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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)contig137854
          (589 letters)

                                                                    Score     E
Sequences producing significant alignments:                         (Bits)  Value

Noname  No definition line                                           312    1E-88

ALIGNMENTS
>Noname No definition line
          Length=1635

 Score = 311.7 bits (157),  Expect = 1E-88
 Identities = 287/330 (87), Gaps = 4/330 (1)
 Strand = Plus/Plus

Query  167  CTCAACATTCTCATTTTGGTTTGTTTGCAAGATAATATTTTTCTTTCTCTCATTTAATAT  226
            |||| |||| || |||||||||||||||| |||||||||||||||||||||| |||||
Sbjct  9    CTCAGCATTTTCCTTTTGGTTTGTTTGCAAAATAATATTTTTCTTTCTCTCATTCAATAT  68

Query  227  CTAAACTTCAATTGCTAATCCTTGAGAAAACTTCCTTAAATGCTTCTCGCAATATATTCC  286
            | ||| |||| | |||||||||  |||||||||||||||||||||||| ||||||||||
Sbjct  69   CCAAATTTCATTAGCTAATCCTCAAGAAAACTTCCTTAAATGCTTCTCGGAATATATTCC  128

Query  287  CACCGATGTAACAAGTCTAAAACT----TACCCTCAAAACAACCAATTGTATATGTCTGT  342
             | | ||  | ||| || |||| |    ||| ||||| || |||||||||||||||||||
Sbjct  129  TAACAATCCAGCAAATCCAAAATTCATATACACTCAACACGACCAATTGTATATGTCTGT  188

Query  343  CCTAAATTCGACAATACACAATCTTAGATTCACCTTTGACACAACCCCAAAACCACTTGT  402
            ||| |||||||||||||| |||||||||||||||| ||| |||||||||||||||||| ||
Sbjct  189  CCTGAATTCGACAATACAAAATCTTAGATTCACCTCTGATACAACCCCAAAACCACTCGT  248

Query  403  TATCGTCACTCCTTCACATGTCTCCCATATCCAAGGCACTATTCTATGCTCCAAGAAAGT  462
            ||| |||||||||||| |||||||||||||||| | || |||||| ||||||||||||||
Sbjct  249  TATTGTCACTCCTTCAAATGTCTCCCATATCCAGGCCAGTATTCTCTGCTCCAAGAAAGT  308

Query  463  TGGCTTGCAAATTCAAACTCAAAGCGGTGG  492
            ||| ||||| |||| ||||| |||||||||
Sbjct  309  TGGTTTGCAGATTCGAACTCGAAGCGGTGG  338
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