 2 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  8227646  ACACTGGAACTGA  8227658


 Features in this part of subject sequence:
    hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  8385919  ACACTGGAACTGA  8385907


 Features flanking this part of subject sequence:
    67381 bp at 5' side: hypothetical protein
    83031 bp at 3' side: kin of IRRE like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  8453358  CTGGAACTGAGAT  8453346


 Features in this part of subject sequence:
    G protein-coupled receptor 161 isoform 2
    G protein-coupled receptor 161 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  18559252  TCACACTGGAACT  18559240


 Features in this part of subject sequence:
    coagulation factor V precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  20021086  GGAACTGAGATAC  20021098


 Features flanking this part of subject sequence:
    37050 bp at 5' side: influenza virus NS1A binding protein isoform b
    388225 bp at 3' side: hemicentin 1
```

```
  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  5         ACTGGAACTGAGA  17
                  |||||||||||||
 Sbjct  35806041  ACTGGAACTGAGA  35806029


  Features flanking this part of subject sequence:
    494450 bp at 5' side: similar to solute carrier family 4 (anion exchanger), mem.
    1895750 bp at 3' side: family with sequence similarity 5, member C


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  3         ACACTGGAACTGA  15
                  |||||||||||||
 Sbjct  38661740  ACACTGGAACTGA  38661752


  Features flanking this part of subject sequence:
    1808214 bp at 5' side: similar to solute carrier family 4 (anion exchanger), mem
    581986 bp at 3' side: family with sequence similarity 5, member C


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  7         TGGAACTGAGATA  19
                  |||||||||||||
 Sbjct  39975504  TGGAACTGAGATA  39975516


  Features in this part of subject sequence:
    zinc finger and BTB domain containing 41


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  8         GGAACTGAGATAC  20
                  |||||||||||||
 Sbjct  47653124  GGAACTGAGATAC  47653112


 >ref|NT_021877.18|Hs1_22033 D Homo sapiens chromosome 1 genomic contig, reference a
 Length=17265625

                                                                Sort alignments for this s
                                                                  E value  Score  Percent i
                                                                  Query start position  Sul

  Features flanking this part of subject sequence:
    661316 bp at 5' side: plexin A2
    352395 bp at 3' side: hypothetical protein


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Minus

 Query  4        CACTGGAACTGAGAT  18
                 |||||||||||||||
 Sbjct  2570376  CACTGGAACTGAGAT  2570362


  Features flanking this part of subject sequence:
    50880 bp at 5' side: Fc alpha/mu receptor
    940 bp at 3' side: specifically androgen-regulated protein


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

 Query  4       CACTGGAACTGAGA  17
                ||||||||||||||
 Sbjct  712129  CACTGGAACTGAGA  712142
```

```
 Features flanking this part of subject sequence:
   41644 bp at 5' side: plexin A2
   972068 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGAG  16
                ||||||||||||||
Sbjct  1950690  ACACTGGAACTGAG  1950703


 Features flanking this part of subject sequence:
   12521 bp at 5' side: SCIRP10-related protein
   156482 bp at 3' side: activating transcription factor 3 delta Zip isoform


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGAT  18
                ||||||||||||||
Sbjct  6149661  ACTGGAACTGAGAT  6149648


 Features in this part of subject sequence:
   IKK-related kinase epsilon
   hypothetical protein LOC574431


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1       TCACACTGGAACTGAGA  17
               ||||||||||| |||||
Sbjct  183756  TCACACTGGAAATGAGA  183772


 Features flanking this part of subject sequence:
   75861 bp at 5' side: H2.0-like homeo box 1
   373259 bp at 3' side: hypothetical protein LOC400804


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  14651698  CACTGGAACTGAG  14651686


 Features flanking this part of subject sequence:
   39084 bp at 5' side: hypothetical protein LOC400823
   154646 bp at 3' side: dispatched A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  16479299  CACTGGAACTGAG  16479287


>ref|NW_926584.1|HsCraAADB02_571 D Homo sapiens chromosome 17 genomic contig, alter
(based on Celera assembly)
Length=15369037

                                                                Sort alignments for this s
                                                                  E value  Score  Percent :
                                                                  Query start position  Su

 Features in this part of subject sequence:
   hypothetical protein LOC9912


 Score = 28.2 bits (14),  Expect =   112
```

```
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  12730646  TGGAACTGAGATAC  12730633


 Features in this part of subject sequence:
   syntaxin 8


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  9211394  ACTGGAACTGAGA  9211406


 Features flanking this part of subject sequence:
   395146 bp at 5' side: hypothetical protein
   21190 bp at 3' side: hypothetical protein LOC388336


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTGAGAT  18
                 |||||||| ||||||||
Sbjct  11072463  CACACTGGCACTGAGAT  11072447


 Features in this part of subject sequence:
   dynein, axonemal, heavy polypeptide 9 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  11473201  GGAACTGAGATAC  11473213


 Features flanking this part of subject sequence:
   59229 bp at 5' side: hypothetical protein LOC400576
   391463 bp at 3' side: peripheral myelin protein 22


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  14684835  TGGAACTGAGATA  14684847


>ref|NW_926462.1|HsCraAADB02_560 D Homo sapiens chromosome 16 genomic contig, alte
(based on Celera assembly)
Length=23685799

                                                                Sort alignments for this s
                                                                  E value  Score  Percent
                                                                  Query start position  Su

 Features flanking this part of subject sequence:
   21351 bp at 5' side: hypothetical protein
   445851 bp at 3' side: cerebellin 1 precursor


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACTG  14
                ||||||||||||||
Sbjct  2444220  TCACACTGGAACTG  2444233


 Features flanking this part of subject sequence:
```

```
   41147 bp at 5' side: zinc finger protein 423
   161473 bp at 3' side: hypothetical protein LOC255919


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACTG  14
                ||||||||||||||
Sbjct  3475640  TCACACTGGAACTG  3475653


 Features flanking this part of subject sequence:
   10486 bp at 5' side: cadherin 5, type 2 preproprotein
   98973 bp at 3' side: thymidine kinase 2, mitochondrial


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGATA  19
                 ||||||||||||||
Sbjct  20018255  CTGGAACTGAGATA  20018268


 Features flanking this part of subject sequence:
   297042 bp at 5' side: hypothetical protein
   170161 bp at 3' side: cerebellin 1 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  2719923  ACTGGAACTGAGA  2719911


 Features in this part of subject sequence:
   naked cuticle homolog 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  4184481  GGAACTGAGATAC  4184493


 Features flanking this part of subject sequence:
   443015 bp at 5' side: sal-like 1
   431257 bp at 3' side: hypothetical protein isoform 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  5209340  CTGGAACTGAGAT  5209352


 Features flanking this part of subject sequence:
   521808 bp at 5' side: sal-like 1
   352464 bp at 3' side: hypothetical protein isoform 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  5288133  TCACACTGGAACT  5288145


 Features flanking this part of subject sequence:
   34960 bp at 5' side: G-protein coupled receptor 114
   39687 bp at 3' side: G protein-coupled receptor 56 isoform a
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  11210519  ACTGGAACTGAGA  11210531


 Features flanking this part of subject sequence:
   1370040 bp at 5' side: hypothetical protein LOC650767
   230553 bp at 3' side: similar to serine palmitoyltransferase subunit 1 isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  13725420  ACACTGGAACTGA  13725408


 Features flanking this part of subject sequence:
   24446 bp at 5' side: hypothetical protein
   1273775 bp at 3' side: cadherin 8, type 2 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  13982907  TCACACTGGAACT  13982919


 Features flanking this part of subject sequence:
   55516 bp at 5' side: hypothetical protein
   1242705 bp at 3' side: cadherin 8, type 2 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  14013977  ACTGGAACTGAGA  14013989


 Features flanking this part of subject sequence:
   1298201 bp at 5' side: hypothetical protein
   20 bp at 3' side: cadherin 8, type 2 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  15256674  CACTGGAACTGAG  15256662


 Features in this part of subject sequence:
   hypothetical protein isoform 4
   hypothetical protein isoform 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  18962007  ACTGGAACTGAGA  18962019


 Features flanking this part of subject sequence:
   13374 bp at 5' side: chemokine-like factor superfamily 4 isoform 2
   75435 bp at 3' side: dynein, cytoplasmic, light intermediate polypeptide 2
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  20255161  ACTGGAACTGAGA  20255149


>ref|NW_926528.1|HsCraAADB02_566 D Homo sapiens chromosome 16 genomic contig, alte
(based on Celera assembly)
Length=13777636

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features in this part of subject sequence:
   c-Maf-inducing protein C-mip isoform
   c-Maf-inducing protein Tc-mip isoform


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAGA  17
                ||||||||||||||
Sbjct  7087086  CACTGGAACTGAGA  7087073


 Features in this part of subject sequence:
   WD repeat domain 59


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1       TCACACTGGAACT  13
               |||||||||||||
Sbjct  526304  TCACACTGGAACT  526316


 Features in this part of subject sequence:
   cadherin 13 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  9194074  CACACTGGAACTG  9194062


>ref|NW_925940.1|HsCraAADB02_513 D Homo sapiens chromosome 15 genomic contig, alte
(based on Celera assembly)
Length=17317633

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   556280 bp at 5' side: similar to ATP/GTP binding protein 1
   291820 bp at 3' side: neurotrophic tyrosine kinase, receptor, type 3 isoform b .


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGAT  18
                ||||||||||||||
Sbjct  3022445  ACTGGAACTGAGAT  3022432


 Features in this part of subject sequence:
   mitochondrial ribosomal protein S11 isoform b
   mitochondrial ribosomal protein S11 isoform a
```

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  1        TCACACTGGAACTG  14
                ||||||||||||||
Sbjct  3912672  TCACACTGGAACTG  3912659


 Features flanking this part of subject sequence:
   190959 bp at 5' side: similar to Solute carrier organic anion transporter famil.
   39938 bp at 3' side: ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTGA  15
                ||||||||||||||
Sbjct  7802023  CACACTGGAACTGA  7802010


 Features flanking this part of subject sequence:
   139472 bp at 5' side: phosphodiesterase 8A isoform 3
   109048 bp at 3' side: similar to Fatty acid-binding protein, epidermal (E-FABP).


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3       ACACTGGAACTGA  15
               |||||||||||||
Sbjct  742178  ACACTGGAACTGA  742190


 Features flanking this part of subject sequence:
   89495 bp at 5' side: similar to ATP/GTP binding protein 1
   758606 bp at 3' side: neurotrophic tyrosine kinase, receptor, type 3 isoform b .


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  2555647  GGAACTGAGATAC  2555659


 Features in this part of subject sequence:
   IQ motif containing GTPase activating protein 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  5889277  CTGGAACTGAGAT  5889289


 Features flanking this part of subject sequence:
   926285 bp at 5' side: hypothetical protein
   15934 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  11706263  AACTGAGATACGG  11706251


 Features flanking this part of subject sequence:
   160796 bp at 5' side: hypothetical protein
   190202 bp at 3' side: hypothetical protein LOC283777


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  13703298  CTGGAACTGAGAT  13703310


 Features flanking this part of subject sequence:
   6335 bp at 5' side: MADS box transcription enhancer factor 2, polypeptide A (...
   10038 bp at 3' side: hypothetical protein LOC145748


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  15171062  ACACTGGAACTGA  15171050


>ref|NW_925506.1|HsCraAADB02_474 D Homo sapiens chromosome 13 genomic contig, alte
(based on Celera assembly)
Length=22380413

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent :
                                                                    Query start position  Sul

 Features flanking this part of subject sequence:
   2015666 bp at 5' side: hypothetical protein
   454994 bp at 3' side: kelch-like 1 protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  6        CTGGAACTGAGATA  19
                ||||||||||||||
Sbjct  5412128  CTGGAACTGAGATA  5412141


 Features flanking this part of subject sequence:
   282850 bp at 5' side: hypothetical protein
   7109 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGATA  19
                 ||||||||||||||
Sbjct  10582338  CTGGAACTGAGATA  10582351


 Features flanking this part of subject sequence:
   224694 bp at 5' side: dachshund homolog 1 isoform b
   615359 bp at 3' side: hypothetical protein isoform 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  8256886  CACTGGAACTGAG  8256874


 Features flanking this part of subject sequence:
   711596 bp at 5' side: dachshund homolog 1 isoform b
   128457 bp at 3' side: hypothetical protein isoform 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  8743776  TCACACTGGAACT  8743788
```

```
 Features flanking this part of subject sequence:
   89946 bp at 5' side: similar to Fatty acid-binding protein, epidermal (E-FABP)..
   217178 bp at 3' side: similar to MAP/microtubule affinity-regulating kinase 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  9352861  ACTGGAACTGAGA  9352873


 Features flanking this part of subject sequence:
   285492 bp at 5' side: slit and trk like 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  22258823  CACACTGGAACTG  22258835


>ref|NW_925495.1|HsCraAADB02_473 D Homo sapiens chromosome 13 genomic contig, alte
(based on Celera assembly)
Length=11111593

                                                         Sort alignments for this s
                                                           E value  Score  Percent 
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   94148 bp at 5' side: protocadherin 20
   897364 bp at 3' side: similar to sequestosome 1 isoform 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACTGAGAT  18
                |||||||||| |||||||
Sbjct  8899964  TCACACTGGATCTGAGAT  8899981


 Features flanking this part of subject sequence:
   1376926 bp at 5' side: olfactomedin 4 precursor
   13516 bp at 3' side: similar to ribosomal protein L13a isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  1844458  ACACTGGAACTGA  1844446


 Features flanking this part of subject sequence:
   251349 bp at 5' side: similar to ribosomal protein L13a isoform 3
   2907831 bp at 3' side: protocadherin 17


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  2109934  TCACACTGGAACT  2109946


 Features flanking this part of subject sequence:
   1538274 bp at 5' side: similar to ribosomal protein L13a isoform 3
   1620906 bp at 3' side: protocadherin 17
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  3396871  CTGGAACTGAGAT  3396859


 Features flanking this part of subject sequence:
   2522784 bp at 5' side: similar to ribosomal protein L13a isoform 3
   636396 bp at 3' side: protocadherin 17


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9        GAACTGAGATACG  21
                |||||||||||||
Sbjct  4381381  GAACTGAGATACG  4381369


>ref|NT_079592.2|Hs7_79657 D Homo sapiens chromosome 7 genomic contig, alternate as
(based on CRA_TCAGchr7v2)
Length=58008433

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent :
                                                                   Query start position  Sul

 Features flanking this part of subject sequence:
   149931 bp at 5' side: hypothetical protein LOC399844
   56570 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  1       TCACACTGGAACTG  14
               ||||||||||||||
Sbjct  179310  TCACACTGGAACTG  179297


 Features flanking this part of subject sequence:
   171168 bp at 5' side: hypothetical protein LOC399844
   35334 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1       TCACACTGGAACT  13
               |||||||||||||
Sbjct  200546  TCACACTGGAACT  200534


 Features in this part of subject sequence:
   COX19 cytochrome c oxidase assembly homolog


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  1016397  ACTGGAACTGAGA  1016385


 Features in this part of subject sequence:
   MAD1-like 1 protein
   MAD1-like 1 protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7        TGGAACTGAGATA  19
                |||||||||||||
Sbjct  2023731  TGGAACTGAGATA  2023743
```

```
 Features in this part of subject sequence:
   TRIAD3 protein isoform a
   TRIAD3 protein isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  5706781  ACTGGAACTGAGA  5706769


 Features flanking this part of subject sequence:
   505951 bp at 5' side: neurexophilin 1 precursor
   473962 bp at 3' side: similar to C3 and PZP-like, alpha-2-macroglobulin domain .


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  9295684  ACACTGGAACTGA  9295696


 Features flanking this part of subject sequence:
   74918 bp at 5' side: PHD finger protein 14 isoform 2
   198217 bp at 3' side: similar to abnormal GONad development family member (gon-.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  11220597  TGGAACTGAGATA  11220609


 Features in this part of subject sequence:
   basic leucine zipper and W2 domains 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  16710942  CACTGGAACTGAG  16710954


 Features in this part of subject sequence:
   hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  17319639  TGGAACTGAGATA  17319627


 Features in this part of subject sequence:
   aryl hydrocarbon receptor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  17354032  AACTGAGATACGG  17354020


 Features in this part of subject sequence:
   sorting nexin 13
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  17878451  TCACACTGGAACT  17878439


 Features flanking this part of subject sequence:
   108176 bp at 5' side: putative binding protein 7a5
   60589 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  20311004  TGGAACTGAGATA  20311016


 Features in this part of subject sequence:
   parathyroid hormone-responsive B1 isoform 3
   parathyroid hormone-responsive B1 isoform 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  33554691  GGAACTGAGATAC  33554703


 Features flanking this part of subject sequence:
   167239 bp at 5' side: T-box transcription factor TBX20
   212527 bp at 3' side: HERPUD family member 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAGATAC  20
                 |||||| ||||||||||
Sbjct  35449569  CACTGGGACTGAGATAC  35449585


 Features in this part of subject sequence:
   cell division cycle 10 isoform 1
   cell division cycle 10 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  35879930  TGGAACTGAGATA  35879942


 Features flanking this part of subject sequence:
   439812 bp at 5' side: similar to CDC14 cell division cycle 14 homolog B
   289507 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  49398923  CACTGGAACTGAG  49398935


 Features in this part of subject sequence:
   growth factor receptor-bound protein 10 isoform a
   growth factor receptor-bound protein 10 isoform b
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  50708730  ACACTGGAACTGA  50708742


 Features flanking this part of subject sequence:
   41445 bp at 5' side: hypothetical protein LOC401337
   689764 bp at 3' side: hypothetical protein LOC222008


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  53876479  CACACTGGAACTG  53876467


 Features flanking this part of subject sequence:
   57330 bp at 5' side: similar to solute carrier family 29 (nucleoside transport..
   36464 bp at 3' side: similar to Zinc finger protein 479 (Zinc finger protein K..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  57105188  TGGAACTGAGATA  57105176


>ref|NW_923095.1|HsCraAADB02_257 D Homo sapiens chromosome 6 genomic contig, alter
(based on Celera assembly)
Length=6269147

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent 
                                                                    Query start position  Su

 Features in this part of subject sequence:
   KH domain-containing, RNA-binding, signal transduction-as...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  1        TCACACTGGAACTG  14
                ||||||||||||||
Sbjct  1210330  TCACACTGGAACTG  1210317


 Features flanking this part of subject sequence:
   98435 bp at 5' side: similar to notch homolog 5
   137188 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATA  19
                ||||||||||||||
Sbjct  4568040  CTGGAACTGAGATA  4568027


>ref|NW_921351.1|HsCraAADB02_10 D Homo sapiens chromosome 1 genomic contig, altern
(based on Celera assembly)
Length=57745789

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent 
                                                                    Query start position  Su

 Features in this part of subject sequence:
   microtubule associated serine/threonine kinase 2
```

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGAG  16
                 ||||||||||||||
Sbjct  20603149  ACACTGGAACTGAG  20603136


 Features flanking this part of subject sequence:
   33381 bp at 5' side: similar to fatty acid amide hydrolase
   28325 bp at 3' side: diencephalon/mesencephalon homeobox 1 isoform a


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
Sbjct  21092593  ACTGGAACTGAGAT  21092606


 Features in this part of subject sequence:
   phosphatidic acid phosphatase type 2B
   phosphatidic acid phosphatase type 2B


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGAT  18
                 ||||||||||||||
Sbjct  31174956  ACTGGAACTGAGAT  31174969


 Features in this part of subject sequence:
   protein tyrosine phosphatase, receptor type, U isoform 1 ...
   protein tyrosine phosphatase, receptor type, U isoform 2 ...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAGATAC  20
                ||||||||||| |||||
Sbjct  3874375  CACTGGAACTGGGATAC  3874391


 Features flanking this part of subject sequence:
   112734 bp at 5' side: pumilio 1 isoform 2
   10296 bp at 3' side: hypothetical protein LOC79570


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  5761519  CACTGGAACTGAG  5761531


 Features flanking this part of subject sequence:
   322391 bp at 5' side: HMG2 like isoform 2
   10704 bp at 3' side: hypothetical protein LOC84970


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTG  14
                |||||||||||||
Sbjct  8785367  CACACTGGAACTG  8785355


 Features flanking this part of subject sequence:
   422745 bp at 5' side: human immunodeficiency virus type I enhancer binding prot.
   145858 bp at 3' side: guanylate cyclase activator 2B (uroguanylin)
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  16616409  TCACACTGGAACT  16616397


 Features in this part of subject sequence:
   nuclease sensitive element binding protein 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  17299387  ACACTGGAACTGA  17299375


 Features flanking this part of subject sequence:
   70388 bp at 5' side: solute carrier family 2 (facilitated glucose transporter)..
   41596 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  17637673  TGGAACTGAGATA  17637661


 Features in this part of subject sequence:
   ATP/GTP binding protein-like 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  23589887  ACTGGAACTGAGA  23589875


 Features flanking this part of subject sequence:
   657119 bp at 5' side: hypothetical protein LOC79656
   692833 bp at 3' side: ELAV-like 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  24028806  TGGAACTGAGATA  24028794


 Features flanking this part of subject sequence:
   634049 bp at 5' side: hypothetical protein LOC127795
   375979 bp at 3' side: nuclear factor I/A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  35321987  CTGGAACTGAGAT  35321975


 Features in this part of subject sequence:
   nuclear factor I/A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  35931500  ACACTGGAACTGA  35931512


 Features flanking this part of subject sequence:
   34592 bp at 5' side: solute carrier family 35 (UDP-glucuronic acid/UDP-N-acety..
   4385 bp at 3' side: hypothetical protein LOC400757


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  41705131  CTGGAACTGAGAT  41705119


 Features flanking this part of subject sequence:
   1703 bp at 5' side: interleukin 12 receptor, beta 2 precursor
   15406 bp at 3' side: SERPINE1 mRNA binding protein 1 isoform 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  42014074  CTGGAACTGAGAT  42014086


 Features flanking this part of subject sequence:
   190492 bp at 5' side: DEP domain containing 1
   1072363 bp at 3' side: leucine rich repeat containing 7


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
Sbjct  43304264  AACTGAGATACGG  43304252


 Features flanking this part of subject sequence:
   70086 bp at 5' side: similar to Triosephosphate isomerase (TIM) (Triose-phosph..
   97018 bp at 3' side: sialyltransferase 7E


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  51336632  ACTGGAACTGAGA  51336644


>ref|NT_010641.15|Hs17_10798 D Homo sapiens chromosome 17 genomic contig, referenc
Length=11472733

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features in this part of subject sequence:
   ATP-binding cassette, sub-family A, member 6


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGAG  16
                ||||||||||||||
Sbjct  1044227  ACACTGGAACTGAG  1044240


 Features flanking this part of subject sequence:
   936094 bp at 5' side: potassium inwardly-rectifying channel J2
   508548 bp at 3' side: similar to Myosin light polypeptide 6 (Smooth muscle and .
```

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGAT  18
                ||||||||||||||
Sbjct  3034843  ACTGGAACTGAGAT  3034830


 Features flanking this part of subject sequence:
   84041 bp at 5' side: similar to R102.4b
   18079 bp at 3' side: suppressor of cytokine signaling 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  10262692  CACACTGGAACTG  10262680


 Features in this part of subject sequence:
   pleckstrin homology, Sec7 and coiled/coil domains 1 isofo...
   pleckstrin homology, Sec7 and coiled/coil domains 1 isofo...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  10699886  ACTGGAACTGAGA  10699898


>ref|NT_010498.15|Hs16_10655 D Homo sapiens chromosome 16 genomic contig, referenc
Length=42003582
                                                                  Sort alignments for this s
                                                                    E value  Score  Percent :
                                                                    Query start position  Sul

 Features flanking this part of subject sequence:
   194309 bp at 5' side: hypothetical protein
   446589 bp at 3' side: cerebellin 1 precursor


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACTG  14
                ||||||||||||||
Sbjct  2480912  TCACACTGGAACTG  2480925


 Features flanking this part of subject sequence:
   41150 bp at 5' side: zinc finger protein 423
   161468 bp at 3' side: hypothetical protein LOC255919


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACTG  14
                ||||||||||||||
Sbjct  3511945  TCACACTGGAACTG  3511958


 Features flanking this part of subject sequence:
   10484 bp at 5' side: cadherin 5, type 2 preproprotein
   98302 bp at 3' side: thymidine kinase 2, mitochondrial


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGATA  19
```

```
                 ||||||||||||||
Sbjct  20061755  CTGGAACTGAGATA  20061768


 Features in this part of subject sequence:
   c-Maf-inducing protein C-mip isoform
   c-Maf-inducing protein Tc-mip isoform


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  35163955  CACTGGAACTGAGA  35163942


 Features flanking this part of subject sequence:
   471322 bp at 5' side: hypothetical protein
   169577 bp at 3' side: cerebellin 1 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5        ACTGGAACTGAGA  17
                |||||||||||||
Sbjct  2757937  ACTGGAACTGAGA  2757925


 Features in this part of subject sequence:
   naked cuticle homolog 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  4218562  GGAACTGAGATAC  4218574


 Features flanking this part of subject sequence:
   444404 bp at 5' side: sal-like 1
   430712 bp at 3' side: hypothetical protein isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  5243755  CTGGAACTGAGAT  5243767


 Features flanking this part of subject sequence:
   523044 bp at 5' side: sal-like 1
   352072 bp at 3' side: hypothetical protein isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  5322395  TCACACTGGAACT  5322407


 Features flanking this part of subject sequence:
   35051 bp at 5' side: G-protein coupled receptor 114
   39687 bp at 3' side: G protein-coupled receptor 56 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  11258700  ACTGGAACTGAGA  11258712
```

```
 Features flanking this part of subject sequence:
   1370636 bp at 5' side: hypothetical protein LOC650767
   230579 bp at 3' side: similar to serine palmitoyltransferase subunit 1 isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  13774738  ACACTGGAACTGA  13774726


 Features flanking this part of subject sequence:
   19855 bp at 5' side: similar to nuclear pore membrane glycoprotein 121
   1274039 bp at 3' side: cadherin 8, type 2 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  14027660  TCACACTGGAACT  14027672


 Features flanking this part of subject sequence:
   50923 bp at 5' side: similar to nuclear pore membrane glycoprotein 121
   1242971 bp at 3' side: cadherin 8, type 2 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  14058728  ACTGGAACTGAGA  14058740


 Features flanking this part of subject sequence:
   1293874 bp at 5' side: similar to nuclear pore membrane glycoprotein 121
   20 bp at 3' side: cadherin 8, type 2 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  15301691  CACTGGAACTGAG  15301679


 Features in this part of subject sequence:
   hypothetical protein isoform 2
   hypothetical protein isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  19002590  ACTGGAACTGAGA  19002602


 Features in this part of subject sequence:
   chemokine-like factor superfamily 4 isoform 1
   chemokine-like factor superfamily 4 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  20298066  ACTGGAACTGAGA  20298054
```

```
  Features in this part of subject sequence:
    AT-binding transcription factor 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  26602575  ACACTGGAACTGA  26602587


  Features flanking this part of subject sequence:
    721700 bp at 5' side: hypothetical protein LOC388289
    431421 bp at 3' side: proteasome 26S non-ATPase subunit 7


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  27513579  CTGGAACTGAGAT  27513591


  Features flanking this part of subject sequence:
    1096489 bp at 5' side: hypothetical protein LOC388289
    56632 bp at 3' side: proteasome 26S non-ATPase subunit 7


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  27888368  ACACTGGAACTGA  27888380


  Features in this part of subject sequence:
    WD repeat domain 59


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  28607597  TCACACTGGAACT  28607609


  Features in this part of subject sequence:
    cadherin 13 preproprotein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  37266680  CACACTGGAACTG  37266668


>ref|NT_010274.16|Hs15_10431 D Homo sapiens chromosome 15 genomic contig, referenc
Length=13510195

                                                               Sort alignments for this s
                                                                 E value  Score  Percent 
                                                                 Query start position  Su

  Features flanking this part of subject sequence:
    1268524 bp at 5' side: hypothetical protein
    291345 bp at 3' side: neurotrophic tyrosine kinase, receptor, type 3 isoform a .


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus
```

```
Query  5        ACTGGAACTGAGAT  18
                ||||||||||||||
Sbjct  3094348  ACTGGAACTGAGAT  3094335


 Features in this part of subject sequence:
   mitochondrial ribosomal protein S11 isoform b
   mitochondrial ribosomal protein S11 isoform a


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  1        TCACACTGGAACTG  14
                ||||||||||||||
Sbjct  3984831  TCACACTGGAACTG  3984818


 Features flanking this part of subject sequence:
   190950 bp at 5' side: solute carrier organic anion transporter family, member 3A
   39967 bp at 3' side: ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  2        CACACTGGAACTGA  15
                ||||||||||||||
Sbjct  7862855  CACACTGGAACTGA  7862842


 Features flanking this part of subject sequence:
   100979 bp at 5' side: hypothetical protein
   74421 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3       ACACTGGAACTGA  15
               |||||||||||||
Sbjct  815024  ACACTGGAACTGA  815036


 Features flanking this part of subject sequence:
   801282 bp at 5' side: hypothetical protein
   758588 bp at 3' side: neurotrophic tyrosine kinase, receptor, type 3 isoform a .


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        GGAACTGAGATAC  20
                |||||||||||||
Sbjct  2627093  GGAACTGAGATAC  2627105


 Features in this part of subject sequence:
   IQ motif containing GTPase activating protein 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6        CTGGAACTGAGAT  18
                |||||||||||||
Sbjct  5957241  CTGGAACTGAGAT  5957253


 Features flanking this part of subject sequence:
   925897 bp at 5' side: hypothetical protein
   15938 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        AACTGAGATACGG  22
                 |||||||||||||
```

```
Sbjct  11762766  AACTGAGATACGG  11762754


>ref|NT_009952.14|Hs13_10109 D Homo sapiens chromosome 13 genomic contig, referenc
Length=25443670

                                                                Sort alignments for this s
                                                                  E value  Score  Percent 
                                                                  Query start position  Su

 Features flanking this part of subject sequence:
   142939 bp at 5' side: similar to CXXC finger 6
   3355376 bp at 3' side: glypican 5


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAGA  17
                ||||||||||||||
Sbjct  1785588  CACTGGAACTGAGA  1785601


 Features flanking this part of subject sequence:
   95784 bp at 5' side: hypothetical protein
   2088823 bp at 3' side: D-amino acid oxidase activator


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGATA  19
                 ||||||||||||||
Sbjct  17119491  CTGGAACTGAGATA  17119478


 Features in this part of subject sequence:
   glypican 6 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3        ACACTGGAACTGA  15
                |||||||||||||
Sbjct  7413487  ACACTGGAACTGA  7413475


 Features flanking this part of subject sequence:
   116885 bp at 5' side: serine/threonine kinase 24 (STE20 homolog, yeast) isoform 
   45975 bp at 3' side: solute carrier family 15 (oligopeptide transporter), memb..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  12380679  TCACACTGGAACT  12380667


 Features in this part of subject sequence:
   citrate lyase beta like
   citrate lyase beta like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  13440496  ACTGGAACTGAGA  13440484


 Features flanking this part of subject sequence:
   160834 bp at 5' side: hypothetical protein
   2023774 bp at 3' side: D-amino acid oxidase activator
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  17184540  CTGGAACTGAGAT  17184528


 Features flanking this part of subject sequence:
   1492946 bp at 5' side: hypothetical protein
   691662 bp at 3' side: D-amino acid oxidase activator


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  18516640  ACTGGAACTGAGA  18516652


 Features flanking this part of subject sequence:
   191483 bp at 5' side: hypothetical protein
   148333 bp at 3' side: DNA ligase IV


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         TCACACTGGAACT  13
                 |||||||||||||
Sbjct  21802212  TCACACTGGAACT  21802224


 Features flanking this part of subject sequence:
   214789 bp at 5' side: hypothetical protein
   148564 bp at 3' side: alpha 1 type IV collagen preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  23743822  ACACTGGAACTGA  23743810


>ref|NT_029419.11|Hs12_29578 D Homo sapiens chromosome 12 genomic contig, referenc
Length=38648979

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent 
                                                                    Query start position  Su

 Features in this part of subject sequence:
   PDZ domain containing RING finger 4


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query  5        ACTGGAACTGAGATACGG  22
                ||||||||| ||||||||
Sbjct  4000913  ACTGGAACTTAGATACGG  4000930


 Features flanking this part of subject sequence:
   63687 bp at 5' side: prickle-like 1
   817994 bp at 3' side: a disintegrin-like and metalloprotease (reprolysin type) .


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  3        ACACTGGAACTGAG  16
                ||||||||||||||
Sbjct  5073311  ACACTGGAACTGAG  5073324
```

```
 Features flanking this part of subject sequence:
   260357 bp at 5' side: transmembrane 4 superfamily member 3
   22033 bp at 3' side: leucine-rich repeat-containing G protein-coupled receptor 5


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATAC  20
                 ||||||||||||||
Sbjct  33955134  TGGAACTGAGATAC  33955121


 Features in this part of subject sequence:
   YY1 associated factor 2 isoform a
   YY1 associated factor 2 isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  4747555  CACTGGAACTGAG  4747567


 Features flanking this part of subject sequence:
   43317 bp at 5' side: YY1 associated factor 2 isoform b
   31558 bp at 3' side: zinc finger CCHC-type and RNA binding motif 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4        CACTGGAACTGAG  16
                |||||||||||||
Sbjct  4818605  CACTGGAACTGAG  4818617


 Features flanking this part of subject sequence:
   57351 bp at 5' side: developing brain homeobox 2
   64900 bp at 3' side: pleckstrin homology domain containing, family A (phosphoi..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  7645367  TCACACTGGAACT  7645379


 Features in this part of subject sequence:
   transmembrane protease, serine 12


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  13386307  ACTGGAACTGAGA  13386319


 Features in this part of subject sequence:
   SLIT-ROBO Rho GTPase-activating protein 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  26482807  CTGGAACTGAGAT  26482819


 Features in this part of subject sequence:
   leucine-rich repeat-containing G protein-coupled receptor 5
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  34089121  CACTGGAACTGAG  34089109


 Features flanking this part of subject sequence:
   569952 bp at 5' side: thyrotropin-releasing hormone degrading enzyme
   1809154 bp at 3' side: Shaw-related voltage-gated potassium channel protein 2 is


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  35770233  ACACTGGAACTGA  35770245


>ref|NT_007299.12|Hs6_7456 D Homo sapiens chromosome 6 genomic contig, reference as
Length=33500716

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent 
                                                                   Query start position  Su

 Features in this part of subject sequence:
   KH domain-containing, RNA-binding, signal transduction-as...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  1       TCACACTGGAACTG  14
               ||||||||||||||
Sbjct  343224  TCACACTGGAACTG  343211


 Features flanking this part of subject sequence:
   98434 bp at 5' side: similar to notch homolog 5
   137105 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  6        CTGGAACTGAGATA  19
                ||||||||||||||
Sbjct  3690342  CTGGAACTGAGATA  3690329


 Features flanking this part of subject sequence:
   113815 bp at 5' side: hypothetical protein
   119189 bp at 3' side: inhibitor of Bruton's tyrosine kinase


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  4         CACTGGAACTGAGA  17
                 ||||||||||||||
Sbjct  20582124  CACTGGAACTGAGA  20582111


 Features in this part of subject sequence:
   brain-specific angiogenesis inhibitor 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        TCACACTGGAACT  13
                |||||||||||||
Sbjct  7474391  TCACACTGGAACT  7474403
```

```
 Features flanking this part of subject sequence:
   573005 bp at 5' side: CD109
   689889 bp at 3' side: collagen, type XII, alpha 1 long isoform precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         ACTGGAACTGAGA  17
                 |||||||||||||
Sbjct  12926534  ACTGGAACTGAGA  12926546


 Features flanking this part of subject sequence:
   847645 bp at 5' side: 5-hydroxytryptamine (serotonin) receptor 1B
   556517 bp at 3' side: interleukin-1 receptor-associated kinase 1 binding protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6         CTGGAACTGAGAT  18
                 |||||||||||||
Sbjct  16840948  CTGGAACTGAGAT  16840936


 Features in this part of subject sequence:
   SH3 domain binding glutamic acid-rich protein like 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         CACTGGAACTGAG  16
                 |||||||||||||
Sbjct  18175344  CACTGGAACTGAG  18175356


 Features flanking this part of subject sequence:
   50825 bp at 5' side: SH3 domain binding glutamic acid-rich protein like 2
   166262 bp at 3' side: elongation of very long chain fatty acids (FEN1/Elo2, SUR.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         ACACTGGAACTGA  15
                 |||||||||||||
Sbjct  18280234  ACACTGGAACTGA  18280222


 Features flanking this part of subject sequence:
   1381196 bp at 5' side: branched chain keto acid dehydrogenase E1, beta polypepti
   24683 bp at 3' side: family with sequence similarity 46, member A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  20254900  GGAACTGAGATAC  20254888


 Features flanking this part of subject sequence:
   497932 bp at 5' side: 5T4 oncofetal trophoblast glycoprotein
   28856 bp at 3' side: hypothetical protein LOC90025


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         TGGAACTGAGATA  19
                 |||||||||||||
Sbjct  21394056  TGGAACTGAGATA  21394044


 Features flanking this part of subject sequence:
```

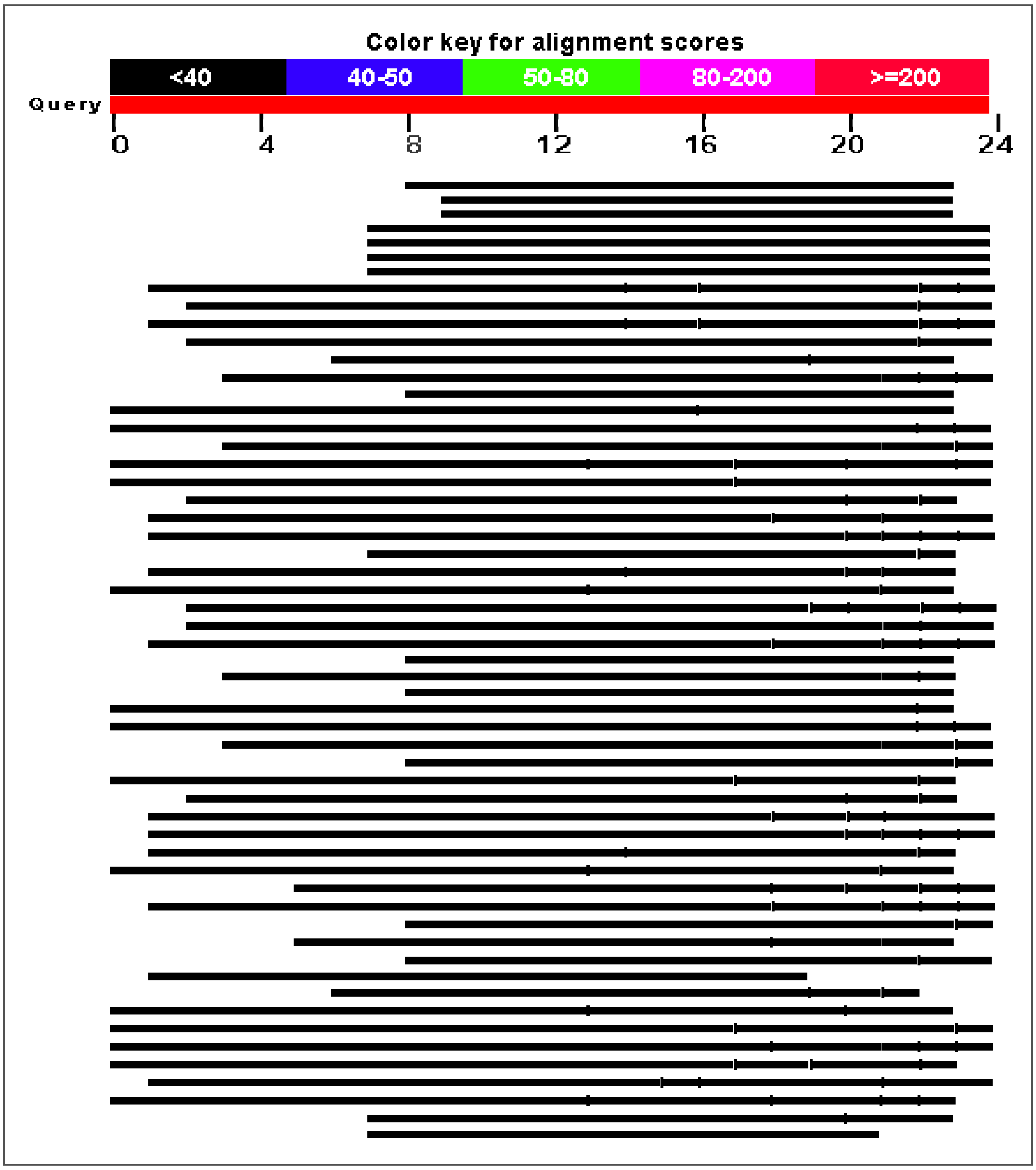
```
    250779 bp at 5' side: similar to T-box transcription factor TBX18 (T-box protei.
    242410 bp at 3' side: similar to ribosomal protein L31


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  23544849  CACACTGGAACTG  23544861


  Features flanking this part of subject sequence:
    41465 bp at 5' side: glycoprotein hormones, alpha polypeptide precursor
    25915 bp at 3' side: similar to Zinc finger protein 292 isoform 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  25659566  GGAACTGAGATAC  25659554


  Features in this part of subject sequence:
    RNA guanylyltransferase and 5'-phosphatase


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  8         GGAACTGAGATAC  20
                 |||||||||||||
Sbjct  27264076  GGAACTGAGATAC  27264088


  Features in this part of subject sequence:
    RNA guanylyltransferase and 5'-phosphatase


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  2         CACACTGGAACTG  14
                 |||||||||||||
Sbjct  27438460  CACACTGGAACTG  27438448


>ref|NT_022517.17|Hs3_22673 D Homo sapiens chromosome 3 genomic contig, reference
Length=66080833

  Features flanking this part of subject sequence:
    24953 bp at 5' side: inositol 1,4,5-triphosphate receptor, type 1
    108529 bp at 3' side: basic helix-loop-helix domain containing, class B, 2


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

Query  5        ACTGGAACTGAGAT  18
                ||||||||||||||
Sbjct  4852875  ACTGGAACTGAGAT  4852862
```

Genome View

Show positions of the BLAST hits in the human genome using the Entrez Genomes MapViewer

Query= BorrprimerA Length=24

Distribution of 1214 Blast Hits on the Query Sequence



Distance tree of results NEW

Legend for links to other resources: U UniGene E GEO G Gene S Structure M M

Sequences producing significant alignments:
(Click headers to sort columns)

