

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)contig18025
(3609 letters)

Sequences producing significant alignments:		Score (Bits)	E Value
Noname	No definition line	1759	0E00
Noname	No definition line	24	3E-01
Noname	No definition line	22	1E00
Noname	No definition line	22	1E00
Noname	No definition line	22	1E00

ALIGNMENTS

>Noname No definition line
Length=1635

Score = 1758.8 bits (887), Expect = 0E00
Identities = 1286/1417 (91), Gaps = 2/1417 (0)
Strand = Plus/Minus

Query	2115	GCGGTGGAAGAGGTGGGATGCTTTGTTCGTTTCTAAAAAATTATTGGGATCAACCTTGG	2174
Sbjct	1627	GCGGTGGAAGAGGTGGGATACTTTGTTCGTTTCTAAAAAATTATTGGGATCAGCTTTGG	1568
Query	2175	TTTTCACCTTAACAAACCTGTAAAATTTTACTAAAATACTTTTCACCCCAAATACATG	2234
Sbjct	1567	TTTTCACCTTAACCTGTTAAAATTTTACCAAATACTTTTCACCCCAAATACGTG	1508
Query	2235	CTTGTGTGTAATTATTAGGACTCTTGGGATTAGTTTTTCTAAATCAAGGTCCCTATAAT	2294
Sbjct	1507	CTTGTGTGTAATTATTAGGACTCTCAGGATTAGTTTTTCTAAATCAAGGTCCCTATAAT	1448
Query	2295	TGAGATATGGGAATCTTTGATTTTAGGACACATAAGGAGTTGTGAAATTATAAACACTTC	2354
Sbjct	1447	TGAGATACCCAATCTTTGATTTTGGGACACATAAGGCGTTGTGAAATTATAAACACTTC	1388
Query	2355	GAACCCAATTTATATGCTTTTGATTATCTTCTTGCTTTTCTAGGTAGCTGCGTACCAA	2414
Sbjct	1387	GAACCCAGTTTATATGCTTTTCGTTATCTTCTTGCTTCTCCAGGTAGCAGTGACCAA	1328
Query	2415	GTTTCATACATGATTCCAGCTCGATGNNNGAATGGAATTGCTGATTCTGAAATCTCATCCA	2474
Sbjct	1327	GTTTCATACATTATTCCAGCTCGATGAGGGAATGGAATTGCTGATTCTGAAATCTCATCCA	1268
Query	2475	TTGTACCGCCGTACAGGATCAAAAGTTACATCCCAACTCCTACATCTTCTTCATATAATT	2534
Sbjct	1267	TTATACCACCGTAAGGGTACAACACATACATCCCAACTCCTACCTCTTCTTCATATAATT	1208
Query	2535	TTTCCAAAATTTTGACCATGCGGTTTTCGGAATTGGGTTCTTAACGTAGTCTAACTTAA	2594

