NCBI Blast: BorrprimerS

BLAST Basic Local Alignment Search Tool
Job Title: BorrprimerS

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

BLASTN 2.2.17 (Aug-26-2007)


**Database**: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences) 6,196,379 sequences; 22,410,130,487 total letters

**Query**= BorrprimerS Length=22

**Distribution of 101 Blast Hits on the Query Sequence**

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![Distribution of 101 Blast Hits on the Query Sequence](image)
**Distance tree of results**

Legend for links to other resources: ‼️ UniGene  🌈 GEO  🧵 Gene  🏙️ Structure  🦜

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

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>gb|EU240885.1| Borrelia sp. BR 2007 16S ribosomal RNA gene, partial sequence
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>gb|EU240883.1| Borrelia theileri 16S ribosomal RNA gene, partial sequence
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>gb|EU132845.1| Uncultured bacterium clone FFCH14064 16S ribosomal RNA gene, partial sequence
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Sbjct  314  TCACACTGGAACTGAGATACGG  335

>gb|EF141021.1| Borrelia sp. BR 16S ribosomal RNA gene, partial sequence
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Sbjct  151  TCACACTGGAACTGAGATACGG  172

>dbj|D89900.1| Borrelia garinii gene for 16S rRNA, partial sequence, strain: Bernie
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Strand=Plus/Plus

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>gb|EU025063.1| Borrelia burgdorferi isolate SCW-59 16S ribosomal RNA (rrs) gene, partial sequence
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Identities = 22/22 (100%), Gaps = 0/22 (0%)
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Query 1    TCACACTGGAACGTGAGATACGG  22
Sbjct 216  TCACACTGGAACGTGAGATACGG  237

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Strand=Plus/Plus

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Sbjct 216  TCACACTGGAACGTGAGATACGG  237

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Identities = 22/22 (100%), Gaps = 0/22 (0%)
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Sbjct 216  TCACACTGGAACGTGAGATACGG  237

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Query 1    TCACACTGGAACGTGAGATACGG  22
Sbjct 216  TCACACTGGAACGTGAGATACGG  237
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Sbjct  216  TCACACTGGAACCTGAGATACGG  237

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Sbjct  216  TCACACTGGAACCTGAGATACGG  237

>gb|EU025044.1| Borrelia burgdorferi isolate SCSC-6 16S ribosomal RNA (rrs) gene, partial sequence
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Sbjct  216  TCACACTGGAACCTGAGATACGG  237

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Sbjct  216  TCACACTGGAACTGAGATACGG  237

>gb|EU025030.1| Borrelia burgdorferi isolate BUL-8 16S ribosomal RNA (rrs) gene, partial sequence
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Sbjct  216  TCACACTGGAACTGAGATACGG  237

>gb|EU025029.1| Borrelia burgdorferi isolate BUL-3 16S ribosomal RNA (rrs) gene, partial sequence
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Strand=Plus/Plus
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Sbjct  216  TCACACTGGAACTGAGATACGG  237

>dbj|AB305505.1| Uncultured bacterium gene for 16S rRNA, partial sequence, clone: p763 b 4.34
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Borrelia burgdorferi isolate SCw-62 16S ribosomal RNA (rrs) gene, partial sequence
Length=1362
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Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Borrelia burgdorferi isolate SCW-53 16S ribosomal RNA (rrs) gene, partial sequence
Length=1362
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Borrelia burgdorferi isolate SCW-25 16S ribosomal RNA (rrs) gene, partial sequence
Length=1362
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Borrelia burgdorferi isolate SI-15 16S ribosomal RNA (rrs) gene, partial sequence
Length=1362
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Borrelia burgdorferi isolate SCI-1 16S ribosomal RNA (rrs) gene, partial sequence
Length=1362
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Borrelia burgdorferi isolate SCCH-19 16S ribosomal RNA (rrs) gene, partial sequence
Length=1362
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Strand=Plus/Plus
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Sbjct 216  TCACACTGGAACGTGATACGG  237

Strand=Plus/Plus
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Sbjct  216  TCACACTGGAAGCGATACGG  237

>gb|EU014802.1| Borrelia burgdorferi isolate SCCH-9 16S ribosomal RNA (rrs) gene, partial sequence
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Length=1362
Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query  1    TCACACTGGAAGCGATACGG  22
  |||||||||||||||||||||
Sbjct  216  TCACACTGGAAGCGATACGG  237

>gb|EU014800.1| Borrelia burgdorferi isolate BUL-10 16S ribosomal RNA (rrs) gene, partial sequence
Length=1362
Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query  1    TCACACTGGAAGCGATACGG  22
  |||||||||||||||||||||
Sbjct  216  TCACACTGGAAGCGATACGG  237