Transcripts

NM_197965.1	Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 6 (SLC10A6), mRNA	30.2	30.2	62%	28	100%	UEGM
NM_173484.2	Homo sapiens Kruppel-like factor 17 (KLF17), mRNA	28.2	28.2	58%	112	100%	
NM_004155.3	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 9 (SERPINB9), mRNA	28.2	28.2	58%	112	100%	UEGM

Genomic sequences [show first]

NW_927195.1	Homo sapiens chromosome 19 genomic contig, alternate assembly (based on Celera assembly)	34.2	193	70%	1.8	100%
NW_927284.1	Homo sapiens chromosome 19 genomic contig, alternate assembly (based on Celera assembly)	34.2	197	70%	1.8	100%
NT_011295.10	Homo sapiens chromosome 19 genomic contig, reference assembly	34.2	193	70%	1.8	100%
NT_011109.15	Homo sapiens chromosome 19 genomic contig, reference assembly	34.2	460	70%	1.8	100%
NW_924062.1	Homo sapiens chromosome 9 genomic contig, alternate assembly (based on Celera assembly)	32.2	512	95%	7.2	100%
NW_922462.1	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on Celera assembly)	32.2	167	91%	7.2	100%
NT_008413.17	Homo sapiens chromosome 9 genomic contig, reference assembly	32.2	486	95%	7.2	100%
NT_019273.18	Homo sapiens chromosome 1 genomic contig, reference assembly	32.2	195	91%	7.2	100%
NW_927713.1	Homo sapiens chromosome X genomic contig, alternate assembly (based on Celera assembly)	30.2	135	70%	28	100%
NW_927700.1	Homo sapiens chromosome X genomic contig, alternate assembly (based on Celera assembly)	30.2	458	87%	28	100%
NW_927406.1	Homo sapiens chromosome 22 genomic contig, alternate assembly (based on Celera assembly)	30.2	30.2	62%	28	100%
NW_927106.1	Homo sapiens chromosome 18 genomic contig, alternate assembly (based on Celera assembly)	30.2	216	95%	28	100%
NW_925884.1	Homo sapiens chromosome 15 genomic contig, alternate assembly (based on Celera assembly)	30.2	484	100%	28	100%
NW_925561.1	Homo sapiens chromosome 14 genomic contig, alternate assembly (based on Celera assembly)	30.2	508	87%	28	100%
NW_925395.1	Homo sapiens chromosome 12 genomic contig, alternate assembly (based on Celera assembly)	30.2	615	100%	28	100%

NW_925106.1	Homo sapiens chromosome 11 genomic contig, alternate assembly (based on Celera assembly)	30.2	296	100%	28	100%
NW_924884.1	Homo sapiens chromosome 10 genomic contig, alternate assembly (based on Celera assembly)	30.2	294	87%	28	100%
NW_924484.1	Homo sapiens chromosome 9 genomic contig, alternate assembly (based on Celera assembly)	30.2	189	95%	28	100%
NW_923929.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on Celera assembly)	30.2	397	95%	28	100%
NW_922984.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on Celera assembly)	30.2	323	66%	28	100%
NW_922217.1	Homo sapiens chromosome 4 genomic contig, alternate assembly (based on Celera assembly)	30.2	482	91%	28	100%
NW_922162.1	Homo sapiens chromosome 4 genomic contig, alternate assembly (based on Celera assembly)	30.2	539	95%	28	100%
NW_921651.1	Homo sapiens chromosome 3 genomic contig, alternate assembly (based on Celera assembly)	30.2	914	91%	28	100%
NW_925683.1	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on Celera assembly)	30.2	112	91%	28	100%
NW_926128.1	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on Celera assembly)	30.2	426	95%	28	100%
NT_011669.16	Homo sapiens chromosome X genomic contig, reference assembly	30.2	58.5	62%	28	100%
NT_011757.15	Homo sapiens chromosome X genomic contig, reference assembly	30.2	432	83%	28	100%
NT_011519.10	Homo sapiens chromosome 22 genomic contig, reference assembly	30.2	56.5	62%	28	100%
NT_025028.13	Homo sapiens chromosome 18 genomic contig, reference assembly	30.2	187	95%	28	100%
NT_010194.16	Homo sapiens chromosome 15 genomic contig, reference assembly	30.2	751	100%	28	100%
NT_026437.11	Homo sapiens chromosome 14 genomic contig, reference assembly	30.2	850	87%	28	100%
NT_009775.16	Homo sapiens chromosome 12 genomic contig, reference assembly	30.2	165	66%	28	100%
NT_033927.7	Homo sapiens chromosome 11 genomic contig, reference assembly	30.2	189	95%	28	100%
NT_030059.12	Homo sapiens chromosome 10 genomic contig, reference assembly	30.2	321	87%	28	100%
NT_008470.18	Homo sapiens chromosome 9 genomic contig, reference assembly	30.2	373	95%	28	100%
NT_008183.18	Homo sapiens chromosome 8 genomic contig, reference assembly	30.2	397	95%	28	100%
NT_007592.14	Homo sapiens chromosome 6 genomic contig, reference assembly	30.2	478	91%	28	100%
NT_016354.18	Homo sapiens chromosome 4 genomic contig, reference assembly	30.2	809	95%	28	100%
NT_022517.17	Homo sapiens chromosome 3 genomic contig, reference assembly	30.2	755	79%	28	100%
NT_004487.18	Homo sapiens chromosome 1 genomic contig, reference assembly	30.2	512	95%	28	100%
NW_926584.1	Homo sapiens chromosome 17 genomic contig, alternate assembly (based on Celera assembly)	28.2	107	66%	112	100%

NW_926462.1	Homo sapiens chromosome 16 genomic contig, alternate assembly (based on Celera assembly)	28.2	185	75%	112	100%
NW_926528.1	Homo sapiens chromosome 16 genomic contig, alternate assembly (based on Celera assembly)	28.2	214	66%	112	100%
NW_925851.1	Homo sapiens chromosome 15 genomic contig, alternate assembly (based on Celera assembly)	28.2	28.2	75%	112	94%
NW_925840.1	Homo sapiens chromosome 15 genomic contig, alternate assembly (based on Celera assembly)	28.2	107	66%	112	100%
NW_925506.1	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on Celera assembly)	28.2	159	95%	112	100%
NW_925473.1	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on Celera assembly)	28.2	290	100%	112	100%
NW_925517.1	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on Celera assembly)	28.2	343	100%	112	100%
NW_925295.1	Homo sapiens chromosome 12 genomic contig, alternate assembly (based on Celera assembly)	28.2	264	95%	112	100%
NW_925006.1	Homo sapiens chromosome 11 genomic contig, alternate assembly (based on Celera assembly)	28.2	478	95%	112	100%
NW_925173.1	Homo sapiens chromosome 11 genomic contig, alternate assembly (based on Celera assembly)	28.2	500	95%	112	100%
NW_924796.1	Homo sapiens chromosome 10 genomic contig, alternate assembly (based on Celera assembly)	28.2	187	66%	112	100%
NW_924606.1	Homo sapiens chromosome 10 genomic contig, alternate assembly (based on Celera assembly)	28.2	28.2	58%	112	100%
NW_924584.1	Homo sapiens chromosome 10 genomic contig, alternate assembly (based on Celera assembly)	28.2	478	91%	112	100%
NW_924573.1	Homo sapiens chromosome 9 genomic contig, alternate assembly (based on Celera assembly)	28.2	212	66%	112	100%
NW_924539.1	Homo sapiens chromosome 9 genomic contig, alternate assembly (based on Celera assembly)	28.2	133	62%	112	100%
NW_923873.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on Celera assembly)	28.2	54.5	58%	112	100%
NW_923984.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on Celera assembly)	28.2	557	95%	112	100%
NW_923796.1	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on Celera assembly)	28.2	54.5	58%	112	100%
NT_079595.2	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on CRA_TCAGchr7v2)	28.2	395	91%	112	100%
NW_923240.1	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on Celera assembly)	28.2	133	83%	112	100%
NW_923707.1	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on Celera assembly)	28.2	54.5	58%	112	100%
NW_923640.1	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on Celera assembly)	28.2	371	91%	112	100%

NT_079592.2	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on CRA_TCAGchr7v2)	28.2	238	83%	112	100%
NW_923574.1	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on Celera assembly)	28.2	343	91%	112	100%
NT_079596.2	Homo sapiens chromosome 7 genomic contig, alternate assembly (based on CRA_TCAGchr7v2)	28.2	506	91%	112	100%
NW_923184.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on Celera assembly)	28.2	878	91%	112	100%
NW_923095.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on Celera assembly)	28.2	54.5	79%	112	100%
NW_922607.1	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on Celera assembly)	28.2	109	95%	112	100%
NW_922596.1	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on Celera assembly)	28.2	216	66%	112	100%
NW_922784.1	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on Celera assembly)	28.2	450	100%	112	100%
NW_922562.1	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on Celera assembly)	28.2	107	87%	112	100%
NW_922518.1	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on Celera assembly)	28.2	82.8	62%	112	100%
NW_922729.1	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on Celera assembly)	28.2	214	62%	112	100%
NW_922073.1	Homo sapiens chromosome 4 genomic contig, alternate assembly (based on Celera assembly)	28.2	397	95%	112	100%
NW_921751.1	Homo sapiens chromosome 3 genomic contig, alternate assembly (based on Celera assembly)	28.2	159	58%	112	100%
NW_921807.1	Homo sapiens chromosome 3 genomic contig, alternate assembly (based on Celera assembly)	28.2	587	95%	112	100%
NW_921585.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on Celera assembly)	28.2	500	83%	112	100%
NW_927719.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on Celera assembly)	28.2	743	100%	112	100%
NW_921618.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on Celera assembly)	28.2	424	91%	112	100%
NW_922017.1	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on Celera assembly)	28.2	28.2	58%	112	100%
NW_923572.1	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on Celera assembly)	28.2	80.8	58%	112	100%
NW_921351.1	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on Celera assembly)	28.2	563	95%	112	100%
NW_927128.1	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on Celera assembly)	28.2	242	70%	112	100%
NT_079573.3	Homo sapiens chromosome X genomic contig, reference assembly	28.2	238	100%	112	100%

NT_010783.14	Homo sapiens chromosome 17 genomic contig, reference assembly	28.2	159	91%	112	100%
NT_010498.15	Homo sapiens chromosome 16 genomic contig, reference assembly	28.2	399	79%	112	100%
NT_009952.14	Homo sapiens chromosome 13 genomic contig, reference assembly	28.2	343	100%	112	100%
NT_024524.13	Homo sapiens chromosome 13 genomic contig, reference assembly	28.2	634	100%	112	100%
NT_029419.11	Homo sapiens chromosome 12 genomic contig, reference assembly	28.2	238	95%	112	100%
NT_025741.14	Homo sapiens chromosome 6 genomic contig, reference assembly	28.2	478	91%	112	100%
NT_005612.15	Homo sapiens chromosome 3 genomic contig, reference assembly	28.2	587	95%	112	100%
NT_022459.14	Homo sapiens chromosome 3 genomic contig, reference assembly	28.2	345	91%	112	100%
NT_005334.15	Homo sapiens chromosome 2 genomic contig, reference assembly	28.2	109	95%	112	100%
NT_005403.16	Homo sapiens chromosome 2 genomic contig, reference assembly	28.2	818	91%	112	100%
NT_022184.14	Homo sapiens chromosome 2 genomic contig, reference assembly	28.2	581	95%	112	100%
NT_022135.15	Homo sapiens chromosome 2 genomic contig, reference assembly	28.2	238	66%	112	100%