Sbjct 1207 TTTCCAAAATTTTGACCATTGCAGTTTCAGGTATTAGTTTCTTAACATAGTCTAACTTAA 1148
 Query 2595 TTGAGAAAGCTGTCTTCGGCCAGCTGATCGATCAAGCAAAATTTCCCTTTTAAAATTAG 2654
 Sbjct 1147 TTGAGAAAGCCGTCTTCTTCCAGCTGATCTATCAAGCAAAATTTCCCTTTTAAAATTAG 1088
 Query 2655 CAGTGTG-AATTTACAATTCCTACTGTAAAAGATGGTGGTATCAATTCAGCTCAATTCTT 2713
 Sbjct 1087 CAGTGTGTAATTTACAACACCCTGTAGAAGATGGTGTATCAATCCAGCTCAATTCTT 1028
 Query 2714 TGCAATCAGTTTTTTTAAATACCCAACCTCAAGAAAGCTCTTGTTTCATCAAGTCAACTAAAC 2773
 Sbjct 1027 TGCAATCAGTTTTTTTAAATACCCAACCTCAGGAAAGCTCTTGTTTCATCAAGTCAACTAGAC 968
 Query 2774 TATCCGCTCCACCATGGAAAATGGAAGGGAAGTAACCGTGTACTGTTGTTTTATTCTTTC 2833
 Sbjct 967 TATCCACTCCACCAAGAAAATGGAAGAGAAGTAACCATGTACTGTAGTCTTATTCTTCC 908
 Query 2834 CTTGATTATCTGTAGTATTTTGGTTATGAAGTGAGTCATGAGTAATAAATCTTTGTCAT 2893
 Sbjct 907 CATGATTATCTGTAATATTTCTAGTTCTGAAGTGAGTCGTGAGCATTAATCTTTGTCAT 848
 Query 2894 ACTTGTAAGCAATATTTTGCCATTTATCAAATAACTTGACAAGCCCATGTATCTCCATAT 2953
 Sbjct 847 ACTTGTAAGCAATATTTTGCCATTTGTTAAATAACTTGACAAGCCCATGTATCTCCATGT 788
 Query 2954 TCTTTTCAACACTGAATATAGTAGACTTTGACATGACATCAACCAGTCTGATTTTCCACA 3013
 Sbjct 787 TCTTTTAAACTGAATATAGTAGCCTTTGATGGGACAACAACAAGTTTGATTTTCCATG 728
 Query 3014 GTGTAATTATTCCAAAGTTT-CTCCTCCACCACCACGTATAGCCCAAACATATCTTCTC 3072
 Sbjct 727 CTGCAATGATTCCAAAGTTTCTCCTCCTCCACCACGTATAGCCCAAATAGATCTTCTC 668
 Query 3073 CCATGGATTTTCGATCTAGAACTTTCCATCAACATTGACTATGTGTGCATCAATGATAT 3132
 Sbjct 667 CCATGGATTTTCGATCTAGAACTTTCCATCAACATTGACTAAGTGTGCATCAATGATAT 608
 Query 3133 TATTAGCCGCGAGGCCATAATTTTCGATCAATGCTCCATAGCCTCCTCCACTAAAGTGTC 3192
 Sbjct 607 TATCAGCCGCAAGGCCATAATTTTCGATCAATGCTCCATAGCCTCCTCCACTAAAGTGTC 548
 Query 3193 CACCTGCGCCAACAGTAGGGCAAACCACCAGGAAAATTAAGATTCTCATTCTTCTCAT 3252
 Sbjct 547 CACCTACGCCAACAGTAGGGCAATACCCACCAGGAAAATTAAGATTCTCATTCTTCTCAT 488
 Query 3253 TGATCCGGAAGTAAACTTCTCCAAGGGTAGCTCCAGCTTCAACCCATGCAGTTTGGCTAC 3312
 Sbjct 487 TGATCCAATAATAAACTTCTCCAAGGGTAGCTCCGGCTTCAACCCACGCAGTTTGGCTAT 428
 Query 3313 GAACATCTATTTGATCAAATGTATGTTTCTCAAGTCTACTATAACGAATGGGACTTGAG 3372
 Sbjct 427 GAATATCTACTTTGACCGTATGCATGTTTCTCAAGTCTACTATAGCAAATGGGACTTGAG 368
 Query 3373 ATATGTAGGACAAACCCTCAGCATCGTGGCTACCGCTTCAAGTTTCAATCTACAAGTCAA 3432
 Sbjct 367 ATATGTAGGACAAACCCTCAGCATCATGGCCACCGCTTCGAGTTTCAATCTGCAAACCAA 308
 Query 3433 CTTTCTTGAGCATAGAATTGGGGCTTGATGTGGGAGACATTTGAAGGAGTGACGATAA 3492
 Sbjct 3433 CTTTCTTGAGCATAGAATTGGGGCTTGATGTGGGAGACATTTGAAGGAGTGACGATAA 3492

Sbjct 307 CTTTCTTGGAGCAGAGAATACTGGCCTGGATATGGGAGACATTTGAAGGAGTGACAATAA 248

Query 3493 CGAGTGGTTTTGGGGTTGCATCAGAGTTGAATCTAAG 3529

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Sbjct 247 CGAGTGGTTTTGGGGTTGTATCAGAGGTGAATCTAAG 211

Score = 24.3 bits (12), Expect = 3E-01
Identities = 12/12 (100), Gaps = 0/12 (0)
Strand = Plus/Plus

Query 2970 TATAGTAGACTT 2981

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Sbjct 384 TATAGTAGACTT 395

Score = 22.3 bits (11), Expect = 1E00
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Minus

Query 1809 AATATTATTTT 1819

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Sbjct 47 AATATTATTTT 37

Score = 22.3 bits (11), Expect = 1E00
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Minus

Query 612 GATGAGGGAAT 622

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Sbjct 1306 GATGAGGGAAT 1296

Score = 22.3 bits (11), Expect = 1E00
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Minus

Query 3014 GTGTAATTATT 3024

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Sbjct 1502 GTGTAATTATT 1492