

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+blHAevSehZTmOPBE+++TI/-Tmp-/tmp-3a65a3f9-9e9c-44f8-8c6d-85cef6b95e96/blastout9597339/206235tmp

Query= Prep7_1-3_1_sequence(paired)contig165876 (1582 letters)

Sequences producing significant alignments:		Score (Bits)	E Value
Noname	No definition line	676	0E00
Noname	No definition line	22	5E-01

ALIGNMENTS

>Noname No definition line
Length=1635

Score = 676.5 bits (341), Expect = 0E00
Identities = 425/453 (94), Gaps = 0/453 (0)
Strand = Plus/Minus

Query	1	GTAGCTCCGGCTTCAACCCACGCAATTTGGCTACGAATATCTATTTTCACCGAATGCATG	60
Sbjct	461	GTAGCTCCGGCTTCAACCCACGCAATTTGGCTATGAATATCTACTTTGACCGTATGCATG	402
Query	61	TTTCTCAAGTCTACTATAACAAATGGGACTTGAGATATGTAGGACAAACCCTCAGCATCA	120
Sbjct	401	TTTCTCAAGTCTACTATAGCAAATGGGACTTGAGATATGTAGGACAAACCCTCAGCATCA	342
Query	121	TGGCCACCGCTTCGAGTTCGAATTTGCAAGCCACTTTCTTGGAGCATAGAATAGTGGCT	180
Sbjct	341	TGGCCACCGCTTCGAGTTCGAATCTGCAAACCAACTTTCTTGGAGCAGAGAATACTGGCC	282
Query	181	TGGATATGGGAGACATTTGAAGGAGTGACAATAACGAGTGGTTTTGGGGTTGTATCAGAG	240
Sbjct	281	TGGATATGGGAGACATTTGAAGGAGTGACAATAACGAGTGGTTTTGGGGTTGTATCAGAG	222
Query	241	GTAAATCTAAGATTTTGTATTTGTCAAATTCAGGACAGACATATACAATTGGTCGTGTTGA	300
Sbjct	221	GTGAATCTAAGATTTTGTATTTGTCAAATTCAGGACAGACATATACAATTGGTCGTGTTGA	162
Query	301	GTGTATACGAGTTTTAGATTTGCTGGATTGTTATGAATATATTGGGAGAAGCATTTTAGG	360
Sbjct	161	GTGTATATGAATTTTGGATTTGCTGGATTGTTAGGAATATATTCCGAGAAGCATTTAAGG	102
Query	361	AAATTTTCTTGGAGATTAGCTATTGAAATTTGGATATTGAATGAGAGAAAGAAAAATATA	420
Sbjct	101	AAGTTTTCTTGGAGATTAGCTAATGAAATTTGGATATTGAATGAGAGAAAGAAAAATATT	42
Query	421	ATTTTGTAAACAAACCTAAAGGAGAATGTTGAG	453
Sbjct	41	ATTTTGTAAACAAACCTAAAGGAAAATGCTGAG	9

Score = 22.3 bits (11), Expect = 5E-01
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Plus

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Query 343 TGGGAGAAGCA 353
          |||
Sbjct 1345 TGGGAGAAGCA 1355
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