Alignments

```
>ref|NM_197965.1| UEGM Homo sapiens solute carrier family 10 (sodium/bile acid c
family), member 6 (SLC10A6), mRNA
Length=1134

 GENE ID: 345274 SLC10A6 | solute carrier family 10 (sodium/bile acid
cotransporter family), member 6 [Homo sapiens] (10 or fewer PubMed links)


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  9     ACCTTCTTCATTCAC  23
             |||||||||||||||
Sbjct  1053  ACCTTCTTCATTCAC  1039


>ref|NM_173484.2|  Homo sapiens Kruppel-like factor 17 (KLF17), mRNA
Length=3188


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10    CCTTCTTCATTCAC  23
             ||||||||||||||
Sbjct  1242  CCTTCTTCATTCAC  1229


>ref|NM_004155.3| UEGM Homo sapiens serpin peptidase inhibitor, clade B (ovalbum
member 9 (SERPINB9), mRNA
Length=4121

 GENE ID: 5272 SERPINB9 | serpin peptidase inhibitor, clade B (ovalbumin),
member 9 [Homo sapiens] (Over 10 PubMed links)


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10    CCTTCTTCATTCAC  23
             ||||||||||||||
Sbjct  1060  CCTTCTTCATTCAC  1047


>ref|NW_927195.1|HsCraAADB02_626 D Homo sapiens chromosome 19 genomic contig, alte
(based on Celera assembly)
Length=15589000

                                                              Sort alignments for this s
                                                                E value  Score  Percent 
                                                                Query start position  Su

 Features flanking this part of subject sequence:
   39278 bp at 5' side: zinc finger protein 560
   13776 bp at 3' side: zinc finger protein 426


 Score = 34.2 bits (17),  Expect = 1.8
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  8       GACCTTCTTCATTCACG  24
               |||||||||||||||||
Sbjct  736972  GACCTTCTTCATTCACG  736988


 Features flanking this part of subject sequence:
   67541 bp at 5' side: zinc finger protein 91
   192353 bp at 3' side: zinc finger protein 675


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
```

```
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  14696362  CCTTCTTCATTCAC  14696349


 Features flanking this part of subject sequence:
   56527 bp at 5' side: mucin 16
   53872 bp at 3' side: olfactory receptor, family 1, subfamily M, member 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11      CTTCTTCATTCAC  23
               |||||||||||||
Sbjct  261728  CTTCTTCATTCAC  261740


 Features flanking this part of subject sequence:
   8591 bp at 5' side: zinc finger protein 627
   21866 bp at 3' side: similar to Zinc finger protein 20 (Zinc finger protein KO..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  8        GACCTTCTTCATTCACG  24
                |||||||||| ||||||
Sbjct  2847708  GACCTTCTTCGTTCACG  2847724


 Features flanking this part of subject sequence:
   9873 bp at 5' side: similar to zinc finger protein 700
   22405 bp at 3' side: zinc finger protein 439


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  3065187  CCTTCTTCATTCA  3065175


 Features flanking this part of subject sequence:
   20527 bp at 5' side: DnaJ (Hsp40) homolog, subfamily B, member 1
   23652 bp at 3' side: similar to Synaptic glycoprotein SC2 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8        GACCTTCTTCATT  20
                |||||||||||||
Sbjct  5760073  GACCTTCTTCATT  5760061


 Features flanking this part of subject sequence:
   26386 bp at 5' side: bromodomain-containing protein 4 isoform short
   55414 bp at 3' side: A-kinase anchor protein 8


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  6522205  CTTCTTCATTCAC  6522193


>ref|NW_927284.1|HsCraAADB02_634 D Homo sapiens chromosome 19 genomic contig, alte
(based on Celera assembly)
Length=8450095

                                                                Sort alignments for this s
                                                                  E value  Score  Percent
                                                                  Query start position  Su
```

```
 Features flanking this part of subject sequence:
   2123 bp at 5' side: zinc finger protein 350
   16380 bp at 3' side: zinc finger protein 615


 Score = 34.2 bits (17),  Expect = 1.8
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  8        GACCTTCTTCATTCACG  24
                |||||||||||||||||
Sbjct  1836595  GACCTTCTTCATTCACG  1836579


 Features in this part of subject sequence:
   myosin, heavy polypeptide 14


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  8       GACCTTCTTCATTCA  22
               |||||||||||||||
Sbjct  104203  GACCTTCTTCATTCA  104217


 Features flanking this part of subject sequence:
   35014 bp at 5' side: zinc finger protein 447
   3184 bp at 3' side: zinc finger protein 329


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  7987279  CCTTCTTCATTCAC  7987266


 Features in this part of subject sequence:
   hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8        GACCTTCTTCATT  20
                |||||||||||||
Sbjct  1561779  GACCTTCTTCATT  1561767


 Features flanking this part of subject sequence:
   41834 bp at 5' side: formyl peptide receptor-like 1
   12188 bp at 3' side: formyl peptide receptor-like 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  1671645  CTTCTTCATTCAC  1671657


 Features flanking this part of subject sequence:
   5577 bp at 5' side: hypothetical protein LOC374928
   14553 bp at 3' side: zinc finger protein 549


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  7375240  CCTTCTTCATTCA  7375252


 Features flanking this part of subject sequence:
   5629 bp at 5' side: hypothetical protein LOC374928
```

```
   14497 bp at 3' side: zinc finger protein 549


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  8        GACCTTCTTCATTCACG  24
                ||||||||||| |||||
Sbjct  7375308  GACCTTCTTCACTCACG  7375292


>ref|NT_011295.10|Hs19_11452 D Homo sapiens chromosome 19 genomic contig, referenc
Length=15825424
                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   39276 bp at 5' side: zinc finger protein 560
   13775 bp at 3' side: zinc finger protein 426


 Score = 34.2 bits (17),  Expect = 1.8
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  8       GACCTTCTTCATTCACG  24
               |||||||||||||||||
Sbjct  888067  GACCTTCTTCATTCACG  888083


 Features flanking this part of subject sequence:
   67585 bp at 5' side: zinc finger protein 91
   190274 bp at 3' side: zinc finger protein 675


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  14839396  CCTTCTTCATTCAC  14839383


 Features flanking this part of subject sequence:
   58794 bp at 5' side: mucin 16
   53301 bp at 3' side: olfactory receptor, family 1, subfamily M, member 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11      CTTCTTCATTCAC  23
               |||||||||||||
Sbjct  413410  CTTCTTCATTCAC  413422


 Features flanking this part of subject sequence:
   8592 bp at 5' side: zinc finger protein 627
   58730 bp at 3' side: hypothetical protein LOC401898


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  8        GACCTTCTTCATTCACG  24
                |||||||||| ||||||
Sbjct  3000098  GACCTTCTTCGTTCACG  3000114


 Features flanking this part of subject sequence:
   9870 bp at 5' side: similar to Zinc finger protein 440
   22402 bp at 3' side: zinc finger protein 439


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  3217372  CCTTCTTCATTCA  3217360


 Features in this part of subject sequence:
   glycoprotein, synaptic 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8        GACCTTCTTCATT  20
                |||||||||||||
Sbjct  5912476  GACCTTCTTCATT  5912464


 Features flanking this part of subject sequence:
   26391 bp at 5' side: bromodomain-containing protein 4 isoform short
   55413 bp at 3' side: A-kinase anchor protein 8


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  6673115  CTTCTTCATTCAC  6673103


>ref|NT_011109.15|Hs19_11266 D Homo sapiens chromosome 19 genomic contig, referenc
Length=31383029
                                                                 Sort alignments for this s
                                                                   E value  Score  Percent :
                                                                   Query start position  Su

 Features flanking this part of subject sequence:
   2123 bp at 5' side: zinc finger protein 350
   16381 bp at 3' side: zinc finger protein 615


 Score = 34.2 bits (17),  Expect = 1.8
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTCACG  24
                 |||||||||||||||||
Sbjct  24747942  GACCTTCTTCATTCACG  24747926


 Features in this part of subject sequence:
   myosin, heavy polypeptide 14


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTCA  22
                 |||||||||||||||
Sbjct  23015239  GACCTTCTTCATTCA  23015253


 Features flanking this part of subject sequence:
   34414 bp at 5' side: zinc finger protein 447
   3184 bp at 3' side: zinc finger protein 329


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  30904251  CCTTCTTCATTCAC  30904238


 Features flanking this part of subject sequence:
   59164 bp at 5' side: hypothetical protein
   943271 bp at 3' side: zinc finger protein 507
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  4168684  CCTTCTTCATTCA  4168672


 Features flanking this part of subject sequence:
   649314 bp at 5' side: hypothetical protein
   353121 bp at 3' side: zinc finger protein 507


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  4758834  ACCTTCTTCATTC  4758822


 Features flanking this part of subject sequence:
   15037 bp at 5' side: carcinoembryonic antigen-related cell adhesion molecule
   17838 bp at 3' side: carcinoembryonic antigen-related cell adhesion molecule 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  14376083  CTTCTTCATTCAC  14376071


 Features in this part of subject sequence:
   carcinoembryonic antigen-related cell adhesion molecule 7


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  14459032  CTTCTTCATTCAC  14459044


 Features in this part of subject sequence:
   carcinoembryonic antigen-related cell adhesion molecule 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  14482152  CTTCTTCATTCAC  14482140


 Features in this part of subject sequence:
   carcinoembryonic antigen-related cell adhesion molecule 6...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  14529061  CTTCTTCATTCAC  14529049


 Features in this part of subject sequence:
   carcinoembryonic antigen-related cell adhesion molecule 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  14570074  CTTCTTCATTCAC  14570062


 Features in this part of subject sequence:
   carcinoembryonic antigen-related cell adhesion molecule 1...
   carcinoembryonic antigen-related cell adhesion molecule 1...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  15299435  CTTCTTCATTCAC  15299447


 Features in this part of subject sequence:
   zinc finger protein 226 isoform b
   zinc finger protein 226 isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  16945797  CCTTCTTCATTCA  16945809


 Features in this part of subject sequence:
   testis-specific kinase substrate


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  22534243  CTTCTTCATTCAC  22534255


 Features in this part of subject sequence:
   hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  24473150  GACCTTCTTCATT  24473138


 Features flanking this part of subject sequence:
   41836 bp at 5' side: formyl peptide receptor-like 1
   12187 bp at 3' side: formyl peptide receptor-like 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  24582993  CTTCTTCATTCAC  24583005


 Features flanking this part of subject sequence:
   5584 bp at 5' side: hypothetical protein LOC374928
   14554 bp at 3' side: zinc finger protein 549


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  30292566  CCTTCTTCATTCA  30292578
```

```
 Features flanking this part of subject sequence:
   5636 bp at 5' side: hypothetical protein LOC374928
   14498 bp at 3' side: zinc finger protein 549


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTCACG  24
                 ||||||||||| |||||
Sbjct  30292634  GACCTTCTTCACTCACG  30292618


>ref|NW_924062.1|HsCraAADB02_344 D Homo sapiens chromosome 9 genomic contig, alter
(based on Celera assembly)
Length=38596040

                                                              Sort alignments for this s
                                                                E value  Score  Percent 
                                                                Query start position  Su

 Features flanking this part of subject sequence:
   878472 bp at 5' side: hypothetical protein
   1202003 bp at 3' side: tyrosinase-related protein 1


 Score = 32.2 bits (16),  Expect = 7.2
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query  7         CGACCTTCTTCATTCA  22
                 ||||||||||||||||
Sbjct  11309095  CGACCTTCTTCATTCA  11309110


 Features in this part of subject sequence:
   GLIS family zinc finger 3


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  3633978  CCTTCTTCATTCAC  3633965


 Features in this part of subject sequence:
   hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  13235773  GACCTTCTTCATTC  13235786


 Features flanking this part of subject sequence:
   516035 bp at 5' side: similar to Nonhistone chromosomal protein HMG-17 (High-mo.
   307427 bp at 3' side: basonuclin 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  15923051  GACCTTCTTCATTC  15923038


 Features flanking this part of subject sequence:
   155702 bp at 5' side: SH3-domain GRB2-like 2
   519943 bp at 3' side: ADAMTS-like 1 isoform 1


 Score = 28.2 bits (14),  Expect =   112
```

```
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCACG  24
                 ||||||||||||||
Sbjct  17764498  CTTCTTCATTCACG  17764511


 Features flanking this part of subject sequence:
   361116 bp at 5' side: regulatory factor X3 isoform a
   71258 bp at 3' side: GLIS family zinc finger 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  3559485  CTTCTTCATTCAC  3559497


 Features flanking this part of subject sequence:
   1338989 bp at 5' side: protein tyrosine phosphatase, receptor type, D isoform 1
   538576 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2        TCTTTCGACCTTC  14
                |||||||||||||
Sbjct  9891742  TCTTTCGACCTTC  9891730


 Features flanking this part of subject sequence:
   479476 bp at 5' side: hypothetical protein
   177941 bp at 3' side: nuclear factor I/B


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  13728417  ACCTTCTTCATTC  13728429


 Features flanking this part of subject sequence:
   677514 bp at 5' side: similar to Nonhistone chromosomal protein HMG-17 (High-mo.
   145949 bp at 3' side: basonuclin 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  16084529  CCTTCTTCATTCA  16084517


 Features in this part of subject sequence:
   hypothetical protein LOC54914


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  20805543  ACCTTCTTCATTC  20805531


 Features flanking this part of subject sequence:
   40542 bp at 5' side: similar to F59E12.9
   251210 bp at 3' side: DMRT-like family A1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  22018663  GACCTTCTTCATT  22018675


 Features flanking this part of subject sequence:
   58505 bp at 5' side: similar to F59E12.9
   233247 bp at 3' side: DMRT-like family A1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  22036638  CTTCTTCATTCAC  22036626


 Features flanking this part of subject sequence:
   494006 bp at 5' side: DMRT-like family A1
   730935 bp at 3' side: ELAV (embryonic lethal, abnormal vision, Drosophila)-like.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  22768736  ACCTTCTTCATTC  22768748


 Features flanking this part of subject sequence:
   1006127 bp at 5' side: DMRT-like family A1
   218814 bp at 3' side: ELAV (embryonic lethal, abnormal vision, Drosophila)-like.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         TTTCGACCTTCTT  16
                 |||||||||||||
Sbjct  23280857  TTTCGACCTTCTT  23280869


 Features flanking this part of subject sequence:
   578693 bp at 5' side: ELAV (embryonic lethal, abnormal vision, Drosophila)-like.
   1341174 bp at 3' side: tumor suppressor candidate 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  24148056  ACCTTCTTCATTC  24148068


 Features flanking this part of subject sequence:
   665769 bp at 5' side: ELAV (embryonic lethal, abnormal vision, Drosophila)-like.
   1254098 bp at 3' side: tumor suppressor candidate 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  24235144  GACCTTCTTCATT  24235132


 Features flanking this part of subject sequence:
   1518714 bp at 5' side: hypothetical protein
   723185 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  29480448  ACCTTCTTCATTC  29480460


 Features flanking this part of subject sequence:
   2091979 bp at 5' side: hypothetical protein
   149920 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  30053725  CCTTCTTCATTCA  30053713


 Features flanking this part of subject sequence:
   22773 bp at 5' side: zinc finger, CCHC domain containing 7
   42710 bp at 3' side: glyoxylate reductase/hydroxypyruvate reductase


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  37197791  CCTTCTTCATTCA  37197779


>ref|NW_922462.1|HsCraAADB02_20 D Homo sapiens chromosome 1 genomic contig, altern
(based on Celera assembly)
Length=11481316

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent 
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   14383 bp at 5' side: epidermal growth factor receptor pathway substrate 8-like..
   134862 bp at 3' side: colony stimulating factor 1 isoform a precursor


 Score = 32.2 bits (16),  Expect = 7.2
 Identities = 19/20 (95%), Gaps = 0/20 (0%)
 Strand=Plus/Minus

Query  3        CTTTCGACCTTCTTCATTCA  22
                ||||| ||||||||||||||
Sbjct  1283598  CTTTCTACCTTCTTCATTCA  1283579


 Features in this part of subject sequence:
   G-protein signalling modulator 2 (AGS3-like, C. elegans)


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  7       CGACCTTCTTCATT  20
               ||||||||||||||
Sbjct  441655  CGACCTTCTTCATT  441642


 Features flanking this part of subject sequence:
   148271 bp at 5' side: mitochondrial tryptophanyl tRNA synthetase 2 isoform 2 pr.
   92136 bp at 3' side: hydroxyacid oxidase 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  10780606  ACCTTCTTCATTCA  10780593


 Features in this part of subject sequence:
   G-protein signalling modulator 2 (AGS3-like, C. elegans)
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8       GACCTTCTTCATT  20
               |||||||||||||
Sbjct  441989  GACCTTCTTCATT  441977


 Features in this part of subject sequence:
   CD53 antigen
   CD53 antigen


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12       TTCTTCATTCACG  24
                |||||||||||||
Sbjct  2405503  TTCTTCATTCACG  2405515


 Features flanking this part of subject sequence:
   356936 bp at 5' side: nerve growth factor, beta polypeptide precursor
   7595 bp at 3' side: vang-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  7133494  CCTTCTTCATTCA  7133482


>ref|NT_008413.17|Hs9_8570 D Homo sapiens chromosome 9 genomic contig, reference as
Length=39653686

                                                                Sort alignments for this s
                                                                  E value  Score  Percent :
                                                                  Query start position  Sul

 Features flanking this part of subject sequence:
   878523 bp at 5' side: hypothetical protein
   1202088 bp at 3' side: tyrosinase-related protein 1


 Score = 32.2 bits (16),  Expect = 7.2
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query  7         CGACCTTCTTCATTCA  22
                 ||||||||||||||||
Sbjct  11481894  CGACCTTCTTCATTCA  11481909


 Features in this part of subject sequence:
   GLIS family zinc finger 3


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  3821495  CCTTCTTCATTCAC  3821482


 Features in this part of subject sequence:
   hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  13408232  GACCTTCTTCATTC  13408245
```

```
 Features flanking this part of subject sequence:
   522604 bp at 5' side: similar to Nonhistone chromosomal protein HMG-17 (High-mo.
   307757 bp at 3' side: basonuclin 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  16101230  GACCTTCTTCATTC  16101217


 Features flanking this part of subject sequence:
   158265 bp at 5' side: SH3-domain GRB2-like 2
   520212 bp at 3' side: ADAMTS-like 1 isoform 3


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCACG  24
                 ||||||||||||||
Sbjct  17944006  CTTCTTCATTCACG  17944019


 Features flanking this part of subject sequence:
   361093 bp at 5' side: regulatory factor X3 isoform a
   71579 bp at 3' side: GLIS family zinc finger 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  3746681  CTTCTTCATTCAC  3746693


 Features flanking this part of subject sequence:
   1338644 bp at 5' side: protein tyrosine phosphatase, receptor type, D isoform 4
   540567 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         TCTTTCGACCTTC  14
                 |||||||||||||
Sbjct  10062499  TCTTTCGACCTTC  10062487


 Features flanking this part of subject sequence:
   479784 bp at 5' side: hypothetical protein
   177112 bp at 3' side: nuclear factor I/B


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  13901184  ACCTTCTTCATTC  13901196


 Features flanking this part of subject sequence:
   684071 bp at 5' side: similar to Nonhistone chromosomal protein HMG-17 (High-mo.
   146291 bp at 3' side: basonuclin 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  16262696  CCTTCTTCATTCA  16262684
```

```
 Features in this part of subject sequence:
   hypothetical protein LOC54914


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  20972727  ACCTTCTTCATTC  20972715


 Features flanking this part of subject sequence:
   58531 bp at 5' side: similar to F59E12.9
   233277 bp at 3' side: DMRT-like family A1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  22203788  CTTCTTCATTCAC  22203776


 Features flanking this part of subject sequence:
   494033 bp at 5' side: DMRT-like family A1
   746600 bp at 3' side: ELAV (embryonic lethal, abnormal vision, Drosophila)-like.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  22935943  ACCTTCTTCATTC  22935955


 Features flanking this part of subject sequence:
   1021823 bp at 5' side: DMRT-like family A1
   218810 bp at 3' side: ELAV (embryonic lethal, abnormal vision, Drosophila)-like.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         TTTCGACCTTCTT  16
                 |||||||||||||
Sbjct  23463733  TTTCGACCTTCTT  23463745


 Features flanking this part of subject sequence:
   578713 bp at 5' side: ELAV (embryonic lethal, abnormal vision, Drosophila)-like.
   1336724 bp at 3' side: tumor suppressor candidate 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  24330945  ACCTTCTTCATTC  24330957


 Features flanking this part of subject sequence:
   665790 bp at 5' side: ELAV (embryonic lethal, abnormal vision, Drosophila)-like.
   1249647 bp at 3' side: tumor suppressor candidate 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  24418034  GACCTTCTTCATT  24418022


 Features flanking this part of subject sequence:
   1716714 bp at 5' side: leucine rich repeat neuronal 6C
```

```
    722672 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  29657383  ACCTTCTTCATTC  29657395


  Features flanking this part of subject sequence:
    2289943 bp at 5' side: leucine rich repeat neuronal 6C
    149443 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  30230624  CCTTCTTCATTCA  30230612


  Features flanking this part of subject sequence:
    22774 bp at 5' side: zinc finger, CCHC domain containing 7
    42697 bp at 3' side: glyoxylate reductase/hydroxypyruvate reductase


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  37370051  CCTTCTTCATTCA  37370039


>ref|NT_019273.18|Hs1_19429 D Homo sapiens chromosome 1 genomic contig, reference a
Length=16604841
                                                                  Sort alignments for this s
                                                                    E value  Score  Percent i
                                                                    Query start position  Sul

  Features flanking this part of subject sequence:
    14381 bp at 5' side: epidermal growth factor receptor pathway substrate 8-like..
    134875 bp at 3' side: colony stimulating factor 1 isoform a precursor


  Score = 32.2 bits (16),  Expect = 7.2
  Identities = 19/20 (95%), Gaps = 0/20 (0%)
  Strand=Plus/Minus

Query  3        CTTTCGACCTTCTTCATTCA  22
                ||||| ||||||||||||||
Sbjct  6226456  CTTTCTACCTTCTTCATTCA  6226437


  Features in this part of subject sequence:
    netrin G1


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

Query  3        CTTTCGACCTTCTT  16
                ||||||||||||||
Sbjct  3642617  CTTTCGACCTTCTT  3642630


  Features in this part of subject sequence:
    G-protein signalling modulator 2 (AGS3-like, C. elegans)


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

Query  7        CGACCTTCTTCATT  20
                ||||||||||||||
```

```
Sbjct  5361553  CGACCTTCTTCATT  5361540


 Features flanking this part of subject sequence:
   148276 bp at 5' side: mitochondrial tryptophanyl tRNA synthetase 2 isoform 2 pr.
   92153 bp at 3' side: hydroxyacid oxidase 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  15739241  ACCTTCTTCATTCA  15739228


 Features in this part of subject sequence:
   G-protein signalling modulator 2 (AGS3-like, C. elegans)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8        GACCTTCTTCATT  20
                |||||||||||||
Sbjct  5361887  GACCTTCTTCATT  5361875


 Features in this part of subject sequence:
   CD53 antigen
   CD53 antigen


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12       TTCTTCATTCACG  24
                |||||||||||||
Sbjct  7347965  TTCTTCATTCACG  7347977


 Features flanking this part of subject sequence:
   357012 bp at 5' side: nerve growth factor, beta polypeptide precursor
   7595 bp at 3' side: vang-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  12094125  CCTTCTTCATTCA  12094113


>ref|NW_927713.1|HsCraAADB02_684 D Homo sapiens chromosome X genomic contig, alter
(based on Celera assembly)
Length=16225840

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features in this part of subject sequence:
   solute carrier family 16, member 2


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTCAC  23
                |||||||||||||||
Sbjct  1491540  ACCTTCTTCATTCAC  1491554


 Features in this part of subject sequence:
   phosphoglycerate kinase 1


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  5138378  CCTTCTTCATTCA  5138366


 Features flanking this part of subject sequence:
   187752 bp at 5' side: POU domain, class 3, transcription factor 4
   164022 bp at 3' side: similar to Cylicin-1 (Cylicin I) (Multiple-band polypepti.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         CGACCTTCTTCAT  19
                 |||||||||||||
Sbjct  10709747  CGACCTTCTTCAT  10709759


 Features in this part of subject sequence:
   dachshund 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  13205226  CCTTCTTCATTCA  13205238


 Features flanking this part of subject sequence:
   435661 bp at 5' side: kelch-like 4 isoform 1
   646539 bp at 3' side: hypothetical protein LOC53336


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  15117082  ACCTTCTTCATTC  15117070


>ref|NW_927700.1|HsCraAADB02_672 D Homo sapiens chromosome X genomic contig, alter
(based on Celera assembly)
Length=35626972

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent 
                                                                   Query start position  Su

 Features flanking this part of subject sequence:
   67775 bp at 5' side: G protein-coupled receptor 64
   208500 bp at 3' side: pyruvate dehydrogenase (lipoamide) alpha 1


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTCA  22
                 |||||||||||||||
Sbjct  17673264  GACCTTCTTCATTCA  17673250


 Features in this part of subject sequence:
   X-linked neuroligin 4
   X-linked neuroligin 4


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  8        GACCTTCTTCATTC  21
                ||||||||||||||
Sbjct  4663426  GACCTTCTTCATTC  4663413
```

```
 Features flanking this part of subject sequence:
   7659 bp at 5' side: motile sperm domain containing 2
   316809 bp at 3' side: ankyrin repeat and SOCS box-containing 9 isoform 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  13459083  GACCTTCTTCATTC  13459096


 Features flanking this part of subject sequence:
   700604 bp at 5' side: similar to Eukaryotic translation initiation factor 1A (e.
   531307 bp at 3' side: connector enhancer of kinase suppressor of Ras 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query  4         TTTCGACCTTCTTCATTC  21
                 |||| |||||||||||||
Sbjct  19381107  TTTCCACCTTCTTCATTC  19381124


 Features flanking this part of subject sequence:
   66332 bp at 5' side: transmembrane 4 superfamily member 10
   219472 bp at 3' side: hypothetical protein LOC170062


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  33266996  GACCTTCTTCATTC  33267009


 Features flanking this part of subject sequence:
   49423 bp at 5' side: adlican
   218596 bp at 3' side: protein kinase, X-linked


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  1990811  CCTTCTTCATTCA  1990799


 Features in this part of subject sequence:
   PDZ domain containing 10


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  11160691  GACCTTCTTCATT  11160703


 Features in this part of subject sequence:
   phosphatidylinositol N-acetylglucosaminyltransferase subu...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  13855175  GACCTTCTTCATT  13855163


 Features flanking this part of subject sequence:
   350127 bp at 5' side: retinoic acid induced 2
```

```
    12863 bp at 3' side: hypothetical protein LOC139105


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  8         GACCTTCTTCATT  20
                  |||||||||||||
 Sbjct  16687871  GACCTTCTTCATT  16687859


  Features flanking this part of subject sequence:
    28784 bp at 5' side: mitogen-activated protein kinase kinase kinase 15
    96306 bp at 3' side: SH3-domain kinase binding protein 1 isoform b


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  11        CTTCTTCATTCAC  23
                  |||||||||||||
 Sbjct  17980052  CTTCTTCATTCAC  17980064


  Features in this part of subject sequence:
    SH3-domain kinase binding protein 1 isoform b


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  11        CTTCTTCATTCAC  23
                  |||||||||||||
 Sbjct  18164677  CTTCTTCATTCAC  18164689


  Features in this part of subject sequence:
    small muscle protein, X-linked


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  20278016  CCTTCTTCATTCA  20278004


  Features flanking this part of subject sequence:
    40559 bp at 5' side: zinc finger protein 645
    121331 bp at 3' side: similar to methyltransferase 5 domain containing 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  11        CTTCTTCATTCAC  23
                  |||||||||||||
 Sbjct  20852042  CTTCTTCATTCAC  20852054


  Features flanking this part of subject sequence:
    9234 bp at 5' side: pyruvate dehydrogenase kinase, isoenzyme 3
    18977 bp at 3' side: phosphate cytidylyltransferase 1, choline, beta


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  12        TTCTTCATTCACG  24
                  |||||||||||||
 Sbjct  23082590  TTCTTCATTCACG  23082602


  Features flanking this part of subject sequence:
    156292 bp at 5' side: interleukin 1 receptor accessory protein-like 1
    101152 bp at 3' side: melanoma antigen family B, 2
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  28655452  CTTCTTCATTCAC  28655440


 Features flanking this part of subject sequence:
   2739865 bp at 5' side: dystrophin Dp40 isoform
   122911 bp at 3' side: hypothetical protein LOC158724


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  32550618  CCTTCTTCATTCA  32550606


 Features flanking this part of subject sequence:
   118416 bp at 5' side: hypothetical protein LOC170062
   648453 bp at 3' side: similar to melanoma antigen family B, 18


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  33606846  CCTTCTTCATTCA  33606834


>ref|NW_927406.1|HsCraAADB02_645 D Homo sapiens chromosome 22 genomic contig, alte
(based on Celera assembly)
Length=1603103

 Features flanking this part of subject sequence:
   41226 bp at 5' side: CDS
   6517 bp at 3' side: GRB2-associated binding protein family, member 4


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  9       ACCTTCTTCATTCAC  23
               |||||||||||||||
Sbjct  392378  ACCTTCTTCATTCAC  392364


>ref|NW_927106.1|HsCraAADB02_618 D Homo sapiens chromosome 18 genomic contig, alte
(based on Celera assembly)
Length=20447294

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features in this part of subject sequence:
   RAB27B, member RAS oncogene family


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  1        ATCTTTCGACCTTCT  15
                |||||||||||||||
Sbjct  7861435  ATCTTTCGACCTTCT  7861421


 Features in this part of subject sequence:
   Sma- and Mad-related protein 2
   Sma- and Mad-related protein 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus
```

```
Query  10      CCTTCTTCATTCAC  23
               ||||||||||||||
Sbjct  813145  CCTTCTTCATTCAC  813132


 Features in this part of subject sequence:
   hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4        TTTCGACCTTCTT  16
                |||||||||||||
Sbjct  4390377  TTTCGACCTTCTT  4390365


 Features flanking this part of subject sequence:
   290600 bp at 5' side: transcription factor 4 isoform b
   151138 bp at 3' side: hypothetical protein LOC642484


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  8855801  CTTCTTCATTCAC  8855789


 Features flanking this part of subject sequence:
   368444 bp at 5' side: hypothetical protein
   138347 bp at 3' side: thioredoxin-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  9442632  CTTCTTCATTCAC  9442620


 Features in this part of subject sequence:
   rabconnectin-3 beta isoform 1
   rabconnectin-3 beta isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  9909220  CCTTCTTCATTCA  9909232


 Features flanking this part of subject sequence:
   86180 bp at 5' side: collagen and calcium binding EGF domains 1
   116658 bp at 3' side: phorbol-12-myristate-13-acetate-induced protein 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  12762397  CCTTCTTCATTCA  12762385


 Features flanking this part of subject sequence:
   499307 bp at 5' side: cadherin 19, type 2 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
```

```
Sbjct  20050302  CCTTCTTCATTCA  20050314


>ref|NW_925884.1|HsCraAADB02_508 D Homo sapiens chromosome 15 genomic contig, alte
(based on Celera assembly)
Length=30328800

                                                                Sort alignments for this s
                                                                  E value  Score  Percent
                                                                  Query start position  Su

 Features in this part of subject sequence:
   acidic (leucine-rich) nuclear phosphoprotein 32 family, m...


 Score = 30.2 bits (15),  Expect =    28
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query  2         TCTTTCGACCTTCTTCATT  20
                 |||||| ||||||||||||
Sbjct  25068334  TCTTTCTACCTTCTTCATT  25068316


 Features flanking this part of subject sequence:
   8883 bp at 3' side: protein disulfide isomerase-associated 3 precursor


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query  2      TCTTTCGACCTTCTTCAT  19
              |||||| |||||||||||
Sbjct  17118  TCTTTCAACCTTCTTCAT  17135


 Features in this part of subject sequence:
   transcription factor 12 isoform b
   transcription factor 12 isoform a


 Score = 28.2 bits (14),  Expect =   112
 Identities = 20/22 (90%), Gaps = 0/22 (0%)
 Strand=Plus/Minus

Query  1         ATCTTTCGACCTTCTTCATTCA  22
                 |||||| |||| ||||||||||
Sbjct  13271929  ATCTTTAGACCATCTTCATTCA  13271908


 Features flanking this part of subject sequence:
   124535 bp at 5' side: talin 2
   77767 bp at 3' side: tropomyosin 1 alpha chain isoform 3


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  2         TCTTTCGACCTTCT  15
                 ||||||||||||||
Sbjct  19234772  TCTTTCGACCTTCT  19234785


 Features in this part of subject sequence:
   thrombospondin, type I, domain containing 4


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  27630734  CCTTCTTCATTCAC  27630747


 Features flanking this part of subject sequence:
   5234 bp at 5' side: Numb-interacting protein
   3707 bp at 3' side: dual oxidase 1 precursor


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  1409699  CCTTCTTCATTCA  1409711


 Features in this part of subject sequence:
   solute carrier family 28 (sodium-coupled nucleoside trans...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  1535333  ACCTTCTTCATTC  1535321


 Features flanking this part of subject sequence:
   917488 bp at 5' side: sulfide dehydrogenase like
   1152549 bp at 3' side: semaphorin 6D isoform 6 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8        GACCTTCTTCATT  20
                |||||||||||||
Sbjct  2889721  GACCTTCTTCATT  2889709


 Features in this part of subject sequence:
   myosin VC


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  8519605  CCTTCTTCATTCA  8519617


 Features flanking this part of subject sequence:
   450405 bp at 5' side: similar to 40S ribosomal protein SA (p40) (34/67 kDa lami.
   180654 bp at 3' side: WD repeat domain 72


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  9621992  CTTCTTCATTCAC  9622004


 Features flanking this part of subject sequence:
   18423 bp at 5' side: suppressor of hairy wing homolog 4 isoform 3
   121653 bp at 3' side: similar to Acyl-CoA-binding protein (ACBP) (Diazepam-bind.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 19/21 (90%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query  2         TCTTTCGACCTTCTTCATTCA  22
                 |||| ||||||||| ||||||
Sbjct  13004929  TCTTACGACCTTCTGCATTCA  13004949


 Features in this part of subject sequence:
   transcription factor 12 isoform b
   transcription factor 12 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  13488267  TTCTTCATTCACG  13488255


 Features flanking this part of subject sequence:
   71289 bp at 5' side: hypothetical protein
   904 bp at 3' side: aquaporin 9


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  14417234  CTTCTTCATTCAC  14417222


 Features flanking this part of subject sequence:
   717365 bp at 5' side: RAR-related orphan receptor A isoform c
   510680 bp at 3' side: vacuolar protein sorting 13C protein isoform 1A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         ATCTTTCGACCTT  13
                 |||||||||||||
Sbjct  17623230  ATCTTTCGACCTT  17623242


 Features flanking this part of subject sequence:
   729386 bp at 5' side: RAR-related orphan receptor A isoform c
   498659 bp at 3' side: vacuolar protein sorting 13C protein isoform 1A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  17635251  CCTTCTTCATTCA  17635263


 Features flanking this part of subject sequence:
   41184 bp at 5' side: guanine nucleotide exchange factor p532
   91760 bp at 3' side: death-associated protein kinase 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  20086177  CCTTCTTCATTCA  20086165


 Features in this part of subject sequence:
   casein kinase 1, gamma 1 isoform S


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  20501500  ACCTTCTTCATTC  20501512


 Features in this part of subject sequence:
   myosin IXA


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  28151315  CTTCTTCATTCAC  28151327
```

```
>ref|NW_925561.1|HsCraAADB02_479 D Homo sapiens chromosome 14 genomic contig, alte
(based on Celera assembly)
Length=53999513

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   1338234 bp at 5' side: hypothetical protein
   1394262 bp at 3' side: hypothetical protein


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTCAC  23
                 |||||||||||||||
Sbjct  31399647  ACCTTCTTCATTCAC  31399633


 Features in this part of subject sequence:
   regulator of G-protein signalling 6


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query  4         TTTCGACCTTCTTCATTC  21
                 |||| |||||||||||||
Sbjct  19254066  TTTCTACCTTCTTCATTC  19254083


 Features flanking this part of subject sequence:
   816893 bp at 5' side: hypothetical protein
   229728 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  29822547  CCTTCTTCATTCAC  29822560


 Features flanking this part of subject sequence:
   946087 bp at 5' side: hypothetical protein
   100530 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Minus

Query  4         TTTCGACCTTCTTCATTC  21
                 |||| |||||||||||||
Sbjct  29951758  TTTCCACCTTCTTCATTC  29951741


 Features flanking this part of subject sequence:
   101401 bp at 5' side: orthodenticle 2 isoform b
   302311 bp at 3' side: SEC10 protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12       TTCTTCATTCACG  24
                |||||||||||||
Sbjct  4177618  TTCTTCATTCACG  4177630


 Features in this part of subject sequence:
   retinoblastoma-binding protein 1 isoform III
   retinoblastoma-binding protein 1 isoform II
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12       TTCTTCATTCACG  24
                |||||||||||||
Sbjct  5597883  TTCTTCATTCACG  5597871


 Features flanking this part of subject sequence:
   165197 bp at 5' side: small nuclear RNA activating complex, polypeptide 1, 43kDa
   35843 bp at 3' side: synaptotagmin XIV-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  9231886  CCTTCTTCATTCA  9231898


 Features in this part of subject sequence:
   synaptotagmin XIV-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  9285233  CTTCTTCATTCAC  9285245


 Features in this part of subject sequence:
   hypothetical protein LOC9766


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  16956299  CTTCTTCATTCAC  16956287


 Features flanking this part of subject sequence:
   71412 bp at 5' side: hypothetical protein
   60283 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  22626882  CCTTCTTCATTCA  22626870


 Features in this part of subject sequence:
   basic leucine zipper transcription factor, ATF-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  22802964  ACCTTCTTCATTC  22802976


 Features in this part of subject sequence:
   serine palmitoyltransferase, long chain base subunit 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
```

```
                    |||||||||||||
Sbjct  24855984  CTTCTTCATTCAC  24855972


 Features in this part of subject sequence:
   neurexin 3 isoform alpha precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  26047079  CCTTCTTCATTCA  26047091


 Features flanking this part of subject sequence:
   1312459 bp at 5' side: hypothetical protein
   1420039 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  31373870  CCTTCTTCATTCA  31373858


 Features in this part of subject sequence:
   calponin like transmembrane domain protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  42588831  ACCTTCTTCATTC  42588843


 Features flanking this part of subject sequence:
   10638 bp at 5' side: hypothetical protein
   1148453 bp at 3' side: hypothetical protein LOC283598


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  44844365  CTTCTTCATTCAC  44844353


 Features flanking this part of subject sequence:
   26423 bp at 5' side: hypothetical protein
   1132668 bp at 3' side: hypothetical protein LOC283598


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  44860150  CTTCTTCATTCAC  44860138


 Features in this part of subject sequence:
   solute carrier family 25, member 29 isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  47578549  CTTCTTCATTCAC  47578537
```

```
 Features in this part of subject sequence:
   WD repeat domain 20 isoform 1
   WD repeat domain 20 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  49484549  GACCTTCTTCATT  49484561


>ref|NW_925395.1|HsCraAADB02_464 D Homo sapiens chromosome 12 genomic contig, alte
(based on Celera assembly)
Length=79994791

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent :
                                                                   Query start position  Sul

 Features flanking this part of subject sequence:
   304017 bp at 5' side: suppressor of defective silencing 3
   263609 bp at 3' side: KIAA1853 protein


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTCAC  23
                 |||||||||||||||
Sbjct  66413049  ACCTTCTTCATTCAC  66413035


 Features flanking this part of subject sequence:
   26126 bp at 5' side: olfactory receptor, family 6, subfamily C, member 76
   16012 bp at 3' side: olfactory receptor, family 6, subfamily C, member 70


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  3122998  CCTTCTTCATTCAC  3122985


 Features flanking this part of subject sequence:
   3090 bp at 5' side: hypothetical protein
   80706 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCACG  24
                 ||||||||||||||
Sbjct  50863419  CTTCTTCATTCACG  50863432


 Features flanking this part of subject sequence:
   256302 bp at 5' side: thyroid hormone receptor associated protein 2
   1043 bp at 3' side: hypothetical protein LOC400077


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  64224652  CCTTCTTCATTCAC  64224665


 Features in this part of subject sequence:
   suppressor of defective silencing 3


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
```

```
 Strand=Plus/Minus

Query  11        CTTCTTCATTCACG  24
                 ||||||||||||||
Sbjct  66093726  CTTCTTCATTCACG  66093713


 Features flanking this part of subject sequence:
   244778 bp at 5' side: similar to heat shock 70kD protein binding protein
   646100 bp at 3' side: leucine-rich repeats and immunoglobulin-like domains 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  5905724  CCTTCTTCATTCA  5905712


 Features flanking this part of subject sequence:
   282376 bp at 5' side: leucine-rich repeats and immunoglobulin-like domains 3
   503131 bp at 3' side: solute carrier family 16, member 7


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        GACCTTCTTCATT  20
                |||||||||||||
Sbjct  6881863  GACCTTCTTCATT  6881875


 Features in this part of subject sequence:
   carboxypeptidase M precursor
   carboxypeptidase M precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  16550547  CCTTCTTCATTCA  16550535


 Features flanking this part of subject sequence:
   182375 bp at 5' side: carboxypeptidase M precursor
   124466 bp at 3' side: cleavage and polyadenylation specific factor 6, 68 kD sub.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  16796621  CTTCTTCATTCAC  16796609


 Features flanking this part of subject sequence:
   297879 bp at 5' side: protein tyrosine phosphatase, receptor type, R isoform 2
   73330 bp at 3' side: transmembrane 4 superfamily member 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  18732935  CCTTCTTCATTCA  18732923


 Features flanking this part of subject sequence:
   44266 bp at 5' side: transmembrane protein vezatin
   130787 bp at 3' side: methionyl aminopeptidase 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  43031882  ACCTTCTTCATTC  43031894


 Features flanking this part of subject sequence:
   647306 bp at 5' side: neural precursor cell expressed, developmentally down-reg.
   885400 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         ATCTTTCGACCTT  13
                 |||||||||||||
Sbjct  45282971  ATCTTTCGACCTT  45282959


 Features in this part of subject sequence:
   cajalin 2 isoform a
   cajalin 2 isoform c


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  46463678  GACCTTCTTCATT  46463690


 Features in this part of subject sequence:
   solute carrier family 17 (sodium-dependent inorganic phos...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  48063642  CCTTCTTCATTCA  48063630


 Features in this part of subject sequence:
   transmembrane protein 16D


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  48596171  CTTCTTCATTCAC  48596159


 Features in this part of subject sequence:
   polymerase (RNA) III (DNA directed) polypeptide B


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  54102645  ACCTTCTTCATTC  54102657


 Features flanking this part of subject sequence:
   31913 bp at 5' side: mitochondrial aldehyde dehydrogenase 2 precursor
   1234 bp at 3' side: mitogen-activated protein kinase-activated protein kinase...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  59528596  TTCTTCATTCACG  59528584
```

```
 Features flanking this part of subject sequence:
   49520 bp at 5' side: hypothetical protein LOC283450
   86124 bp at 3' side: ribosomal protein L6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  60007867  CTTCTTCATTCAC  60007879


 Features flanking this part of subject sequence:
   19953 bp at 5' side: thyroid hormone receptor associated protein 2
   237393 bp at 3' side: hypothetical protein LOC400077


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  63988315  CCTTCTTCATTCA  63988303


 Features flanking this part of subject sequence:
   547980 bp at 5' side: hypothetical protein
   86313 bp at 3' side: similar to CG14446-PA


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1         ATCTTTCGACCTTCTTC  17
                 ||||||| |||||||||
Sbjct  75903038  ATCTTTCCACCTTCTTC  75903054


 Features in this part of subject sequence:
   hypothetical protein LOC121256


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  76961609  ACCTTCTTCATTC  76961597


 Features in this part of subject sequence:
   E1A binding protein p400


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  79688724  ACCTTCTTCATTC  79688712


 Features in this part of subject sequence:
   EP400 N-terminal like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  79832821  ACCTTCTTCATTC  79832809


>ref|NW_925106.1|HsCraAADB02_438 D Homo sapiens chromosome 11 genomic contig, alte
(based on Celera assembly)
```

```
Length=33348968
                                                                 Sort alignments for this s
                                                                   E value  Score  Percent i
                                                                   Query start position  Sul

 Features in this part of subject sequence:
   SH3 and multiple ankyrin repeat domains 2 isoform 1


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  2         TCTTTCGACCTTCTT  16
                 |||||||||||||||
Sbjct  15931797  TCTTTCGACCTTCTT  15931783


 Features flanking this part of subject sequence:
   200575 bp at 5' side: olfactory receptor, family 4, subfamily A, member 15
   1078 bp at 3' side: olfactory receptor, family 4, subfamily C, member 16


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTCA  22
                ||||||||||||||
Sbjct  1028428  ACCTTCTTCATTCA  1028415


 Features flanking this part of subject sequence:
   165036 bp at 5' side: chapsyn-110
   543545 bp at 3' side: hypothetical protein LOC55863


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  30456585  ACCTTCTTCATTCA  30456572


 Features flanking this part of subject sequence:
   14564 bp at 5' side: olfactory receptor, family 5, subfamily B, member 12
   53139 bp at 3' side: olfactory receptor, family 5, subfamily B, member 21


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  3928694  ACCTTCTTCATTC  3928682


 Features flanking this part of subject sequence:
   102728 bp at 5' side: transcobalamin I precursor
   54691 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  8        GACCTTCTTCATTCACG  24
                |||||||| ||||||||
Sbjct  5447521  GACCTTCTGCATTCACG  5447505


 Features flanking this part of subject sequence:
   174691 bp at 5' side: two pore segment channel 2
   35610 bp at 3' side: myeloma overexpressed


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
```

```
                  |||||||||||||
Sbjct  14718274  CTTCTTCATTCAC  14718286


 Features flanking this part of subject sequence:
   303610 bp at 5' side: similar to odd Oz/ten-m homolog 4
   3316666 bp at 3' side: similar to 40S ribosomal protein S28 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  1         ATCTTTCGACCTTCTTC  17
                 |||||||||||| ||||
Sbjct  24741862  ATCTTTCGACCTCCTTC  24741846


 Features flanking this part of subject sequence:
   763183 bp at 5' side: similar to odd Oz/ten-m homolog 4
   2857097 bp at 3' side: similar to 40S ribosomal protein S28 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  25201419  ACCTTCTTCATTC  25201431


 Features flanking this part of subject sequence:
   1410511 bp at 5' side: similar to odd Oz/ten-m homolog 4
   2209769 bp at 3' side: similar to 40S ribosomal protein S28 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  25848747  ACCTTCTTCATTC  25848759


 Features flanking this part of subject sequence:
   2228100 bp at 5' side: similar to odd Oz/ten-m homolog 4
   1392180 bp at 3' side: similar to 40S ribosomal protein S28 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  26666336  CCTTCTTCATTCA  26666348


 Features in this part of subject sequence:
   chapsyn-110


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  30260172  CTTCTTCATTCAC  30260184


>ref|NW_924884.1|HsCraAADB02_418 D Homo sapiens chromosome 10 genomic contig, alte
(based on Celera assembly)
Length=44859570

                                                         Sort alignments for this s
                                                           E value  Score  Percent 
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   75496 bp at 5' side: hypothetical protein LOC143384
   41733 bp at 3' side: similar to 60S ribosomal protein L17 (L23) (Amino acid st..
```

```
 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTCA  22
                 |||||||||||||||
Sbjct  31323239  GACCTTCTTCATTCA  31323253


 Features flanking this part of subject sequence:
   2051 bp at 5' side: cytochrome P450, family 2, subfamily C, polypeptide 9
   47052 bp at 3' side: cytochrome P450, family 2, subfamily C, polypeptide 8 iso..


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query  3        CTTTCGACCTTCTTCATT  20
                ||||| ||||||||||||
Sbjct  7493768  CTTTCAACCTTCTTCATT  7493785


 Features flanking this part of subject sequence:
   5001 bp at 5' side: interferon-induced protein with tetratricopeptide repeats...
   2959 bp at 3' side: interferon-induced protein with tetratricopeptide repeats...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  1899146  CTTCTTCATTCAC  1899134


 Features in this part of subject sequence:
   SEC15-like 1 isoform b
   SEC15-like 1 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  5561975  CTTCTTCATTCAC  5561987


 Features in this part of subject sequence:
   cytochrome P450, family 2, subfamily C, polypeptide 19


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  7347628  CTTCTTCATTCAC  7347640


 Features in this part of subject sequence:
   B-cell linker


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  8747480  CCTTCTTCATTCA  8747492


 Features in this part of subject sequence:
   beta-transducin repeat containing protein isoform 2
   beta-transducin repeat containing protein isoform 1


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  13874755  ACCTTCTTCATTC  13874743


 Features in this part of subject sequence:
   hypothetical protein LOC80217


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  16692844  ACCTTCTTCATTC  16692856


 Features flanking this part of subject sequence:
   961760 bp at 5' side: SORCS receptor 1 isoform a
   1731488 bp at 3' side: X-prolyl aminopeptidase (aminopeptidase P) 1, soluble


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  20627943  CTTCTTCATTCAC  20627955


 Features in this part of subject sequence:
   mitochondrial glycerol 3-phosphate acyltransferase


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  24656781  CCTTCTTCATTCA  24656769


 Features flanking this part of subject sequence:
   123611 bp at 5' side: antigen identified by monoclonal antibody Ki-67
   665303 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  40721856  CCTTCTTCATTCA  40721844


>ref|NW_924484.1|HsCraAADB02_382 D Homo sapiens chromosome 9 genomic contig, alter
(based on Celera assembly)
Length=25897798

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   39230 bp at 5' side: protein tyrosine phosphatase domain containing 1 protein ..
   145125 bp at 3' side: zinc finger protein 169


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCACG  24
                 |||||||||||||||
Sbjct  25731061  CCTTCTTCATTCACG  25731047


 Features flanking this part of subject sequence:
```

```
   314446 bp at 5' side: neurotrophic tyrosine kinase, receptor, type 2 isoform c .
   210938 bp at 3' side: ATP/GTP binding protein 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  16901361  GACCTTCTTCATTC  16901348


 Features flanking this part of subject sequence:
   951405 bp at 5' side: annexin I
   377886 bp at 3' side: RAR-related orphan receptor B


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  5689101  CCTTCTTCATTCA  5689113


 Features flanking this part of subject sequence:
   727009 bp at 5' side: phosphoserine aminotransferase isoform 1
   335285 bp at 3' side: similar to Coiled-coil-helix-coiled-coil-helix domain-con.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  10628322  GACCTTCTTCATT  10628334


 Features flanking this part of subject sequence:
   61276 bp at 5' side: hypothetical protein LOC401535
   279157 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  18784664  CTTCTTCATTCAC  18784652


 Features flanking this part of subject sequence:
   65451 bp at 5' side: hypothetical protein
   42039 bp at 3' side: Di-Ras2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  22148146  CCTTCTTCATTCA  22148134


 Features flanking this part of subject sequence:
   170899 bp at 5' side: nuclear factor, interleukin 3 regulated
   37841 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  2         TCTTTCGACCTTCTTCA  18
                 |||||| ||||||||||
Sbjct  23158609  TCTTTCTACCTTCTTCA  23158593


>ref|NW_923929.1|HsCraAADB02_332 D Homo sapiens chromosome 8 genomic contig, alter
```

```
(based on Celera assembly)
Length=39695605

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features in this part of subject sequence:
   staufen homolog 2


 Score = 30.2 bits (15),  Expect =    28
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query  2         TCTTTCGACCTTCTTCATT  20
                 |||||| ||||||||||||
Sbjct  27726887  TCTTTCCACCTTCTTCATT  27726869


 Features in this part of subject sequence:
   hypothetical protein LOC23514


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  1504131  ACCTTCTTCATTC  1504119


 Features flanking this part of subject sequence:
   211801 bp at 5' side: ubiquitin-conjugating enzyme E2 variant 2
   319908 bp at 3' side: hypothetical protein LOC401459


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  2303501  CTTCTTCATTCAC  2303489


 Features flanking this part of subject sequence:
   23835 bp at 5' side: coiled-coil-helix-coiled-coil-helix domain containing 7 i..
   60860 bp at 3' side: epidermal retinal dehydrogenase 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         CTTTCGACCTTCT  15
                 |||||||||||||
Sbjct  10276656  CTTTCGACCTTCT  10276668


 Features flanking this part of subject sequence:
   353073 bp at 5' side: thymus high mobility group box protein TOX
   736282 bp at 3' side: carbonic anhydrase VIII


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  13509171  TTCTTCATTCACG  13509159


 Features flanking this part of subject sequence:
   40151 bp at 5' side: chromodomain helicase DNA binding protein 7
   393845 bp at 3' side: hypothetical protein LOC157807


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
```

```
                 |||||||||||||
Sbjct  14941439  ACCTTCTTCATTC  14941451


 Features in this part of subject sequence:
   hypothetical protein LOC286183


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  16508374  CCTTCTTCATTCA  16508362


 Features flanking this part of subject sequence:
   1139084 bp at 5' side: YTH domain family, member 3
   20833 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  18385062  CCTTCTTCATTCA  18385050


 Features flanking this part of subject sequence:
   178205 bp at 5' side: carboxypeptidase B precursor
   28095 bp at 3' side: DEP domain containing 2 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  21962864  CTTCTTCATTCAC  21962876


 Features flanking this part of subject sequence:
   5184 bp at 5' side: PR domain containing 14
   38575 bp at 3' side: nuclear receptor coactivator 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  24118025  GACCTTCTTCATT  24118013


 Features flanking this part of subject sequence:
   442116 bp at 5' side: ankyrin-like protein 1
   53606 bp at 3' side: potassium voltage-gated channel, Shab-related subfamily, ..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  26562307  CTTCTTCATTCAC  26562295


 Features in this part of subject sequence:
   potassium voltage-gated channel, Shab-related subfamily, ...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  26703703  CTTCTTCATTCAC  26703691
```

```
 Features in this part of subject sequence:
   potassium voltage-gated channel, Shab-related subfamily, ...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  26944689  CCTTCTTCATTCA  26944677


 Features flanking this part of subject sequence:
   431883 bp at 5' side: cocoacrisp
   79269 bp at 3' side: hepatocyte nuclear factor 4, gamma


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  29504677  CCTTCTTCATTCA  29504689


 Features flanking this part of subject sequence:
   907011 bp at 5' side: peroxisomal membrane protein 3
   717537 bp at 3' side: cAMP-dependent protein kinase inhibitor alpha isoform 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  31929866  TTCTTCATTCACG  31929878


>ref|NW_922984.1|HsCraAADB02_247 D Homo sapiens chromosome 6 genomic contig, alter
(based on Celera assembly)
Length=26292868

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   10302 bp at 5' side: H4 histone family, member H
   72349 bp at 3' side: butyrophilin, subfamily 3, member A2 precursor


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTCA  22
                 |||||||||||||||
Sbjct  25920592  GACCTTCTTCATTCA  25920606


 Features in this part of subject sequence:
   serine (or cysteine) proteinase inhibitor, clade B (ovalb...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  2514751  CCTTCTTCATTCAC  2514764


 Features flanking this part of subject sequence:
   7223 bp at 5' side: testis-specific histone H2B
   27436 bp at 3' side: solute carrier family 17 (sodium phosphate), member 4


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
```

```
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  25357224  CCTTCTTCATTCAC  25357211


 Features in this part of subject sequence:
   phenylalanine-tRNA synthetase 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  5270223  CCTTCTTCATTCA  5270235


 Features flanking this part of subject sequence:
   372196 bp at 5' side: hypothetical protein
   432921 bp at 3' side: MRDS1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  9087508  ACCTTCTTCATTC  9087520


 Features flanking this part of subject sequence:
   265245 bp at 5' side: neural precursor cell expressed, developmentally down-reg.
   216226 bp at 3' side: hypothetical protein LOC84830


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  11121731  CCTTCTTCATTCA  11121743


 Features flanking this part of subject sequence:
   75858 bp at 5' side: human immunodeficiency virus type I enhancer binding prot..
   50306 bp at 3' side: endothelin 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  11863866  CTTCTTCATTCAC  11863854


 Features flanking this part of subject sequence:
   71103 bp at 5' side: endothelin 1
   146923 bp at 3' side: similar to ribosomal protein L15 isoform 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  11990716  CTTCTTCATTCAC  11990728


 Features in this part of subject sequence:
   dystrobrevin binding protein 1 isoform c
   dystrobrevin binding protein 1 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  15199894  ACCTTCTTCATTC  15199906


 Features flanking this part of subject sequence:
   662704 bp at 5' side: ataxin 1
   138242 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  16624319  CTTCTTCATTCAC  16624331


 Features flanking this part of subject sequence:
   558563 bp at 5' side: hypothetical protein
   857663 bp at 3' side: vesicular membrane protein p24


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  22905436  CCTTCTTCATTCA  22905448


 Features flanking this part of subject sequence:
   799482 bp at 5' side: hypothetical protein
   616744 bp at 3' side: vesicular membrane protein p24


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  23146355  CCTTCTTCATTCA  23146367


>ref|NW_922217.1|HsCraAADB02_178 D Homo sapiens chromosome 4 genomic contig, alter
(based on Celera assembly)
Length=70496567

                                                                   Sort alignments for this s
                                                                     E value  Score  Percent
                                                                     Query start position  Su

 Features flanking this part of subject sequence:
   33295 bp at 5' side: endothelin receptor type A
   42038 bp at 3' side: transmembrane protein 34


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTCAC  23
                 |||||||||||||||
Sbjct  28075640  ACCTTCTTCATTCAC  28075654


 Features flanking this part of subject sequence:
   5970 bp at 5' side: Sm protein F
   21314 bp at 3' side: similar to stromal cell derived factor receptor 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  26693735  GACCTTCTTCATTC  26693722


 Features flanking this part of subject sequence:
```

```
   489361 bp at 5' side: acidic nuclear phosphoprotein 32C
   255683 bp at 3' side: similar to nascent polypeptide-associated complex alpha p.


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  45198254  ACCTTCTTCATTCA  45198267


 Features flanking this part of subject sequence:
   215612 bp at 5' side: glycoprotein M6A isoform 2
   68527 bp at 3' side: WD repeat domain 17 isoform 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  56534627  GACCTTCTTCATTC  56534640


 Features flanking this part of subject sequence:
   54467 bp at 5' side: annexin 5
   9270 bp at 3' side: hypothetical protein LOC132332


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  2315216  CTTCTTCATTCAC  2315204


 Features in this part of subject sequence:
   spermatogenesis associated factor SPAF


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  3857223  CCTTCTTCATTCA  3857211


 Features flanking this part of subject sequence:
   332506 bp at 5' side: hypothetical protein isoform 1
   670067 bp at 3' side: ankyrin repeat domain 50


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  4558164  CCTTCTTCATTCA  4558176


 Features flanking this part of subject sequence:
   772008 bp at 5' side: hypothetical protein
   2537358 bp at 3' side: protocadherin 10 isoform 1 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  11130415  GACCTTCTTCATT  11130427


 Features flanking this part of subject sequence:
   152976 bp at 5' side: similar to poly(A) binding protein, cytoplasmic 4 (induci.
   586091 bp at 3' side: similar to Ubiquinol-cytochrome c reductase complex ubiqu.
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  14872197  CTTCTTCATTCAC  14872209


 Features flanking this part of subject sequence:
   489937 bp at 5' side: hypothetical protein
   767668 bp at 3' side: similar to Telomeric repeat-binding factor 1 (TTAGGG repe.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  16101202  CTTCTTCATTCAC  16101214


 Features flanking this part of subject sequence:
   112085 bp at 5' side: nuclear receptor subfamily 3, group C, member 2
   962774 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  29048904  ACCTTCTTCATTC  29048916


 Features flanking this part of subject sequence:
   487174 bp at 5' side: PET112-like
   74588 bp at 3' side: F-box protein FBW7 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         TCTTTCGACCTTC  14
                 |||||||||||||
Sbjct  32750703  TCTTTCGACCTTC  32750691


 Features flanking this part of subject sequence:
   750411 bp at 5' side: hypothetical protein
   301859 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  4         TTTCGACCTTCTTCATT  20
                 |||| ||||||||||||
Sbjct  43318168  TTTCAACCTTCTTCATT  43318152


 Features flanking this part of subject sequence:
   23616 bp at 5' side: tolloid-like 1
   611941 bp at 3' side: testican 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  46638547  ACCTTCTTCATTC  46638535


 Features in this part of subject sequence:
   SH3 domain containing ring finger 1
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  49654803  CCTTCTTCATTCA  49654791


 Features in this part of subject sequence:
   polypeptide N-acetylgalactosaminyltransferase 7


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  53766989  ACCTTCTTCATTC  53766977


 Features flanking this part of subject sequence:
   1548564 bp at 5' side: hypothetical protein
   1037513 bp at 3' side: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomp


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  60044870  ACCTTCTTCATTC  60044858


 Features flanking this part of subject sequence:
   58511 bp at 5' side: dCMP deaminase isoform b
   63003 bp at 3' side: similar to CG6405-PA


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  63486866  CCTTCTTCATTCA  63486854


>ref|NW_922162.1|HsCraAADB02_173 D Homo sapiens chromosome 4 genomic contig, alter
(based on Celera assembly)
Length=66459542

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent 
                                                                    Query start position  Su

 Features in this part of subject sequence:
   sodium-dependent organic anion transporter


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTCAC  23
                 |||||||||||||||
Sbjct  34859455  ACCTTCTTCATTCAC  34859469


 Features flanking this part of subject sequence:
   44399 bp at 5' side: ankyrin repeat domain 56
   7665 bp at 3' side: septin 11


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  24989740  ACCTTCTTCATTCA  24989727
```

```
 Features in this part of subject sequence:
   family with sequence similarity 13, member A1 isoform a
   family with sequence similarity 13, member A1 isoform b


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  36850807  CCTTCTTCATTCAC  36850794


 Features in this part of subject sequence:
   glutamate receptor, ionotropic, delta 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  40764932  CCTTCTTCATTCAC  40764919


 Features in this part of subject sequence:
   glutamate receptor, ionotropic, delta 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  41482621  CCTTCTTCATTCAC  41482608


 Features in this part of subject sequence:
   protein phosphatase 3 (formerly 2B), catalytic subunit, a...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  49251016  ACCTTCTTCATTCA  49251029


 Features in this part of subject sequence:
   kinase insert domain receptor (a type III receptor tyrosi...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8        GACCTTCTTCATT  20
                |||||||||||||
Sbjct  3282350  GACCTTCTTCATT  3282338


 Features flanking this part of subject sequence:
   75938 bp at 5' side: kinase insert domain receptor (a type III receptor tyrosi..
   145012 bp at 3' side: steroid 5 alpha-reductase 2-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  3        CTTTCGACCTTCTTCAT  19
                ||||| |||||||||||
Sbjct  3394299  CTTTCAACCTTCTTCAT  3394283


 Features in this part of subject sequence:
   ADAM metallopeptidase with thrombospondin type 1 motif, 3...


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  20476991  CTTCTTCATTCAC  20476979


 Features flanking this part of subject sequence:
   138441 bp at 5' side: betacellulin
   596 bp at 3' side: DKFZP564O0823 protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  22978176  GACCTTCTTCATT  22978164


 Features flanking this part of subject sequence:
   787404 bp at 5' side: hypothetical protein LOC84803
   90274 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         ATCTTTCGACCTT  13
                 |||||||||||||
Sbjct  32428730  ATCTTTCGACCTT  32428742


 Features in this part of subject sequence:
   Rho GTPase activating protein 24 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  33647770  CCTTCTTCATTCA  33647782


 Features flanking this part of subject sequence:
   45545 bp at 5' side: hypothetical protein LOC285513
   431758 bp at 3' side: alpha-synuclein isoform NACP140


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  37337945  CTTCTTCATTCAC  37337933


 Features flanking this part of subject sequence:
   737470 bp at 5' side: hypothetical protein
   242383 bp at 3' side: glutamate receptor, ionotropic, delta 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  40099086  ACCTTCTTCATTC  40099074


 Features in this part of subject sequence:
   glutamate receptor, ionotropic, delta 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  40509275  ACCTTCTTCATTC  40509263


 Features in this part of subject sequence:
   alcohol dehydrogenase 1B (class I), beta polypeptide


 Score = 26.3 bits (13),  Expect =   444
 Identities = 19/21 (90%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query  1         ATCTTTCGACCTTCTTCATTC  21
                 ||||||| ||||| |||||||
Sbjct  47353989  ATCTTTCCACCTTTTTCATTC  47354009


 Features flanking this part of subject sequence:
   51052 bp at 5' side: hypothetical protein isoform 2
   62890 bp at 3' side: hypothetical protein LOC54790


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  53216458  ACCTTCTTCATTC  53216470


 Features flanking this part of subject sequence:
   47484 bp at 5' side: glutamyl aminopeptidase (aminopeptidase A)
   9106 bp at 3' side: paired-like homeodomain transcription factor 2 isoform c


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  4         TTTCGACCTTCTTCATT  20
                 |||| ||||||||||||
Sbjct  58648973  TTTCCACCTTCTTCATT  58648957


 Features flanking this part of subject sequence:
   1966643 bp at 5' side: N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4
   39910 bp at 3' side: translocation associated membrane protein 1-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  3         CTTTCGACCTTCTTCAT  19
                 |||||| ||||||||||
Sbjct  65082701  CTTTCGCCCTTCTTCAT  65082685


 Features flanking this part of subject sequence:
   512323 bp at 5' side: translocation associated membrane protein 1-like 1
   455316 bp at 3' side: N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  65636043  CCTTCTTCATTCA  65636055


>ref|NW_921651.1|HsCraAADB02_127 D Homo sapiens chromosome 3 genomic contig, alter
(based on Celera assembly)
Length=75540080

                                                            Sort alignments for this s
                                                              E value  Score  Percent 
                                                              Query start position  Su

 Features flanking this part of subject sequence:
   585552 bp at 5' side: 3-oxoacyl-ACP synthase, mitochondrial
```

```
   242431 bp at 3' side: hypothetical protein


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTCA  22
                 |||||||||||||||
Sbjct  26358424  GACCTTCTTCATTCA  26358410


 Features flanking this part of subject sequence:
   99190 bp at 5' side: similar to zinc finger protein 160
   17617 bp at 3' side: glycerol-3-phosphate dehydrogenase 1-like


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTCA  22
                 |||||||||||||||
Sbjct  32068247  GACCTTCTTCATTCA  32068261


 Features in this part of subject sequence:
   special AT-rich sequence binding protein 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  18352814  CCTTCTTCATTCAC  18352801


 Features flanking this part of subject sequence:
   249647 bp at 5' side: shugoshin-like 1 isoform C1
   988497 bp at 3' side: zinc finger protein 659


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  7         CGACCTTCTTCATT  20
                 ||||||||||||||
Sbjct  20415785  CGACCTTCTTCATT  20415798


 Features flanking this part of subject sequence:
   14543 bp at 5' side: hypothetical protein
   70821 bp at 3' side: leucine rich repeat containing 3B


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  26616941  ACCTTCTTCATTCA  26616928


 Features flanking this part of subject sequence:
   129794 bp at 5' side: cholecystokinin preproprotein
   4878 bp at 3' side: lysozyme-like 4


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  42374296  CCTTCTTCATTCAC  42374283


 Features flanking this part of subject sequence:
   32044 bp at 5' side: XC chemokine receptor 1
   149222 bp at 3' side: chemokine (C-C motif) receptor 1
```

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCACG  24
                 ||||||||||||||
Sbjct  46032845  CTTCTTCATTCACG  46032858


 Features in this part of subject sequence:
   protein tyrosine phosphatase, receptor type, G precursor


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  61983616  CCTTCTTCATTCAC  61983629


 Features flanking this part of subject sequence:
   156290 bp at 5' side: hypothetical protein
   148513 bp at 3' side: SHQ1 homolog


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCACG  24
                 ||||||||||||||
Sbjct  72585085  CTTCTTCATTCACG  72585072


 Features in this part of subject sequence:
   contactin 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  1353293  ACCTTCTTCATTC  1353281


 Features in this part of subject sequence:
   inositol 1,4,5-triphosphate receptor, type 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7        CGACCTTCTTCAT  19
                |||||||||||||
Sbjct  4575530  CGACCTTCTTCAT  4575518


 Features flanking this part of subject sequence:
   650604 bp at 5' side: hypothetical protein
   24616 bp at 3' side: similar to Retinoic acid receptor beta (RAR-beta) (RAR-ep..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  25127434  GACCTTCTTCATT  25127422


 Features flanking this part of subject sequence:
   516815 bp at 5' side: 3-oxoacyl-ACP synthase, mitochondrial
   311170 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  26289673  CTTCTTCATTCAC  26289685


 Features flanking this part of subject sequence:
   78740 bp at 5' side: hypothetical protein
   6625 bp at 3' side: leucine rich repeat containing 3B


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  26681137  CTTCTTCATTCAC  26681125


 Features flanking this part of subject sequence:
   106621 bp at 5' side: glutamate decarboxylase-like 1
   497485 bp at 3' side: similar to Thyroid hormone receptor-associated protein 3 .


