

NCBI/BLAST/tblast/Formatting Results - 8643463S012

Your search is limited to records matching entrez query: txid138 [ORGN].

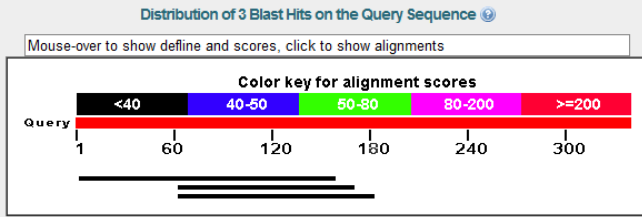
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gb|dq132793.1| (339 letters)

Query ID: [gi|73427170|gb|DQ132793.1](#) Database Name: nr
 Description: Homo sapiens transfection product sequence Description: All GenBank+EMBL+DBJ+PDB sequences (but no EGS, environmental samples or phase 0, 1 or 2 HTGS sequences)
 Molecule type: nucleic acid Program: TBLASTX 2.2.25+ [Citation](#)
 Query Length: 339

Other reports: [Search Summary](#) [Taxonomy reports](#)

Graphic Summary



Descriptions

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer [P](#) PubChem BioAssay

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	N	Link
CP001567.1	Borrelia burgdorferi Bol26 plasmid Bol26_lp36, complete sequence	27.2	27.2	46%	8.9	1	
CP001432.1	Borrelia valaisiana VS116 plasmid VS116_cp26, complete sequence	27.2	27.2	31%	8.9	1	
CP000014.1	Borrelia garinii PBi plasmid cp26, complete sequence	27.2	27.2	35%	8.9	1	

Alignments

Select All [Get selected sequences](#)

```
>gb|CP001567.1| D Borrelia burgdorferi Bol26 plasmid Bol26_lp36, complete sequence
Length=36936
Score = 27.2 bits (53), Expect = 8.9
Identities = 13/52 (25%), Positives = 26/52 (50%), Gaps = 0/52 (0%)
Frame = -1/-1
Query 159  FLTCPPYYASRELSFSIMVREIGNAVEXALNLRNSQSWQEKASTSYMLAV 4
             P CPP+Y S E S+ + + + + + + L+ + S K S+ L+
Sbjct 18141 PSICPPFYCSTE*FSSKIDFSKDSIFASVELSSIEESLFFIKIKKSFKLLI 17986

>gb|CP001432.1| D Borrelia valaisiana VS116 plasmid VS116_cp26, complete sequence
Length=26875
Score = 27.2 bits (53), Expect = 8.9
Identities = 12/36 (33%), Positives = 17/36 (47%), Gaps = 0/36 (0%)
Frame = -1/+1
Query 171  TRPELTCPPYYASRELSFSIMVREIGNAVEXALNL 64
             TRP+ PP Y + + P + +G E AL L
Sbjct 2863 TRPKVAPLPPIYINESRNFPAKINGSGRLSERALIL 2970

>gb|CP000014.1| D Borrelia garinii PBi plasmid cp26, complete sequence
Length=27108
Score = 27.2 bits (53), Expect = 8.9
Identities = 13/40 (33%), Positives = 18/40 (45%), Gaps = 0/40 (0%)
Frame = -1/+3
Query 183  IKVYTRPELTCPPYYASRELSFSIMVREIGNAVEXALNL 64
             I TRP+ PP Y + + P + +G E AL L
Sbjct 2838 IMAITRKPVEFAPPIYINESRNFPAKI*GSGRLSERALIL 2957
```

Select All [Get selected sequences](#)

