

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)contig32061  
(1719 letters)

Sequences producing significant alignments:		Score	E
		(Bits)	Value
Noname	No definition line	1388	0E00
Noname	No definition line	26	3E-02

ALIGNMENTS

>Noname No definition line  
Length=1635

Score = 1388.1 bits (700), Expect = 0E00  
Identities = 946/1028 (92), Gaps = 0/1028 (0)  
Strand = Plus/Minus

Query	8	GTATCAATCCAGCTCAACTGTTTGC	67
Sbjct	1049	GTATCAATCCAGCTCAATTCTTTGC	990
Query	68	TTGTTCATCAAGTCGACTAGACTAT	127
Sbjct	989	TTGTTCATCAAGTCGACTAGACTAT	930
Query	128	TGTATTGTGTCTTATTCTTCCCTT	187
Sbjct	929	TGTACTGTAGTCTTATTCTTCCCAT	870
Query	188	AAGAGTAATAATTCTTTTCATACA	247
Sbjct	869	GTGAGCATTAAATCTTTGTCATACT	810
Query	248	ACAAGCTCATGTATCTCCATGTTCT	307
Sbjct	809	ACAAGCCCATGTATCTCCATGTTCT	750
Query	308	GCAACAAGTCTAATTTCCACGCTG	367
Sbjct	749	ACAACAAGTTTGATTTCCATGCTGC	690
Query	368	ATAGCCCCAAAACAAATCTTCCCC	427
Sbjct	689	ATAGCCCCAAAATAGATCTTCTCC	630
Query	428	ACTAAGTGCGCATCAATGATATTAT	487
Sbjct	629	ACTAAGTGCGCATCAATGATATTAT	570
Query	488	TAGCCTCCTCCACTAAAGTGTTCC	547

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Sbjct 569  |||||
TAGCCTCCTCCACTAAAGTGTCCACCTACGCCAACAGTAGGGCAATACCCACCAGGAAAA 510

Query 548  CTAAGATTCTCATTGTTCTCATTGATCCAATAATAAACTTCTCCAAGGGTAGCTCCGGCT 607
Sbjct 509  |||||
CTAAAATTCTCATTTCATCTCATTGATCCAATAATAAACTTCTCCAAGGGTAGCTCCGGCT 450

Query 608  TCAACCCATGCAGTTTGGCTATGAACATCTATTTTGACCGAATGCATGTTTCTCAAGTCT 667
Sbjct 449  |||||
TCAACCCACGCAGTTTGGCTATGAATATCTACTTTGACCGTATGCATGTTTCTCAAGTCT 390

Query 668  ACTATAACAAATGGGACTTGAGATATGTAGGACATGCCCTCAGCATCATGACCACCGCTT 727
Sbjct 389  |||||
ACTATAGCAAATGGGACTTGAGATATGTAGGACAAACCTCAGCATCATGGCCACCGCTT 330

Query 728  CGAGTTCGAATCTGCAAGCCAACCTTTCTGGAGCATAGAATAGTGCCTTGGATATGGGAG 787
Sbjct 329  |||||
CGAGTTCGAATCTGCAAACCAACCTTTCTGGAGCAGAGAATACTGGCCTGGATATGGGAG 270

Query 788  ACATTTAAAGGAGTGATGATAACAAGTGGTTTTGGGGTTGTGTGTCAGAGGTAAATCTAAGA 847
Sbjct 269  |||||
ACATTTGAAGGAGTGACAATAACGAGTGGTTTTGGGGTTGTATCAGAGGTGAATCTAAGA 210

Query 848  TTTTGTATGGTTCGAATTTAGGATAGACATATAAAATTGGTTCGTGTTGAGTGTATACGAGT 907
Sbjct 209  |||||
TTTTGTATTGTCGAATTCAGGACAGACATATAACAATTGGTTCGTGTTGAGTGTATATGAAT 150

Query 908  TTTGCATTTGTTACATTGGTGGGAATATATTGTGAGAAGCATTTAAGGAAGTTTTCTTGA 967
Sbjct 149  |||||
TTTGGATTTGCTGGATTGTTAGGAATATATTCCGAGAAGCATTTAAGGAAGTTTTCTTGA 90

Query 968  GGATTAGCTATTGAAATTTGGATATTGAATGAGAGAAAGAAAAATATTATCTTGCAAACA 1027
Sbjct 89  |||||
GGATTAGCTAATGAAATTTGGATATTGAATGAGAGAAAGAAAAATATTATTTTGCAAACA 30

Query 1028  TACCAAAA 1035
Sbjct 29  |||||
AACCAAAA 22

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Score = 26.3 bits (13), Expect = 3E-02  
Identities = 13/13 (100), Gaps = 0/13 (0)  
Strand = Plus/Minus

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Query 1197  TTTTACCAAAAAT 1209
Sbjct 1541  |||||
TTTTTACCAAAAAT 1529

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