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  30935196  ACCTTCTTCATTC  30935184


 Features flanking this part of subject sequence:
   1348370 bp at 5' side: programmed cell death 6 interacting protein
   420542 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         TCGACCTTCTTCA  18
                 |||||||||||||
Sbjct  35199265  TCGACCTTCTTCA  35199277


 Features flanking this part of subject sequence:
   50016 bp at 5' side: cyclic AMP-regulated phosphoprotein, 21 kD isoform 1
   537601 bp at 3' side: SH3 and cysteine rich domain


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  35827446  CTTCTTCATTCAC  35827434


 Features in this part of subject sequence:
   integrin, alpha 9 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  37584808  CTTCTTCATTCAC  37584820


 Features flanking this part of subject sequence:
   25497 bp at 5' side: similar to voltage-gated sodium channel type V alpha isof..
   38594 bp at 3' side: sodium channel, voltage-gated, type X, alpha


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
```

```
                 |||||||||||||
Sbjct  38639307  CCTTCTTCATTCA  38639295


 Features in this part of subject sequence:
   natural killer-tumor recognition sequence isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  42623962  CCTTCTTCATTCA  42623974


 Features flanking this part of subject sequence:
   11375 bp at 5' side: zinc finger protein 502
   584 bp at 3' side: zinc finger protein 501


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  44713317  CCTTCTTCATTCA  44713305


 Features flanking this part of subject sequence:
   17928 bp at 5' side: chemokine (C-C motif) receptor-like 2
   9206 bp at 3' side: lactotransferrin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  46405852  CTTCTTCATTCAC  46405840


 Features in this part of subject sequence:
   huntingtin interacting protein B


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  47068025  CCTTCTTCATTCA  47068037


 Features flanking this part of subject sequence:
   7247 bp at 5' side: chondroitin sulfate proteoglycan 5 (neuroglycan C)
   2258 bp at 3' side: SWI/SNF-related matrix-associated actin-dependent regulat...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  47569219  CCTTCTTCATTCA  47569231


 Features flanking this part of subject sequence:
   65882 bp at 5' side: family with sequence similarity 3, member D
   20997 bp at 3' side: hypothetical protein LOC200844


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  58720641  GACCTTCTTCATT  58720629
```

```
 Features in this part of subject sequence:
   fragile histidine triad gene


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  60450516  GACCTTCTTCATT  60450528


 Features in this part of subject sequence:
   protein tyrosine phosphatase, receptor type, G precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  62046593  TTCTTCATTCACG  62046581


 Features flanking this part of subject sequence:
   133072 bp at 5' side: hypothetical protein
   479648 bp at 3' side: membrane associated guanylate kinase, WW and PDZ domain c.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  64878652  GACCTTCTTCATT  64878640


 Features flanking this part of subject sequence:
   111600 bp at 5' side: T-cell activation kelch repeat protein
   253364 bp at 3' side: succinate-CoA ligase, GDP-forming, beta subunit


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  67115901  CCTTCTTCATTCA  67115913


 Features flanking this part of subject sequence:
   15968 bp at 5' side: hypothetical protein LOC401072
   327750 bp at 3' side: forkhead box P1 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  3         CTTTCGACCTTCTTCAT  19
                 ||||| |||||||||||
Sbjct  70607554  CTTTCAACCTTCTTCAT  70607570


 Features in this part of subject sequence:
   forkhead box P1 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  70999144  ACCTTCTTCATTC  70999156


 Features in this part of subject sequence:
   SHQ1 homolog
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  72821135  CTTCTTCATTCAC  72821123


 Features flanking this part of subject sequence:
   584101 bp at 5' side: similar to PDZ domain containing RING finger 3
   56153 bp at 3' side: contactin 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  74192755  CCTTCTTCATTCA  74192767


 Features flanking this part of subject sequence:
   699355 bp at 5' side: contactin 3
   155566 bp at 3' side: similar to Protein C21orf63 precursor (SUE21)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  75204528  CCTTCTTCATTCA  75204540


>ref|NW_925683.1|HsCraAADB02_49 D Homo sapiens chromosome 1 genomic contig, alterna
(based on Celera assembly)
Length=11514521

                                                                   Sort alignments for this s
                                                                     E value  Score  Percent
                                                                     Query start position  Su

 Features in this part of subject sequence:
   GA repeat binding protein, beta 2


 Score = 30.2 bits (15),  Expect =    28
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Plus

Query  4        TTTCGACCTTCTTCATTCA  22
                ||||||||| |||||||||
Sbjct  1232550  TTTCGACCTACTTCATTCA  1232568


 Features flanking this part of subject sequence:
   25378 bp at 5' side: CD1D antigen, d polypeptide
   45103 bp at 3' side: CD1A antigen precursor


 Score = 30.2 bits (15),  Expect =    28
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query  3        CTTTCGACCTTCTTCATTC  21
                ||||| |||||||||||||
Sbjct  8287234  CTTTCTACCTTCTTCATTC  8287216


 Features flanking this part of subject sequence:
   10384 bp at 5' side: small proline-rich protein 2G
   43933 bp at 3' side: late cornified envelope-like proline-rich 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12       TTCTTCATTCACG  24
                |||||||||||||
```

```
Sbjct  3240564  TTCTTCATTCACG  3240576


 Features in this part of subject sequence:
   Est1p-like protein B


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  6339907  CCTTCTTCATTCA  6339895


>ref|NW_926128.1|HsCraAADB02_53 D Homo sapiens chromosome 1 genomic contig, altern
(based on Celera assembly)
Length=44521323
                                                                Sort alignments for this s
                                                                  E value  Score  Percent
                                                                  Query start position  Su

 Features in this part of subject sequence:
   family with sequence similarity 5, member C


 Score = 30.2 bits (15),  Expect =    28
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query  3         CTTTCGACCTTCTTCATTC  21
                 ||||||||||||| |||||
Sbjct  28540142  CTTTCGACCTTCTCCATTC  28540124


 Features in this part of subject sequence:
   LIM homeobox transcription factor 1, alpha isoform a


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTCA  22
                ||||||||||||||
Sbjct  3593167  ACCTTCTTCATTCA  3593154


 Features flanking this part of subject sequence:
   316836 bp at 5' side: dermatopontin precursor
   59757 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  7379793  CTTCTTCATTCAC  7379805


 Features in this part of subject sequence:
   kinesin-associated protein 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  2        TCTTTCGACCTTCTTCA  18
                |||||| ||||||||||
Sbjct  8280825  TCTTTCCACCTTCTTCA  8280809


 Features in this part of subject sequence:
   kinesin-associated protein 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  8332862  CTTCTTCATTCAC  8332874


 Features in this part of subject sequence:
   ring finger and WD repeat domain 2 isoform d24
   ring finger and WD repeat domain 2 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  14282533  CCTTCTTCATTCA  14282545


 Features flanking this part of subject sequence:
   267788 bp at 5' side: ring finger and WD repeat domain 2 isoform a
   80960 bp at 3' side: pappalysin 2 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  14809321  CTTCTTCATTCAC  14809309


 Features flanking this part of subject sequence:
   225737 bp at 5' side: similar to protein tyrosine phosphatase 4a1
   21730 bp at 3' side: astrotactin isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  15176476  CTTCTTCATTCAC  15176464


 Features flanking this part of subject sequence:
   121493 bp at 5' side: regucalcin gene promotor region related protein
   5055 bp at 3' side: RAS protein activator like 2 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  16422278  CTTCTTCATTCAC  16422266


 Features flanking this part of subject sequence:
   21793 bp at 5' side: immediate early response 5
   206664 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  19442460  CTTCTTCATTCAC  19442472


 Features in this part of subject sequence:
   chromosome 1 open reading frame 21


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
```

```
Sbjct  22934236  GACCTTCTTCATT  22934224


 Features flanking this part of subject sequence:
   69232 bp at 5' side: UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase 2
   2976870 bp at 3' side: potassium channel, subfamily T, member 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  31584294  GACCTTCTTCATT  31584282


 Features flanking this part of subject sequence:
   47336 bp at 5' side: DENN/MADD domain containing 1B
   119654 bp at 3' side: hypothetical protein LOC388722


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  36129777  TTCTTCATTCACG  36129789


 Features in this part of subject sequence:
   hypothetical protein LOC55765


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         TTCGACCTTCTTC  17
                 |||||||||||||
Sbjct  39239843  TTCGACCTTCTTC  39239855


 Features flanking this part of subject sequence:
   3515 bp at 5' side: hypothetical protein LOC284573
   68078 bp at 3' side: SRY-box 13


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  42403968  CCTTCTTCATTCA  42403956


 Features flanking this part of subject sequence:
   110192 bp at 5' side: phosphoinositol 3-phosphate-binding protein-3
   22161 bp at 3' side: protein phosphatase 1, regulatory subunit 15B


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  42743256  CTTCTTCATTCAC  42743244


>ref|NT_011669.16|HsX_11826 D Homo sapiens chromosome X genomic contig, reference
Length=14971611
                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

 Features in this part of subject sequence:
   solute carrier family 16, member 2


 Score = 30.2 bits (15),  Expect =    28
```

```
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTCAC  23
                 |||||||||||||||
Sbjct  12005753  ACCTTCTTCATTCAC  12005767


 Features flanking this part of subject sequence:
   62345 bp at 5' side: similar to RNA binding motif protein, X-linked
   2709 bp at 3' side: V-set and immunoglobulin domain containing 4


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  3557371  CCTTCTTCATTCAC  3557384


>ref|NT_011757.15|HsX_11914 D Homo sapiens chromosome X genomic contig, reference
Length=34879939
                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   67615 bp at 5' side: G protein-coupled receptor 64
   207575 bp at 3' side: pyruvate dehydrogenase (lipoamide) alpha 1


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTCA  22
                 |||||||||||||||
Sbjct  16936264  GACCTTCTTCATTCA  16936250


 Features in this part of subject sequence:
   X-linked neuroligin 4
   X-linked neuroligin 4


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  8        GACCTTCTTCATTC  21
                ||||||||||||||
Sbjct  3921724  GACCTTCTTCATTC  3921711


 Features flanking this part of subject sequence:
   7659 bp at 5' side: motile sperm domain containing 2
   317025 bp at 3' side: ankyrin repeat and SOCS box-containing 9 isoform 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  12727273  GACCTTCTTCATTC  12727286


 Features flanking this part of subject sequence:
   574162 bp at 5' side: ribosomal protein S6 kinase, 90kDa, polypeptide 3
   534087 bp at 3' side: connector enhancer of kinase suppressor of Ras 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query  4         TTTCGACCTTCTTCATTC  21
                 |||| |||||||||||||
Sbjct  18640595  TTTCCACCTTCTTCATTC  18640612
```

```
 Features flanking this part of subject sequence:
   66329 bp at 5' side: transmembrane 4 superfamily member 10
   219461 bp at 3' side: hypothetical protein LOC170062


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  32523158  GACCTTCTTCATTC  32523171


 Features flanking this part of subject sequence:
   49418 bp at 5' side: adlican
   218937 bp at 3' side: protein kinase, X-linked


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  1193066  CCTTCTTCATTCA  1193054


 Features in this part of subject sequence:
   PDZ domain containing 10


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  10430770  GACCTTCTTCATT  10430782


 Features in this part of subject sequence:
   phosphatidylinositol N-acetylglucosaminyltransferase subu...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  13123072  GACCTTCTTCATT  13123060


 Features flanking this part of subject sequence:
   350128 bp at 5' side: retinoic acid induced 2
   12859 bp at 3' side: hypothetical protein LOC139105


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  15951953  GACCTTCTTCATT  15951941


 Features flanking this part of subject sequence:
   29116 bp at 5' side: mitogen-activated protein kinase kinase kinase 15
   93908 bp at 3' side: SH3-domain kinase binding protein 1 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  17242298  CTTCTTCATTCAC  17242310


 Features in this part of subject sequence:
   SH3-domain kinase binding protein 1 isoform a
```

```
    SH3-domain kinase binding protein 1 isoform b


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  17424698  CTTCTTCATTCAC  17424710


  Features in this part of subject sequence:
    small muscle protein, X-linked


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  19540133  CCTTCTTCATTCA  19540121


  Features flanking this part of subject sequence:
    40560 bp at 5' side: zinc finger protein 645
    121216 bp at 3' side: similar to methyltransferase 5 domain containing 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  20114629  CTTCTTCATTCAC  20114641


  Features flanking this part of subject sequence:
    161608 bp at 5' side: interleukin 1 receptor accessory protein-like 1
    101141 bp at 3' side: melanoma antigen family B, 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  27917240  CTTCTTCATTCAC  27917228


  Features flanking this part of subject sequence:
    2740141 bp at 5' side: dystrophin Dp40 isoform
    122921 bp at 3' side: hypothetical protein LOC158724


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  31806782  CCTTCTTCATTCA  31806770


  Features flanking this part of subject sequence:
    118220 bp at 5' side: hypothetical protein LOC170062
    648277 bp at 3' side: similar to melanoma antigen family B, 18


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  32862801  CCTTCTTCATTCA  32862789


>ref|NT_011519.10|Hs22_11676 D Homo sapiens chromosome 22 genomic contig, referenc
Length=3661581

                                                            Sort alignments for this s
```

```
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   41223 bp at 5' side: CDS
   6517 bp at 3' side: GRB2-associated binding protein family, member 4


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  9       ACCTTCTTCATTCAC  23
               |||||||||||||||
Sbjct  589256  ACCTTCTTCATTCAC  589242


 Features flanking this part of subject sequence:
   3282 bp at 5' side: similar to carbonic anhydrase 15
   300 bp at 3' side: integral membrane protein DGCR2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  2178216  ACCTTCTTCATTC  2178228


>ref|NT_025028.13|Hs18_25184 D Homo sapiens chromosome 18 genomic contig, referenc
Length=20074199
                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features in this part of subject sequence:
   RAB27B, member RAS oncogene family


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  1       ATCTTTCGACCTTCT  15
               |||||||||||||||
Sbjct  341134  ATCTTTCGACCTTCT  341120


 Features flanking this part of subject sequence:
   290563 bp at 5' side: transcription factor 4 isoform b
   151149 bp at 3' side: hypothetical protein LOC642484


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  1335786  CTTCTTCATTCAC  1335774


 Features flanking this part of subject sequence:
   368557 bp at 5' side: hypothetical protein
   138380 bp at 3' side: thioredoxin-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  1922742  CTTCTTCATTCAC  1922730


 Features in this part of subject sequence:
   rabconnectin-3 beta isoform 1
   rabconnectin-3 beta isoform 2
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  2389396  CCTTCTTCATTCA  2389408


 Features flanking this part of subject sequence:
   86165 bp at 5' side: collagen and calcium binding EGF domains 1
   116659 bp at 3' side: phorbol-12-myristate-13-acetate-induced protein 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  5241597  CCTTCTTCATTCA  5241585


 Features flanking this part of subject sequence:
   498539 bp at 5' side: cadherin 19, type 2 preproprotein
   440215 bp at 3' side: hypothetical protein LOC92126


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  12528826  CCTTCTTCATTCA  12528838


 Features in this part of subject sequence:
   cytochrome b-5 isoform 1
   cytochrome b-5 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  19719826  CTTCTTCATTCAC  19719838


>ref|NT_010194.16|Hs15_10351 D Homo sapiens chromosome 15 genomic contig, referenc
Length=53619965

                                                         Sort alignments for this s
                                                           E value  Score  Percent :
                                                           Query start position  Sul

 Features in this part of subject sequence:
   acidic (leucine-rich) nuclear phosphoprotein 32 family, m...


 Score = 30.2 bits (15),  Expect =    28
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query  2         TCTTTCGACCTTCTTCATT  20
                 |||||| ||||||||||||
Sbjct  39871641  TCTTTCTACCTTCTTCATT  39871623


 Features in this part of subject sequence:
   fibrous sheath interacting protein 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  10766187  GACCTTCTTCATTC  10766200


 Features in this part of subject sequence:
```

sperm-associated cation channel 2 isoform 2
sperm-associated cation channel 2 isoform 1

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query  2         TCTTTCGACCTTCTTCAT  19
                 |||||| |||||||||||
Sbjct  14724214  TCTTTCAACCTTCTTCAT  14724231
```

Features flanking this part of subject sequence:
38552 bp at 5' side: creatine kinase, mitochondrial 1A precursor
8882 bp at 3' side: protein disulfide isomerase-associated 3 precursor

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query  2         TCTTTCGACCTTCTTCAT  19
                 |||||| |||||||||||
Sbjct  14820396  TCTTTCAACCTTCTTCAT  14820413
```

Features in this part of subject sequence:
transcription factor 12 isoform b
transcription factor 12 isoform a

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 20/22 (90%), Gaps = 0/22 (0%)
 Strand=Plus/Minus

Query  1         ATCTTTCGACCTTCTTCATTCA  22
                 |||||| |||| ||||||||||
Sbjct  28074396  ATCTTTAGACCATCTTCATTCA  28074375
```

Features flanking this part of subject sequence:
124452 bp at 5' side: talin 2
77755 bp at 3' side: tropomyosin 1 alpha chain isoform 3

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  2         TCTTTCGACCTTCT  15
                 ||||||||||||||
Sbjct  34047579  TCTTTCGACCTTCT  34047592
```

Features in this part of subject sequence:
thrombospondin, type I, domain containing 4

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  42432016  CCTTCTTCATTCAC  42432029
```

Features flanking this part of subject sequence:
38230 bp at 5' side: hypothetical protein LOC400359
515349 bp at 3' side: hypothetical protein LOC400360

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  9819533  CCTTCTTCATTCA  9819545
```

Features in this part of subject sequence:
spectrin, beta, non-erythrocytic 5

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  12943128  CCTTCTTCATTCA  12943116


 Features in this part of subject sequence:
   similar to StAR-related lipid transfer protein 9 (StARD9)...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         CGACCTTCTTCAT  19
                 |||||||||||||
Sbjct  13776556  CGACCTTCTTCAT  13776568


 Features flanking this part of subject sequence:
   5234 bp at 5' side: Numb-interacting protein
   3707 bp at 3' side: dual oxidase 1 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  16211003  CCTTCTTCATTCA  16211015


 Features in this part of subject sequence:
   solute carrier family 28 (sodium-coupled nucleoside trans...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  16336787  ACCTTCTTCATTC  16336775


 Features flanking this part of subject sequence:
   915243 bp at 5' side: sulfide dehydrogenase like
   1153513 bp at 3' side: semaphorin 6D isoform 6 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  17689040  GACCTTCTTCATT  17689028


 Features in this part of subject sequence:
   myosin VC


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  23317892  CCTTCTTCATTCA  23317904


 Features flanking this part of subject sequence:
   450539 bp at 5' side: similar to 40S ribosomal protein SA (p40) (34/67 kDa lami.
   180675 bp at 3' side: WD repeat domain 72


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  24419766  CTTCTTCATTCAC  24419778


 Features flanking this part of subject sequence:
   18422 bp at 5' side: suppressor of hairy wing homolog 4 isoform 3
   120789 bp at 3' side: similar to Acyl-CoA-binding protein (ACBP) (Diazepam-bind.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 19/21 (90%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query  2         TCTTTCGACCTTCTTCATTCA  22
                 |||| ||||||||| ||||||
Sbjct  27808286  TCTTACGACCTTCTGCATTCA  27808306


 Features in this part of subject sequence:
   transcription factor 12 isoform b
   transcription factor 12 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  28290729  TTCTTCATTCACG  28290717


 Features flanking this part of subject sequence:
   71297 bp at 5' side: hypothetical protein
   904 bp at 3' side: aquaporin 9


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  29220418  CTTCTTCATTCAC  29220406


 Features flanking this part of subject sequence:
   114588 bp at 5' side: RAR-related orphan receptor A isoform a
   510639 bp at 3' side: vacuolar protein sorting 13C protein isoform 1A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         ATCTTTCGACCTT  13
                 |||||||||||||
Sbjct  32426562  ATCTTTCGACCTT  32426574


 Features flanking this part of subject sequence:
   126579 bp at 5' side: RAR-related orphan receptor A isoform a
   498648 bp at 3' side: vacuolar protein sorting 13C protein isoform 1A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  32438553  CCTTCTTCATTCA  32438565


 Features flanking this part of subject sequence:
   41188 bp at 5' side: guanine nucleotide exchange factor p532
   91697 bp at 3' side: death-associated protein kinase 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  34899340  CCTTCTTCATTCA  34899328


 Features in this part of subject sequence:
   casein kinase 1, gamma 1 isoform S


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  35315057  ACCTTCTTCATTC  35315069


 Features in this part of subject sequence:
   myosin IXA


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  42957483  CTTCTTCATTCAC  42957495


 Features flanking this part of subject sequence:
   211 bp at 5' side: cytochrome P450, family 1, subfamily A, polypeptide 1
   26419 bp at 3' side: cytochrome P450, family 1, subfamily A, polypeptide 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  45805967  CCTTCTTCATTCA  45805979


 Features in this part of subject sequence:
   similar to taste receptor protein 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  4         TTTCGACCTTCTTCATT  20
                 |||| ||||||||||||
Sbjct  46329702  TTTCAACCTTCTTCATT  46329718


 Features in this part of subject sequence:
   transcriptional co-repressor Sin3A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  4         TTTCGACCTTCTTCATT  20
                 |||| ||||||||||||
Sbjct  46464806  TTTCAACCTTCTTCATT  46464822


 Features in this part of subject sequence:
   neuregulin 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  47050676  CTTCTTCATTCAC  47050664


 Features flanking this part of subject sequence:
```

```
    48701 bp at 5' side: similar to uncharacterized protein family UPF0227 member ..
    70797 bp at 3' side: KIAA1199


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  51885732  TTCTTCATTCACG  51885744


>ref|NT_026437.11|Hs14_26604 D Homo sapiens chromosome 14 genomic contig, referenc
Length=88290585

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

  Features flanking this part of subject sequence:
    1336324 bp at 5' side: hypothetical protein
    1394502 bp at 3' side: hypothetical protein


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Minus

Query  9         ACCTTCTTCATTCAC  23
                 |||||||||||||||
Sbjct  65600278  ACCTTCTTCATTCAC  65600264


  Features in this part of subject sequence:
    regulator of G-protein signalling 6


  Score = 28.2 bits (14),  Expect =   112
  Identities = 17/18 (94%), Gaps = 0/18 (0%)
  Strand=Plus/Plus

Query  4         TTTCGACCTTCTTCATTC  21
                 |||| |||||||||||||
Sbjct  53436078  TTTCTACCTTCTTCATTC  53436095


  Features flanking this part of subject sequence:
    815198 bp at 5' side: hypothetical protein
    230413 bp at 3' side: hypothetical protein


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  64024403  CCTTCTTCATTCAC  64024416


  Features flanking this part of subject sequence:
    945069 bp at 5' side: hypothetical protein
    100538 bp at 3' side: hypothetical protein


  Score = 28.2 bits (14),  Expect =   112
  Identities = 17/18 (94%), Gaps = 0/18 (0%)
  Strand=Plus/Minus

Query  4         TTTCGACCTTCTTCATTC  21
                 |||| |||||||||||||
Sbjct  64154291  TTTCCACCTTCTTCATTC  64154274


  Features flanking this part of subject sequence:
    24153 bp at 5' side: olfactory receptor, family 4, subfamily K, member 13
    1122 bp at 3' side: olfactory receptor, family 4, subfamily L, member 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus
```

```
Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  1526910  CCTTCTTCATTCA  1526922


 Features flanking this part of subject sequence:
   6825 bp at 5' side: olfactory receptor, family 11, subfamily G, member 2
   18500 bp at 3' side: olfactory receptor, family 11, subfamily H, member 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4        TTTCGACCTTCTT  16
                |||||||||||||
Sbjct  1673209  TTTCGACCTTCTT  1673197


 Features flanking this part of subject sequence:
   34609 bp at 5' side: ribonuclease, RNase A family, 12 (non-active)
   15352 bp at 3' side: olfactory receptor, family 6, subfamily S, member 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  2093343  ACCTTCTTCATTC  2093331


 Features in this part of subject sequence:
   solute carrier family 7 (cationic amino acid transporter,...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  4272016  CCTTCTTCATTCA  4272028


 Features flanking this part of subject sequence:
   22418 bp at 5' side: homeodomain leucine zipper protein
   1851 bp at 3' side: similar to Protein phosphatase 1 regulatory subunit 3D (P...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  4768634  CCTTCTTCATTCA  4768622


 Features flanking this part of subject sequence:
   22077 bp at 5' side: dehydrogenase/reductase (SDR family) member 2 isoform 2
   157202 bp at 3' side: similar to dehydrogenase/reductase (SDR family) member 2 .


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  5136379  CCTTCTTCATTCA  5136391


 Features flanking this part of subject sequence:
   13446 bp at 5' side: amisyn
   278788 bp at 3' side: similar to Nonhistone chromosomal protein HMG-17 (High-mo.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
```

```
Sbjct  6457310  CCTTCTTCATTCA  6457322


 Features flanking this part of subject sequence:
   7320 bp at 5' side: adaptor-related protein complex 4, sigma 1 subunit
   8716 bp at 3' side: HECT domain containing 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  12561159  CCTTCTTCATTCA  12561171


 Features flanking this part of subject sequence:
   72853 bp at 5' side: MAM domain containing 1
   470248 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  28673550  ACCTTCTTCATTC  28673562


 Features flanking this part of subject sequence:
   350911 bp at 5' side: MAM domain containing 1
   192190 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  28951608  CCTTCTTCATTCA  28951620


 Features flanking this part of subject sequence:
   1841974 bp at 5' side: hypothetical protein
   52072 bp at 3' side: ribosomal protein S29 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  30992208  ACCTTCTTCATTC  30992196


 Features flanking this part of subject sequence:
   97109 bp at 5' side: ADP-ribosylation factor 6
   919 bp at 3' side: hypothetical protein LOC283551


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  31457841  CTTCTTCATTCAC  31457853


 Features flanking this part of subject sequence:
   63009 bp at 5' side: nidogen 2
   23859 bp at 3' side: similar to Integrin alpha-3 precursor (Galactoprotein B3)..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  33598471  CTTCTTCATTCAC  33598483
```

```
 Features flanking this part of subject sequence:
   101368 bp at 5' side: orthodenticle 2 isoform b
   301773 bp at 3' side: SEC10 protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  38373295  TTCTTCATTCACG  38373307


 Features in this part of subject sequence:
   retinoblastoma-binding protein 1 isoform III
   retinoblastoma-binding protein 1 isoform II


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  39793142  TTCTTCATTCACG  39793130


 Features flanking this part of subject sequence:
   165187 bp at 5' side: small nuclear RNA activating complex, polypeptide 1, 43kDa
   35838 bp at 3' side: synaptotagmin XIV-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  43426641  CCTTCTTCATTCA  43426653


 Features in this part of subject sequence:
   synaptotagmin XIV-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  43479980  CTTCTTCATTCAC  43479992


 Features in this part of subject sequence:
   hypothetical protein LOC9766


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  51137413  CTTCTTCATTCAC  51137401


 Features flanking this part of subject sequence:
   86130 bp at 5' side: v-fos FBJ murine osteosarcoma viral oncogene homolog
   60285 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  56834022  CCTTCTTCATTCA  56834010


 Features in this part of subject sequence:
```

```
    basic leucine zipper transcription factor, ATF-like


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  9         ACCTTCTTCATTC  21
                  |||||||||||||
 Sbjct  57010097  ACCTTCTTCATTC  57010109


  Features in this part of subject sequence:
    serine palmitoyltransferase, long chain base subunit 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  11        CTTCTTCATTCAC  23
                  |||||||||||||
 Sbjct  59062684  CTTCTTCATTCAC  59062672


  Features in this part of subject sequence:
    neurexin 3 isoform alpha precursor


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  60254484  CCTTCTTCATTCA  60254496


  Features flanking this part of subject sequence:
    1310519 bp at 5' side: hypothetical protein
    1420309 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  65574471  CCTTCTTCATTCA  65574459


  Features in this part of subject sequence:
    calponin like transmembrane domain protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  9         ACCTTCTTCATTC  21
                  |||||||||||||
 Sbjct  76777911  ACCTTCTTCATTC  76777923


  Features flanking this part of subject sequence:
    10638 bp at 5' side: hypothetical protein
    1148090 bp at 3' side: hypothetical protein LOC283598


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  11        CTTCTTCATTCAC  23
                  |||||||||||||
 Sbjct  79034192  CTTCTTCATTCAC  79034180


  Features flanking this part of subject sequence:
    26423 bp at 5' side: hypothetical protein
    1132305 bp at 3' side: hypothetical protein LOC283598


  Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  79049977  CTTCTTCATTCAC  79049965


 Features in this part of subject sequence:
   solute carrier family 25, member 29 isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  81769145  CTTCTTCATTCAC  81769133


 Features in this part of subject sequence:
   WD repeat domain 20 isoform 1
   WD repeat domain 20 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  83675266  GACCTTCTTCATT  83675278


>ref|NT_009775.16|Hs12_9932 D Homo sapiens chromosome 12 genomic contig, reference
Length=13091146

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

 Features flanking this part of subject sequence:
   303856 bp at 5' side: suppressor of defective silencing 3
   263580 bp at 3' side: KIAA1853 protein


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTCAC  23
                |||||||||||||||
Sbjct  9725617  ACCTTCTTCATTCAC  9725603


 Features flanking this part of subject sequence:
   256440 bp at 5' side: thyroid hormone receptor associated protein 2
   1043 bp at 3' side: hypothetical protein LOC400077


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  7540885  CCTTCTTCATTCAC  7540898


 Features in this part of subject sequence:
   suppressor of defective silencing 3


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCACG  24
                ||||||||||||||
Sbjct  9406455  CTTCTTCATTCACG  9406442


 Features flanking this part of subject sequence:
```

```
    31913 bp at 5' side: mitochondrial aldehyde dehydrogenase 2 precursor
    1234 bp at 3' side: mitogen-activated protein kinase-activated protein kinase...


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  12       TTCTTCATTCACG  24
                 |||||||||||||
 Sbjct  2848813  TTCTTCATTCACG  2848801


  Features flanking this part of subject sequence:
    48752 bp at 5' side: hypothetical protein LOC283450
    86057 bp at 3' side: ribosomal protein L6


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  11       CTTCTTCATTCAC  23
                 |||||||||||||
 Sbjct  3326468  CTTCTTCATTCAC  3326480


  Features flanking this part of subject sequence:
    19995 bp at 5' side: thyroid hormone receptor associated protein 2
    237489 bp at 3' side: hypothetical protein LOC400077


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10       CCTTCTTCATTCA  22
                 |||||||||||||
 Sbjct  7304452  CCTTCTTCATTCA  7304440


 >ref|NT_033927.7|Hs11_34082 D Homo sapiens chromosome 11 genomic contig, reference
 Length=17911127
                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

  Features in this part of subject sequence:
    SH3 and multiple ankyrin repeat domains 2 isoform 1


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Minus

 Query  2       TCTTTCGACCTTCTT  16
                |||||||||||||||
 Sbjct  545285  TCTTTCGACCTTCTT  545271


  Features flanking this part of subject sequence:
    165048 bp at 5' side: chapsyn-110
    543517 bp at 3' side: hypothetical protein LOC55863


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

 Query  9         ACCTTCTTCATTCA  22
                  ||||||||||||||
 Sbjct  15021972  ACCTTCTTCATTCA  15021959


  Features flanking this part of subject sequence:
    303665 bp at 5' side: similar to odd Oz/ten-m homolog 4
    1280287 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 16/17 (94%), Gaps = 0/17 (0%)
  Strand=Plus/Minus
```

```
Query  1        ATCTTTCGACCTTCTTC  17
                |||||||||||| ||||
Sbjct  9307419  ATCTTTCGACCTCCTTC  9307403


 Features flanking this part of subject sequence:
   763264 bp at 5' side: similar to odd Oz/ten-m homolog 4
   820692 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  9767002  ACCTTCTTCATTC  9767014


 Features flanking this part of subject sequence:
   1410731 bp at 5' side: similar to odd Oz/ten-m homolog 4
   173225 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  10414469  ACCTTCTTCATTC  10414481


 Features flanking this part of subject sequence:
   644135 bp at 5' side: hypothetical protein
   1391327 bp at 3' side: similar to 40S ribosomal protein S28 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  11232011  CCTTCTTCATTCA  11232023


 Features in this part of subject sequence:
   chapsyn-110


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  14825547  CTTCTTCATTCAC  14825559


>ref|NT_030059.12|Hs10_30314 D Homo sapiens chromosome 10 genomic contig, referenc
Length=44617998

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   75539 bp at 5' side: hypothetical protein LOC143384
   41734 bp at 3' side: similar to 60S ribosomal protein L17 (L23) (Amino acid st..


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTCA  22
                 |||||||||||||||
Sbjct  39338339  GACCTTCTTCATTCA  39338353


 Features flanking this part of subject sequence:
   2051 bp at 5' side: cytochrome P450, family 2, subfamily C, polypeptide 9
   46032 bp at 3' side: cytochrome P450, family 2, subfamily C, polypeptide 8 iso..
```

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query  3         CTTTCGACCTTCTTCATT  20
                 ||||| ||||||||||||
Sbjct  15499362  CTTTCAACCTTCTTCATT  15499379


 Features in this part of subject sequence:
   neuregulin 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  2484648  CCTTCTTCATTCA  2484660


 Features in this part of subject sequence:
   neuregulin 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  2659954  CCTTCTTCATTCA  2659942


 Features flanking this part of subject sequence:
   5003 bp at 5' side: interferon-induced protein with tetratricopeptide repeats...
   2960 bp at 3' side: interferon-induced protein with tetratricopeptide repeats...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  9898026  CTTCTTCATTCAC  9898014


 Features in this part of subject sequence:
   SEC15-like 1 isoform b
   SEC15-like 1 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  13566481  CTTCTTCATTCAC  13566493


 Features in this part of subject sequence:
   cytochrome P450, family 2, subfamily C, polypeptide 19


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  15353227  CTTCTTCATTCAC  15353239


 Features in this part of subject sequence:
   B-cell linker


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  16751994  CCTTCTTCATTCA  16752006


 Features in this part of subject sequence:
   beta-transducin repeat containing protein isoform 2
   beta-transducin repeat containing protein isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  21881715  ACCTTCTTCATTC  21881703


 Features in this part of subject sequence:
   hypothetical protein LOC80217


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  24697700  ACCTTCTTCATTC  24697712


 Features flanking this part of subject sequence:
   961800 bp at 5' side: SORCS receptor 1 isoform a
   1738846 bp at 3' side: X-prolyl aminopeptidase (aminopeptidase P) 1, soluble


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  28634610  CTTCTTCATTCAC  28634622


 Features in this part of subject sequence:
   mitochondrial glycerol 3-phosphate acyltransferase


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  32674932  CCTTCTTCATTCA  32674920


>ref|NT_008470.18|Hs9_8627 D Homo sapiens chromosome 9 genomic contig, reference as
Length=40394265

                                                               Sort alignments for this s
                                                                 E value  Score  Percent i
                                                                 Query start position  Sul

 Features flanking this part of subject sequence:
   39230 bp at 5' side: protein tyrosine phosphatase domain containing 1 protein ..
   145159 bp at 3' side: zinc finger protein 169


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCACG  24
                |||||||||||||||
Sbjct  4230675  CCTTCTTCATTCACG  4230661


 Features in this part of subject sequence:
   hypothetical protein LOC552891
```

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  21730036  CCTTCTTCATTCAC  21730023


 Features flanking this part of subject sequence:
   65418 bp at 5' side: hypothetical protein
   42064 bp at 3' side: Di-Ras2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10      CCTTCTTCATTCA  22
               |||||||||||||
Sbjct  654650  CCTTCTTCATTCA  654638


 Features flanking this part of subject sequence:
   170921 bp at 5' side: nuclear factor, interleukin 3 regulated
   141991 bp at 3' side: receptor tyrosine kinase-like orphan receptor 2 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  2        TCTTTCGACCTTCTTCA  18
                |||||| ||||||||||
Sbjct  1665158  TCTTTCTACCTTCTTCA  1665142


 Features flanking this part of subject sequence:
   1028681 bp at 5' side: protein phosphatase 3 regulatory subunit B, beta isoform
   371758 bp at 3' side: cylicin 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  12707098  CTTCTTCATTCAC  12707110


 Features flanking this part of subject sequence:
   53164 bp at 5' side: olfactory receptor, family 13, subfamily C, member 9
   23042 bp at 3' side: olfactory receptor, family 13, subfamily D, member 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  14754866  ACCTTCTTCATTC  14754854


 Features flanking this part of subject sequence:
   340474 bp at 5' side: hypothetical protein LOC644602
   522611 bp at 3' side: zinc finger protein 462


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  16484247  ACCTTCTTCATTC  16484259


 Features in this part of subject sequence:
   hypothetical protein LOC401546


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  20287232  ACCTTCTTCATTC  20287244


 Features flanking this part of subject sequence:
   58774 bp at 5' side: regulator of G-protein signalling 3 isoform 4
   380623 bp at 3' side: zinc finger protein 618


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  23739224  GACCTTCTTCATT  23739212


 Features in this part of subject sequence:
   tenascin C (hexabrachion)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  25117356  CCTTCTTCATTCA  25117344


 Features flanking this part of subject sequence:
   828457 bp at 5' side: toll-like receptor 4 precursor
   623967 bp at 3' side: deleted in bladder cancer 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  28626600  CTTCTTCATTCAC  28626588


 Features flanking this part of subject sequence:
   1165288 bp at 5' side: toll-like receptor 4 precursor
   287136 bp at 3' side: deleted in bladder cancer 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  28963419  CTTCTTCATTCAC  28963431


 Features flanking this part of subject sequence:
   75961 bp at 5' side: DENN/MADD domain containing 1A isoform 2
   6471 bp at 3' side: LIM homeobox protein 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  34089362  CCTTCTTCATTCA  34089350


 Features in this part of subject sequence:
   mitogen-activated protein kinase associated protein 1 iso...
   mitogen-activated protein kinase associated protein 1 iso...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  35650091  CTTCTTCATTCAC  35650103


>ref|NT_008183.18|Hs8_8340 D Homo sapiens chromosome 8 genomic contig, reference a
Length=38454502

                                                             Sort alignments for this s
                                                               E value  Score  Percent
                                                               Query start position  Su

 Features in this part of subject sequence:
   staufen homolog 2


 Score = 30.2 bits (15),  Expect =    28
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query  2         TCTTTCGACCTTCTTCATT  20
                 |||||| ||||||||||||
Sbjct  26449502  TCTTTCCACCTTCTTCATT  26449484


 Features in this part of subject sequence:
   hypothetical protein LOC23514


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9       ACCTTCTTCATTC  21
               |||||||||||||
Sbjct  239207  ACCTTCTTCATTC  239195


 Features flanking this part of subject sequence:
   209806 bp at 5' side: ubiquitin-conjugating enzyme E2 variant 2
   319903 bp at 3' side: hypothetical protein LOC401459


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  1036558  CTTCTTCATTCAC  1036546


 Features flanking this part of subject sequence:
   23890 bp at 5' side: coiled-coil-helix-coiled-coil-helix domain containing 7 i..
   61073 bp at 3' side: epidermal retinal dehydrogenase 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3        CTTTCGACCTTCT  15
                |||||||||||||
Sbjct  9006307  CTTTCGACCTTCT  9006319


 Features flanking this part of subject sequence:
   352628 bp at 5' side: thymus high mobility group box protein TOX
   737158 bp at 3' side: carbonic anhydrase VIII


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  12237539  TTCTTCATTCACG  12237527


 Features flanking this part of subject sequence:
   40144 bp at 5' side: chromodomain helicase DNA binding protein 7
   393739 bp at 3' side: hypothetical protein LOC157807
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  13671989  ACCTTCTTCATTC  13672001


 Features in this part of subject sequence:
   hypothetical protein LOC286183


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  15238641  CCTTCTTCATTCA  15238629


 Features flanking this part of subject sequence:
   1139687 bp at 5' side: YTH domain family, member 3
   19876 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  17115316  CCTTCTTCATTCA  17115304


 Features flanking this part of subject sequence:
   178251 bp at 5' side: carboxypeptidase B precursor
   28003 bp at 3' side: DEP domain containing 2 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  20689968  CTTCTTCATTCAC  20689980


 Features flanking this part of subject sequence:
   5184 bp at 5' side: PR domain containing 14
   38576 bp at 3' side: nuclear receptor coactivator 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  22840644  GACCTTCTTCATT  22840632


 Features flanking this part of subject sequence:
   438715 bp at 5' side: ankyrin-like protein 1
   53599 bp at 3' side: potassium voltage-gated channel, Shab-related subfamily, ..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  25279724  CTTCTTCATTCAC  25279712


 Features in this part of subject sequence:
   potassium voltage-gated channel, Shab-related subfamily, ...


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  25421139  CTTCTTCATTCAC  25421127


 Features in this part of subject sequence:
   potassium voltage-gated channel, Shab-related subfamily, ...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  25667832  CCTTCTTCATTCA  25667820


 Features flanking this part of subject sequence:
   432282 bp at 5' side: cocoacrisp
   79298 bp at 3' side: hepatocyte nuclear factor 4, gamma


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  28230113  CCTTCTTCATTCA  28230125


 Features flanking this part of subject sequence:
   900405 bp at 5' side: peroxisomal membrane protein 3
   713789 bp at 3' side: cAMP-dependent protein kinase inhibitor alpha isoform 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  30650173  TTCTTCATTCACG  30650185


>ref|NT_007592.14|Hs6_7749 D Homo sapiens chromosome 6 genomic contig, reference as
Length=48945890

                                                             Sort alignments for this s
                                                               E value  Score  Percent 
                                                               Query start position  Sul

 Features flanking this part of subject sequence:
   10302 bp at 5' side: H4 histone family, member H
   72368 bp at 3' side: butyrophilin, subfamily 3, member A2 precursor


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTCA  22
                 |||||||||||||||
Sbjct  17154280  GACCTTCTTCATTCA  17154294


 Features flanking this part of subject sequence:
   7225 bp at 5' side: testis-specific histone H2B
   27433 bp at 3' side: solute carrier family 17 (sodium phosphate), member 4


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  16593009  CCTTCTTCATTCAC  16592996
```

```
 Features flanking this part of subject sequence:
   432921 bp at 3' side: MRDS1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9       ACCTTCTTCATTC  21
               |||||||||||||
Sbjct  322442  ACCTTCTTCATTC  322454


 Features flanking this part of subject sequence:
   265257 bp at 5' side: neural precursor cell expressed, developmentally down-reg.
   216694 bp at 3' side: hypothetical protein LOC84830


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  2356263  CCTTCTTCATTCA  2356275


 Features flanking this part of subject sequence:
   75849 bp at 5' side: human immunodeficiency virus type I enhancer binding prot..
   50308 bp at 3' side: endothelin 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  3098813  CTTCTTCATTCAC  3098801


 Features flanking this part of subject sequence:
   71102 bp at 5' side: endothelin 1
   146928 bp at 3' side: similar to ribosomal protein L15 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  3225660  CTTCTTCATTCAC  3225672


 Features in this part of subject sequence:
   dystrobrevin binding protein 1 isoform a
   dystrobrevin binding protein 1 isoform c


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  6424936  ACCTTCTTCATTC  6424948


 Features flanking this part of subject sequence:
   662647 bp at 5' side: ataxin 1
   138227 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  7849439  CTTCTTCATTCAC  7849451


 Features flanking this part of subject sequence:
   558519 bp at 5' side: hypothetical protein
```

```
    858030 bp at 3' side: vesicular membrane protein p24


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  14134765  CCTTCTTCATTCA  14134777


  Features flanking this part of subject sequence:
    605909 bp at 5' side: hypothetical protein
    810640 bp at 3' side: vesicular membrane protein p24


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  9         ACCTTCTTCATTC  21
                  |||||||||||||
 Sbjct  14182155  ACCTTCTTCATTC  14182167


  Features flanking this part of subject sequence:
    800197 bp at 5' side: hypothetical protein
    616352 bp at 3' side: vesicular membrane protein p24


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  14376443  CCTTCTTCATTCA  14376455


  Features flanking this part of subject sequence:
    2149 bp at 5' side: hypothetical protein LOC285830
    76715 bp at 3' side: major histocompatibility complex, class I, G precursor


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  9         ACCTTCTTCATTC  21
                  |||||||||||||
 Sbjct  20577158  ACCTTCTTCATTC  20577146


  Features flanking this part of subject sequence:
    12348 bp at 5' side: tripartite motif protein 31 isoform beta
    11872 bp at 3' side: tripartite motif-containing 40


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  20951193  CCTTCTTCATTCA  20951181


  Features in this part of subject sequence:
    testis expressed sequence 27


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  11        CTTCTTCATTCAC  23
                  |||||||||||||
 Sbjct  28710803  CTTCTTCATTCAC  28710791


  Features flanking this part of subject sequence:
    13612 bp at 5' side: hypothetical protein LOC401263
    1349477 bp at 3' side: methylmalonyl Coenzyme A mutase precursor
```

```
  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  38908195  CCTTCTTCATTCA  38908183


  Features in this part of subject sequence:
    hypothetical protein LOC55166


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  8         GACCTTCTTCATT  20
                  |||||||||||||
 Sbjct  40307010  GACCTTCTTCATT  40306998


  Features flanking this part of subject sequence:
    82211 bp at 5' side: defensin, beta 112
    583182 bp at 3' side: transcription factor AP-2 beta-like 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  2         TCTTTCGACCTTC  14
                  |||||||||||||
 Sbjct  40956806  TCTTTCGACCTTC  40956818


  Features flanking this part of subject sequence:
    543289 bp at 5' side: transcription factor AP-2 beta (activating enhancer bindi.
    129473 bp at 3' side: polyductin isoform 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  42212625  CCTTCTTCATTCA  42212637


 >ref|NT_016354.18|Hs4_16510 D Homo sapiens chromosome 4 genomic contig, reference a
 Length=92123751

                                                                Sort alignments for this s
                                                                  E value  Score  Percent i
                                                                  Query start position  Sul

  Features in this part of subject sequence:
    sodium-dependent organic anion transporter


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Plus

 Query  9         ACCTTCTTCATTCAC  23
                  |||||||||||||||
 Sbjct  12292643  ACCTTCTTCATTCAC  12292657


  Features flanking this part of subject sequence:
    33289 bp at 5' side: endothelin receptor type A
    42035 bp at 3' side: transmembrane protein 34


  Score = 30.2 bits (15),  Expect =    28
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Plus

 Query  9         ACCTTCTTCATTCAC  23
                  |||||||||||||||
 Sbjct  73045206  ACCTTCTTCATTCAC  73045220
```

```
 Features flanking this part of subject sequence:
   44377 bp at 5' side: ankyrin repeat domain 56
   7665 bp at 3' side: septin 11


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTCA  22
                ||||||||||||||
Sbjct  2411113  ACCTTCTTCATTCA  2411100


 Features in this part of subject sequence:
   family with sequence similarity 13, member A1 isoform a
   family with sequence similarity 13, member A1 isoform b


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  14277489  CCTTCTTCATTCAC  14277476


 Features in this part of subject sequence:
   glutamate receptor, ionotropic, delta 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  18191066  CCTTCTTCATTCAC  18191053


 Features in this part of subject sequence:
   glutamate receptor, ionotropic, delta 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  18908993  CCTTCTTCATTCAC  18908980


 Features in this part of subject sequence:
   protein phosphatase 3 (formerly 2B), catalytic subunit, a...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  26674486  ACCTTCTTCATTCA  26674499


 Features flanking this part of subject sequence:
   5970 bp at 5' side: Sm protein F
   21314 bp at 3' side: similar to stromal cell derived factor receptor 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  71664938  GACCTTCTTCATTC  71664925


 Features flanking this part of subject sequence:
   489418 bp at 5' side: acidic nuclear phosphoprotein 32C
   256148 bp at 3' side: similar to nascent polypeptide-associated complex alpha p.
```