>gb|EU014799.1| Borrelia burgdorferi isolate BUL-6 16S ribosomal RNA (rrs) gene, partial sequence
Length=1362
Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query  1    TCACACTGGAAGCGATACGG  22
  |||||||||||||||||||||
Sbjct  216  TCACACTGGAAGCGATACGG  237

>gb|EU014798.1| Borrelia burgdorferi isolate BUL-5 16S ribosomal RNA (rrs) gene, partial sequence
Length=1362
Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query  1    TCACACTGGAAGCGATACGG  22
  |||||||||||||||||||||
Sbjct  216  TCACACTGGAAGCGATACGG  237

>gb|EU014797.1| Borrelia burgdorferi isolate BUL-4 16S ribosomal RNA (rrs) gene, partial sequence
Length=1362
Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query 1    TCACACTGGAACTGAGATACGG  22
Sbjct 216  TCACACTGGAACTGAGATACGG  237

>gb|EU014796.1| Borrelia burgdorferi isolate BUL-1 16S ribosomal RNA (rrs) gene, partial sequence
Length=1362
 Score = 44.1 bits (22), Expect = 0.005
 Identities = 22/22 (100%), Gaps = 0/22 (0%)
 Strand=Plus/Plus
Query 1    TCACACTGGAACTGAGATACGG  22
Sbjct 216  TCACACTGGAACTGAGATACGG  237

>gb|EF665487.1| Uncultured proteobacterium clone GASP-MB2W3_E06 16S ribosomal RNA gene, partial sequence
Length=829
 Score = 44.1 bits (22), Expect = 0.005
 Identities = 22/22 (100%), Gaps = 0/22 (0%)
 Strand=Plus/Plus
Query 1    TCACACTGGAACTGAGATACGG  22
Sbjct 226  TCACACTGGAACTGAGATACGG  247

>gb|EF641295.1| Borrelia hermsii strain LPO 16S ribosomal RNA gene, partial sequence
Length=1257
 Score = 44.1 bits (22), Expect = 0.005
 Identities = 22/22 (100%), Gaps = 0/22 (0%)
 Strand=Plus/Plus
Query 1    TCACACTGGAACTGAGATACGG  22
Sbjct 241  TCACACTGGAACTGAGATACGG  262

>gb|DQ981010.1| Uncultured bacterium clone layman_l22 16S ribosomal RNA gene, partial sequence
Length=783
 Score = 44.1 bits (22), Expect = 0.005
 Identities = 22/22 (100%), Gaps = 0/22 (0%)
 Strand=Plus/Plus
Query 1    TCACACTGGAACTGAGATACGG  22
Sbjct 284  TCACACTGGAACTGAGATACGG  305

>gb|DQ981000.1| Uncultured bacterium clone layman_j22 16S ribosomal RNA gene, partial sequence
Length=923
 Score = 44.1 bits (22), Expect = 0.005
 Identities = 22/22 (100%), Gaps = 0/22 (0%)
 Strand=Plus/Plus
Query 1    TCACACTGGAACTGAGATACGG  22
Sbjct 263  TCACACTGGAACTGAGATACGG  284

>gb|EF541175.1| Borrelia afzelii strain Nov1105 16S ribosomal RNA gene, partial sequence
Length=1294
 Score = 44.1 bits (22), Expect = 0.005
 Identities = 22/22 (100%), Gaps = 0/22 (0%)
 Strand=Plus/Plus
Query 1    TCACACTGGAACTGAGATACGG  22
Sbjct 241  TCACACTGGAACTGAGATACGG  262

>gb|EF541174.1| Borrelia afzelii strain Nov11506 16S ribosomal RNA gene, partial sequence
Length=1294
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1  TCACACTGGAACTGAGATACGG  22
Sbjct 241 TCACACTGGAACTGAGATACGG  262

>gb|DQ676372.1| Uncultured candidate division TM6 bacterium clone MVP-110 16S ribosomal RNA gene, partial sequence
Length=1444
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1  TCACACTGGAACTGAGATACGG  22
Sbjct 271 TCACACTGGAACTGAGATACGG  292

>gb|DQ676349.1| Uncultured candidate division TM6 bacterium clone MVP-50 16S ribosomal RNA gene, partial sequence
Length=1434
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1  TCACACTGGAACTGAGATACGG  22
Sbjct 258 TCACACTGGAACTGAGATACGG  279

>gb|EF507535.1| Borrelia lonesartia clone pBLS1082 16S ribosomal RNA gene, partial sequence; hypothetical protein genes, complete cds; and putative proline dipeptidase gene, partial cds
Length=3500
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1  TCACACTGGAACTGAGATACGG  22
Sbjct 370 TCACACTGGAACTGAGATACGG  349

