

BLASTN 2.2.25+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: local

Database: /var/folders/OV/OVxMj+b1HAevSehZTmOPBE+++TI/-Tmp-/tmp-3a65a3f9-9e9c-44f8-8c6d-85cef6b95e96/blastout9597339/206235tmp
Query= Prep7_1-3_1_sequence(paired)contig19853
(2722 letters)

Sequences producing significant alignments:		Score (Bits)	E Value
Noname	No definition line	302	6E-85
Noname	No definition line	264	1E-73
Noname	No definition line	28	1E-02
Noname	No definition line	28	1E-02
Noname	No definition line	26	5E-02
Noname	No definition line	26	5E-02
Noname	No definition line	24	2E-01
Noname	No definition line	22	9E-01
Noname	No definition line	22	9E-01
Noname	No definition line	22	9E-01
Noname	No definition line	22	9E-01
Noname	No definition line	22	9E-01
Noname	No definition line	22	9E-01

ALIGNMENTS

>Noname No definition line
Length=1635

Score = 301.8 bits (152), Expect = 6E-85
Identities = 551/683 (81), Gaps = 2/683 (0)
Strand = Plus/Plus

Query	749	TATATCTCTGTCCTAAATTCAACTATACAAAACCTTAGATTTCGCTTCTCCATCAACACCA	808
Sbjct	178	TATATGTCTGTCCTGAATTTCGACAATACAAAATCTTAGATTTCACCTCTGATACAACCCCA	237
Query	809	AAACCACTAGTTATCATCACACCTTCAAATACATCCCATGTCCAAGCCTGTGTTTTATGC	868
Sbjct	238	AAACCACTCGTTATTGTCACTCCTTCAAATGTCTCCCATATCCAGGCCAGTATTCTCTGC	297
Query	869	TCCAAGAAATATGGCTTGCAGATTTCGAACTCGAAGCGGTGGCCATGACTTTGAGGGTGCC	928
Sbjct	298	TCCAAGAAAGTTGGTTTGCAGATTTCGAACTCGAAGCGGTGGCCATGATGCTGAGGGTTTG	357
Query	929	TCCTATGTGTCTAAAGTCCCATTTGTGATATTAGATATGAGAAATCTACGTTCAATCACT	988
Sbjct	358	TCCTACATATCTCAAGTCCCATTTGTCTATAGTAGACTTGAGAAACATGCATACGGTCAAA	417
Query	989	GTAGACGTAGATAACAAAACCTGCATGGGTTGAAGCTGGAGCTACCATTGGTGAACTTTAT	1048
Sbjct	418	GTAGATATTCATAGCCAAAACCTGCGTGGGTTGAAGCCGGAGCTACCCTTGGAGAAGTTTAT	477
Query	1049	TATAGGATTGCTGAGAAAAATGGGAATCTGAGTTTTCTCTGCTGGGTACTGTCGTACTGTT	1108

Sbjct 1609 ATCCCACCTCTTC 1621
||||||| |||

Score = 28.2 bits (14), Expect = 1E-02
Identities = 14/14 (100), Gaps = 0/14 (0)
Strand = Plus/Minus

Query 137 CATCAATGATATTA 150
Sbjct 619 CATCAATGATATTA 606
||||||| |||

Score = 28.2 bits (14), Expect = 1E-02
Identities = 14/14 (100), Gaps = 0/14 (0)
Strand = Plus/Plus

Query 1563 TTCCTGAGTTGGG 1576
Sbjct 994 TTCCTGAGTTGGG 1007
||||||| |||

Score = 26.3 bits (13), Expect = 5E-02
Identities = 13/13 (100), Gaps = 0/13 (0)
Strand = Plus/Plus

Query 1993 CTACATATCTCAA 2005
Sbjct 360 CTACATATCTCAA 372
||||||| |||

Score = 26.3 bits (13), Expect = 5E-02
Identities = 13/13 (100), Gaps = 0/13 (0)
Strand = Plus/Plus

Query 1364 GAGATGAATGAGA 1376
Sbjct 490 GAGATGAATGAGA 502
||||||| |||

Score = 24.3 bits (12), Expect = 2E-01
Identities = 12/12 (100), Gaps = 0/12 (0)
Strand = Plus/Plus

Query 2284 AAATAATATTTT 2295
Sbjct 38 AAATAATATTTT 49
||||||| |||

Score = 22.3 bits (11), Expect = 9E-01
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Plus

Query 248 AGATATTCATA 258
Sbjct 420 AGATATTCATA 430
||||||| |||

Score = 22.3 bits (11), Expect = 9E-01
Identities = 11/11 (100), Gaps = 0/11 (0)

```

Strand = Plus/Plus

Query  1758  TTGGAGAAGTT  1768
          |||
Sbjct  464   TTGGAGAAGTT  474

Score = 22.3 bits (11), Expect = 9E-01
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Minus

Query  554   CAAGAAAAATG  564
          |||
Sbjct  955   CAAGAAAAATG  945

Score = 22.3 bits (11), Expect = 9E-01
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Minus

Query  2240  CCTTTTTAAAA  2250
          |||
Sbjct  1102  CCTTTTTAAAA  1092

Score = 22.3 bits (11), Expect = 9E-01
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Plus

Query  2092  GTATGAACTTT  2102
          |||
Sbjct  1320  GTATGAACTTT  1330

Score = 22.3 bits (11), Expect = 9E-01
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Plus

Query  342   AGAAGATAACG  352
          |||
Sbjct  1356  AGAAGATAACG  1366

```