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  90156428  ACCTTCTTCATTCA  90156441


 Features flanking this part of subject sequence:
   138395 bp at 5' side: betacellulin
   596 bp at 3' side: DKFZP564O0823 protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8       GACCTTCTTCATT  20
               |||||||||||||
Sbjct  405663  GACCTTCTTCATT  405651


 Features flanking this part of subject sequence:
   787666 bp at 5' side: hypothetical protein LOC84803
   100844 bp at 3' side: NK6 transcription factor related, locus 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        ATCTTTCGACCTT  13
                |||||||||||||
Sbjct  9861307  ATCTTTCGACCTT  9861319


 Features in this part of subject sequence:
   Rho GTPase activating protein 24 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  11080746  CCTTCTTCATTCA  11080758


 Features flanking this part of subject sequence:
   45513 bp at 5' side: hypothetical protein LOC285513
   430993 bp at 3' side: alpha-synuclein isoform NACP140


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  14764506  CTTCTTCATTCAC  14764494


 Features flanking this part of subject sequence:
   737051 bp at 5' side: hypothetical protein
   242388 bp at 3' side: glutamate receptor, ionotropic, delta 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  17531140  ACCTTCTTCATTC  17531128


 Features in this part of subject sequence:
   glutamate receptor, ionotropic, delta 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
```

```
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  17938179  ACCTTCTTCATTC  17938167


 Features in this part of subject sequence:
   alcohol dehydrogenase 1B (class I), beta polypeptide


 Score = 26.3 bits (13),  Expect =   444
 Identities = 19/21 (90%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query  1         ATCTTTCGACCTTCTTCATTC  21
                 ||||||| ||||| |||||||
Sbjct  24779559  ATCTTTCCACCTTTTTCATTC  24779579


 Features flanking this part of subject sequence:
   51090 bp at 5' side: hypothetical protein isoform 2
   62889 bp at 3' side: hypothetical protein LOC54790


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  30640345  ACCTTCTTCATTC  30640357


 Features flanking this part of subject sequence:
   47442 bp at 5' side: glutamyl aminopeptidase (aminopeptidase A)
   9109 bp at 3' side: paired-like homeodomain transcription factor 2 isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  4         TTTCGACCTTCTTCATT  20
                 |||| ||||||||||||
Sbjct  36078318  TTTCTACCTTCTTCATT  36078302


 Features flanking this part of subject sequence:
   1967324 bp at 5' side: N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4
   39907 bp at 3' side: translocation associated membrane protein 1-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  3         CTTTCGACCTTCTTCAT  19
                 |||||| ||||||||||
Sbjct  42513678  CTTTCGCCCTTCTTCAT  42513662


 Features flanking this part of subject sequence:
   512628 bp at 5' side: translocation associated membrane protein 1-like 1
   455877 bp at 3' side: N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  43067322  CCTTCTTCATTCA  43067334


 Features flanking this part of subject sequence:
   54423 bp at 5' side: annexin 5
   9270 bp at 3' side: hypothetical protein LOC132332


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  47220326  CTTCTTCATTCAC  47220314


 Features in this part of subject sequence:
   spermatogenesis associated factor SPAF


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  48765336  CCTTCTTCATTCA  48765324


 Features flanking this part of subject sequence:
   332485 bp at 5' side: hypothetical protein isoform 1
   671929 bp at 3' side: ankyrin repeat domain 50


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  49466348  CCTTCTTCATTCA  49466360


 Features flanking this part of subject sequence:
   772194 bp at 5' side: hypothetical protein
   2579399 bp at 3' side: protocadherin 10 isoform 1 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  56040032  GACCTTCTTCATT  56040044


 Features flanking this part of subject sequence:
   153019 bp at 5' side: similar to poly(A) binding protein, cytoplasmic 4 (induci.
   590255 bp at 3' side: similar to Ubiquinol-cytochrome c reductase complex ubiqu.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  59823340  CTTCTTCATTCAC  59823352


 Features flanking this part of subject sequence:
   490186 bp at 5' side: hypothetical protein
   767664 bp at 3' side: similar to Telomeric repeat-binding factor 1 (TTAGGG repe.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  61057029  CTTCTTCATTCAC  61057041


 Features flanking this part of subject sequence:
   112999 bp at 5' side: nuclear receptor subfamily 3, group C, member 2
   964825 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
```

```
Sbjct  74019158  ACCTTCTTCATTC  74019170


 Features flanking this part of subject sequence:
   487215 bp at 5' side: PET112-like
   74672 bp at 3' side: F-box protein FBW7 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2         TCTTTCGACCTTC  14
                 |||||||||||||
Sbjct  77717508  TCTTTCGACCTTC  77717496


 Features flanking this part of subject sequence:
   750758 bp at 5' side: hypothetical protein
   300960 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  4         TTTCGACCTTCTTCATT  20
                 |||| ||||||||||||
Sbjct  88277163  TTTCAACCTTCTTCATT  88277147


 Features flanking this part of subject sequence:
   23615 bp at 5' side: tolloid-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  91593802  ACCTTCTTCATTC  91593790


>ref|NT_022517.17|Hs3_22673 D Homo sapiens chromosome 3 genomic contig, reference a
Length=66080833

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent i
                                                                    Query start position  Sul

 Features flanking this part of subject sequence:
   585726 bp at 5' side: 3-oxoacyl-ACP synthase, mitochondrial
   242536 bp at 3' side: hypothetical protein


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTCA  22
                 |||||||||||||||
Sbjct  26361729  GACCTTCTTCATTCA  26361715


 Features flanking this part of subject sequence:
   98085 bp at 5' side: similar to zinc finger protein 611
   17635 bp at 3' side: glycerol-3-phosphate dehydrogenase 1-like


 Score = 30.2 bits (15),  Expect =    28
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTCA  22
                 |||||||||||||||
Sbjct  32070559  GACCTTCTTCATTCA  32070573


 Features in this part of subject sequence:
   special AT-rich sequence binding protein 1


 Score = 28.2 bits (14),  Expect =   112
```

```
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  18354668  CCTTCTTCATTCAC  18354655


 Features flanking this part of subject sequence:
   249479 bp at 5' side: shugoshin-like 1 isoform C1
   412731 bp at 3' side: similar to Mediator of DNA damage checkpoint protein 1 (N.


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  7         CGACCTTCTTCATT  20
                 ||||||||||||||
Sbjct  20415002  CGACCTTCTTCATT  20415015


 Features flanking this part of subject sequence:
   14549 bp at 5' side: hypothetical protein
   70811 bp at 3' side: leucine rich repeat containing 3B


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  26620357  ACCTTCTTCATTCA  26620344


 Features flanking this part of subject sequence:
   128744 bp at 5' side: cholecystokinin preproprotein
   4878 bp at 3' side: lysozyme-like 4


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  42373883  CCTTCTTCATTCAC  42373870


 Features flanking this part of subject sequence:
   32054 bp at 5' side: XC chemokine receptor 1
   149231 bp at 3' side: chemokine (C-C motif) receptor 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCACG  24
                 ||||||||||||||
Sbjct  46035497  CTTCTTCATTCACG  46035510


 Features in this part of subject sequence:
   protein tyrosine phosphatase, receptor type, G precursor


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  61906580  CCTTCTTCATTCAC  61906593


 Features in this part of subject sequence:
   contactin 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  1352908  ACCTTCTTCATTC  1352896


 Features in this part of subject sequence:
   inositol 1,4,5-triphosphate receptor, type 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7        CGACCTTCTTCAT  19
                |||||||||||||
Sbjct  4577432  CGACCTTCTTCAT  4577420


 Features flanking this part of subject sequence:
   650199 bp at 5' side: hypothetical protein
   24623 bp at 3' side: similar to Retinoic acid receptor beta (RAR-beta) (RAR-ep..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  25131270  GACCTTCTTCATT  25131258


 Features flanking this part of subject sequence:
   516929 bp at 5' side: 3-oxoacyl-ACP synthase, mitochondrial
   311335 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  26292918  CTTCTTCATTCAC  26292930


 Features flanking this part of subject sequence:
   78736 bp at 5' side: hypothetical protein
   6625 bp at 3' side: leucine rich repeat containing 3B


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  26684543  CTTCTTCATTCAC  26684531


 Features flanking this part of subject sequence:
   702231 bp at 5' side: hypothetical protein LOC285322
   3112 bp at 3' side: RNA binding motif, single stranded interacting protein 3 ...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  29260065  CCTTCTTCATTCA  29260053


 Features flanking this part of subject sequence:
   106613 bp at 5' side: glutamate decarboxylase-like 1
   497262 bp at 3' side: similar to Thyroid hormone receptor-associated protein 3 .


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
```

```
Sbjct  30938215  ACCTTCTTCATTC  30938203


 Features flanking this part of subject sequence:
   1349229 bp at 5' side: programmed cell death 6 interacting protein
   420579 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         TCGACCTTCTTCA  18
                 |||||||||||||
Sbjct  35197250  TCGACCTTCTTCA  35197262


 Features flanking this part of subject sequence:
   50034 bp at 5' side: cyclic AMP-regulated phosphoprotein, 21 kD isoform 1
   536640 bp at 3' side: SH3 and cysteine rich domain


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  35825500  CTTCTTCATTCAC  35825488


 Features in this part of subject sequence:
   integrin, alpha 9 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  37591275  CTTCTTCATTCAC  37591287


 Features flanking this part of subject sequence:
   25378 bp at 5' side: voltage-gated sodium channel type V alpha isoform b
   38652 bp at 3' side: sodium channel, voltage-gated, type X, alpha


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  38640192  CCTTCTTCATTCA  38640180


 Features in this part of subject sequence:
   natural killer-tumor recognition sequence isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  42623581  CCTTCTTCATTCA  42623593


 Features flanking this part of subject sequence:
   11374 bp at 5' side: zinc finger protein 502
   584 bp at 3' side: zinc finger protein 501


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  44715334  CCTTCTTCATTCA  44715322
```

```
 Features flanking this part of subject sequence:
   17929 bp at 5' side: chemokine (C-C motif) receptor-like 2
   9140 bp at 3' side: lactotransferrin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  46408550  CTTCTTCATTCAC  46408538


 Features in this part of subject sequence:
   huntingtin interacting protein B


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  47069533  CCTTCTTCATTCA  47069545


 Features flanking this part of subject sequence:
   7247 bp at 5' side: chondroitin sulfate proteoglycan 5 (neuroglycan C)
   2257 bp at 3' side: SWI/SNF-related matrix-associated actin-dependent regulat...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  47567434  CCTTCTTCATTCA  47567446


 Features flanking this part of subject sequence:
   65888 bp at 5' side: family with sequence similarity 3, member D
   20997 bp at 3' side: hypothetical protein LOC200844


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  58647230  GACCTTCTTCATT  58647218


 Features in this part of subject sequence:
   fragile histidine triad gene


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  60377141  GACCTTCTTCATT  60377153


 Features in this part of subject sequence:
   protein tyrosine phosphatase, receptor type, G precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  61969557  TTCTTCATTCACG  61969545


 Features flanking this part of subject sequence:
   133066 bp at 5' side: hypothetical protein
   480001 bp at 3' side: membrane associated guanylate kinase, WW and PDZ domain c.
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  64802092  GACCTTCTTCATT  64802080


>ref|NT_004487.18|Hs1_4644 D Homo sapiens chromosome 1 genomic contig, reference a
Length=56413061

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent 
                                                                    Query start position  Su

 Features in this part of subject sequence:
   GA repeat binding protein, beta 2


 Score = 30.2 bits (15),  Expect =    28
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Plus

Query  4        TTTCGACCTTCTTCATTCA  22
                ||||||||| |||||||||
Sbjct  1570801  TTTCGACCTACTTCATTCA  1570819


 Features flanking this part of subject sequence:
   25395 bp at 5' side: CD1D antigen, d polypeptide
   45107 bp at 3' side: CD1A antigen precursor


 Score = 30.2 bits (15),  Expect =    28
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query  3        CTTTCGACCTTCTTCATTC  21
                ||||| |||||||||||||
Sbjct  8669708  CTTTCTACCTTCTTCATTC  8669690


 Features in this part of subject sequence:
   family with sequence similarity 5, member C


 Score = 30.2 bits (15),  Expect =    28
 Identities = 18/19 (94%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query  3         CTTTCGACCTTCTTCATTC  21
                 ||||||||||||| |||||
Sbjct  40667119  CTTTCGACCTTCTCCATTC  40667101


 Features in this part of subject sequence:
   LIM homeobox transcription factor 1, alpha isoform a


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  15723567  ACCTTCTTCATTCA  15723554


 Features in this part of subject sequence:
   Est1p-like protein B


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  6720454  CCTTCTTCATTCA  6720442


 Features flanking this part of subject sequence:
   316874 bp at 5' side: dermatopontin precursor
```

```
   59452 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  19505641  CTTCTTCATTCAC  19505653


 Features in this part of subject sequence:
   kinesin-associated protein 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  2         TCTTTCGACCTTCTTCA  18
                 |||||| ||||||||||
Sbjct  20406642  TCTTTCCACCTTCTTCA  20406626


 Features in this part of subject sequence:
   kinesin-associated protein 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  20458654  CTTCTTCATTCAC  20458666


 Features in this part of subject sequence:
   ring finger and WD repeat domain 2 isoform d24
   ring finger and WD repeat domain 2 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  26407401  CCTTCTTCATTCA  26407413


 Features flanking this part of subject sequence:
   267818 bp at 5' side: ring finger and WD repeat domain 2 isoform a
   81518 bp at 3' side: pappalysin 2 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  26934298  CTTCTTCATTCAC  26934286


 Features flanking this part of subject sequence:
   225750 bp at 5' side: similar to protein tyrosine phosphatase 4a1
   21742 bp at 3' side: astrotactin isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  27302032  CTTCTTCATTCAC  27302020


 Features flanking this part of subject sequence:
   121499 bp at 5' side: regucalcin gene promotor region related protein
   5055 bp at 3' side: RAS protein activator like 2 isoform 2
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  28548981  CTTCTTCATTCAC  28548969


 Features flanking this part of subject sequence:
   21790 bp at 5' side: immediate early response 5
   206451 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  31571166  CTTCTTCATTCAC  31571178


 Features in this part of subject sequence:
   chromosome 1 open reading frame 21


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  35058890  GACCTTCTTCATT  35058878


 Features flanking this part of subject sequence:
   69216 bp at 5' side: UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase 2
   2977434 bp at 3' side: potassium channel, subfamily T, member 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  43710274  GACCTTCTTCATT  43710262


 Features flanking this part of subject sequence:
   47333 bp at 5' side: DENN/MADD domain containing 1B
   119668 bp at 3' side: hypothetical protein LOC388722


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  48242454  TTCTTCATTCACG  48242466


 Features in this part of subject sequence:
   hypothetical protein LOC55765


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5         TTCGACCTTCTTC  17
                 |||||||||||||
Sbjct  51351367  TTCGACCTTCTTC  51351379


 Features flanking this part of subject sequence:
   3523 bp at 5' side: hypothetical protein LOC284573
   68247 bp at 3' side: SRY-box 13


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  54504151  CCTTCTTCATTCA  54504139


 Features flanking this part of subject sequence:
   110197 bp at 5' side: phosphoinositol 3-phosphate-binding protein-3
   22156 bp at 3' side: protein phosphatase 1, regulatory subunit 15B


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  54843418  CTTCTTCATTCAC  54843406


>ref|NW_926584.1|HsCraAADB02_571 D Homo sapiens chromosome 17 genomic contig, alte
(based on Celera assembly)
Length=15369037

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features in this part of subject sequence:
   methyltransferase 10 domain containing


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  2317631  CCTTCTTCATTCAC  2317618


 Features in this part of subject sequence:
   kinesin family member 1C


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  4859098  ACCTTCTTCATTC  4859086


 Features in this part of subject sequence:
   syntaxin 8


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12       TTCTTCATTCACG  24
                |||||||||||||
Sbjct  9184523  TTCTTCATTCACG  9184535


 Features in this part of subject sequence:
   dynein, axonemal, heavy polypeptide 9 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  11724615  CTTCTTCATTCAC  11724603


>ref|NW_926462.1|HsCraAADB02_560 D Homo sapiens chromosome 16 genomic contig, alte
(based on Celera assembly)
Length=23685799
```

```
                                                                  Sort alignments for this s
                                                                    E value  Score  Percent 
                                                                    Query start position  Su

          Features flanking this part of subject sequence:
            800976 bp at 5' side: sal-like 1
            73295 bp at 3' side: hypothetical protein isoform 4


          Score = 28.2 bits (14),  Expect =   112
          Identities = 14/14 (100%), Gaps = 0/14 (0%)
          Strand=Plus/Plus

         Query  10       CCTTCTTCATTCAC  23
                         ||||||||||||||
         Sbjct  5567301  CCTTCTTCATTCAC  5567314


          Features in this part of subject sequence:
            T-cell immunomodulatory protein


          Score = 26.3 bits (13),  Expect =   444
          Identities = 13/13 (100%), Gaps = 0/13 (0%)
          Strand=Plus/Plus

         Query  11       CTTCTTCATTCAC  23
                         |||||||||||||
         Sbjct  1032859  CTTCTTCATTCAC  1032871


          Features in this part of subject sequence:
            hypothetical protein LOC23322


          Score = 26.3 bits (13),  Expect =   444
          Identities = 13/13 (100%), Gaps = 0/13 (0%)
          Strand=Plus/Minus

         Query  6        TCGACCTTCTTCA  18
                         |||||||||||||
         Sbjct  7312747  TCGACCTTCTTCA  7312735


          Features in this part of subject sequence:
            similar to fatso isoform 5


          Score = 26.3 bits (13),  Expect =   444
          Identities = 13/13 (100%), Gaps = 0/13 (0%)
          Strand=Plus/Minus

         Query  11       CTTCTTCATTCAC  23
                         |||||||||||||
         Sbjct  7673483  CTTCTTCATTCAC  7673471


          Features flanking this part of subject sequence:
            71798 bp at 5' side: calpain small subunit 2
            17368 bp at 3' side: solute carrier family 6 member 2


          Score = 26.3 bits (13),  Expect =   444
          Identities = 13/13 (100%), Gaps = 0/13 (0%)
          Strand=Plus/Plus

         Query  11       CTTCTTCATTCAC  23
                         |||||||||||||
         Sbjct  9252235  CTTCTTCATTCAC  9252247


          Features in this part of subject sequence:
            guanine nucleotide binding protein, alpha activating poly...
            guanine nucleotide binding protein, alpha activating poly...


          Score = 26.3 bits (13),  Expect =   444
          Identities = 13/13 (100%), Gaps = 0/13 (0%)
          Strand=Plus/Plus

         Query  9        ACCTTCTTCATTC  21
                         |||||||||||||
         Sbjct  9811975  ACCTTCTTCATTC  9811987
```

```
 Features in this part of subject sequence:
   cirhin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  22759708  ACCTTCTTCATTC  22759720


>ref|NW_926528.1|HsCraAADB02_566 D Homo sapiens chromosome 16 genomic contig, alte
(based on Celera assembly)
Length=13777636

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent 
                                                                   Query start position  Su

 Features flanking this part of subject sequence:
   446487 bp at 5' side: M-phase phosphoprotein 6
   9703 bp at 3' side: cadherin 13 preproprotein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTCA  22
                ||||||||||||||
Sbjct  8188956  ACCTTCTTCATTCA  8188943


 Features in this part of subject sequence:
   hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCACG  24
                 ||||||||||||||
Sbjct  12741126  CTTCTTCATTCACG  12741113


 Features flanking this part of subject sequence:
   196658 bp at 5' side: similar to LSM3 homolog, U6 small nuclear RNA associated
   659856 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  4126408  CCTTCTTCATTCA  4126420


 Features flanking this part of subject sequence:
   815483 bp at 5' side: similar to LSM3 homolog, U6 small nuclear RNA associated
   41031 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12       TTCTTCATTCACG  24
                |||||||||||||
Sbjct  4745233  TTCTTCATTCACG  4745245

 Features in this part of subject sequence:
   cadherin 13 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  8415819  CCTTCTTCATTCA  8415807


 Features in this part of subject sequence:
   membrane-bound transcription factor site-1 protease isofo...
   membrane-bound transcription factor site-1 protease isofo...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  9667673  ACCTTCTTCATTC  9667685


 Features in this part of subject sequence:
   coactosin-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  10161222  CTTCTTCATTCAC  10161234


 Features flanking this part of subject sequence:
   9169 bp at 5' side: cytochrome c oxidase subunit IV isoform 1 precursor
   86878 bp at 3' side: interferon regulatory factor 8


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  11392641  ACCTTCTTCATTC  11392653


>ref|NW_925851.1|HsCraAADB02_505 D Homo sapiens chromosome 15 genomic contig, alte
(based on Celera assembly)
Length=42577


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Minus

Query  2      TCTTTCGACCTTCTTCAT  19
              |||||| |||||||||||
Sbjct  18208  TCTTTCAACCTTCTTCAT  18191


>ref|NW_925840.1|HsCraAADB02_504 D Homo sapiens chromosome 15 genomic contig, alte
(based on Celera assembly)
Length=10907654

                                                             Sort alignments for this s
                                                               E value  Score  Percent
                                                               Query start position  Su


 Features in this part of subject sequence:
   fibrous sheath interacting protein 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8        GACCTTCTTCATTC  21
                ||||||||||||||
Sbjct  7021238  GACCTTCTTCATTC  7021251


 Features flanking this part of subject sequence:
   38219 bp at 5' side: hypothetical protein LOC400359
   509836 bp at 3' side: hypothetical protein LOC400360
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  6078739  CCTTCTTCATTCA  6078751


 Features in this part of subject sequence:
   spectrin, beta, non-erythrocytic 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  9202982  CCTTCTTCATTCA  9202970


 Features in this part of subject sequence:
   similar to StAR-related lipid transfer protein 9 (StARD9)...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         CGACCTTCTTCAT  19
                 |||||||||||||
Sbjct  10036479  CGACCTTCTTCAT  10036491


>ref|NW_925506.1|HsCraAADB02_474 D Homo sapiens chromosome 13 genomic contig, alte
(based on Celera assembly)
Length=22380413

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   197176 bp at 3' side: protocadherin 9 isoform 1 precursor


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  2272560  CCTTCTTCATTCAC  2272573


 Features flanking this part of subject sequence:
   2012208 bp at 3' side: protocadherin 9 isoform 1 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8       GACCTTCTTCATT  20
               |||||||||||||
Sbjct  457541  GACCTTCTTCATT  457529


 Features in this part of subject sequence:
   dachshund homolog 1 isoform c
   dachshund homolog 1 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  7881702  CTTCTTCATTCAC  7881714
```

```
 Features flanking this part of subject sequence:
   73990 bp at 5' side: hypothetical protein
   215970 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  10373490  CTTCTTCATTCAC  10373478


 Features flanking this part of subject sequence:
   73085 bp at 5' side: endothelin receptor type B isoform 1
   604987 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  14153014  CTTCTTCATTCAC  14153026


 Features flanking this part of subject sequence:
   237816 bp at 5' side: hypothetical protein
   25541 bp at 3' side: sprouty 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         ATCTTTCGACCTT  13
                 |||||||||||||
Sbjct  16476381  ATCTTTCGACCTT  16476393


>ref|NW_925473.1|HsCraAADB02_471 D Homo sapiens chromosome 13 genomic contig, alte
(based on Celera assembly)
Length=33583425

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   42694 bp at 5' side: doublecortin and CaM kinase-like 1
   494 bp at 3' side: spermatogenesis and oogenesis specific basic helix-loop-h...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  17545072  CCTTCTTCATTCAC  17545059


 Features flanking this part of subject sequence:
   194390 bp at 5' side: similar to Protein C21orf70 homolog
   108204 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12      TTCTTCATTCACG  24
               |||||||||||||
Sbjct  272024  TTCTTCATTCACG  272012


 Features flanking this part of subject sequence:
   741687 bp at 5' side: fibroblast growth factor 9 precursor
   360126 bp at 3' side: similar to 60S ribosomal protein L7a (Surfeit locus prote.


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3        CTTTCGACCTTCT  15
                |||||||||||||
Sbjct  3814882  CTTTCGACCTTCT  3814894


 Features flanking this part of subject sequence:
   72827 bp at 5' side: ubiquitin specific peptidase like 1
   3398 bp at 3' side: arachidonate 5-lipoxygenase-activating protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3         CTTTCGACCTTCT  15
                 |||||||||||||
Sbjct  12110532  CTTTCGACCTTCT  12110544


 Features flanking this part of subject sequence:
   26919 bp at 5' side: klotho isoform b
   17998 bp at 3' side: START domain containing 13 isoform alpha


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  14463785  CTTCTTCATTCAC  14463797


 Features in this part of subject sequence:
   START domain containing 13 isoform alpha
   START domain containing 13 isoform delta


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  14578555  CCTTCTTCATTCA  14578543


 Features in this part of subject sequence:
   doublecortin and CaM kinase-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  17182901  CCTTCTTCATTCA  17182913


 Features in this part of subject sequence:
   FRAS1 related extracellular matrix protein 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  20150311  CTTCTTCATTCAC  20150323


 Features flanking this part of subject sequence:
   402526 bp at 5' side: 5-hydroxytryptamine (serotonin) receptor 2A
   643728 bp at 3' side: succinate-CoA ligase, ADP-forming, beta subunit


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  28663757  CCTTCTTCATTCA  28663745


 Features flanking this part of subject sequence:
   506221 bp at 5' side: 5-hydroxytryptamine (serotonin) receptor 2A
   540029 bp at 3' side: succinate-CoA ligase, ADP-forming, beta subunit


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1         ATCTTTCGACCTTCTTC  17
                 ||||||| |||||||||
Sbjct  28767440  ATCTTTCCACCTTCTTC  28767456


 Features flanking this part of subject sequence:
   1006193 bp at 5' side: 5-hydroxytryptamine (serotonin) receptor 2A
   40061 bp at 3' side: succinate-CoA ligase, ADP-forming, beta subunit


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  29267424  CCTTCTTCATTCA  29267412


>ref|NW_925517.1|HsCraAADB02_475 D Homo sapiens chromosome 13 genomic contig, alte
(based on Celera assembly)
Length=28042733

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features in this part of subject sequence:
   glypican 5


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Minus

Query  1        ATCTTTCGACCTTCTTCA  18
                ||||||| ||||||||||
Sbjct  5375428  ATCTTTCAACCTTCTTCA  5375411


 Features flanking this part of subject sequence:
   2656110 bp at 5' side: similar to CXXC finger 6
   853876 bp at 3' side: glypican 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  4297557  CTTCTTCATTCAC  4297545


 Features flanking this part of subject sequence:
   2735728 bp at 5' side: similar to CXXC finger 6
   774258 bp at 3' side: glypican 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  4377163  CCTTCTTCATTCA  4377175


 Features in this part of subject sequence:
   G protein-coupled receptor 180 precursor
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  8356609  CTTCTTCATTCAC  8356597


 Features flanking this part of subject sequence:
   1720 bp at 5' side: DAZ interacting protein 1 isoform 2
   33498 bp at 3' side: DnaJ (Hsp40) homolog, subfamily C, member 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12       TTCTTCATTCACG  24
                |||||||||||||
Sbjct  9397008  TTCTTCATTCACG  9396996


 Features in this part of subject sequence:
   fibroblast growth factor 14 isoform 1B
   fibroblast growth factor 14 isoform 1A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  15522001  ACCTTCTTCATTC  15521989


 Features flanking this part of subject sequence:
   1177701 bp at 5' side: hypothetical protein
   1007096 bp at 3' side: D-amino acid oxidase activator


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  18209090  CCTTCTTCATTCA  18209102


 Features in this part of subject sequence:
   ephrin B2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  20264778  CCTTCTTCATTCA  20264790


 Features flanking this part of subject sequence:
   316603 bp at 5' side: tumor necrosis factor (ligand) superfamily, member 13b
   42356 bp at 3' side: myosin heavy chain Myr 8


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  22373849  CCTTCTTCATTCA  22373837


 Features flanking this part of subject sequence:
   150487 bp at 5' side: myosin heavy chain Myr 8
   398754 bp at 3' side: insulin receptor substrate 2
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  23107378  CCTTCTTCATTCA  23107366


 Features flanking this part of subject sequence:
   509205 bp at 5' side: myosin heavy chain Myr 8
   40036 bp at 3' side: insulin receptor substrate 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  23466084  ACCTTCTTCATTC  23466096


 Features flanking this part of subject sequence:
   20132 bp at 5' side: RAB20, member RAS oncogene family
   34002 bp at 3' side: hypothetical protein LOC55739


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  24333257  TTCTTCATTCACG  24333269


 Features in this part of subject sequence:
   ankyrin repeat domain 10


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  24638262  ACCTTCTTCATTC  24638274


>ref|NW_925295.1|HsCraAADB02_455 D Homo sapiens chromosome 12 genomic contig, alte
(based on Celera assembly)
Length=12881912

                                                              Sort alignments for this s
                                                                E value  Score  Percent
                                                                Query start position  Su

 Features flanking this part of subject sequence:
   179580 bp at 5' side: hypothetical protein
   64571 bp at 3' side: neurotrophin 3 precursor


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTCA  22
                ||||||||||||||
Sbjct  5363108  ACCTTCTTCATTCA  5363121


 Features in this part of subject sequence:
   beta 1,4-N-acetylgalactosaminyltransferase-transferase-III


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  5       TTCGACCTTCTTC  17
               |||||||||||||
Sbjct  431157  TTCGACCTTCTTC  431169
```

```
  Features in this part of subject sequence:
    beta 1,4-N-acetylgalactosaminyltransferase-transferase-III


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  5       TTCGACCTTCTTC  17
                |||||||||||||
 Sbjct  431453  TTCGACCTTCTTC  431465


  Features in this part of subject sequence:
    beta 1,4-N-acetylgalactosaminyltransferase-transferase-III


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  5       TTCGACCTTCTTC  17
                |||||||||||||
 Sbjct  431491  TTCGACCTTCTTC  431503


  Features in this part of subject sequence:
    beta 1,4-N-acetylgalactosaminyltransferase-transferase-III


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  5       TTCGACCTTCTTC  17
                |||||||||||||
 Sbjct  431793  TTCGACCTTCTTC  431805


  Features in this part of subject sequence:
    beta 1,4-N-acetylgalactosaminyltransferase-transferase-III


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  5       TTCGACCTTCTTC  17
                |||||||||||||
 Sbjct  431936  TTCGACCTTCTTC  431948


  Features flanking this part of subject sequence:
    101037 bp at 5' side: hypothetical protein
    24250 bp at 3' side: HMT1 hnRNP methyltransferase-like 4


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  7        CGACCTTCTTCAT  19
                 |||||||||||||
 Sbjct  3393905  CGACCTTCTTCAT  3393893


  Features flanking this part of subject sequence:
    8519 bp at 5' side: RAD51 associated protein 1
    23649 bp at 3' side: dual-specificity tyrosine-(Y)-phosphorylation regulated k..


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  11       CTTCTTCATTCAC  23
                 |||||||||||||
 Sbjct  4502317  CTTCTTCATTCAC  4502305


  Features in this part of subject sequence:
    microfibrillar associated protein 5


  Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1        ATCTTTCGACCTTCTTC  17
                ||||||| |||||||||
Sbjct  8542710  ATCTTTCTACCTTCTTC  8542726


 Features flanking this part of subject sequence:
   26460 bp at 5' side: hypothetical protein
   46708 bp at 3' side: similar to cDNA sequence BC048546


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7        CGACCTTCTTCAT  19
                |||||||||||||
Sbjct  9256031  CGACCTTCTTCAT  9256043


>ref|NW_925006.1|HsCraAADB02_429 D Homo sapiens chromosome 11 genomic contig, alte
(based on Celera assembly)
Length=46519059

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent 
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   329504 bp at 5' side: inscuteable
   397315 bp at 3' side: SRY (sex determining region Y)-box 6 isoform 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  2         TCTTTCGACCTTCT  15
                 ||||||||||||||
Sbjct  11224601  TCTTTCGACCTTCT  11224588


 Features flanking this part of subject sequence:
   80457 bp at 5' side: lin-7 homolog C
   70998 bp at 3' side: brain-derived neurotrophic factor isoform b preproprotein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  23254788  GACCTTCTTCATTC  23254801


 Features flanking this part of subject sequence:
   194207 bp at 5' side: olfactory receptor, family 4, subfamily C, member 45


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  45901115  CCTTCTTCATTCAC  45901102


 Features flanking this part of subject sequence:
   2878 bp at 5' side: olfactory receptor, family 51, subfamily S, member 1
   29721 bp at 3' side: olfactory receptor, family 51, subfamily T, member 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4       TTTCGACCTTCTT  16
               |||||||||||||
Sbjct  497452  TTTCGACCTTCTT  497440
```

```
  Features flanking this part of subject sequence:
    11436 bp at 5' side: synaptotagmin IX
    7676 bp at 3' side: olfactomedin-like 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  10       CCTTCTTCATTCA  22
                 |||||||||||||
 Sbjct  3118873  CCTTCTTCATTCA  3118885


  Features in this part of subject sequence:
    SET binding factor 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  9        ACCTTCTTCATTC  21
                 |||||||||||||
 Sbjct  5689561  ACCTTCTTCATTC  5689573


  Features in this part of subject sequence:
    ubiquitin specific protease 47


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10       CCTTCTTCATTCA  22
                 |||||||||||||
 Sbjct  7550322  CCTTCTTCATTCA  7550310


  Features in this part of subject sequence:
    phosphodiesterase 3B, cGMP-inhibited


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  10353225  CCTTCTTCATTCA  10353213


  Features in this part of subject sequence:
    phosphoinositide-3-kinase, class 2, alpha polypeptide


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  11        CTTCTTCATTCAC  23
                  |||||||||||||
 Sbjct  12747284  CTTCTTCATTCAC  12747272


  Features in this part of subject sequence:
    nel-like 1 precursor


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  16802941  CCTTCTTCATTCA  16802929


  Features flanking this part of subject sequence:
    40369 bp at 5' side: gamma-butyrobetaine hydroxylase
    170751 bp at 3' side: coiled-coil domain containing 34 isoform 1
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  22834355  CCTTCTTCATTCA  22834367


 Features in this part of subject sequence:
   paired box gene 6 isoform a
   paired box gene 6 isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  27470608  CCTTCTTCATTCA  27470620


 Features in this part of subject sequence:
   F-box only protein 3 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  29412321  CTTCTTCATTCAC  29412333


 Features flanking this part of subject sequence:
   117977 bp at 5' side: pyruvate dehydrogenase complex, component X
   26131 bp at 3' side: CD44 antigen isoform 1 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  30782345  CCTTCTTCATTCA  30782357


 Features flanking this part of subject sequence:
   6071 bp at 5' side: similar to zinc finger, CCHC domain containing 9
   24314 bp at 3' side: netrin-G1 ligand


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  35765477  CTTCTTCATTCAC  35765465


 Features flanking this part of subject sequence:
   170379 bp at 5' side: hypothetical protein LOC399886
   107292 bp at 3' side: carbohydrate (keratan sulfate Gal-6) sulfotransferase 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTCACG  24
                 ||||||||||| |||||
Sbjct  41211624  GACCTTCTTCAGTCACG  41211608


 Features flanking this part of subject sequence:
   19340 bp at 5' side: solute carrier family 35, member C1
   16821 bp at 3' side: cryptochrome 2 (photolyase-like)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
```

```
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  41500153  CCTTCTTCATTCA  41500141


 Features flanking this part of subject sequence:
   67675 bp at 5' side: similar to mitochondrial carrier protein MGC4399
   55388 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  45174489  CCTTCTTCATTCA  45174477


>ref|NW_925173.1|HsCraAADB02_444 D Homo sapiens chromosome 11 genomic contig, alte
(based on Celera assembly)
Length=44976370

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent 
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   6474 bp at 5' side: KDEL (Lys-Asp-Glu-Leu) containing 2
   4678 bp at 3' side: exophilin 5


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  18399391  GACCTTCTTCATTC  18399404


 Features flanking this part of subject sequence:
   1129091 bp at 5' side: cysteine and histidine-rich domain (CHORD)-containing, zi
   872720 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  1254637  CCTTCTTCATTCA  1254649


 Features in this part of subject sequence:
   mastermind-like 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  6136176  CTTCTTCATTCAC  6136164


 Features flanking this part of subject sequence:
   871493 bp at 5' side: jerky homolog-like
   2299194 bp at 3' side: contactin 5 isoform short


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  7165993  CCTTCTTCATTCA  7165981
```

```
 Features flanking this part of subject sequence:
   31756 bp at 5' side: caspase-1 dominant-negative inhibitor pseudo-ICE isoform 2
   22309 bp at 3' side: inhibitory caspase recruitment domain (CARD) protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  14980853  CCTTCTTCATTCA  14980865


 Features flanking this part of subject sequence:
   5712 bp at 5' side: inhibitory caspase recruitment domain (CARD) protein
   31675 bp at 3' side: ICEBERG caspase-1 inhibitor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  15010937  CCTTCTTCATTCA  15010949


 Features in this part of subject sequence:
   ataxia telangiectasia mutated protein isoform 1
   ataxia telangiectasia mutated protein isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  2         TCTTTCGACCTTCTTCA  18
                 ||||| |||||||||||
Sbjct  18204720  TCTTTAGACCTTCTTCA  18204736


 Features in this part of subject sequence:
   hypothetical protein LOC160140


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  18278155  CTTCTTCATTCAC  18278167


 Features flanking this part of subject sequence:
   147537 bp at 5' side: DEAD (Asp-Glu-Ala-Asp) box polypeptide 10
   335011 bp at 3' side: hypothetical protein LOC399947


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  18982448  CCTTCTTCATTCA  18982460


 Features in this part of subject sequence:
   DIX domain containing 1 isoform a
   DIX domain containing 1 isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  21878303  CCTTCTTCATTCA  21878315


 Features flanking this part of subject sequence:
   34278 bp at 5' side: succinate dehydrogenase complex, subunit D precursor
```

```
    14381 bp at 3' side: interleukin 18 proprotein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  22022064  CCTTCTTCATTCA  22022076


  Features flanking this part of subject sequence:
    466283 bp at 5' side: hypothetical protein
    234721 bp at 3' side: neural cell adhesion molecule 1 isoform 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  22619486  CCTTCTTCATTCA  22619498


  Features flanking this part of subject sequence:
    171645 bp at 5' side: sortilin-related receptor containing LDLR class A repeats.
    316722 bp at 3' side: BRCC2 protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  6         TCGACCTTCTTCA  18
                  |||||||||||||
 Sbjct  31699150  TCGACCTTCTTCA  31699162


  Features in this part of subject sequence:
    kin of IRRE like 3


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  36766151  CCTTCTTCATTCA  36766139


  Features flanking this part of subject sequence:
    550747 bp at 5' side: proline rich 10
    906853 bp at 3' side: v-ets erythroblastosis virus E26 oncogene homolog 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  11        CTTCTTCATTCAC  23
                  |||||||||||||
 Sbjct  37460596  CTTCTTCATTCAC  37460608


  Features flanking this part of subject sequence:
    1082738 bp at 5' side: proline rich 10
    374862 bp at 3' side: v-ets erythroblastosis virus E26 oncogene homolog 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  2         TCTTTCGACCTTC  14
                  |||||||||||||
 Sbjct  37992587  TCTTTCGACCTTC  37992599


  Features flanking this part of subject sequence:
    89274 bp at 5' side: v-ets erythroblastosis virus E26 oncogene homolog 1
    82894 bp at 3' side: Friend leukemia virus integration 1
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         ATCTTTCGACCTT  13
                 |||||||||||||
Sbjct  38516332  ATCTTTCGACCTT  38516320


 Features in this part of subject sequence:
   opioid binding protein/cell adhesion molecule-like isofor...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  43093870  GACCTTCTTCATT  43093858


 Features in this part of subject sequence:
   KIAA0056 protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  44128750  GACCTTCTTCATT  44128738


>ref|NW_924796.1|HsCraAADB02_410 D Homo sapiens chromosome 10 genomic contig, alte
(based on Celera assembly)
Length=28940744

                                                                Sort alignments for this s
                                                                  E value  Score  Percent
                                                                  Query start position  Sul

 Features flanking this part of subject sequence:
   64048 bp at 5' side: receptor expression enhancing protein 3
   485822 bp at 3' side: similar to activator of S phase kinase


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  12906417  CCTTCTTCATTCAC  12906404


 Features flanking this part of subject sequence:
   86226 bp at 5' side: discs large homolog 5
   22041 bp at 3' side: polymerase (RNA) III (DNA directed) polypeptide A, 155kDa


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  27196030  CCTTCTTCATTCAC  27196017


 Features flanking this part of subject sequence:
   1757335 bp at 5' side: ZW10 interactor isoform c
   79587 bp at 3' side: inositol polyphosphate multikinase


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  7335747  CCTTCTTCATTCA  7335735
```

```
  Features flanking this part of subject sequence:
    111810 bp at 5' side: Rho-related BTB domain containing 1
    387201 bp at 3' side: transmembrane protein 26


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  8         GACCTTCTTCATT  20
                  |||||||||||||
 Sbjct  10244107  GACCTTCTTCATT  10244119


  Features flanking this part of subject sequence:
    250240 bp at 5' side: Rho-related BTB domain containing 1
    248771 bp at 3' side: transmembrane protein 26


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  10382549  CCTTCTTCATTCA  10382537


  Features in this part of subject sequence:
    catenin, alpha 3


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  8         GACCTTCTTCATT  20
                  |||||||||||||
 Sbjct  15172603  GACCTTCTTCATT  15172615


  Features in this part of subject sequence:
    catenin, alpha 3


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  11        CTTCTTCATTCAC  23
                  |||||||||||||
 Sbjct  16416707  CTTCTTCATTCAC  16416719


 >ref|NW_924606.1|HsCraAADB02_393 D Homo sapiens chromosome 10 genomic contig, alte
 (based on Celera assembly)
 Length=3630937