>gb|EF523250.1| Borrelia hermsii strain CC1 16S ribosomal RNA gene, partial sequence
Length=1239
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1  TCACACTGGAACTGAGATACGG  22
Sbjct 253 TCACACTGGAACTGAGATACGG  274

>gb|EF515541.1| Uncultured bacterium clone 29h07 16S ribosomal RNA gene, partial sequence
Length=1307
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1  TCACACTGGAACTGAGATACGG  22
Sbjct 201 TCACACTGGAACTGAGATACGG  222

>gb|EF488992.1| Borrelia sp. 57Nsk 16S ribosomal RNA gene, partial sequence
Length=1293
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1  TCACACTGGAACTGAGATACGG  22
Sbjct 201 TCACACTGGAACTGAGATACGG  222
Sbjct 239 TCACACTGGAACTGAGATACGG 260

>gb|EF488991.1| Borrelia garinii strain Nov9906 16S ribosomal RNA gene, partial sequence
Length=1292
Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query 1 TCACACTGGAACTGAGATACGG 22
Sbjct 239 TCACACTGGAACTGAGATACGG 260

>gb|EF488990.1| Borrelia garinii strain Nov7006 16S ribosomal RNA gene, partial sequence
Length=1292
Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query 1 TCACACTGGAACTGAGATACGG 22
Sbjct 239 TCACACTGGAACTGAGATACGG 260

>gb|EF488989.1| Borrelia garinii strain Nov14506 16S ribosomal RNA gene, partial sequence
Length=1292
Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query 1 TCACACTGGAACTGAGATACGG 22
Sbjct 239 TCACACTGGAACTGAGATACGG 260

>gb|EF509402.1| Uncultured bacterium clone P7D1-446 16S ribosomal RNA gene, partial sequence
Length=1507
Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query 1 TCACACTGGAACTGAGATACGG 22
Sbjct 298 TCACACTGGAACTGAGATACGG 319

>gb|DQ463373.1| Borrelia garinii strain 05-F35P 16S ribosomal RNA gene, partial sequence
Length=388
Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query 1 TCACACTGGAACTGAGATACGG 22
Sbjct 103 TCACACTGGAACTGAGATACGG 124

>gb|EF018807.1| Uncultured bacterium clone Amb_16S_1277 16S ribosomal RNA gene, partial sequence
Length=1381
Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query 1 TCACACTGGAACTGAGATACGG 22
Sbjct 291 TCACACTGGAACTGAGATACGG 312

>gb|DQ803342.1| Uncultured bacterium clone RL311_aam24c07 16S ribosomal RNA gene, partial sequence
Length=1396
NCBI Blast: BorrprimerS

>emb|AM182231.1| Borrelia spielmanii partial 16S rRNA gene, strain PJes
Length=1389

Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1    TCACACTGGAACTGAGATACGG 22
Sbjct 298 TCACACTGGAACTGAGATACGG 319

>emb|AM182230.1| Borrelia spielmanii partial 16S rRNA gene, strain PAnz
Length=1389

Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1    TCACACTGGAACTGAGATACGG 22
Sbjct 230 TCACACTGGAACTGAGATACGG 251

>emb|AM182229.1| Borrelia spielmanii partial 16S rRNA gene, strain PMai
Length=1411

Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1    TCACACTGGAACTGAGATACGG 22
Sbjct 229 TCACACTGGAACTGAGATACGG 250

>emb|AM182228.1| Borrelia spielmanii partial 16S rRNA gene, strain PMew
Length=1409

Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1    TCACACTGGAACTGAGATACGG 22
Sbjct 229 TCACACTGGAACTGAGATACGG 250

>emb|AM182227.1| Borrelia spielmanii partial 16S rRNA gene, strain PHap
Length=1412

Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1    TCACACTGGAACTGAGATACGG 22
Sbjct 229 TCACACTGGAACTGAGATACGG 250

>emb|AM182226.1| Borrelia spielmanii partial 16S rRNA gene, strain PSigII
Length=1389

Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1    TCACACTGGAACTGAGATACGG 22
Sbjct 229 TCACACTGGAACTGAGATACGG 250

>emb|AM418456.1| Borrelia sp. Ir-3519 partial 16S rRNA gene, isolate Ir-3519
Length=1420

Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query  1    TCACACTGGAACGTGATACGG  22
Sbjct  201  TCACACTGGAACGTGATACGG  222

>emb|AM418454.1|  Borrelia sp. Ir-4721 partial 16S rRNA gene, isolate Ir-4721
Length=1481
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query  1    TCACACTGGAACGTGATACGG  22
Sbjct  262  TCACACTGGAACGTGATACGG  283

