

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)contig54345
(1024 letters)

Sequences producing significant alignments:		Score (Bits)	E Value
Noname	No definition line	445	2E-128
Noname	No definition line	22	3E-01
Noname	No definition line	22	3E-01
Noname	No definition line	22	3E-01
Noname	No definition line	22	3E-01

ALIGNMENTS

>Noname No definition line
Length=1635

Score = 444.5 bits (224), Expect = 2E-128
Identities = 423/488 (87), Gaps = 1/488 (0)
Strand = Plus/Minus

Query	538	ATGACGATGCGGTGGAAGAGGTGGGATGCTTTGTTTCATTTCTAAAAAGATTATTGAAATC	597
Sbjct	1635	ATGATGATGCGGTGGAAGAGGTGGGATACTTTGTTTCGTTTCTAAAAAATTATTGGGATC	1576
Query	598	AACCAGGGTTTTCACTTTTACTAGCCTGTCAAATTTTTTACC-AAAGATTTCTCACCCCA	656
Sbjct	1575	AGCTTTGGTTTTCACTTAACCTAACCTGTTAAATTTTTTACCAAAATACTTTTCACCCCA	1516
Query	657	AATACATGCTTCTGTGTAATTATTTTACTCTTTGGGATCATTTATTCCTATATCAAGATG	716
Sbjct	1515	AATACGTGCTTGTGTGTAATTATTAGGACTCTCAGGATTAGTTTTTCTAAATCAAGGTC	1456
Query	717	TCTATAATTGAGATATGTCAATCTTGGATTTTGGGACACATAAGGAGTCATGAAGTTATC	776
Sbjct	1455	CCTATAATTGAGATACGCCAATCTTGGATTTTGGGACACATAAGGCCTTGTGAAATTATA	1396
Query	777	AACATTTCGAATCCAGTTTAGATACTTTTCTTTATCTTCGTGCTTCTCCCAGCTACATGT	836
Sbjct	1395	AACACTTCGAACCCAGTTTATATGCTTTTCGTTATCTTCTTGCTTCTCCCAGGTAGCAGT	1336
Query	837	GTACCATAATTCATACATGATTCCAACCTCGATGAGGGAATGGAATTGCTGATTCTGAAAT	896
Sbjct	1335	GTACCAAAGTTTCATACATTATTCCAGCTCGATGAGGGAATGGAATTGCTGATTCTGAAAT	1276
Query	897	CTCATCCATTATACAACCGTAAGGTGTACAACGCATACATCCCAACTCCTTCATCTTCTTC	956
Sbjct	1275	CTCATCCATTATACCACCGTAAGGGTACAACACATACATCCCAACTCCTACCTCTTCTTC	1216
Query	957	ATATAATTTTCCAAAATTTTGACAAACGCAGATTCTGGAATTGGTTTCTTAACGTAGTC	1016

Sbjct 1215 ATATAATTTTTCCAAAATTTTGACCATTGCAGTTTCAGGTATTAGTTTCTTAACATAGTC 1156

Query 1017 TAACTTAA 1024

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Sbjct 1155 TAACTTAA 1148

Score = 22.3 bits (11), Expect = 3E-01
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Plus

Query 328 AAAATAATATT 338

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Sbjct 37 AAAATAATATT 47

Score = 22.3 bits (11), Expect = 3E-01
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Minus

Query 724 TTGAGATATGT 734

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Sbjct 372 TTGAGATATGT 362

Score = 22.3 bits (11), Expect = 3E-01
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Plus

Query 517 AAGATCTATTT 527

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Sbjct 671 AAGATCTATTT 681

Score = 22.3 bits (11), Expect = 3E-01
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Plus

Query 625 GTCAAAATTTT 635

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Sbjct 1192 GTCAAAATTTT 1202