  Features flanking this part of subject sequence:
    83596 bp at 5' side: hypothetical protein
    349654 bp at 3' side: hypothetical protein


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

 Query  8        GACCTTCTTCATTC  21
                 ||||||||||||||
 Sbjct  1843481  GACCTTCTTCATTC  1843468


 >ref|NW_924584.1|HsCraAADB02_391 D Homo sapiens chromosome 10 genomic contig, alte
 (based on Celera assembly)
 Length=38429485
                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

  Features flanking this part of subject sequence:
    167610 bp at 5' side: metalloprotease 1
    438236 bp at 3' side: Kruppel-like factor 6
```

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  3328360  CCTTCTTCATTCAC  3328373


 Features flanking this part of subject sequence:
   49110 bp at 5' side: hypothetical protein
   97704 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Minus

Query  3        CTTTCGACCTTCTTCATT  20
                |||| |||||||||||||
Sbjct  3822166  CTTTTGACCTTCTTCATT  3822149


 Features in this part of subject sequence:
   G protein-coupled receptor 158


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  25481192  GACCTTCTTCATTC  25481205


 Features flanking this part of subject sequence:
   334744 bp at 5' side: metalloprotease 1
   271103 bp at 3' side: Kruppel-like factor 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3        CTTTCGACCTTCT  15
                |||||||||||||
Sbjct  3495494  CTTTCGACCTTCT  3495506


 Features in this part of subject sequence:
   similar to Aldo-keto reductase family 1 member C3 (Trans-...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  4875026  CCTTCTTCATTCA  4875038


 Features flanking this part of subject sequence:
   201217 bp at 5' side: hypothetical protein
   381666 bp at 3' side: Scm-like with four mbt domains 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12       TTCTTCATTCACG  24
                |||||||||||||
Sbjct  6749767  TTCTTCATTCACG  6749755


 Features in this part of subject sequence:
   hypothetical protein LOC221061


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
```

```
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  15268556  CTTCTTCATTCAC  15268568


 Features flanking this part of subject sequence:
   488780 bp at 5' side: chromosome 10 open reading frame 97
   135256 bp at 3' side: phosphotriesterase related


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  16324335  CCTTCTTCATTCA  16324323


 Features flanking this part of subject sequence:
   354364 bp at 5' side: plexin domain containing 2 precursor
   152173 bp at 3' side: nebulette sarcomeric isoform


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  20609204  CTTCTTCATTCAC  20609192


 Features flanking this part of subject sequence:
   4762 bp at 5' side: COMM domain containing 3
   1694 bp at 3' side: polycomb group ring finger 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  22301410  CCTTCTTCATTCA  22301398


 Features flanking this part of subject sequence:
   16917 bp at 5' side: armadillo repeat containing 3
   41147 bp at 3' side: methionine sulfoxide reductase B2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  6         TCGACCTTCTTCA  18
                 |||||||||||||
Sbjct  23030971  TCGACCTTCTTCA  23030983


 Features in this part of subject sequence:
   abl-interactor 1 isoform b
   abl-interactor 1 isoform c


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  26810961  CTTCTTCATTCAC  26810949


 Features flanking this part of subject sequence:
   73740 bp at 5' side: patched domain containing 3
   16285 bp at 3' side: RAB18, member RAS oncogene family


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus
```

```
Query  3         CTTTCGACCTTCTTCAT  19
                 ||||||| |||||||||
Sbjct  27540610  CTTTCGATCTTCTTCAT  27540626


 Features flanking this part of subject sequence:
   49966 bp at 5' side: armadillo repeat containing 4
   8945 bp at 3' side: palmitoylated membrane protein 7


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  28097439  CCTTCTTCATTCA  28097451


 Features flanking this part of subject sequence:
   232981 bp at 5' side: similar to ribosomal protein L21
   156728 bp at 3' side: lysozyme-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  29186956  TTCTTCATTCACG  29186968


 Features flanking this part of subject sequence:
   36548 bp at 5' side: PAP associated domain containing 1
   53093 bp at 3' side: mitogen-activated protein kinase kinase kinase 8


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  4         TTTCGACCTTCTTCATT  20
                 |||| ||||||||||||
Sbjct  30439697  TTTCAACCTTCTTCATT  30439681


 Features in this part of subject sequence:
   Rho GTPase activating protein 12


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  31960685  GACCTTCTTCATT  31960673


 Features flanking this part of subject sequence:
   32682 bp at 5' side: neuropilin 1 isoform c
   744125 bp at 3' side: partitioning-defective protein 3 homolog


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  33421337  CCTTCTTCATTCA  33421349


>ref|NW_924573.1|HsCraAADB02_390 D Homo sapiens chromosome 9 genomic contig, alter
(based on Celera assembly)
Length=25070985

                                                           Sort alignments for this s
                                                             E value  Score  Percent
                                                             Query start position  Su

 Features flanking this part of subject sequence:
```

```
    4522 bp at 5' side: uridine-cytidine kinase 1
    9770 bp at 3' side: hypothetical protein


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

 Query  8         GACCTTCTTCATTC  21
                  ||||||||||||||
 Sbjct  18439106  GACCTTCTTCATTC  18439093


  Features flanking this part of subject sequence:
    58801 bp at 5' side: regulator of G-protein signalling 3 isoform 4
    380307 bp at 3' side: zinc finger protein 618


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  8       GACCTTCTTCATT  20
                |||||||||||||
 Sbjct  553461  GACCTTCTTCATT  553449


  Features in this part of subject sequence:
    tenascin C (hexabrachion)


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10       CCTTCTTCATTCA  22
                 |||||||||||||
 Sbjct  1931443  CCTTCTTCATTCA  1931431


  Features flanking this part of subject sequence:
    828346 bp at 5' side: toll-like receptor 4 precursor
    624113 bp at 3' side: deleted in bladder cancer 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  11       CTTCTTCATTCAC  23
                 |||||||||||||
 Sbjct  5440882  CTTCTTCATTCAC  5440870


  Features flanking this part of subject sequence:
    1165209 bp at 5' side: toll-like receptor 4 precursor
    287250 bp at 3' side: deleted in bladder cancer 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  11       CTTCTTCATTCAC  23
                 |||||||||||||
 Sbjct  5777733  CTTCTTCATTCAC  5777745


  Features flanking this part of subject sequence:
    75957 bp at 5' side: DENN/MADD domain containing 1A isoform 2
    6471 bp at 3' side: LIM homeobox protein 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  10903242  CCTTCTTCATTCA  10903230


  Features in this part of subject sequence:
    mitogen-activated protein kinase associated protein 1 iso...
    mitogen-activated protein kinase associated protein 1 iso...
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  12465844  CTTCTTCATTCAC  12465856


 Features in this part of subject sequence:
   v-abl Abelson murine leukemia viral oncogene homolog 1 is...
   v-abl Abelson murine leukemia viral oncogene homolog 1 is...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  17775531  CCTTCTTCATTCA  17775543


>ref|NW_924539.1|HsCraAADB02_387 D Homo sapiens chromosome 9 genomic contig, alter
(based on Celera assembly)
Length=15704581

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features in this part of subject sequence:
   hypothetical protein LOC552891


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  14617598  CCTTCTTCATTCAC  14617585


 Features flanking this part of subject sequence:
   1018300 bp at 5' side: protein phosphatase 3 regulatory subunit B, beta isoform
   372577 bp at 3' side: cylicin 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  5599471  CTTCTTCATTCAC  5599483


 Features flanking this part of subject sequence:
   52851 bp at 5' side: olfactory receptor, family 13, subfamily C, member 9
   23042 bp at 3' side: olfactory receptor, family 13, subfamily D, member 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  7648665  ACCTTCTTCATTC  7648653


 Features flanking this part of subject sequence:
   340989 bp at 5' side: hypothetical protein LOC644602
   521389 bp at 3' side: zinc finger protein 462


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTC  21
```

```
                    |||||||||||||
Sbjct  9378197  ACCTTCTTCATTC  9378209


 Features in this part of subject sequence:
   hypothetical protein LOC401546


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  13177360  ACCTTCTTCATTC  13177372


>ref|NW_923873.1|HsCraAADB02_327 D Homo sapiens chromosome 8 genomic contig, alter
(based on Celera assembly)
Length=3916416

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

 Features flanking this part of subject sequence:
   43902 bp at 5' side: retinitis pigmentosa 1-like 1
   5702 bp at 3' side: hypothetical protein LOC203076


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTCA  22
                ||||||||||||||
Sbjct  2439649  ACCTTCTTCATTCA  2439662


 Features in this part of subject sequence:
   tankyrase, TRF1-interacting ankyrin-related ADP-ribose po...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  1400960  CCTTCTTCATTCA  1400972


>ref|NW_923984.1|HsCraAADB02_337 D Homo sapiens chromosome 8 genomic contig, alter
(based on Celera assembly)
Length=55887796

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

 Features flanking this part of subject sequence:
   281696 bp at 5' side: TSPY-like 5
   84689 bp at 3' side: LYRIC/3D3


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  2         TCTTTCGACCTTCT  15
                 ||||||||||||||
Sbjct  11723351  TCTTTCGACCTTCT  11723364


 Features flanking this part of subject sequence:
   196034 bp at 5' side: metastasis suppressor 1
   51849 bp at 3' side: zinc finger protein 572


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCAC  23
```

```
                 ||||||||||||||
Sbjct  39089676  CCTTCTTCATTCAC  39089689


 Features in this part of subject sequence:
   hypothetical protein LOC401478


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  52117054  CCTTCTTCATTCAC  52117067


 Features flanking this part of subject sequence:
   195045 bp at 5' side: cyclic nucleotide binding domain containing 1
   23606 bp at 3' side: similar to mitochondrial isoleucine tRNA synthetase


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  1749962  CTTCTTCATTCAC  1749950


 Features flanking this part of subject sequence:
   131454 bp at 5' side: OTU domain containing 6B
   32359 bp at 3' side: solute carrier family 26, member 7 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8        GACCTTCTTCATT  20
                |||||||||||||
Sbjct  5388906  GACCTTCTTCATT  5388894


 Features flanking this part of subject sequence:
   392902 bp at 5' side: neurocalcin delta
   11117 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  16275002  CTTCTTCATTCAC  16274990


 Features in this part of subject sequence:
   oxidation resistance 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  20878353  CCTTCTTCATTCA  20878365


 Features in this part of subject sequence:
   CUB and Sushi multiple domains 3 isoform 1
   CUB and Sushi multiple domains 3 isoform 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  26981056  ACCTTCTTCATTC  26981044
```

```
 Features in this part of subject sequence:
   exostosin 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  32211516  TTCTTCATTCACG  32211528


 Features flanking this part of subject sequence:
   108225 bp at 5' side: sterile alpha motif domain containing 12
   31843 bp at 3' side: similar to 40S ribosomal protein S26


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  32895888  CTTCTTCATTCAC  32895900


 Features flanking this part of subject sequence:
   98109 bp at 5' side: mal, T-cell differentiation protein 2
   74954 bp at 3' side: nov precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  33508553  GACCTTCTTCATT  33508541


 Features in this part of subject sequence:
   DEP domain containing 6


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  34171001  CTTCTTCATTCAC  34170989


 Features flanking this part of subject sequence:
   730604 bp at 5' side: breast cancer membrane protein 101
   448535 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  41445560  ACCTTCTTCATTC  41445572


 Features flanking this part of subject sequence:
   846801 bp at 5' side: breast cancer membrane protein 101
   332338 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  41561769  CTTCTTCATTCAC  41561757


 Features flanking this part of subject sequence:
   679572 bp at 5' side: hypothetical protein LOC641384
```

```
    588199 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  42785962  CCTTCTTCATTCA  42785974


  Features flanking this part of subject sequence:
    915770 bp at 5' side: hypothetical protein LOC641384
    352001 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  11        CTTCTTCATTCAC  23
                  |||||||||||||
 Sbjct  43022160  CTTCTTCATTCAC  43022172


  Features flanking this part of subject sequence:
    7393 bp at 5' side: similar to Otoconin 90 precursor (Oc90) (Phospholipase A2...
    71974 bp at 3' side: potassium voltage-gated channel KQT-like protein 3


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  11        CTTCTTCATTCAC  23
                  |||||||||||||
 Sbjct  46210543  CTTCTTCATTCAC  46210531


  Features in this part of subject sequence:
    potassium voltage-gated channel KQT-like protein 3


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  46490866  CCTTCTTCATTCA  46490854


  Features flanking this part of subject sequence:
    318235 bp at 5' side: collagen, type XXII, alpha 1
    417880 bp at 3' side: potassium channel, subfamily K, member 9


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  53346140  CCTTCTTCATTCA  53346152


  Features in this part of subject sequence:
    NIK and IKK(beta) binding protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  8         GACCTTCTTCATT  20
                  |||||||||||||
 Sbjct  54438799  GACCTTCTTCATT  54438787


  Features flanking this part of subject sequence:
    97493 bp at 5' side: similar to proton-associated sugar transporter A isoform 4
    16997 bp at 3' side: hypothetical protein
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  55469309  CTTCTTCATTCAC  55469297


>ref|NW_923796.1|HsCraAADB02_320 D Homo sapiens chromosome 7 genomic contig, alter
(based on Celera assembly)
Length=5180218

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   692472 bp at 5' side: sonic hedgehog preproprotein
   102626 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  2341951  CCTTCTTCATTCAC  2341938


 Features in this part of subject sequence:
   protein tyrosine phosphatase, receptor type, N polypeptid...
   protein tyrosine phosphatase, receptor type, N polypeptid...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  4315416  CCTTCTTCATTCA  4315404


>ref|NT_079595.2|Hs7_79660 D Homo sapiens chromosome 7 genomic contig, alternate a
(based on CRA_TCAGchr7v2)
Length=25815644

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features in this part of subject sequence:
   membrane associated guanylate kinase, WW and PDZ domain c...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  3424482  CCTTCTTCATTCAC  3424495


 Features in this part of subject sequence:
   similar to opposite strand transcription unit to Stag3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9      ACCTTCTTCATTC  21
              |||||||||||||
Sbjct  83040  ACCTTCTTCATTC  83052


 Features in this part of subject sequence:
   membrane associated guanylate kinase, WW and PDZ domain c...


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  3292252  CCTTCTTCATTCA  3292264


 Features in this part of subject sequence:
   guanine nucleotide binding protein (G protein), alpha inh...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12       TTCTTCATTCACG  24
                |||||||||||||
Sbjct  5034692  TTCTTCATTCACG  5034680


 Features in this part of subject sequence:
   calcium channel, voltage-dependent, alpha 2/delta subunit 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  7046358  CCTTCTTCATTCA  7046346


 Features in this part of subject sequence:
   Rap2-binding protein 9


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  12492171  GACCTTCTTCATT  12492183


 Features flanking this part of subject sequence:
   32626 bp at 5' side: similar to Importin alpha-2 subunit (Karyopherin alpha-2 ..
   161905 bp at 3' side: hypothetical protein LOC219578


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  13459705  CCTTCTTCATTCA  13459693


 Features in this part of subject sequence:
   hypothetical protein LOC219578


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  3         CTTTCGACCTTCTTCAT  19
                 ||||| |||||||||||
Sbjct  13695128  CTTTCTACCTTCTTCAT  13695112


 Features flanking this part of subject sequence:
   810964 bp at 5' side: hypothetical protein LOC219557
   553530 bp at 3' side: six transmembrane epithelial antigen of the prostate


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         TTTCGACCTTCTT  16
                 |||||||||||||
```

```
Sbjct  14467551  TTTCGACCTTCTT  14467539


 Features in this part of subject sequence:
   paraoxonase 2 isoform 1
   paraoxonase 2 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  20281761  ACCTTCTTCATTC  20281749


 Features in this part of subject sequence:
   solute carrier family 25, member 13 (citrin)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  21169879  CCTTCTTCATTCA  21169891


 Features flanking this part of subject sequence:
   11358 bp at 5' side: hypothetical protein LOC401388
   181261 bp at 3' side: candidate for split hand/foot malformation type 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  21367057  ACCTTCTTCATTC  21367069


 Features in this part of subject sequence:
   Smad ubiquitination regulatory factor 1 isoform 1
   Smad ubiquitination regulatory factor 1 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  23894891  CCTTCTTCATTCA  23894903


 Features in this part of subject sequence:
   opposite strand transcription unit to STAG3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  25116371  ACCTTCTTCATTC  25116383


 Features flanking this part of subject sequence:
   57221 bp at 5' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  25811546  CTTCTTCATTCAC  25811558


>ref|NW_923240.1|HsCraAADB02_270 D Homo sapiens chromosome 7 genomic contig, alter
```

```
(based on Celera assembly)
Length=37175744

                                                          Sort alignments for this s
                                                            E value  Score  Percent i
                                                            Query start position  Sul

 Features flanking this part of subject sequence:
   403779 bp at 5' side: hypothetical protein LOC79783
   425414 bp at 3' side: inhibin beta A precursor


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query  6         TCGACCTTCTTCATTCAC  23
                 |||||| |||||||||||
Sbjct  34465471  TCGACCCTCTTCATTCAC  34465488


 Features in this part of subject sequence:
   sorting nexin 13


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         TTTCGACCTTCTT  16
                 |||||||||||||
Sbjct  11055234  TTTCGACCTTCTT  11055222


 Features in this part of subject sequence:
   similar to Rap guanine nucleotide exchange factor 5 (Guan...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  15421510  CTTCTTCATTCAC  15421522


 Features flanking this part of subject sequence:
   28556 bp at 5' side: src family associated phosphoprotein 2
   201500 bp at 3' side: homeobox A1 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  20092361  CTTCTTCATTCAC  20092349


 Features in this part of subject sequence:
   BMP-binding endothelial regulator precursor protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  27144856  CTTCTTCATTCAC  27144844


>ref|NW_923707.1|HsCraAADB02_312 D Homo sapiens chromosome 7 genomic contig, alter
(based on Celera assembly)
Length=5539637

                                                          Sort alignments for this s
                                                            E value  Score  Percent i
                                                            Query start position  Sul

 Features flanking this part of subject sequence:
   10816 bp at 5' side: rho guanine nucleotide exchange factor 5
```

```
    8055 bp at 3' side: similar to OG2 homeobox


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

Query  9      ACCTTCTTCATTCA  22
              ||||||||||||||
Sbjct  28199  ACCTTCTTCATTCA  28186


  Features in this part of subject sequence:
    cell recognition molecule Caspr2 precursor


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  2549682  CCTTCTTCATTCA  2549694


>ref|NW_923640.1|HsCraAADB02_306 D Homo sapiens chromosome 7 genomic contig, alter
(based on Celera assembly)
Length=39238468

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

  Features in this part of subject sequence:
    component of oligomeric golgi complex 5 isoform 2
    component of oligomeric golgi complex 5 isoform 1


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  4499111  CCTTCTTCATTCAC  4499124


  Features flanking this part of subject sequence:
    158584 bp at 5' side: forkhead box P2 isoform III
    73936 bp at 3' side: MyoD family inhibitor domain containing isoform p40


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  12053838  ACCTTCTTCATTCA  12053825


  Features in this part of subject sequence:
    lipoma HMGIC fusion partner-like 3


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  1730900  CCTTCTTCATTCA  1730888


  Features flanking this part of subject sequence:
    14043 bp at 5' side: cAMP-dependent protein kinase, regulatory subunit beta 2
    6267 bp at 3' side: HMG-box transcription factor 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
```

```
                    |||||||||||||
Sbjct  4378108  CCTTCTTCATTCA  4378120


 Features flanking this part of subject sequence:
   1443065 bp at 5' side: hypothetical protein LOC154907
   335683 bp at 3' side: IMP2 inner mitochondrial membrane protease-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  7539358  ACCTTCTTCATTC  7539346


 Features in this part of subject sequence:
   IMP2 inner mitochondrial membrane protease-like


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8        GACCTTCTTCATT  20
                |||||||||||||
Sbjct  8202386  GACCTTCTTCATT  8202374


 Features flanking this part of subject sequence:
   87097 bp at 5' side: MyoD family inhibitor domain containing isoform p40
   838279 bp at 3' side: transcription factor EC isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  12308453  CCTTCTTCATTCA  12308441


 Features flanking this part of subject sequence:
   89724 bp at 5' side: capping protein (actin filament) muscle Z-line, alpha 2
   271231 bp at 3' side: wingless-type MMTV integration site family member 2 precu.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         TCTTTCGACCTTC  14
                 |||||||||||||
Sbjct  14213895  TCTTTCGACCTTC  14213907


 Features flanking this part of subject sequence:
   49696 bp at 5' side: ankyrin repeat, SAM and basic leucine zipper domain conta..
   2920 bp at 3' side: cystic fibrosis transmembrane conductance regulator, ATP-...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  14684159  CTTCTTCATTCAC  14684147


 Features flanking this part of subject sequence:
   54951 bp at 5' side: leptin precursor
   904 bp at 3' side: RNA binding motif protein 28


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  25511815  CTTCTTCATTCAC  25511803
```

```
  Features flanking this part of subject sequence:
    111081 bp at 5' side: CCR4-NOT transcription complex, subunit 4 isoform b
    8523 bp at 3' side: nucleoporin 205kDa


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  32730344  ACCTTCTTCATTC  32730356


  Features flanking this part of subject sequence:
    586325 bp at 5' side: similar to transient receptor potential cation channel, s.
    23686 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  34030155  GACCTTCTTCATT  34030143


  Features in this part of subject sequence:
    mitochondrial ribosomal protein S33
    mitochondrial ribosomal protein S33


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  38187125  CCTTCTTCATTCA  38187113


  Features flanking this part of subject sequence:
    25300 bp at 5' side: hypothetical protein LOC401410
    113806 bp at 3' side: multiple substrate lipid kinase


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  38621841  ACCTTCTTCATTC  38621829


>ref|NT_079592.2|Hs7_79657 D Homo sapiens chromosome 7 genomic contig, alternate a
(based on CRA_TCAGchr7v2)
Length=58008433

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

  Features flanking this part of subject sequence:
    403784 bp at 5' side: hypothetical protein LOC79783
    425418 bp at 3' side: inhibin beta A precursor


  Score = 28.2 bits (14),  Expect =   112
  Identities = 17/18 (94%), Gaps = 0/18 (0%)
  Strand=Plus/Plus

Query  6         TCGACCTTCTTCATTCAC  23
                 |||||| |||||||||||
Sbjct  41293679  TCGACCCTCTTCATTCAC  41293696


  Features in this part of subject sequence:
    sorting nexin 13
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         TTTCGACCTTCTT  16
                 |||||||||||||
Sbjct  17907690  TTTCGACCTTCTT  17907678


 Features in this part of subject sequence:
   similar to Rap guanine nucleotide exchange factor 5 (Guan...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  22266298  CTTCTTCATTCAC  22266310


 Features flanking this part of subject sequence:
   28554 bp at 5' side: src family associated phosphoprotein 2
   201440 bp at 3' side: homeobox A1 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  26933772  CTTCTTCATTCAC  26933760


 Features in this part of subject sequence:
   BMP-binding endothelial regulator precursor protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  33987170  CTTCTTCATTCAC  33987158


 Features flanking this part of subject sequence:
   239365 bp at 5' side: hypothetical protein
   1369559 bp at 3' side: hypothetical protein LOC285877


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  51689214  CCTTCTTCATTCA  51689226


 Features flanking this part of subject sequence:
   358479 bp at 5' side: hypothetical protein
   1250445 bp at 3' side: hypothetical protein LOC285877


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  51808328  CTTCTTCATTCAC  51808340


 Features flanking this part of subject sequence:
   23746 bp at 5' side: similar to zinc finger protein 678
   26957 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  56782276  CTTCTTCATTCAC  56782288


 Features flanking this part of subject sequence:
   284929 bp at 5' side: similar to zinc finger protein 682
   1195 bp at 3' side: similar to zinc finger protein 679


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  4         TTTCGACCTTCTTCATT  20
                 |||| ||||||||||||
Sbjct  57472586  TTTCAACCTTCTTCATT  57472602


>ref|NW_923574.1|HsCraAADB02_300 D Homo sapiens chromosome 7 genomic contig, alter
(based on Celera assembly)
Length=23851963

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features in this part of subject sequence:
   membrane associated guanylate kinase, WW and PDZ domain c...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  1430873  CCTTCTTCATTCAC  1430886


 Features in this part of subject sequence:
   membrane associated guanylate kinase, WW and PDZ domain c...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  1298657  CCTTCTTCATTCA  1298669


 Features in this part of subject sequence:
   guanine nucleotide binding protein (G protein), alpha inh...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12       TTCTTCATTCACG  24
                |||||||||||||
Sbjct  3041681  TTCTTCATTCACG  3041669


 Features in this part of subject sequence:
   calcium channel, voltage-dependent, alpha 2/delta subunit 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  5051887  CCTTCTTCATTCA  5051875


 Features in this part of subject sequence:
   Rap2-binding protein 9


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  10503296  GACCTTCTTCATT  10503308


 Features flanking this part of subject sequence:
   32625 bp at 5' side: similar to Importin alpha-2 subunit (Karyopherin alpha-2 ..
   161909 bp at 3' side: hypothetical protein LOC219578


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  11471232  CCTTCTTCATTCA  11471220


 Features in this part of subject sequence:
   hypothetical protein LOC219578


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  3         CTTTCGACCTTCTTCAT  19
                 ||||| |||||||||||
Sbjct  11706622  CTTTCTACCTTCTTCAT  11706606


 Features flanking this part of subject sequence:
   810792 bp at 5' side: hypothetical protein LOC219557
   553486 bp at 3' side: similar to Six transmembrane epithelial antigen of prosta.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         TTTCGACCTTCTT  16
                 |||||||||||||
Sbjct  12478908  TTTCGACCTTCTT  12478896


 Features in this part of subject sequence:
   paraoxonase 2 isoform 1
   paraoxonase 2 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  18289290  ACCTTCTTCATTC  18289278


 Features in this part of subject sequence:
   solute carrier family 25, member 13 (citrin)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  19178704  CCTTCTTCATTCA  19178716


 Features flanking this part of subject sequence:
   11359 bp at 5' side: hypothetical protein LOC401388
   181242 bp at 3' side: candidate for split hand/foot malformation type 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  19376034  ACCTTCTTCATTC  19376046


 Features in this part of subject sequence:
   Smad ubiquitination regulatory factor 1 isoform 1
   Smad ubiquitination regulatory factor 1 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  21905527  CCTTCTTCATTCA  21905539


 Features in this part of subject sequence:
   opposite strand transcription unit to STAG3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  23129446  ACCTTCTTCATTC  23129458


>ref|NT_079596.2|Hs7_79661 D Homo sapiens chromosome 7 genomic contig, alternate as
(based on CRA_TCAGchr7v2)
Length=58365407

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent :
                                                                    Query start position  Sul

 Features in this part of subject sequence:
   component of oligomeric golgi complex 5 isoform 1
   component of oligomeric golgi complex 5 isoform 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10      CCTTCTTCATTCAC  23
               ||||||||||||||
Sbjct  6331740  CCTTCTTCATTCAC  6331753


 Features flanking this part of subject sequence:
   158587 bp at 5' side: forkhead box P2 isoform III
   73925 bp at 3' side: MyoD family inhibitor domain containing isoform p40


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTCA  22
                ||||||||||||||
Sbjct  13919382  ACCTTCTTCATTCA  13919369


 Features flanking this part of subject sequence:
   10815 bp at 5' side: rho guanine nucleotide exchange factor 5
   8055 bp at 3' side: similar to OG2 homeobox


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTCA  22
                ||||||||||||||
Sbjct  43461804  ACCTTCTTCATTCA  43461791


 Features flanking this part of subject sequence:
   236635 bp at 5' side: hypothetical protein
```

```
    102620 bp at 3' side: hypothetical protein


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  55560737  CCTTCTTCATTCAC  55560724


  Features in this part of subject sequence:
    lipoma HMGIC fusion partner-like 3


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  3562212  CCTTCTTCATTCA  3562200


  Features flanking this part of subject sequence:
    14043 bp at 5' side: cAMP-dependent protein kinase, regulatory subunit beta 2
    6267 bp at 3' side: HMG-box transcription factor 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  6210715  CCTTCTTCATTCA  6210727


  Features flanking this part of subject sequence:
    1443229 bp at 5' side: hypothetical protein LOC154907
    335672 bp at 3' side: IMP2 inner mitochondrial membrane protease-like


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  9370697  ACCTTCTTCATTC  9370685


  Features in this part of subject sequence:
    IMP2 inner mitochondrial membrane protease-like


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  10034011  GACCTTCTTCATT  10033999


  Features flanking this part of subject sequence:
    87106 bp at 5' side: MyoD family inhibitor domain containing isoform p40
    837605 bp at 3' side: transcription factor EC isoform a


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  14173980  CCTTCTTCATTCA  14173968


  Features in this part of subject sequence:
    suppression of tumorigenicity 7 isoform b
    suppression of tumorigenicity 7 isoform a
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         TCTTTCGACCTTC  14
                 |||||||||||||
Sbjct  16078084  TCTTTCGACCTTC  16078096


 Features flanking this part of subject sequence:
   49696 bp at 5' side: ankyrin repeat, SAM and basic leucine zipper domain conta..
   2920 bp at 3' side: cystic fibrosis transmembrane conductance regulator, ATP-...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  16548231  CTTCTTCATTCAC  16548219


 Features flanking this part of subject sequence:
   55107 bp at 5' side: leptin precursor
   904 bp at 3' side: RNA binding motif protein 28


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  27368624  CTTCTTCATTCAC  27368612


 Features flanking this part of subject sequence:
   111058 bp at 5' side: CCR4-NOT transcription complex, subunit 4 isoform b
   8521 bp at 3' side: nucleoporin 205kDa


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  34614059  ACCTTCTTCATTC  34614071


 Features flanking this part of subject sequence:
   584369 bp at 5' side: similar to transient receptor potential cation channel, s.
   23755 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  35912039  GACCTTCTTCATT  35912027


 Features in this part of subject sequence:
   mitochondrial ribosomal protein S33
   mitochondrial ribosomal protein S33


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  40080240  CCTTCTTCATTCA  40080228


 Features flanking this part of subject sequence:
   25295 bp at 5' side: hypothetical protein LOC401410
   113803 bp at 3' side: multiple substrate lipid kinase


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  40514750  ACCTTCTTCATTC  40514738


 Features in this part of subject sequence:
   cell recognition molecule Caspr2 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  45984049  CCTTCTTCATTCA  45984061


 Features flanking this part of subject sequence:
   444288 bp at 5' side: actin-related protein 3-beta isoform 1
   114560 bp at 3' side: hypothetical protein LOC346547


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  52358586  CCTTCTTCATTCA  52358574


 Features in this part of subject sequence:
   protein tyrosine phosphatase, receptor type, N polypeptid...
   protein tyrosine phosphatase, receptor type, N polypeptid...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  57511440  CCTTCTTCATTCA  57511428


>ref|NW_923184.1|HsCraAADB02_265 D Homo sapiens chromosome 6 genomic contig, alter
(based on Celera assembly)
Length=103786604

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   311289 bp at 5' side: similar to ribosomal protein S14
   35865 bp at 3' side: RNA guanylyltransferase and 5'-phosphatase


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  21773094  CCTTCTTCATTCAC  21773081


 Features flanking this part of subject sequence:
   306033 bp at 5' side: mitogen-activated protein kinase kinase kinase 7 isoform C
   2350659 bp at 3' side: ephrin receptor EphA7


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  24091807  ACCTTCTTCATTCA  24091794
```

```
 Features flanking this part of subject sequence:
   1638182 bp at 5' side: mitogen-activated protein kinase kinase kinase 7 isoform
   1018510 bp at 3' side: ephrin receptor EphA7


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  25423956  CCTTCTTCATTCAC  25423943


 Features flanking this part of subject sequence:
   113712 bp at 5' side: activator of cAMP-responsive element modulator (CREM) in .
   68932 bp at 3' side: G protein-coupled receptor 63


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  29888066  GACCTTCTTCATTC  29888053


 Features in this part of subject sequence:
   glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  39802953  ACCTTCTTCATTCA  39802940


 Features in this part of subject sequence:
   glutamate receptor, metabotropic 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  79298671  GACCTTCTTCATTC  79298684


 Features flanking this part of subject sequence:
   89623 bp at 5' side: regulating synaptic membrane exocytosis 1
   131835 bp at 3' side: potassium voltage-gated channel, KQT-like subfamily, memb.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  5662087  ACCTTCTTCATTC  5662075


 Features in this part of subject sequence:
   solute carrier family 17 (anion/sugar transporter), member 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  6781617  CTTCTTCATTCAC  6781605


 Features flanking this part of subject sequence:
   101464 bp at 5' side: inhibitor of Bruton's tyrosine kinase
   33195 bp at 3' side: 5T4 oncofetal trophoblast glycoprotein
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  15543163  GACCTTCTTCATT  15543175


 Features flanking this part of subject sequence:
   131704 bp at 5' side: mitogen-activated protein kinase kinase kinase 7 isoform C
   2524989 bp at 3' side: ephrin receptor EphA7


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  23917477  GACCTTCTTCATT  23917465


 Features flanking this part of subject sequence:
   768467 bp at 5' side: mitogen-activated protein kinase kinase kinase 7 isoform C
   1888226 bp at 3' side: ephrin receptor EphA7


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  24554240  GACCTTCTTCATT  24554228


 Features flanking this part of subject sequence:
   1423860 bp at 5' side: mitogen-activated protein kinase kinase kinase 7 isoform
   1232833 bp at 3' side: ephrin receptor EphA7


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  25209633  TTCTTCATTCACG  25209621


 Features flanking this part of subject sequence:
   2247317 bp at 5' side: mitogen-activated protein kinase kinase kinase 7 isoform
   409376 bp at 3' side: ephrin receptor EphA7


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  26033090  CCTTCTTCATTCA  26033078


 Features flanking this part of subject sequence:
   219403 bp at 5' side: similar to mannosidase, endo-alpha
   378415 bp at 3' side: fucosyltransferase 9 (alpha (1,3) fucosyltransferase)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  28983297  GACCTTCTTCATT  28983285


 Features flanking this part of subject sequence:
   572795 bp at 5' side: similar to mannosidase, endo-alpha
   25019 bp at 3' side: fucosyltransferase 9 (alpha (1,3) fucosyltransferase)
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  5         TTCGACCTTCTTCATTC  21
                 |||| ||||||||||||
Sbjct  29336677  TTCGTCCTTCTTCATTC  29336693


 Features in this part of subject sequence:
   cyclin-dependent kinase (CDC2-like) 11


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         CTTTCGACCTTCT  15
                 |||||||||||||
Sbjct  43801554  CTTTCGACCTTCT  43801542


 Features flanking this part of subject sequence:
   29483 bp at 5' side: TSPY-like 1
   89937 bp at 3' side: squamous cell carcinoma antigen recognized by T cells 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  49442123  GACCTTCTTCATT  49442111


 Features in this part of subject sequence:
   karyopherin alpha 5 (importin alpha 6)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  49851009  GACCTTCTTCATT  49851021


 Features flanking this part of subject sequence:
   557 bp at 5' side: HD domain containing 2
   67831 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  58437289  CTTCTTCATTCAC  58437277


 Features flanking this part of subject sequence:
   30646 bp at 5' side: hypothetical protein LOC253582
   128265 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  63027982  CCTTCTTCATTCA  63027970


 Features in this part of subject sequence:
   A-kinase anchor protein 7 isoform gamma


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  4         TTTCGACCTTCTT  16
                 |||||||||||||
Sbjct  64352492  TTTCGACCTTCTT  64352504


 Features flanking this part of subject sequence:
   354097 bp at 5' side: eyes absent 4 isoform b
   6320 bp at 3' side: transcription factor 21


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  67013891  CTTCTTCATTCAC  67013879


 Features flanking this part of subject sequence:
   32551 bp at 5' side: v-myb myeloblastosis viral oncogene homolog
   35113 bp at 3' side: jouberin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  68380636  CTTCTTCATTCAC  68380624


 Features flanking this part of subject sequence:
   746274 bp at 5' side: utrophin
   28473 bp at 3' side: laforin isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  78727310  ACCTTCTTCATTC  78727322


 Features in this part of subject sequence:
   laforin isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  78756147  GACCTTCTTCATT  78756159


 Features flanking this part of subject sequence:
   675498 bp at 5' side: hypothetical protein LOC389432
   103550 bp at 3' side: SAM and SH3 domain containing 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  81370153  ACCTTCTTCATTC  81370165


 Features flanking this part of subject sequence:
   83438 bp at 5' side: hypothetical protein LOC80129
   106311 bp at 3' side: estrogen receptor 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12        TTCTTCATTCACG  24
```

```
                     |||||||||||||
Sbjct  84825198  TTCTTCATTCACG  84825186


 Features flanking this part of subject sequence:
   535168 bp at 5' side: similar to 60S ribosomal protein L27a
   221436 bp at 3' side: opioid receptor, mu 1 isoform MOR-1O


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  86942124  CTTCTTCATTCAC  86942112


 Features flanking this part of subject sequence:
   28757 bp at 5' side: sorting nexin 9
   10330 bp at 3' side: synaptojanin 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  91110132  CCTTCTTCATTCA  91110120


 Features in this part of subject sequence:
   parkin isoform 3
   parkin isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  94630830  CCTTCTTCATTCA  94630842


 Features flanking this part of subject sequence:
   21168 bp at 5' side: hypothetical protein
   904170 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  97578883  CCTTCTTCATTCA  97578895


 Features flanking this part of subject sequence:
   356 bp at 5' side: phosphodiesterase 10A
   412758 bp at 3' side: hypothetical protein LOC441177


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  98796986  ACCTTCTTCATTC  98796998


 Features flanking this part of subject sequence:
   49264 bp at 5' side: phosphodiesterase 10A
   363850 bp at 3' side: hypothetical protein LOC441177


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
```

```
Sbjct  98845894  CCTTCTTCATTCA  98845906


>ref|NW_923095.1|HsCraAADB02_257 D Homo sapiens chromosome 6 genomic contig, alter
(based on Celera assembly)
Length=6269147

                                                          Sort alignments for this s
                                                            E value  Score  Percent
                                                            Query start position  Su

 Features flanking this part of subject sequence:
   2698 bp at 5' side: KH domain-containing, RNA-binding, signal transduction-as...
   258850 bp at 3' side: similar to 40S ribosomal protein S17


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTCA  22
                ||||||||||||||
Sbjct  1687026  ACCTTCTTCATTCA  1687013


 Features flanking this part of subject sequence:
   197092 bp at 5' side: similar to Alcohol dehydrogenase class 3 chi chain (Alcoh.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4        TTTCGACCTTCTT  16
                |||||||||||||
Sbjct  5454487  TTTCGACCTTCTT  5454499


>ref|NW_922607.1|HsCraAADB02_213 D Homo sapiens chromosome 5 genomic contig, alter
(based on Celera assembly)
Length=11134560

                                                          Sort alignments for this s
                                                            E value  Score  Percent
                                                            Query start position  Su

 Features flanking this part of subject sequence:
   193106 bp at 5' side: similar to poly (ADP-ribose) polymerase family, member 8
   343886 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9       ACCTTCTTCATTCA  22
               ||||||||||||||
Sbjct  892915  ACCTTCTTCATTCA  892902


 Features in this part of subject sequence:
   cAMP-specific phosphodiesterase 4D


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTCA  22
                ||||||||||||||
Sbjct  8872215  ACCTTCTTCATTCA  8872202


 Features flanking this part of subject sequence:
   1751 bp at 5' side: mesoderm induction early response 1, family member 3
   219387 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        ATCTTTCGACCTT  13
                |||||||||||||
```

```
Sbjct  6819286  ATCTTTCGACCTT  6819298


 Features flanking this part of subject sequence:
   474266 bp at 5' side: hypothetical protein LOC345651
   141155 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  7823042  CTTCTTCATTCAC  7823054


>ref|NW_922596.1|HsCraAADB02_212 D Homo sapiens chromosome 5 genomic contig, alter
(based on Celera assembly)
Length=12039450

                                                                Sort alignments for this s
                                                                  E value  Score  Percent 
                                                                  Query start position  Su

 Features flanking this part of subject sequence:
   287611 bp at 5' side: hypothetical protein LOC202151
   20641 bp at 3' side: solute carrier family 1 (glial high affinity glutamate tr..


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTCA  22
                ||||||||||||||
Sbjct  2185327  ACCTTCTTCATTCA  2185314


 Features flanking this part of subject sequence:
   36051 bp at 5' side: disabled homolog 2
   1249520 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  5028440  CCTTCTTCATTCAC  5028427


 Features flanking this part of subject sequence:
   58880 bp at 5' side: hypothetical protein LOC133558
   13066 bp at 3' side: Complement component 6 precursor


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  6728942  CCTTCTTCATTCAC  6728955


 Features in this part of subject sequence:
   KPL2 protein isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  1399950  ACCTTCTTCATTC  1399962


 Features in this part of subject sequence:
   hypothetical protein LOC133584 isoform 1
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  3907416  ACCTTCTTCATTC  3907428


 Features flanking this part of subject sequence:
   481372 bp at 5' side: disabled homolog 2
   804200 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  5473748  CTTCTTCATTCAC  5473760


 Features flanking this part of subject sequence:
   287305 bp at 5' side: F-box only protein 4 isoform 2
   345385 bp at 3' side: growth hormone receptor precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        GACCTTCTTCATT  20
                |||||||||||||
Sbjct  7820549  GACCTTCTTCATT  7820561


 Features flanking this part of subject sequence:
   463047 bp at 5' side: similar to 60S ribosomal protein L29 (Cell surface hepari.
   174577 bp at 3' side: fibroblast growth factor 10 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        GACCTTCTTCATT  20
                |||||||||||||
Sbjct  9733300  GACCTTCTTCATT  9733312


>ref|NW_922784.1|HsCraAADB02_229 D Homo sapiens chromosome 5 genomic contig, alter
(based on Celera assembly)
Length=48999907

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent 
                                                                   Query start position  Sul

 Features flanking this part of subject sequence:
   345518 bp at 5' side: similar to Probable phospholipid-transporting ATPase VB
   251159 bp at 3' side: gamma-aminobutyric acid (GABA) A receptor, beta 2 isoform


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  34129793  GACCTTCTTCATTC  34129780


 Features in this part of subject sequence:
   RAN binding protein 17


 Score = 28.2 bits (14),  Expect =   112
 Identities = 20/22 (90%), Gaps = 0/22 (0%)
 Strand=Plus/Minus

Query  2         TCTTTCGACCTTCTTCATTCAC  23
                 ||||| |||||| |||||||||
Sbjct  44167576  TCTTTTGACCTTTTTCATTCAC  44167555
```

```
 Features in this part of subject sequence:
   ADAM metallopeptidase with thrombospondin type 1 motif, 1...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  2814571  CTTCTTCATTCAC  2814583


 Features flanking this part of subject sequence:
   402646 bp at 5' side: chondroitin sulfate synthase 3
   570971 bp at 3' side: histidine triad nucleotide binding protein 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  3682563  ACCTTCTTCATTC  3682551


 Features in this part of subject sequence:
   solute carrier family 22 member 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  5396327  ACCTTCTTCATTC  5396315


 Features flanking this part of subject sequence:
   18074 bp at 5' side: SMAD, mothers against DPP homolog 5
   17874 bp at 3' side: putative capacitative calcium channel


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  9284002  CTTCTTCATTCAC  9283990


 Features flanking this part of subject sequence:
   280516 bp at 5' side: putative capacitative calcium channel
   340878 bp at 3' side: sparc/osteonectin, cwcv and kazal-like domains proteoglyc.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  9726362  ACCTTCTTCATTC  9726374


 Features in this part of subject sequence:
   potassium channel tetramerisation domain containing 16


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  17337650  ACCTTCTTCATTC  17337638


 Features in this part of subject sequence:
   potassium channel tetramerisation domain containing 16
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  17411951  CTTCTTCATTCAC  17411963


 Features flanking this part of subject sequence:
   10737 bp at 5' side: leucyl-tRNA synthetase
   145876 bp at 3' side: POU domain, class 4, transcription factor 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  19280733  CTTCTTCATTCAC  19280745


 Features in this part of subject sequence:
   beta isoform of regulatory subunit B55, protein phosphata...
   beta isoform of regulatory subunit B55, protein phosphata...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  19984679  CTTCTTCATTCAC  19984691


 Features flanking this part of subject sequence:
   544829 bp at 5' side: neuromedin U receptor 2
   541106 bp at 3' side: glutamate receptor, ionotropic, AMPA 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  26032891  CTTCTTCATTCAC  26032879


 Features flanking this part of subject sequence:
   149944 bp at 5' side: glutamate receptor, ionotropic, AMPA 1
   31829 bp at 3' side: hypothetical protein LOC10827


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  27044245  GACCTTCTTCATT  27044257


 Features flanking this part of subject sequence:
   652796 bp at 5' side: methionine adenosyltransferase II, beta isoform 1
   3404700 bp at 3' side: similar to odd Oz/ten-m homolog 2 isoform 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  37260288  TTCTTCATTCACG  37260276


 Features flanking this part of subject sequence:
   3112802 bp at 5' side: methionine adenosyltransferase II, beta isoform 1
   944694 bp at 3' side: similar to odd Oz/ten-m homolog 2 isoform 5
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  39720282  CCTTCTTCATTCA  39720294


 Features in this part of subject sequence:
   slit homolog 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         ATCTTTCGACCTT  13
                 |||||||||||||
Sbjct  42173768  ATCTTTCGACCTT  42173780


 Features in this part of subject sequence:
   fibroblast growth factor 18 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  44515099  ACCTTCTTCATTC  44515087


>ref|NW_922562.1|HsCraAADB02_209 D Homo sapiens chromosome 5 genomic contig, alter
(based on Celera assembly)
Length=12667399

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

 Features flanking this part of subject sequence:
   451160 bp at 5' side: hypothetical protein
   28083 bp at 3' side: threonyl-tRNA synthetase


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Minus

Query  4         TTTCGACCTTCTTCATTC  21
                 |||| |||||||||||||
Sbjct  11856889  TTTCTACCTTCTTCATTC  11856872


 Features flanking this part of subject sequence:
   975005 bp at 5' side: cadherin 12, type 2 preproprotein
   272010 bp at 3' side: similar to protein tyrosine phosphatase, non-receptor typ.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12       TTCTTCATTCACG  24
                |||||||||||||
Sbjct  1483411  TTCTTCATTCACG  1483399


 Features flanking this part of subject sequence:
   87068 bp at 5' side: PR domain containing 9
   868456 bp at 3' side: cadherin 10, type 2 preproprotein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  2066915  CTTCTTCATTCAC  2066903
```

```
 Features flanking this part of subject sequence:
   121336 bp at 5' side: cadherin 9, type 2 preproprotein
   1814571 bp at 3' side: similar to Striatin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  5557778  CCTTCTTCATTCA  5557790


>ref|NW_922518.1|HsCraAADB02_205 D Homo sapiens chromosome 5 genomic contig, altern
(based on Celera assembly)
Length=16646378

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent i
                                                                    Query start position  Sul

 Features flanking this part of subject sequence:
   52626 bp at 5' side: AKAP-associated sperm protein
   44756 bp at 3' side: similar to ankyrin repeat domain 33


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  9658223  CCTTCTTCATTCAC  9658210


 Features in this part of subject sequence:
   catenin (cadherin-associated protein), delta 2 (neural pl...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  10566493  ACCTTCTTCATTCA  10566480


 Features in this part of subject sequence:
   catenin (cadherin-associated protein), delta 2 (neural pl...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  10443548  CCTTCTTCATTCA  10443560


>ref|NW_922729.1|HsCraAADB02_224 D Homo sapiens chromosome 5 genomic contig, altern
(based on Celera assembly)
Length=28665942

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent i
                                                                    Query start position  Sul

 Features flanking this part of subject sequence:
   217210 bp at 5' side: similar to RAS related protein 1b
   14848 bp at 3' side: IQ motif containing GTPase activating protein 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTCA  22
                ||||||||||||||
Sbjct  4978031  ACCTTCTTCATTCA  4978044
```

```
  Features flanking this part of subject sequence:
    99601 bp at 5' side: hypothetical protein LOC153396
    173810 bp at 3' side: hypothetical protein


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

 Query  10        CCTTCTTCATTCAC  23
                  ||||||||||||||
 Sbjct  16955797  CCTTCTTCATTCAC  16955810


  Features in this part of subject sequence:
    phosphodiesterase 8B isoform 3
    phosphodiesterase 8B isoform 5


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  9        ACCTTCTTCATTC  21
                 |||||||||||||
 Sbjct  5861412  ACCTTCTTCATTC  5861400


  Features flanking this part of subject sequence:
    1279507 bp at 5' side: EGF-like repeats and discoidin I-like domains-containing
    940983 bp at 3' side: cytochrome c oxidase subunit VIIc precursor


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  14264679  CCTTCTTCATTCA  14264691


  Features flanking this part of subject sequence:
    171268 bp at 5' side: cytochrome c oxidase subunit VIIc precursor
    258935 bp at 3' side: hypothetical protein LOC645261


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  15378355  CCTTCTTCATTCA  15378367


  Features flanking this part of subject sequence:
    8544 bp at 5' side: arrestin domain containing 3
    85102 bp at 3' side: similar to Ras-related protein Rab-5C (RAB5L) (L1880)


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  11        CTTCTTCATTCAC  23
                  |||||||||||||
 Sbjct  19989363  CTTCTTCATTCAC  19989351


  Features flanking this part of subject sequence:
    505470 bp at 5' side: hypothetical protein LOC134187
    273228 bp at 3' side: hypothetical protein LOC285600


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  9         ACCTTCTTCATTC  21
                  |||||||||||||
 Sbjct  22842760  ACCTTCTTCATTC  22842772
```

```
  Features in this part of subject sequence:
    chromodomain helicase DNA binding protein 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  11        CTTCTTCATTCAC  23
                  |||||||||||||
 Sbjct  27523594  CTTCTTCATTCAC  27523582


>ref|NW_922073.1|HsCraAADB02_165 D Homo sapiens chromosome 4 genomic contig, alter
(based on Celera assembly)
Length=39674885

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

  Features in this part of subject sequence:
    peroxisome proliferative activated receptor gamma coactiv...


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

 Query  8         GACCTTCTTCATTC  21
                  ||||||||||||||
 Sbjct  14419439  GACCTTCTTCATTC  14419452


  Features flanking this part of subject sequence:
    1770011 bp at 5' side: hypothetical protein
    988795 bp at 3' side: similar to ribosomal protein L31


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

 Query  11        CTTCTTCATTCACG  24
                  ||||||||||||||
 Sbjct  23547423  CTTCTTCATTCACG  23547410


  Features flanking this part of subject sequence:
    229992 bp at 5' side: WD repeat-containing protein 1 isoform 1
    78860 bp at 3' side: hypothetical protein LOC85460


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10      CCTTCTTCATTCA  22
                |||||||||||||
 Sbjct  957403  CCTTCTTCATTCA  957391


  Features in this part of subject sequence:
    mast cell immunoreceptor signal transducer


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  12       TTCTTCATTCACG  24
                 |||||||||||||
 Sbjct  1113949  TTCTTCATTCACG  1113937


  Features flanking this part of subject sequence:
    352320 bp at 5' side: hypothetical protein
    1208936 bp at 3' side: heat shock protein HSP 90-beta


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus
```

```
Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  2719058  ACCTTCTTCATTC  2719046


 Features flanking this part of subject sequence:
   794849 bp at 5' side: hypothetical protein
   67119 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  2        TCTTTCGACCTTC  14
                |||||||||||||
Sbjct  5527930  TCTTTCGACCTTC  5527918


 Features flanking this part of subject sequence:
   51494 bp at 5' side: CD38 antigen
   35732 bp at 3' side: fibroblast growth factor binding protein 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  6493093  CCTTCTTCATTCA  6493105


 Features flanking this part of subject sequence:
   1302392 bp at 5' side: hypothetical protein
   107025 bp at 3' side: slit homolog 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTCACG  24
                 ||||||||| |||||||
Sbjct  10732271  GACCTTCTTTATTCACG  10732255


 Features flanking this part of subject sequence:
   1406385 bp at 5' side: Kv channel interacting protein 4 isoform 3
   124762 bp at 3' side: similar to Probable G-protein coupled receptor 125 precurs


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  12841887  CCTTCTTCATTCA  12841899


 Features flanking this part of subject sequence:
   10354 bp at 5' side: solute carrier family 34 (sodium phosphate), member 2
   61302 bp at 3' side: hypothetical protein LOC23231


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  16263538  CTTCTTCATTCAC  16263550


 Features flanking this part of subject sequence:
   1836503 bp at 5' side: similar to mesoderm specific transcript isoform b
   64497 bp at 3' side: protocadherin 7 isoform c precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
```

```
                     |||||||||||||
Sbjct  21238875  CTTCTTCATTCAC  21238863


 Features flanking this part of subject sequence:
   125915 bp at 5' side: hypothetical protein LOC54502
   187002 bp at 3' side: NOL1/NOP2/Sun domain family, member 7


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  31135081  ACCTTCTTCATTC  31135093


 Features flanking this part of subject sequence:
   473107 bp at 5' side: similar to glutaredoxin cysteine-rich 1 protein
   394740 bp at 3' side: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomp.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  34080252  CTTCTTCATTCAC  34080264


 Features flanking this part of subject sequence:
   133949 bp at 5' side: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomp.
   140959 bp at 3' side: potassium channel tetramerisation domain containing 8


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  34610098  CTTCTTCATTCAC  34610086


 Features flanking this part of subject sequence:
   227336 bp at 5' side: glucosamine-6-phosphate deaminase 2
   1093637 bp at 3' side: gamma-aminobutyric acid A receptor, gamma 1 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  35526337  CTTCTTCATTCAC  35526325


>ref|NW_921751.1|HsCraAADB02_136 D Homo sapiens chromosome 3 genomic contig, alter
(based on Celera assembly)
Length=15218730

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Sul

 Features flanking this part of subject sequence:
   433181 bp at 5' side: glucan (1,4-alpha-), branching enzyme 1 (glycogen branchi.
   2765965 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  6675346  CCTTCTTCATTCAC  6675359


 Features flanking this part of subject sequence:
   42807 bp at 5' side: hypothetical protein
```

```
    15365 bp at 3' side: hypothetical protein LOC642198


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  11      CTTCTTCATTCAC  23
               |||||||||||||
Sbjct  198221  CTTCTTCATTCAC  198233


  Features in this part of subject sequence:
    roundabout, axon guidance receptor, homolog 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  1899101  CCTTCTTCATTCA  1899113


  Features in this part of subject sequence:
    roundabout, axon guidance receptor, homolog 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  2070609  CTTCTTCATTCAC  2070621


  Features in this part of subject sequence:
    roundabout 1 isoform a


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  3997839  CTTCTTCATTCAC  3997851


  Features flanking this part of subject sequence:
    791841 bp at 5' side: hypothetical protein LOC285237
    453 bp at 3' side: similar to NMDA receptor regulated 2 isoform a


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  13440220  CTTCTTCATTCAC  13440208


>ref|NW_921807.1|HsCraAADB02_141 D Homo sapiens chromosome 3 genomic contig, alter
(based on Celera assembly)
Length=101945515

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

  Features flanking this part of subject sequence:
    980769 bp at 5' side: similar to synovial sarcoma, X breakpoint 2 interacting p.
    848215 bp at 3' side: activated leukocyte cell adhesion molecule


  Score = 28.2 bits (14),  Expect =   112
  Identities = 17/18 (94%), Gaps = 0/18 (0%)
  Strand=Plus/Minus

Query  3         CTTTCGACCTTCTTCATT  20
                 ||||| ||||||||||||
Sbjct  10822104  CTTTCTACCTTCTTCATT  10822087
```

```
 Features flanking this part of subject sequence:
   3952 bp at 5' side: hypothetical protein
   126144 bp at 3' side: testes development-related NYD-SP17


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  13552295  ACCTTCTTCATTCA  13552308


 Features flanking this part of subject sequence:
   2076 bp at 5' side: urocanase domain containing 1
   4521 bp at 3' side: carbohydrate (chondroitin 4) sulfotransferase 13


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  32849155  CCTTCTTCATTCAC  32849142


 Features in this part of subject sequence:
   monoglyceride lipase isoform 1
   monoglyceride lipase isoform 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  34106451  CCTTCTTCATTCAC  34106438


 Features flanking this part of subject sequence:
   1500772 bp at 5' side: hypothetical protein LOC205428
   573609 bp at 3' side: procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2 isofor.


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Minus

Query  4         TTTCGACCTTCTTCATTC  21
                 |||| |||||||||||||
Sbjct  51817904  TTTCTACCTTCTTCATTC  51817887


 Features flanking this part of subject sequence:
   178150 bp at 5' side: NOL1/NOP2/Sun domain family, member 3
   202237 bp at 3' side: similar to SVH protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11      CTTCTTCATTCAC  23
               |||||||||||||
Sbjct  592812  CTTCTTCATTCAC  592800


 Features flanking this part of subject sequence:
   540488 bp at 5' side: similar to synovial sarcoma, X breakpoint 2 interacting p.
   1288501 bp at 3' side: activated leukocyte cell adhesion molecule


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         TTTCGACCTTCTT  16
                 |||||||||||||
Sbjct  10381818  TTTCGACCTTCTT  10381806
```

```
  Features flanking this part of subject sequence:
    399229 bp at 5' side: hypothetical protein
    89594 bp at 3' side: growth associated protein 43


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  21846491  CCTTCTTCATTCA  21846503


  Features in this part of subject sequence:
    DNA polymerase theta


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  1         ATCTTTCGACCTT  13
                  |||||||||||||
 Sbjct  27859460  ATCTTTCGACCTT  27859448


  Features flanking this part of subject sequence:
    120834 bp at 5' side: CD86 antigen isoform 2 precursor
    13768 bp at 3' side: calcium-sensing receptor


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  7         CGACCTTCTTCAT  19
                  |||||||||||||
 Sbjct  28554573  CGACCTTCTTCAT  28554561


  Features in this part of subject sequence:
    similar to Integrin beta-5 precursor


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  9         ACCTTCTTCATTC  21
                  |||||||||||||
 Sbjct  31144293  ACCTTCTTCATTC  31144281


  Features flanking this part of subject sequence:
    241267 bp at 5' side: hypothetical protein LOC389152
    54811 bp at 3' side: mitochondrial ribosomal protein S22


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  45616681  CCTTCTTCATTCA  45616669


  Features in this part of subject sequence:
    calsyntenin 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

 Query  10        CCTTCTTCATTCA  22
                  |||||||||||||
 Sbjct  46405020  CCTTCTTCATTCA  46405008


  Features in this part of subject sequence:
    similar to Serine/threonine-protein kinase ATR (Ataxia te...
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  48820019  CTTCTTCATTCAC  48820031


 Features flanking this part of subject sequence:
   604044 bp at 5' side: hypothetical protein isoform 3
   713367 bp at 3' side: angiotensin II receptor, type 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  54341467  CCTTCTTCATTCA  54341455


 Features flanking this part of subject sequence:
   837747 bp at 5' side: hypothetical protein isoform 3
   479664 bp at 3' side: angiotensin II receptor, type 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         CGACCTTCTTCAT  19
                 |||||||||||||
Sbjct  54575170  CGACCTTCTTCAT  54575158


 Features in this part of subject sequence:
   hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  56660641  CCTTCTTCATTCA  56660629


 Features flanking this part of subject sequence:
   120410 bp at 5' side: hypothetical protein
   12425 bp at 3' side: similar to A-kinase anchor protein 5 (A-kinase anchor pro..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  66484890  CTTCTTCATTCAC  66484902


 Features flanking this part of subject sequence:
   178519 bp at 5' side: hypothetical protein
   171222 bp at 3' side: calcium-activated potassium channel beta 2 subunit


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  84940625  CCTTCTTCATTCA  84940637


 Features flanking this part of subject sequence:
   702111 bp at 5' side: translocase of the inner mitochondrial membrane 14 isoform
   21883 bp at 3' side: sex-determining region Y-box 2


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  88027609  ACCTTCTTCATTC  88027621


 Features in this part of subject sequence:
   Ymer protein short isoform
   Ymer protein long isoform


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  97666602  CCTTCTTCATTCA  97666590


 Features flanking this part of subject sequence:
   146505 bp at 5' side: hypothetical protein LOC151963
   180569 bp at 3' side: HRAS-like suppressor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  99393799  CCTTCTTCATTCA  99393811


>ref|NW_921585.1|HsCraAADB02_121 D Homo sapiens chromosome 2 genomic contig, alter
(based on Celera assembly)
Length=63105981

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Sul

 Features in this part of subject sequence:
   RAB3 GTPase-activating protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  3752207  CCTTCTTCATTCAC  3752220


 Features flanking this part of subject sequence:
   289798 bp at 5' side: hypothetical protein LOC401013
   444435 bp at 3' side: alpha-1,3(6)-mannosylglycoprotein beta-1,6-N-acetyl-gluco.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  2469944  ACCTTCTTCATTC  2469956


 Features flanking this part of subject sequence:
   442484 bp at 5' side: ADP-ribosylation-like factor 6 interacting protein 6
   275809 bp at 3' side: reprimo, TP53 dependant G2 arrest mediator candidate


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  21863191  CCTTCTTCATTCA  21863203
```

```
 Features flanking this part of subject sequence:
   201383 bp at 5' side: reprimo, TP53 dependant G2 arrest mediator candidate
   264623 bp at 3' side: UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylga.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  22340736  CTTCTTCATTCAC  22340724


 Features flanking this part of subject sequence:
   597232 bp at 5' side: glycerol-3-phosphate dehydrogenase 2 (mitochondrial)
   77818 bp at 3' side: UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylga..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  25839730  CTTCTTCATTCAC  25839742


 Features in this part of subject sequence:
   lymphocyte antigen 75


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  28494538  CTTCTTCATTCAC  28494550


 Features in this part of subject sequence:
   phospholipase A2 receptor 1 isoform 1 precursor
   phospholipase A2 receptor 1 isoform 2 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  28695201  CTTCTTCATTCAC  28695213


 Features in this part of subject sequence:
   phospholipase A2 receptor 1 isoform 1 precursor
   phospholipase A2 receptor 1 isoform 2 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  28700877  CTTCTTCATTCAC  28700865


 Features in this part of subject sequence:
   potassium voltage-gated channel, subfamily H, member 7 is...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  31076408  CCTTCTTCATTCA  31076420


 Features in this part of subject sequence:
   potassium voltage-gated channel, subfamily H, member 7 is...
```

```
     potassium voltage-gated channel, subfamily H, member 7 is...

  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  31184991  CCTTCTTCATTCA  31185003


  Features flanking this part of subject sequence:
    158 bp at 5' side: longevity assurance homolog 6
    32820 bp at 3' side: nitric oxide synthase trafficking isoform 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  37424448  CTTCTTCATTCAC  37424436


  Features flanking this part of subject sequence:
    12626 bp at 5' side: longevity assurance homolog 6
    20352 bp at 3' side: nitric oxide synthase trafficking isoform 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  37436916  CCTTCTTCATTCA  37436904


  Features flanking this part of subject sequence:
    286549 bp at 5' side: similar to peptidylprolyl isomerase A isoform 1
    108176 bp at 3' side: similar to Ciliary dynein heavy chain 11 (Axonemal beta d.


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  42440772  CCTTCTTCATTCA  42440784


  Features in this part of subject sequence:
    hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  45301871  CCTTCTTCATTCA  45301859


  Features flanking this part of subject sequence:
    71104 bp at 5' side: hypothetical protein LOC285025
    160650 bp at 3' side: SEC14 and spectrin domains 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  47598176  ACCTTCTTCATTC  47598164


  Features in this part of subject sequence:
    hypothetical protein
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  49824480  GACCTTCTTCATT  49824468


 Features in this part of subject sequence:
   phosphodiesterase 1A, calmodulin-dependent isoform 1
   phosphodiesterase 1A, calmodulin-dependent isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  50834236  CCTTCTTCATTCA  50834224


 Features flanking this part of subject sequence:
   195605 bp at 5' side: similar to E74-like factor 2 (ets domain transcription fa.
   2408 bp at 3' side: fibrous sheath interacting protein 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         TTTCGACCTTCTT  16
                 |||||||||||||
Sbjct  54393439  TTTCGACCTTCTT  54393451


 Features flanking this part of subject sequence:
   392682 bp at 5' side: tissue factor pathway inhibitor (lipoprotein-associated c.
   580133 bp at 3' side: GULP, engulfment adaptor PTB domain containing 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  56547106  CTTCTTCATTCAC  56547094


>ref|NW_927719.1|HsCraAADB02_69 D Homo sapiens chromosome 2 genomic contig, altern
(based on Celera assembly)
Length=86821413

                                                          Sort alignments for this s
                                                            E value  Score  Percent i
                                                            Query start position  Sul

 Features in this part of subject sequence:
   thymidylate kinase family LPS-inducible member


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query  2        TCTTTCGACCTTCTTCAT  19
                |||||| |||||||||||
Sbjct  6846791  TCTTTCTACCTTCTTCAT  6846808


 Features flanking this part of subject sequence:
   117513 bp at 5' side: hypothetical protein LOC339789
   241509 bp at 3' side: inhibitor of DNA binding 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCACG  24
                ||||||||||||||
Sbjct  8426512  CTTCTTCATTCACG  8426499
```

```
 Features flanking this part of subject sequence:
   749 bp at 5' side: hypothetical protein LOC388939
   40182 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  29074222  CCTTCTTCATTCAC  29074209


 Features in this part of subject sequence:
   EH domain binding protein 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  62978716  CCTTCTTCATTCAC  62978729


 Features flanking this part of subject sequence:
   11557 bp at 5' side: similar to hepatoma-derived growth factor-related protein 2
   385989 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  2729178  CCTTCTTCATTCA  2729190


 Features flanking this part of subject sequence:
   566325 bp at 5' side: hypothetical protein LOC400940
   181280 bp at 3' side: hypothetical protein LOC400941


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3        CTTTCGACCTTCT  15
                |||||||||||||
Sbjct  6535896  CTTTCGACCTTCT  6535908


 Features in this part of subject sequence:
   lipin 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  11771589  CTTCTTCATTCAC  11771577


 Features in this part of subject sequence:
   hypothetical protein LOC81553


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  16556632  CCTTCTTCATTCA  16556644


 Features flanking this part of subject sequence:
   131174 bp at 5' side: similar to Zinc finger FYVE domain-containing protein 9 (.
```

```
   94862 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  17408958  CCTTCTTCATTCA  17408946


 Features flanking this part of subject sequence:
   45302 bp at 5' side: hypothetical protein
   253000 bp at 3' side: nuclear receptor coactivator 1 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  3         CTTTCGACCTTCTTCAT  19
                 ||||| |||||||||||
Sbjct  24401325  CTTTCTACCTTCTTCAT  24401341


 Features in this part of subject sequence:
   spastin isoform 1
   spastin isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  32108481  CCTTCTTCATTCA  32108493


 Features flanking this part of subject sequence:
   1868392 bp at 5' side: hypothetical protein LOC25940
   893376 bp at 3' side: cysteine-rich motor neuron 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  35463331  CCTTCTTCATTCA  35463319


 Features flanking this part of subject sequence:
   2107024 bp at 5' side: hypothetical protein LOC25940
   654744 bp at 3' side: cysteine-rich motor neuron 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         TCTTTCGACCTTC  14
                 |||||||||||||
Sbjct  35701951  TCTTTCGACCTTC  35701963


 Features flanking this part of subject sequence:
   3116 bp at 5' side: sterolin 2
   7566 bp at 3' side: leucine-rich PPR motif-containing protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  43878836  CCTTCTTCATTCA  43878824


 Features in this part of subject sequence:
   luteinizing hormone/choriogonadotropin receptor precursor
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1         ATCTTTCGACCTTCTTC  17
                 |||||| ||||||||||
Sbjct  48735703  ATCTTTAGACCTTCTTC  48735719


 Features in this part of subject sequence:
   neurexin 1 isoform alpha precursor
   neurexin 1 isoform beta precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  49926337  GACCTTCTTCATT  49926325


 Features flanking this part of subject sequence:
   208830 bp at 5' side: hypothetical protein
   855382 bp at 3' side: B-cell CLL/lymphoma 11A isoform 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  59599842  CCTTCTTCATTCA  59599854


 Features flanking this part of subject sequence:
   605058 bp at 5' side: hypothetical protein
   459150 bp at 3' side: B-cell CLL/lymphoma 11A isoform 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  1         ATCTTTCGACCTTCTTC  17
                 |||||| ||||||||||
Sbjct  59996086  ATCTTTAGACCTTCTTC  59996070


 Features flanking this part of subject sequence:
   6049 bp at 5' side: pellino protein
   234066 bp at 3' side: similar to 60S ribosomal protein L23a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  64118690  ACCTTCTTCATTC  64118702


 Features flanking this part of subject sequence:
   856566 bp at 5' side: hypothetical protein LOC440867
   89132 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  5         TTCGACCTTCTTC  17
                 |||||||||||||
Sbjct  66345483  TTCGACCTTCTTC  66345471


 Features flanking this part of subject sequence:
   128435 bp at 5' side: hypothetical protein isoform 2
   53731 bp at 3' side: ETAA16 protein
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  67351514  GACCTTCTTCATT  67351502


 Features flanking this part of subject sequence:
```