>emb|AM418453.1|  Borrelia garinii partial 16S rRNA gene, isolate Ir-2200
Length=1478
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query  1    TCACACTGGAACGTGATACGG  22
Sbjct  259  TCACACTGGAACGTGATACGG  280

>gb|DQ872186.1|  Borrelia theileri 16S ribosomal RNA (rrs) gene, partial sequence
Length=1183
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query  1    TCACACTGGAACGTGATACGG  22
Sbjct  199  TCACACTGGAACGTGATACGG  220

>gb|DQ833491.1|  Uncultured bacterium clone 35-52 16S ribosomal RNA gene, partial sequence
Length=1521
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query  1    TCACACTGGAACGTGATACGG  22
Sbjct  311  TCACACTGGAACGTGATACGG  332

>gb|DQ855530.1|  Borrelia hermsii isolate MAT 16S ribosomal RNA gene, complete sequence
Length=1273
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query  1    TCACACTGGAACGTGATACGG  22
Sbjct  210  TCACACTGGAACGTGATACGG  231

>gb|DQ855529.1|  Borrelia hermsii isolate LAK-5 16S ribosomal RNA gene, complete sequence
Length=1273
Score = 44.1 bits (22),  Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query  1    TCACACTGGAACGTGATACGG  22
Sbjct  210  TCACACTGGAACGTGATACGG  231

>gb|DQ855528.1|  Borrelia hermsii isolate LAK-4 16S ribosomal RNA gene, complete sequence
Length=1273
Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1 TCACACTGGAACGTGATACGG 22
Sbjct 210 TCACACTGGAACGTGATACGG 231

>gb|DQ855527.1| Borrelia hermsii isolate LAK-3 16S ribosomal RNA gene, complete sequence
Length=1273
Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1 TCACACTGGAACGTGATACGG 22
Sbjct 210 TCACACTGGAACGTGATACGG 231

>gb|CP000395.1| Borrelia afzelii PKo, complete genome
Length=905394

Features in this part of subject sequence:

rRNA-16S ribosomal RNA

Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 TCACACTGGAACGTGATACGG 22
Sbjct 449662 TCACACTGGAACGTGATACGG 449641

Features flanking this part of subject sequence:

735 bp at 5' side: hypothetical protein
691 bp at 3' side: rRNA-16S ribosomal RNA

Score = 36.2 bits (18), Expect = 1.1
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Minus

Query 1 TCACACTGGAACGTGAT 18
Sbjct 447741 TCACACTGGAACGTGAT 447724

>gb|DQ379485.1| Borrelia lusitaniae strain RB-La1N1 16S ribosomal RNA gene, partial sequence
Length=470
Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1 TCACACTGGAACGTGATACGG 22
Sbjct 254 TCACACTGGAACGTGATACGG 275

>gb|DQ379484.1| Borrelia lusitaniae strain RB-Pm2N6 16S ribosomal RNA gene, partial sequence
Length=468
Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1 TCACACTGGAACGTGATACGG 22
Sbjct 254 TCACACTGGAACGTGATACGG 275

>gb|DQ650329.1| Borrelia afzelii strain DB19N7-04 16S ribosomal RNA gene, partial sequence
Length=423

Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query  1    TCACACTGGAACTGAGATACGG  22
Sbjct  258  TCACACTGGAACTGAGATACGG  279

>gb|DQ650328.1|  Borrelia garinii strain DB18N6-04 16S ribosomal RNA gene, partial sequence
Length=430

Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query  1    TCACACTGGAACTGAGATACGG  22
Sbjct  264  TCACACTGGAACTGAGATACGG  285

>gb|DQ650327.1|  Borrelia miyamotoi strain DB15F6-04 16S ribosomal RNA gene, partial sequence
Length=423

Score = 44.1 bits (22), Expect = 0.005
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query  1    TCACACTGGAACTGAGATACGG  22
Sbjct  258  TCACACTGGAACTGAGATACGG  279

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
Posted date:  Dec 19, 2007  5:48 PM
Number of letters in database: 935,294,007
Number of sequences in database:  6,196,379
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: 6196379
Number of Hits to DB: 8891836
Number of extensions: 3494946
Number of successful extensions: 58625
Number of sequences better than 1000: 14972
Number of HSP's better than 1000 without gapping: 0
Number of HSP's gapped: 58624
Number of HSP's successfully gapped: 15066
Length of query: 22
Length of database: 22410130487
Length adjustment: 18
Effective length of query: 4
Effective length of database: 22298595665
Effective search space: 89194382660
Effective search space used: 89194382660
A: 0
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 11 (22.3 bits)
S2: 14 (28.2 bits)