

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)contig108128
(623 letters)

Sequences producing significant alignments:		Score	E
		(Bits)	Value
Noname	No definition line	252	1E-70

ALIGNMENTS

>Noname No definition line
Length=1635

Score = 252.3 bits (127), Expect = 1E-70
Identities = 188/207 (91), Gaps = 1/207 (0)
Strand = Plus/Minus

Query	204	CTAAGATTTTCGTATTTTTGAATTCAGGACAGACATATACAAGTGGTCATTATGAGTGTAT	263
Sbjct	215	CTAAGATTTTGTATTGTCGAATTCAGGACAGACATATACAATTGGTCGTGTTGAGTGTAT	156
Query	264	ACGAGTTTTGGATTTGCTGCATTGTTGGGAATATGTTGCGAGAAGCATTTAAGGAAGTTT	323
Sbjct	155	ATGAATTTTGGATTTGCTGGATTGTTAGGAATATATCCGAGAAGCATTTAAGGAAGTTT	96
Query	324	TCTCGAGGATTAGCTATGGAAATTTGGATA-TGAATGAGAGAAAAGAAAATATTATTTTG	382
Sbjct	95	TCTTGAGGATTAGCTAATGAAATTTGGATATTGAATGAGAGAAAAGAAAATATTATTTTG	36
Query	383	CAAACAAACCAAAGAAAATGTTGAG	409
Sbjct	35	CAAACAAACCAAAGAAAATGCTGAG	9