51835 bp at 5' side: similar to Exocyst complex component Sec15B isoform 3
10492 bp at 3' side: sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidore..

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  72886838  CCTTCTTCATTCA  72886850


 Features in this part of subject sequence:
```

empty spiracles homolog 1 isoform 2
empty spiracles homolog 1 isoform 1

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  72939791  ACCTTCTTCATTC  72939803


 Features flanking this part of subject sequence:
```

13060 bp at 5' side: RAB11 family interacting protein 5 (class I)
76800 bp at 3' side: similar to notochord

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  73135755  CCTTCTTCATTCA  73135743


 Features flanking this part of subject sequence:
```

56686 bp at 5' side: hypothetical protein LOC6936
491957 bp at 3' side: similar to Purine nucleoside phosphorylase (Inosine phosp.

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  75757884  CCTTCTTCATTCA  75757896


 Features flanking this part of subject sequence:
```

644203 bp at 5' side: similar to Leucine-rich repeat transmembrane neuronal pro.
125096 bp at 3' side: leucine rich repeat transmembrane neuronal 4

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  77382585  CCTTCTTCATTCA  77382597


 Features flanking this part of subject sequence:
```

1155107 bp at 5' side: leucine rich repeat transmembrane neuronal 1
124346 bp at 3' side: hypothetical protein LOC647291

```
 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  81446636  ACCTTCTTCATTC  81446624


 Features flanking this part of subject sequence:
   94255 bp at 5' side: sialyltransferase 9
   69784 bp at 3' side: polymerase (RNA) I polypeptide A, 194kDa


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  85944878  CTTCTTCATTCAC  85944866


>ref|NW_921618.1|HsCraAADB02_124 D Homo sapiens chromosome 2 genomic contig, alter
(based on Celera assembly)
Length=47628048

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent 
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   158948 bp at 5' side: phospholipase C-like 1
   966054 bp at 3' side: SATB family member 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTCA  22
                ||||||||||||||
Sbjct  3840930  ACCTTCTTCATTCA  3840943


 Features in this part of subject sequence:
   amyotrophic lateral sclerosis 2 (juvenile) chromosome reg...
   amyotrophic lateral sclerosis 2 (juvenile) chromosome reg...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  10153516  GACCTTCTTCATTC  10153503


 Features flanking this part of subject sequence:
   201128 bp at 5' side: hypothetical protein
   96231 bp at 3' side: phospholipase C-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  3522602  CTTCTTCATTCAC  3522590


 Features flanking this part of subject sequence:
   402475 bp at 5' side: phospholipase C-like 1
   722528 bp at 3' side: SATB family member 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  4084469  CCTTCTTCATTCA  4084457
```

```
 Features flanking this part of subject sequence:
   46585 bp at 5' side: nucleolar protein NOP5/NOP58
   27312 bp at 3' side: bone morphogenetic protein receptor type II precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  7881193  CCTTCTTCATTCA  7881181


 Features flanking this part of subject sequence:
   86596 bp at 5' side: amyotrophic lateral sclerosis 2 (juvenile) chromosome reg..
   61980 bp at 3' side: neurobeachin-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4        TTTCGACCTTCTT  16
                |||||||||||||
Sbjct  8606041  TTTCGACCTTCTT  8606053


 Features flanking this part of subject sequence:
   4709 bp at 5' side: hypothetical protein
   742 bp at 3' side: similar to cytotoxic T-lymphocyte-associated protein 4 is...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  2        TCTTTCGACCTTCTTCA  18
                ||||| |||||||||||
Sbjct  9401259  TCTTTGGACCTTCTTCA  9401275


 Features flanking this part of subject sequence:
   28528 bp at 5' side: carbamoyl-phosphate synthetase 1, mitochondrial
   677196 bp at 3' side: v-erb-a erythroblastic leukemia viral oncogene homolog 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  16253662  CCTTCTTCATTCA  16253650


 Features in this part of subject sequence:
   hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  21241301  CCTTCTTCATTCA  21241313


 Features flanking this part of subject sequence:
   480020 bp at 5' side: solute carrier family 4, anion exchanger, member 3 isoform
   1302451 bp at 3' side: ephrin receptor EphA4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  25670979  CCTTCTTCATTCA  25670967
```

```
  Features in this part of subject sequence:
    hypothetical protein LOC56947


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  32888129  GACCTTCTTCATT  32888117


  Features in this part of subject sequence:
    SP140 nuclear body protein isoform 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  35824954  CCTTCTTCATTCA  35824942


  Features flanking this part of subject sequence:
    139128 bp at 5' side: nuclear antigen Sp100
    70425 bp at 3' side: similar to barrier to autointegration factor 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  36210398  CTTCTTCATTCAC  36210386


  Features in this part of subject sequence:
    neuronal guanine nucleotide exchange factor


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  38488033  ACCTTCTTCATTC  38488021


  Features in this part of subject sequence:
    transient receptor potential cation channel, subfamily M,...


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  7         CGACCTTCTTCAT  19
                 |||||||||||||
Sbjct  39521518  CGACCTTCTTCAT  39521530


  Features flanking this part of subject sequence:
    27177 bp at 5' side: alpha 3 type VI collagen isoform 5 precursor
    5165 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  42960901  CTTCTTCATTCAC  42960889


>ref|NW_922017.1|HsCraAADB02_16 D Homo sapiens chromosome 1 genomic contig, alterna
(based on Celera assembly)
Length=4472039

  Features in this part of subject sequence:
```

```
    netrin G1


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

 Query  3        CTTTCGACCTTCTT  16
                 ||||||||||||||
 Sbjct  3439974  CTTTCGACCTTCTT  3439987


 >ref|NW_923572.1|HsCraAADB02_3 D Homo sapiens chromosome 1 genomic contig, alternat
 (based on Celera assembly)
 Length=9603050

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent i
                                                                   Query start position  Sub

  Features flanking this part of subject sequence:
    935652 bp at 5' side: transmembrane protein SHREW1
    156099 bp at 3' side: nephroretinin


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

 Query  10       CCTTCTTCATTCAC  23
                 ||||||||||||||
 Sbjct  2451371  CCTTCTTCATTCAC  2451384


  Features in this part of subject sequence:
    calmodulin-binding transcription activator 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  11       CTTCTTCATTCAC  23
                 |||||||||||||
 Sbjct  4457126  CTTCTTCATTCAC  4457138


  Features in this part of subject sequence:
    vacuolar protein sorting 13D isoform 2
    vacuolar protein sorting 13D isoform 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  11       CTTCTTCATTCAC  23
                 |||||||||||||
 Sbjct  9039980  CTTCTTCATTCAC  9039992


 >ref|NW_921351.1|HsCraAADB02_10 D Homo sapiens chromosome 1 genomic contig, alterna
 (based on Celera assembly)
 Length=57745789

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent i
                                                                   Query start position  Sub

  Features flanking this part of subject sequence:
    1153 bp at 5' side: coiled-coil domain containing 23
    12797 bp at 3' side: erythroblast membrane-associated protein


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

 Query  9         ACCTTCTTCATTCA  22
                  ||||||||||||||
 Sbjct  17426150  ACCTTCTTCATTCA  17426163


  Features flanking this part of subject sequence:
```

```
    2482 bp at 5' side: zinc finger protein 393
    80334 bp at 3' side: DNA methyltransferase 1 associated protein 1


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

 Query  10        CCTTCTTCATTCAC  23
                  ||||||||||||||
 Sbjct  18743273  CCTTCTTCATTCAC  18743260


  Features in this part of subject sequence:
    ATP/GTP binding protein-like 4


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

 Query  3         CTTTCGACCTTCTT  16
                  ||||||||||||||
 Sbjct  23326616  CTTTCGACCTTCTT  23326603


  Features in this part of subject sequence:
    AMP-activated protein kinase alpha 2 catalytic subunit


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

 Query  9         ACCTTCTTCATTCA  22
                  ||||||||||||||
 Sbjct  31314832  ACCTTCTTCATTCA  31314845


  Features in this part of subject sequence:
    AMP-activated protein kinase alpha 2 catalytic subunit


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

 Query  9         ACCTTCTTCATTCA  22
                  ||||||||||||||
 Sbjct  31314888  ACCTTCTTCATTCA  31314901


  Features flanking this part of subject sequence:
    69672 bp at 5' side: hypothetical protein
    24290 bp at 3' side: APG4 autophagy 4 homolog C


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

 Query  8         GACCTTCTTCATTC  21
                  ||||||||||||||
 Sbjct  37394857  GACCTTCTTCATTC  37394870


  Features flanking this part of subject sequence:
    3839 bp at 5' side: zinc finger protein 31
    20156 bp at 3' side: CUB and Sushi multiple domains 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

 Query  11       CTTCTTCATTCAC  23
                 |||||||||||||
 Sbjct  8097595  CTTCTTCATTCAC  8097607


  Features in this part of subject sequence:
    CUB and Sushi multiple domains 2


  Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  8130914  CTTCTTCATTCAC  8130902


 Features in this part of subject sequence:
   CUB and Sushi multiple domains 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  8364305  CCTTCTTCATTCA  8364317


 Features flanking this part of subject sequence:
   388908 bp at 5' side: hypothetical protein LOC84970
   151239 bp at 3' side: gap junction protein, beta 5 (connexin 31.1)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12       TTCTTCATTCACG  24
                |||||||||||||
Sbjct  9206275  TTCTTCATTCACG  9206263


 Features in this part of subject sequence:
   arginine/proline rich coiled-coil 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  10771816  CTTCTTCATTCAC  10771804


 Features flanking this part of subject sequence:
   12242 bp at 5' side: hypothetical protein LOC339541
   3287 bp at 3' side: kinesin family member 2C


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  19346061  ACCTTCTTCATTC  19346073


 Features in this part of subject sequence:
   hypothetical protein LOC199920


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  31419948  CCTTCTTCATTCA  31419960


 Features flanking this part of subject sequence:
   132565 bp at 5' side: hypothetical protein
   99252 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
```

```
                 |||||||||||||
Sbjct  33648149  CTTCTTCATTCAC  33648137


 Features in this part of subject sequence:
   nuclear factor I/A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 19/21 (90%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query  2         TCTTTCGACCTTCTTCATTCA  22
                 ||||| |||||| ||||||||
Sbjct  35917061  TCTTTTGACCTTGTTCATTCA  35917081


 Features in this part of subject sequence:
   InaD-like protein isoform 1
   InaD-like protein isoform 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  36496192  TTCTTCATTCACG  36496180


 Features in this part of subject sequence:
   WD repeat domain 78 isoform 1
   WD repeat domain 78 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  41502610  TTCTTCATTCACG  41502622


 Features flanking this part of subject sequence:
   700812 bp at 5' side: DEP domain containing 1
   562043 bp at 3' side: leucine rich repeat containing 7


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  43814572  CTTCTTCATTCAC  43814584


 Features in this part of subject sequence:
   prostaglandin E receptor 3, subtype EP3 isoform 6
   prostaglandin E receptor 3, subtype EP3 isoform 7


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  45644955  CCTTCTTCATTCA  45644967


 Features in this part of subject sequence:
   neuronal growth regulator 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  46218674  CTTCTTCATTCAC  46218662
```

```
 Features flanking this part of subject sequence:
   55792 bp at 5' side: interferon-induced, hepatitis C-associated microtubular a..
   170268 bp at 3' side: similar to EGF, latrophilin and seven transmembrane domai.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  53285661  CCTTCTTCATTCA  53285673


>ref|NW_927128.1|HsCraAADB02_62 D Homo sapiens chromosome 1 genomic contig, alterna
(based on Celera assembly)
Length=18989345

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

 Features in this part of subject sequence:
   ryanodine receptor 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  13790594  CCTTCTTCATTCAC  13790607


 Features in this part of subject sequence:
   ryanodine receptor 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  13790630  CCTTCTTCATTCAC  13790643


 Features flanking this part of subject sequence:
   135232 bp at 5' side: cholinergic receptor, muscarinic 3
   385918 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  15521473  GACCTTCTTCATTC  15521486


 Features flanking this part of subject sequence:
   66048 bp at 5' side: hypothetical protein LOC126731
   22967 bp at 3' side: alpha 1 actin precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  5393749  ACCTTCTTCATTC  5393761


 Features flanking this part of subject sequence:
   384774 bp at 5' side: disrupted in schizophrenia 1 isoform Es
   295738 bp at 3' side: signal-induced proliferation-associated 1 like 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
```

```
 Strand=Plus/Minus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  8089053  ACCTTCTTCATTC  8089041


 Features flanking this part of subject sequence:
   285798 bp at 5' side: hypothetical protein
   299387 bp at 3' side: similar to solute carrier family 35, member F3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  9903522  CCTTCTTCATTCA  9903534


 Features flanking this part of subject sequence:
   88708 bp at 5' side: zona pellucida glycoprotein 4 preproprotein
   506634 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  13973319  CCTTCTTCATTCA  13973307


 Features flanking this part of subject sequence:
   158793 bp at 5' side: hypothetical protein
   742606 bp at 3' side: cholinergic receptor, muscarinic 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  7         CGACCTTCTTCAT  19
                 |||||||||||||
Sbjct  14643018  CGACCTTCTTCAT  14643030


 Features flanking this part of subject sequence:
   284217 bp at 5' side: phospholipase D family, member 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  18632283  CTTCTTCATTCAC  18632295


>ref|NT_079573.3|HsX_79638 D Homo sapiens chromosome X genomic contig, reference a
Length=12096764

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent
                                                                    Query start position  Su

 Features flanking this part of subject sequence:
   73796 bp at 5' side: ornithine carbamoyltransferase precursor
   66656 bp at 3' side: tetraspanin 7


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  1205898  CCTTCTTCATTCAC  1205911


 Features flanking this part of subject sequence:
```

```
   78954 bp at 5' side: hypothetical protein
   283050 bp at 3' side: BCL-6 interacting corepressor isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  2480067  CCTTCTTCATTCA  2480079


 Features flanking this part of subject sequence:
   161281 bp at 5' side: hypothetical protein
   200723 bp at 3' side: BCL-6 interacting corepressor isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  2562394  CTTCTTCATTCAC  2562406


 Features flanking this part of subject sequence:
   306337 bp at 5' side: hypothetical protein
   55667 bp at 3' side: BCL-6 interacting corepressor isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  2707450  CTTCTTCATTCAC  2707462


 Features flanking this part of subject sequence:
   89410 bp at 5' side: hypothetical protein
   329791 bp at 3' side: ATPase, H+ transporting, lysosomal accessory protein 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12       TTCTTCATTCACG  24
                |||||||||||||
Sbjct  2962294  TTCTTCATTCACG  2962282


 Features flanking this part of subject sequence:
   306274 bp at 5' side: hypothetical protein
   112927 bp at 3' side: ATPase, H+ transporting, lysosomal accessory protein 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  3179146  CTTCTTCATTCAC  3179158


 Features flanking this part of subject sequence:
   43378 bp at 5' side: hypothetical protein
   1689108 bp at 3' side: monoamine oxidase A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  4678249  CTTCTTCATTCAC  4678237


 Features in this part of subject sequence:
   amine oxidase (flavin-containing)
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1        ATCTTTCGACCTT  13
                |||||||||||||
Sbjct  6505112  ATCTTTCGACCTT  6505124


 Features in this part of subject sequence:
   ornithine aminotransferase-like 1 isoform 2
   ornithine aminotransferase-like 1 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  11265025  GACCTTCTTCATT  11265037


>ref|NT_010783.14|Hs17_10940 D Homo sapiens chromosome 17 genomic contig, referenc
Length=24793602

                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   293572 bp at 5' side: hypothetical protein
   72522 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  3         CTTTCGACCTTCTT  16
                 ||||||||||||||
Sbjct  10011544  CTTTCGACCTTCTT  10011531


 Features in this part of subject sequence:
   hypothetical protein LOC284058


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  2792927  CTTCTTCATTCAC  2792939


 Features flanking this part of subject sequence:
   4820 bp at 5' side: C/EBP-induced protein
   19916 bp at 3' side: MYST histone acetyltransferase 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  6499547  CCTTCTTCATTCA  6499559


 Features in this part of subject sequence:
   carbonic anhydrase X


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  8864533  CCTTCTTCATTCA  8864521
```

```
 Features in this part of subject sequence:
   ankyrin-repeat and fibronectin type III domain containing 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  13191120  ACCTTCTTCATTC  13191132


 Features in this part of subject sequence:
   protein kinase C, alpha


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  23333883  TTCTTCATTCACG  23333871


>ref|NT_010498.15|Hs16_10655 D Homo sapiens chromosome 16 genomic contig, referenc
Length=42003582

                                                                Sort alignments for this s
                                                                  E value  Score  Percent
                                                                  Query start position  Su

 Features flanking this part of subject sequence:
   801788 bp at 5' side: sal-like 1
   73327 bp at 3' side: hypothetical protein isoform 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  5601139  CCTTCTTCATTCAC  5601152


 Features flanking this part of subject sequence:
   447202 bp at 5' side: M-phase phosphoprotein 6
   9703 bp at 3' side: cadherin 13 preproprotein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  36265194  ACCTTCTTCATTCA  36265181


 Features in this part of subject sequence:
   hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCACG  24
                 ||||||||||||||
Sbjct  40815571  CTTCTTCATTCACG  40815558


 Features in this part of subject sequence:
   T-cell immunomodulatory protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
```

```
Sbjct  1074315  CTTCTTCATTCAC  1074327


 Features in this part of subject sequence:
   hypothetical protein LOC23322


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  6        TCGACCTTCTTCA  18
                |||||||||||||
Sbjct  7347556  TCGACCTTCTTCA  7347544


 Features in this part of subject sequence:
   similar to fatso isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  7708414  CTTCTTCATTCAC  7708402


 Features flanking this part of subject sequence:
   71805 bp at 5' side: calpain small subunit 2
   17375 bp at 3' side: solute carrier family 6 member 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  9287419  CTTCTTCATTCAC  9287431


 Features in this part of subject sequence:
   guanine nucleotide binding protein, alpha activating poly...
   guanine nucleotide binding protein, alpha activating poly...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  9864564  ACCTTCTTCATTC  9864576


 Features in this part of subject sequence:
   cirhin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  22799784  ACCTTCTTCATTC  22799796


 Features flanking this part of subject sequence:
   196920 bp at 5' side: similar to LSM3 homolog, U6 small nuclear RNA associated
   659977 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  32200850  CCTTCTTCATTCA  32200862


 Features flanking this part of subject sequence:
```

```
    815882 bp at 5' side: similar to LSM3 homolog, U6 small nuclear RNA associated
    41015 bp at 3' side: hypothetical protein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  32819812  TTCTTCATTCACG  32819824


  Features in this part of subject sequence:
    cadherin 13 preproprotein


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  36492055  CCTTCTTCATTCA  36492043


  Features in this part of subject sequence:
    membrane-bound transcription factor site-1 protease isofo...
    membrane-bound transcription factor site-1 protease isofo...


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  37740043  ACCTTCTTCATTC  37740055


  Features in this part of subject sequence:
    coactosin-like 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  38233731  CTTCTTCATTCAC  38233743


  Features flanking this part of subject sequence:
    9168 bp at 5' side: cytochrome c oxidase subunit IV isoform 1 precursor
    86962 bp at 3' side: interferon regulatory factor 8


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  39463847  ACCTTCTTCATTC  39463859


>ref|NT_009952.14|Hs13_10109 D Homo sapiens chromosome 13 genomic contig, referenc
Length=25443670

                                                              Sort alignments for this
                                                                E value  Score  Percent
                                                                Query start position  Su

  Features in this part of subject sequence:
    glypican 5


  Score = 28.2 bits (14),  Expect =   112
  Identities = 17/18 (94%), Gaps = 0/18 (0%)
  Strand=Plus/Minus

Query  1        ATCTTTCGACCTTCTTCA  18
                ||||||| ||||||||||
```

```
Sbjct  5364703  ATCTTTCAACCTTCTTCA  5364686


 Features flanking this part of subject sequence:
   2645874 bp at 5' side: similar to CXXC finger 6
   852442 bp at 3' side: glypican 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  4288535  CTTCTTCATTCAC  4288523


 Features flanking this part of subject sequence:
   2725486 bp at 5' side: similar to CXXC finger 6
   772830 bp at 3' side: glypican 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  4368135  CCTTCTTCATTCA  4368147


 Features in this part of subject sequence:
   G protein-coupled receptor 180 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  8345114  CTTCTTCATTCAC  8345102


 Features flanking this part of subject sequence:
   1720 bp at 5' side: DAZ interacting protein 1 isoform 2
   33495 bp at 3' side: DnaJ (Hsp40) homolog, subfamily C, member 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12       TTCTTCATTCACG  24
                |||||||||||||
Sbjct  9385691  TTCTTCATTCACG  9385679


 Features in this part of subject sequence:
   fibroblast growth factor 14 isoform 1B
   fibroblast growth factor 14 isoform 1A


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  15515682  ACCTTCTTCATTC  15515670


 Features flanking this part of subject sequence:
   1177124 bp at 5' side: hypothetical protein
   1007484 bp at 3' side: D-amino acid oxidase activator


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  18200818  CCTTCTTCATTCA  18200830
```

```
  Features in this part of subject sequence:
    ephrin B2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  20257020  CCTTCTTCATTCA  20257032


  Features flanking this part of subject sequence:
    316610 bp at 5' side: tumor necrosis factor (ligand) superfamily, member 13b
    42364 bp at 3' side: myosin heavy chain Myr 8


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  22365584  CCTTCTTCATTCA  22365572


  Features flanking this part of subject sequence:
    150471 bp at 5' side: myosin heavy chain Myr 8
    398984 bp at 3' side: insulin receptor substrate 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  23099343  CCTTCTTCATTCA  23099331


  Features flanking this part of subject sequence:
    509428 bp at 5' side: myosin heavy chain Myr 8
    40027 bp at 3' side: insulin receptor substrate 2


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  23458288  ACCTTCTTCATTC  23458300


  Features flanking this part of subject sequence:
    20126 bp at 5' side: RAB20, member RAS oncogene family
    34018 bp at 3' side: hypothetical protein LOC55739


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  24323668  TTCTTCATTCACG  24323680


  Features in this part of subject sequence:
    ankyrin repeat domain 10


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  24628530  ACCTTCTTCATTC  24628542


>ref|NT_024524.13|Hs13_24680 D Homo sapiens chromosome 13 genomic contig, referenc
Length=67740325
```

```
                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

          Features flanking this part of subject sequence:
            42390 bp at 5' side: doublecortin and CaM kinase-like 1
            494 bp at 3' side: spermatogenesis and oogenesis specific basic helix-loop-h...


          Score = 28.2 bits (14),  Expect =   112
          Identities = 14/14 (100%), Gaps = 0/14 (0%)
          Strand=Plus/Minus

         Query  10        CCTTCTTCATTCAC  23
                          ||||||||||||||
         Sbjct  17722677  CCTTCTTCATTCAC  17722664


          Features flanking this part of subject sequence:
            2275666 bp at 5' side: hypothetical protein
            195982 bp at 3' side: protocadherin 9 isoform 2 precursor


          Score = 28.2 bits (14),  Expect =   112
          Identities = 14/14 (100%), Gaps = 0/14 (0%)
          Strand=Plus/Plus

         Query  10        CCTTCTTCATTCAC  23
                          ||||||||||||||
         Sbjct  47662793  CCTTCTTCATTCAC  47662806


          Features flanking this part of subject sequence:
            3166 bp at 5' side: hypothetical protein
            65707 bp at 3' side: similar to telomeric repeat binding factor 1 isoform 2


          Score = 26.3 bits (13),  Expect =   444
          Identities = 13/13 (100%), Gaps = 0/13 (0%)
          Strand=Plus/Plus

         Query  10      CCTTCTTCATTCA  22
                        |||||||||||||
         Sbjct  168910  CCTTCTTCATTCA  168922


          Features flanking this part of subject sequence:
            66792 bp at 5' side: hypothetical protein
            108469 bp at 3' side: hypothetical protein


          Score = 26.3 bits (13),  Expect =   444
          Identities = 13/13 (100%), Gaps = 0/13 (0%)
          Strand=Plus/Minus

         Query  12      TTCTTCATTCACG  24
                        |||||||||||||
         Sbjct  454687  TTCTTCATTCACG  454675


          Features flanking this part of subject sequence:
            741617 bp at 5' side: fibroblast growth factor 9 precursor
            360265 bp at 3' side: similar to 60S ribosomal protein L7a (Surfeit locus prote.


          Score = 26.3 bits (13),  Expect =   444
          Identities = 13/13 (100%), Gaps = 0/13 (0%)
          Strand=Plus/Plus

         Query  3        CTTTCGACCTTCT  15
                         |||||||||||||
         Sbjct  3997191  CTTTCGACCTTCT  3997203


          Features flanking this part of subject sequence:
            72839 bp at 5' side: ubiquitin specific peptidase like 1
            3399 bp at 3' side: arachidonate 5-lipoxygenase-activating protein


          Score = 26.3 bits (13),  Expect =   444
          Identities = 13/13 (100%), Gaps = 0/13 (0%)
          Strand=Plus/Plus

         Query  3         CTTTCGACCTTCT  15
```

```
                  |||||||||||||
Sbjct  12286332  CTTTCGACCTTCT  12286344


 Features flanking this part of subject sequence:
   26895 bp at 5' side: klotho isoform b
   18003 bp at 3' side: START domain containing 13 isoform alpha


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  14641715  CTTCTTCATTCAC  14641727


 Features in this part of subject sequence:
   START domain containing 13 isoform alpha
   START domain containing 13 isoform delta


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  14756773  CCTTCTTCATTCA  14756761


 Features in this part of subject sequence:
   doublecortin and CaM kinase-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  17360778  CCTTCTTCATTCA  17360790


 Features in this part of subject sequence:
   FRAS1 related extracellular matrix protein 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  20341391  CTTCTTCATTCAC  20341403


 Features flanking this part of subject sequence:
   402745 bp at 5' side: 5-hydroxytryptamine (serotonin) receptor 2A
   644708 bp at 3' side: succinate-CoA ligase, ADP-forming, beta subunit


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  28852799  CCTTCTTCATTCA  28852787


 Features flanking this part of subject sequence:
   506460 bp at 5' side: 5-hydroxytryptamine (serotonin) receptor 2A
   540989 bp at 3' side: succinate-CoA ligase, ADP-forming, beta subunit


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1         ATCTTTCGACCTTCTTC  17
                 ||||||| |||||||||
Sbjct  28956502  ATCTTTCCACCTTCTTC  28956518
```

```
 Features flanking this part of subject sequence:
   1007390 bp at 5' side: 5-hydroxytryptamine (serotonin) receptor 2A
   40063 bp at 3' side: succinate-CoA ligase, ADP-forming, beta subunit


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  29457444  CCTTCTTCATTCA  29457432


 Features flanking this part of subject sequence:
   1884675 bp at 5' side: olfactomedin 4 precursor
   2205846 bp at 3' side: hypothetical protein LOC122183


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  36489582  CCTTCTTCATTCA  36489594


 Features flanking this part of subject sequence:
   2288293 bp at 5' side: olfactomedin 4 precursor
   1802228 bp at 3' side: hypothetical protein LOC122183


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  36893200  CCTTCTTCATTCA  36893212


 Features flanking this part of subject sequence:
   3682816 bp at 5' side: olfactomedin 4 precursor
   407705 bp at 3' side: hypothetical protein LOC122183


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  38287735  CCTTCTTCATTCA  38287723


 Features flanking this part of subject sequence:
   689603 bp at 5' side: protocadherin 17
   1359260 bp at 3' side: diaphanous homolog 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  39969032  CTTCTTCATTCAC  39969044


 Features flanking this part of subject sequence:
   1067747 bp at 5' side: protocadherin 17
   981116 bp at 3' side: diaphanous homolog 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  40347176  CCTTCTTCATTCA  40347188
```

```
 Features flanking this part of subject sequence:
   1284392 bp at 5' side: protocadherin 17
   764471 bp at 3' side: diaphanous homolog 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  40563833  CTTCTTCATTCAC  40563821


 Features flanking this part of subject sequence:
   460306 bp at 5' side: hypothetical protein
   2011343 bp at 3' side: protocadherin 9 isoform 2 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  45847445  GACCTTCTTCATT  45847433


 Features in this part of subject sequence:
   dachshund homolog 1 isoform b
   dachshund homolog 1 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  53270354  CTTCTTCATTCAC  53270366


 Features flanking this part of subject sequence:
   73964 bp at 5' side: hypothetical protein
   216025 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  55764436  CTTCTTCATTCAC  55764424


 Features flanking this part of subject sequence:
   73103 bp at 5' side: endothelin receptor type B isoform 1
   604464 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  59545812  CTTCTTCATTCAC  59545824


 Features flanking this part of subject sequence:
   237789 bp at 5' side: hypothetical protein
   25542 bp at 3' side: sprouty 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  1         ATCTTTCGACCTT  13
                 |||||||||||||
Sbjct  61865340  ATCTTTCGACCTT  61865352
```

```
>ref|NT_029419.11|Hs12_29578 D Homo sapiens chromosome 12 genomic contig, referenc
Length=38648979

                                                            Sort alignments for this s
                                                              E value  Score  Percent
                                                              Query start position  Su

 Features flanking this part of subject sequence:
   24 bp at 5' side: olfactory receptor, family 6, subfamily C, member 2
   16011 bp at 3' side: olfactory receptor, family 6, subfamily C, member 70


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  17990279  CCTTCTTCATTCAC  17990266


 Features flanking this part of subject sequence:
   35939 bp at 5' side: hypothetical protein LOC283461
   2824 bp at 3' side: solute carrier family 2 (facilitated glucose transporter)...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8        GACCTTCTTCATT  20
                |||||||||||||
Sbjct  2294298  GACCTTCTTCATT  2294310


 Features flanking this part of subject sequence:
   559550 bp at 5' side: prickle-like 1
   322128 bp at 3' side: a disintegrin-like and metalloprotease (reprolysin type) .


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1        ATCTTTCGACCTTCTTC  17
                |||||| ||||||||||
Sbjct  5569174  ATCTTTTGACCTTCTTC  5569190


 Features in this part of subject sequence:
   AT rich interactive domain 2 (ARID, RFX-like)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  8365273  CTTCTTCATTCAC  8365285


 Features flanking this part of subject sequence:
   234207 bp at 5' side: similar to heat shock 70kD protein binding protein
   653627 bp at 3' side: leucine-rich repeats and immunoglobulin-like domains 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  20756033  CCTTCTTCATTCA  20756021


 Features flanking this part of subject sequence:
   282394 bp at 5' side: leucine-rich repeats and immunoglobulin-like domains 3
   502161 bp at 3' side: solute carrier family 16, member 7


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  21739716  GACCTTCTTCATT  21739728


 Features in this part of subject sequence:
   carboxypeptidase M precursor
   carboxypeptidase M precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  31406210  CCTTCTTCATTCA  31406198


 Features flanking this part of subject sequence:
   182392 bp at 5' side: carboxypeptidase M precursor
   124406 bp at 3' side: cleavage and polyadenylation specific factor 6, 68 kD sub.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  31652327  CTTCTTCATTCAC  31652315


 Features flanking this part of subject sequence:
   297803 bp at 5' side: protein tyrosine phosphatase, receptor type, R isoform 2
   73326 bp at 3' side: transmembrane 4 superfamily member 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  33589094  CCTTCTTCATTCA  33589082


>ref|NT_025741.14|Hs6_25897 D Homo sapiens chromosome 6 genomic contig, reference 
Length=61645385

                                                               Sort alignments for this s
                                                                 E value  Score  Percent 
                                                                 Query start position  Su

 Features flanking this part of subject sequence:
   113754 bp at 5' side: activator of cAMP-responsive element modulator (CREM) in .
   68933 bp at 3' side: G protein-coupled receptor 63


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  8        GACCTTCTTCATTC  21
                ||||||||||||||
Sbjct  1346872  GACCTTCTTCATTC  1346859


 Features in this part of subject sequence:
   glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  11282883  ACCTTCTTCATTCA  11282870


 Features in this part of subject sequence:
   glutamate receptor, metabotropic 1
```

```
 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  50594108  GACCTTCTTCATTC  50594121


 Features flanking this part of subject sequence:
   219188 bp at 5' side: mannosidase, endo-alpha
   377551 bp at 3' side: fucosyltransferase 9 (alpha (1,3) fucosyltransferase)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8       GACCTTCTTCATT  20
               |||||||||||||
Sbjct  442938  GACCTTCTTCATT  442926


 Features flanking this part of subject sequence:
   572745 bp at 5' side: mannosidase, endo-alpha
   23990 bp at 3' side: fucosyltransferase 9 (alpha (1,3) fucosyltransferase)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  5       TTCGACCTTCTTCATTC  21
               |||| ||||||||||||
Sbjct  796483  TTCGTCCTTCTTCATTC  796499


 Features in this part of subject sequence:
   cyclin-dependent kinase (CDC2-like) 11


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  3         CTTTCGACCTTCT  15
                 |||||||||||||
Sbjct  15155795  CTTTCGACCTTCT  15155783


 Features flanking this part of subject sequence:
   29526 bp at 5' side: TSPY-like 1
   89883 bp at 3' side: squamous cell carcinoma antigen recognized by T cells 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  20799960  GACCTTCTTCATT  20799948


 Features in this part of subject sequence:
   karyopherin alpha 5 (importin alpha 6)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  21208773  GACCTTCTTCATT  21208785


 Features flanking this part of subject sequence:
   557 bp at 5' side: HD domain containing 2
   67833 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  29728082  CTTCTTCATTCAC  29728070


 Features flanking this part of subject sequence:
   30644 bp at 5' side: hypothetical protein LOC253582
   128242 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  34317418  CCTTCTTCATTCA  34317406


 Features in this part of subject sequence:
   A-kinase anchor protein 7 isoform gamma


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         TTTCGACCTTCTT  16
                 |||||||||||||
Sbjct  35641682  TTTCGACCTTCTT  35641694


 Features flanking this part of subject sequence:
   354258 bp at 5' side: eyes absent 4 isoform b
   6323 bp at 3' side: transcription factor 21


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  38308642  CTTCTTCATTCAC  38308630


 Features flanking this part of subject sequence:
   32573 bp at 5' side: v-myb myeloblastosis viral oncogene homolog
   35080 bp at 3' side: jouberin


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  39676132  CTTCTTCATTCAC  39676120


 Features flanking this part of subject sequence:
   746212 bp at 5' side: utrophin
   28474 bp at 3' side: laforin isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  50022774  ACCTTCTTCATTC  50022786


 Features in this part of subject sequence:
   laforin isoform b


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  50051612  GACCTTCTTCATT  50051624


 Features flanking this part of subject sequence:
   675032 bp at 5' side: hypothetical protein LOC389432
   103568 bp at 3' side: SAM and SH3 domain containing 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  52665053  ACCTTCTTCATTC  52665065


 Features flanking this part of subject sequence:
   83468 bp at 5' side: hypothetical protein LOC80129
   106286 bp at 3' side: estrogen receptor 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  12        TTCTTCATTCACG  24
                 |||||||||||||
Sbjct  56127191  TTCTTCATTCACG  56127179


 Features flanking this part of subject sequence:
   535187 bp at 5' side: similar to 60S ribosomal protein L27a
   145160 bp at 3' side: hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  58243496  CTTCTTCATTCAC  58243484


>ref|NT_005612.15|Hs3_5769 D Homo sapiens chromosome 3 genomic contig, reference a
Length=100530253

                                                                 Sort alignments for this s
                                                                   E value  Score  Percent
                                                                   Query start position  Su

 Features flanking this part of subject sequence:
   979823 bp at 5' side: similar to synovial sarcoma, X breakpoint 2 interacting p.
   847892 bp at 3' side: activated leukocyte cell adhesion molecule


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Minus

Query  3         CTTTCGACCTTCTTCATT  20
                 ||||| ||||||||||||
Sbjct  10733507  CTTTCTACCTTCTTCATT  10733490


 Features flanking this part of subject sequence:
   3951 bp at 5' side: hypothetical protein
   128448 bp at 3' side: testes development-related NYD-SP17


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  13463120  ACCTTCTTCATTCA  13463133


 Features flanking this part of subject sequence:
   2076 bp at 5' side: urocanase domain containing 1
```

```
   4525 bp at 3' side: carbohydrate (chondroitin 4) sulfotransferase 13


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  32733797  CCTTCTTCATTCAC  32733784


 Features in this part of subject sequence:
   monoglyceride lipase isoform 1
   monoglyceride lipase isoform 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  33989083  CCTTCTTCATTCAC  33989070


 Features flanking this part of subject sequence:
   1501785 bp at 5' side: hypothetical protein LOC205428
   578019 bp at 3' side: procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2 isofor.


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Minus

Query  4         TTTCGACCTTCTTCATTC  21
                 |||| |||||||||||||
Sbjct  51705631  TTTCTACCTTCTTCATTC  51705614


 Features flanking this part of subject sequence:
   178150 bp at 5' side: NOL1/NOP2/Sun domain family, member 3
   202114 bp at 3' side: similar to SVH protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11      CTTCTTCATTCAC  23
               |||||||||||||
Sbjct  518642  CTTCTTCATTCAC  518630


 Features flanking this part of subject sequence:
   539655 bp at 5' side: similar to synovial sarcoma, X breakpoint 2 interacting p.
   1288065 bp at 3' side: activated leukocyte cell adhesion molecule


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  4         TTTCGACCTTCTT  16
                 |||||||||||||
Sbjct  10293334  TTTCGACCTTCTT  10293322


 Features flanking this part of subject sequence:
   1182219 bp at 5' side: zinc finger and BTB domain containing 20
   89601 bp at 3' side: growth associated protein 43


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  21748070  CCTTCTTCATTCA  21748082


 Features in this part of subject sequence:
   DNA polymerase theta
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  1         ATCTTTCGACCTT  13
                 |||||||||||||
Sbjct  27759488  ATCTTTCGACCTT  27759476


 Features flanking this part of subject sequence:
   120900 bp at 5' side: CD86 antigen isoform 2 precursor
   13744 bp at 3' side: calcium-sensing receptor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         CGACCTTCTTCAT  19
                 |||||||||||||
Sbjct  28454439  CGACCTTCTTCAT  28454427


 Features in this part of subject sequence:
   integrin, beta 5


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  31047292  ACCTTCTTCATTC  31047280


 Features flanking this part of subject sequence:
   244581 bp at 5' side: hypothetical protein LOC389152
   54814 bp at 3' side: mitochondrial ribosomal protein S22


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  45503201  CCTTCTTCATTCA  45503189


 Features in this part of subject sequence:
   calsyntenin 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  46291069  CCTTCTTCATTCA  46291057


 Features in this part of subject sequence:
   ataxia telangiectasia and Rad3 related protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  48705965  CTTCTTCATTCAC  48705977


 Features flanking this part of subject sequence:
   602322 bp at 5' side: hypothetical protein isoform 1
   717200 bp at 3' side: angiotensin II receptor, type 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  54236769  CCTTCTTCATTCA  54236757


 Features flanking this part of subject sequence:
   836038 bp at 5' side: hypothetical protein isoform 1
   483484 bp at 3' side: angiotensin II receptor, type 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  7         CGACCTTCTTCAT  19
                 |||||||||||||
Sbjct  54470485  CGACCTTCTTCAT  54470473


 Features in this part of subject sequence:
   hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  56557090  CCTTCTTCATTCA  56557078


 Features flanking this part of subject sequence:
   120785 bp at 5' side: hypothetical protein
   12425 bp at 3' side: similar to A-kinase anchor protein 5 (A-kinase anchor pro..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  66373002  CTTCTTCATTCAC  66373014


 Features flanking this part of subject sequence:
   178536 bp at 5' side: hypothetical protein
   171746 bp at 3' side: calcium-activated potassium channel beta 2 subunit


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  84848590  CCTTCTTCATTCA  84848602


 Features flanking this part of subject sequence:
   700883 bp at 5' side: translocase of the inner mitochondrial membrane 14 isoform
   21864 bp at 3' side: sex-determining region Y-box 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  87903423  ACCTTCTTCATTC  87903435


 Features in this part of subject sequence:
   Ymer protein short isoform
   Ymer protein long isoform


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
```

```
                  |||||||||||||
Sbjct  97547290  CCTTCTTCATTCA  97547278


  Features flanking this part of subject sequence:
    147142 bp at 5' side: hypothetical protein LOC151963
    190663 bp at 3' side: HRAS-like suppressor


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  99277915  CCTTCTTCATTCA  99277927


>ref|NT_022459.14|Hs3_22615 D Homo sapiens chromosome 3 genomic contig, reference a
Length=24211711
                                                                 Sort alignments for this s
                                                                   E value  Score  Percent i
                                                                   Query start position  Sul

  Features flanking this part of subject sequence:
    155163 bp at 5' side: RING1 and YY1 binding protein
    148485 bp at 3' side: SHQ1 homolog


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Minus

Query  11       CTTCTTCATTCACG  24
                ||||||||||||||
Sbjct  6357807  CTTCTTCATTCACG  6357794


  Features flanking this part of subject sequence:
    433547 bp at 5' side: glucan (1,4-alpha-), branching enzyme 1 (glycogen branchi.
    2761927 bp at 3' side: hypothetical protein


  Score = 28.2 bits (14),  Expect =   112
  Identities = 14/14 (100%), Gaps = 0/14 (0%)
  Strand=Plus/Plus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  15951072  CCTTCTTCATTCAC  15951085


  Features flanking this part of subject sequence:
    113588 bp at 5' side: T-cell activation kelch repeat protein
    253759 bp at 3' side: succinate-CoA ligase, GDP-forming, beta subunit


  Score = 26.3 bits (13),  Expect =   444
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus

Query  10      CCTTCTTCATTCA  22
               |||||||||||||
Sbjct  879254  CCTTCTTCATTCA  879266


  Features flanking this part of subject sequence:
    15959 bp at 5' side: hypothetical protein LOC401072
    327660 bp at 3' side: forkhead box P1 isoform 1


  Score = 26.3 bits (13),  Expect =   444
  Identities = 16/17 (94%), Gaps = 0/17 (0%)
  Strand=Plus/Plus

Query  3        CTTTCGACCTTCTTCAT  19
                ||||| |||||||||||
Sbjct  4387579  CTTTCAACCTTCTTCAT  4387595


  Features in this part of subject sequence:
    forkhead box P1 isoform 1
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9        ACCTTCTTCATTC  21
                |||||||||||||
Sbjct  4779105  ACCTTCTTCATTC  4779117


 Features in this part of subject sequence:
   SHQ1 homolog


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  6593845  CTTCTTCATTCAC  6593833


 Features flanking this part of subject sequence:
   583406 bp at 5' side: PDZ domain containing RING finger 3
   56158 bp at 3' side: contactin 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  7964239  CCTTCTTCATTCA  7964251


 Features flanking this part of subject sequence:
   696713 bp at 5' side: contactin 3
   155472 bp at 3' side: similar to Protein C21orf63 precursor (SUE21)


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  8973833  CCTTCTTCATTCA  8973845


 Features flanking this part of subject sequence:
   42962 bp at 5' side: hypothetical protein
   15371 bp at 3' side: hypothetical protein LOC642198


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  9472841  CTTCTTCATTCAC  9472853


 Features in this part of subject sequence:
   roundabout, axon guidance receptor, homolog 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  11175003  CCTTCTTCATTCA  11175015


 Features in this part of subject sequence:
   roundabout, axon guidance receptor, homolog 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus
```

```
Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  11346709  CTTCTTCATTCAC  11346721


 Features in this part of subject sequence:
   roundabout 1 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  13272327  CTTCTTCATTCAC  13272339


 Features flanking this part of subject sequence:
   791772 bp at 5' side: hypothetical protein LOC285237
   453 bp at 3' side: similar to NMDA receptor regulated 2 isoform a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  22704426  CTTCTTCATTCAC  22704414


>ref|NT_005334.15|Hs2_5491 D Homo sapiens chromosome 2 genomic contig, reference a
Length=11088087
                                                         Sort alignments for this s
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features in this part of subject sequence:
   thymidylate kinase family LPS-inducible member


 Score = 28.2 bits (14),  Expect =   112
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query  2        TCTTTCGACCTTCTTCAT  19
                |||||| |||||||||||
Sbjct  1836041  TCTTTCTACCTTCTTCAT  1836058


 Features flanking this part of subject sequence:
   117193 bp at 5' side: hypothetical protein LOC339789
   240328 bp at 3' side: inhibitor of DNA binding 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCACG  24
                ||||||||||||||
Sbjct  3416103  CTTCTTCATTCACG  3416090


 Features flanking this part of subject sequence:
   311753 bp at 5' side: hypothetical protein
   181276 bp at 3' side: hypothetical protein LOC400941


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  3        CTTTCGACCTTCT  15
                |||||||||||||
Sbjct  1525127  CTTTCGACCTTCT  1525139


 Features in this part of subject sequence:
   lipin 1
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  6756651  CTTCTTCATTCAC  6756639


>ref|NT_005403.16|Hs2_5560 D Homo sapiens chromosome 2 genomic contig, reference as
Length=84213157

                                                                  Sort alignments for this s
                                                                    E value  Score  Percent i
                                                                    Query start position  Sul

 Features flanking this part of subject sequence:
   159001 bp at 5' side: phospholipase C-like 1
   966234 bp at 3' side: SATB family member 2


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTCA  22
                 ||||||||||||||
Sbjct  49380104  ACCTTCTTCATTCA  49380117


 Features in this part of subject sequence:
   amyotrophic lateral sclerosis 2 (juvenile) chromosome reg...
   amyotrophic lateral sclerosis 2 (juvenile) chromosome reg...


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATTC  21
                 ||||||||||||||
Sbjct  55693334  GACCTTCTTCATTC  55693321


 Features flanking this part of subject sequence:
   442477 bp at 5' side: ADP-ribosylation-like factor 6 interacting protein 6
   275907 bp at 3' side: reprimo, TP53 dependant G2 arrest mediator candidate


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10       CCTTCTTCATTCA  22
                |||||||||||||
Sbjct  4268249  CCTTCTTCATTCA  4268261


 Features flanking this part of subject sequence:
   201604 bp at 5' side: reprimo, TP53 dependant G2 arrest mediator candidate
   264316 bp at 3' side: UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylga.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
Sbjct  4746113  CTTCTTCATTCAC  4746101


 Features flanking this part of subject sequence:
   597319 bp at 5' side: glycerol-3-phosphate dehydrogenase 2 (mitochondrial)
   77834 bp at 3' side: UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylga..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11       CTTCTTCATTCAC  23
                |||||||||||||
```

```
Sbjct  8246167  CTTCTTCATTCAC  8246179


 Features in this part of subject sequence:
   lymphocyte antigen 75


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  10902300  CTTCTTCATTCAC  10902312


 Features in this part of subject sequence:
   phospholipase A2 receptor 1 isoform 1 precursor
   phospholipase A2 receptor 1 isoform 2 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  11103312  CTTCTTCATTCAC  11103324


 Features in this part of subject sequence:
   phospholipase A2 receptor 1 isoform 1 precursor
   phospholipase A2 receptor 1 isoform 2 precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  11109001  CTTCTTCATTCAC  11108989


 Features in this part of subject sequence:
   potassium voltage-gated channel, subfamily H, member 7 is...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  13485691  CCTTCTTCATTCA  13485703


 Features in this part of subject sequence:
   potassium voltage-gated channel, subfamily H, member 7 is...
   potassium voltage-gated channel, subfamily H, member 7 is...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  13594257  CCTTCTTCATTCA  13594269


 Features flanking this part of subject sequence:
   158 bp at 5' side: longevity assurance homolog 6
   32815 bp at 3' side: nitric oxide synthase trafficking isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  19835760  CTTCTTCATTCAC  19835748
```

```
 Features flanking this part of subject sequence:
   12626 bp at 5' side: longevity assurance homolog 6
   20347 bp at 3' side: nitric oxide synthase trafficking isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  19848228  CCTTCTTCATTCA  19848216


 Features flanking this part of subject sequence:
   286556 bp at 5' side: similar to peptidylprolyl isomerase A isoform 1
   108072 bp at 3' side: similar to Ciliary dynein heavy chain 11 (Axonemal beta d.


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  24847064  CCTTCTTCATTCA  24847076


 Features in this part of subject sequence:
   hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  27718702  CCTTCTTCATTCA  27718690


 Features flanking this part of subject sequence:
   71102 bp at 5' side: hypothetical protein LOC285025
   160648 bp at 3' side: SEC14 and spectrin domains 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  30023395  ACCTTCTTCATTC  30023383


 Features in this part of subject sequence:
   hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  32247984  GACCTTCTTCATT  32247972


 Features in this part of subject sequence:
   phosphodiesterase 1A, calmodulin-dependent isoform 1
   phosphodiesterase 1A, calmodulin-dependent isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  33258117  CCTTCTTCATTCA  33258105


 Features flanking this part of subject sequence:
   195573 bp at 5' side: similar to E74-like factor 2 (ets domain transcription fa.
   2410 bp at 3' side: fibrous sheath interacting protein 2
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         TTTCGACCTTCTT  16
                 |||||||||||||
Sbjct  36817280  TTTCGACCTTCTT  36817292


 Features flanking this part of subject sequence:
   393023 bp at 5' side: tissue factor pathway inhibitor (lipoprotein-associated c.
   580900 bp at 3' side: GULP, engulfment adaptor PTB domain containing 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  38970947  CTTCTTCATTCAC  38970935


 Features flanking this part of subject sequence:
   201125 bp at 5' side: hypothetical protein
   96234 bp at 3' side: phospholipase C-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  49061719  CTTCTTCATTCAC  49061707


 Features flanking this part of subject sequence:
   402437 bp at 5' side: phospholipase C-like 1
   722799 bp at 3' side: SATB family member 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  49623552  CCTTCTTCATTCA  49623540


 Features flanking this part of subject sequence:
   46716 bp at 5' side: nucleolar protein NOP5/NOP58
   27311 bp at 3' side: bone morphogenetic protein receptor type II precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  53424304  CCTTCTTCATTCA  53424292


 Features flanking this part of subject sequence:
   86349 bp at 5' side: amyotrophic lateral sclerosis 2 (juvenile) chromosome reg..
   61978 bp at 3' side: neurobeachin-like 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  4         TTTCGACCTTCTT  16
                 |||||||||||||
Sbjct  54147971  TTTCGACCTTCTT  54147983


 Features flanking this part of subject sequence:
   4709 bp at 5' side: hypothetical protein
   742 bp at 3' side: cytotoxic T-lymphocyte-associated protein 4 isoform a pre...
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  2         TCTTTCGACCTTCTTCA  18
                 ||||| |||||||||||
Sbjct  54941325  TCTTTGGACCTTCTTCA  54941341


 Features flanking this part of subject sequence:
   28526 bp at 5' side: carbamoyl-phosphate synthetase 1, mitochondrial
   677093 bp at 3' side: v-erb-a erythroblastic leukemia viral oncogene homolog 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  61780664  CCTTCTTCATTCA  61780652


 Features in this part of subject sequence:
   hypothetical protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  66766762  CCTTCTTCATTCA  66766774


 Features flanking this part of subject sequence:
   480107 bp at 5' side: solute carrier family 4, anion exchanger, member 3 isoform
   1304179 bp at 3' side: ephrin receptor EphA4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  71195985  CCTTCTTCATTCA  71195973


 Features in this part of subject sequence:
   hypothetical protein LOC56947


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  78413878  GACCTTCTTCATT  78413866


 Features in this part of subject sequence:
   SP140 nuclear body protein isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  81343702  CCTTCTTCATTCA  81343690


 Features flanking this part of subject sequence:
   139052 bp at 5' side: nuclear antigen Sp100
   70439 bp at 3' side: similar to barrier to autointegration factor 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
```

```
Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  81728835  CTTCTTCATTCAC  81728823


 Features in this part of subject sequence:
   neuronal guanine nucleotide exchange factor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  84018628  ACCTTCTTCATTC  84018616


>ref|NT_022184.14|Hs2_22340 D Homo sapiens chromosome 2 genomic contig, reference
Length=68373980

                                                         Sort alignments for this
                                                           E value  Score  Percent
                                                           Query start position  Su

 Features flanking this part of subject sequence:
   749 bp at 5' side: hypothetical protein LOC388939
   40173 bp at 3' side: hypothetical protein


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query  10       CCTTCTTCATTCAC  23
                ||||||||||||||
Sbjct  8113822  CCTTCTTCATTCAC  8113809


 Features in this part of subject sequence:
   EH domain binding protein 1


 Score = 28.2 bits (14),  Expect =   112
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  42018161  CCTTCTTCATTCAC  42018174


 Features flanking this part of subject sequence:
   75426 bp at 5' side: hypothetical protein
   252562 bp at 3' side: nuclear receptor coactivator 1 isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  3        CTTTCGACCTTCTTCAT  19
                ||||| |||||||||||
Sbjct  3444902  CTTTCTACCTTCTTCAT  3444918


 Features in this part of subject sequence:
   spastin isoform 1
   spastin isoform 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  11147593  CCTTCTTCATTCA  11147605


 Features flanking this part of subject sequence:
   1868994 bp at 5' side: hypothetical protein LOC25940
   890142 bp at 3' side: cysteine-rich motor neuron 1
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  14509227  CCTTCTTCATTCA  14509215


 Features flanking this part of subject sequence:
   2107682 bp at 5' side: hypothetical protein LOC25940
   651454 bp at 3' side: cysteine-rich motor neuron 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  2         TCTTTCGACCTTC  14
                 |||||||||||||
Sbjct  14747903  TCTTTCGACCTTC  14747915


 Features flanking this part of subject sequence:
   3116 bp at 5' side: sterolin 2
   7559 bp at 3' side: leucine-rich PPR motif-containing protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  22924113  CCTTCTTCATTCA  22924101


 Features in this part of subject sequence:
   luteinizing hormone/choriogonadotropin receptor precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1         ATCTTTCGACCTTCTTC  17
                 |||||| ||||||||||
Sbjct  27779404  ATCTTTAGACCTTCTTC  27779420


 Features in this part of subject sequence:
   neurexin 1 isoform alpha precursor
   neurexin 1 isoform beta precursor


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  28970130  GACCTTCTTCATT  28970118


 Features flanking this part of subject sequence:
   208955 bp at 5' side: hypothetical protein
   855489 bp at 3' side: B-cell CLL/lymphoma 11A isoform 3


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  38640132  CCTTCTTCATTCA  38640144


 Features flanking this part of subject sequence:
   605228 bp at 5' side: hypothetical protein
   459212 bp at 3' side: B-cell CLL/lymphoma 11A isoform 3
```

```
 Score = 26.3 bits (13),  Expect =   444
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query  1         ATCTTTCGACCTTCTTC  17
                 |||||| ||||||||||
Sbjct  39036421  ATCTTTAGACCTTCTTC  39036405


 Features flanking this part of subject sequence:
   6045 bp at 5' side: pellino protein
   232899 bp at 3' side: similar to 60S ribosomal protein L23a


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  43157422  ACCTTCTTCATTC  43157434


 Features flanking this part of subject sequence:
   128452 bp at 5' side: hypothetical protein isoform 2
   53725 bp at 3' side: ETAA16 protein


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  8         GACCTTCTTCATT  20
                 |||||||||||||
Sbjct  46386789  GACCTTCTTCATT  46386777


 Features flanking this part of subject sequence:
   50786 bp at 5' side: similar to Exocyst complex component Sec15B isoform 1
   10494 bp at 3' side: sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidore..


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  51919993  CCTTCTTCATTCA  51920005


 Features in this part of subject sequence:
   empty spiracles homolog 1 isoform 2
   empty spiracles homolog 1 isoform 1


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  51972950  ACCTTCTTCATTC  51972962


 Features flanking this part of subject sequence:
   13060 bp at 5' side: RAB11 family interacting protein 5 (class I)
   76818 bp at 3' side: similar to notochord


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  52168914  CCTTCTTCATTCA  52168902


 Features flanking this part of subject sequence:
   56696 bp at 5' side: hypothetical protein LOC6936
   490801 bp at 3' side: similar to Purine nucleoside phosphorylase (Inosine phosp.


 Score = 26.3 bits (13),  Expect =   444
```

```
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  54810614  CCTTCTTCATTCA  54810626


 Features flanking this part of subject sequence:
   644244 bp at 5' side: similar to Leucine-rich repeat transmembrane neuronal pro.
   125140 bp at 3' side: leucine rich repeat transmembrane neuronal 4


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCA  22
                 |||||||||||||
Sbjct  56436223  CCTTCTTCATTCA  56436235


 Features flanking this part of subject sequence:
   1154918 bp at 5' side: leucine rich repeat transmembrane neuronal 1
   124351 bp at 3' side: hypothetical protein LOC647291


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  60501814  ACCTTCTTCATTC  60501802


 Features flanking this part of subject sequence:
   94248 bp at 5' side: sialyltransferase 9
   69764 bp at 3' side: polymerase (RNA) I polypeptide A, 194kDa


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  11        CTTCTTCATTCAC  23
                 |||||||||||||
Sbjct  65000722  CTTCTTCATTCAC  65000710


 Features in this part of subject sequence:
   RANBP2-like and GRIP domain containing 2


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  66028576  ACCTTCTTCATTC  66028564


 Features in this part of subject sequence:
   similar to RANBP2-like and GRIP domain containing 2 isofo...
   similar to RANBP2-like and GRIP domain containing 2 isofo...


 Score = 26.3 bits (13),  Expect =   444
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query  9         ACCTTCTTCATTC  21
                 |||||||||||||
Sbjct  66827473  ACCTTCTTCATTC  66827485


>ref|NT_022135.15|Hs2_22291 D Homo sapiens chromosome 2 genomic contig, reference
Length=38390280

 Features in this part of subject sequence:
   RAB3 GTPase-activating protein


 Score = 28.2 bits (14),  Expect =   112
```

```
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Plus

Query  10        CCTTCTTCATTCAC  23
                 ||||||||||||||
Sbjct  24557396  CCTTCTTCATTCAC  24557409
```

```
  Database: human build 36 RNA, reference and alternate assemblies
    Posted date:  Aug 28, 2007  9:42 AM
  Number of letters in database: 1,663,010,206
  Number of sequences in database:  46,285
Lambda     K      H
    1.37    0.711     1.31
Gapped
Lambda     K      H
    1.37    0.711     1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 46285
Number of Hits to DB: 8841127
Number of extensions: 3425664
Number of successful extensions: 466
Number of sequences better than 1000: 34
Number of HSP's better than 1000 without gapping: 0
Number of HSP's gapped: 466
Number of HSP's successfully gapped: 466
Length of database: 5957977502
A: 0
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 13 (26.3 bits)
```