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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)contig69418
          (632 letters)

                                                                    Score     E
Sequences producing significant alignments:                         (Bits)  Value

Noname  No definition line                                           653    0E00
Noname  No definition line                                           24    5E-02
Noname  No definition line                                           22    2E-01
Noname  No definition line                                           22    2E-01

ALIGNMENTS
>Noname No definition line
          Length=1635

 Score = 652.7 bits (329),  Expect = 0E00
 Identities = 559/633 (88), Gaps = 2/633 (0)
 Strand = Plus/Plus

Query  1    ATACACAATCTTAGATTCACCTCTAACACAACCCCAAAACCACTTGTTATCGTCACTCCT  60
            ||||| |||||||||||||||||| | |||||||||||||||||| ||||| |||||||||
Sbjct  202  ATACAAAATCTTAGATTCACCTCTGATACAACCCCAAAACCACTCGTTATTGTCACTCCT  261

Query  61   TCACATGTCTCCCATATCCAAGGCACTATTCTATG-TCCAAGAAAATTGGTTTGCAAATT  119
            ||| |||||||||||||||| | || |||||| || ||||||||| |||||||||| |||
Sbjct  262  TCAAATGTCTCCCATATCCAGGCCAGTATTCTCTGCTCCAAGAAAGTTGGTTTGCAGATT  321

Query  120  CAAACTCGAAACGGTGGTCATGATTCTGAAGGCATGTCCCACATATCTCAAGTCCCATTT  179
            | |||||||| |||||| |||||| |||| ||  ||||| ||||||||||||||||||||
Sbjct  322  CGAACTCGAAGCGGTGGCCATGATGCTGAGGGTTTGTCCTACATATCTCAAGTCCCATTT  381

Query  180  GTTATAGTAGACTTGAGAAACATGCATTCAATCAAAATAGATGTTCATAGCCAAACTACA  239
            | |||||||||||||||||||||||||| |  ||||| ||||| ||||||||||||||| |
Sbjct  382  GCTATAGTAGACTTGAGAAACATGCATACGGTCAAAGTAGATATTCATAGCCAAACTGCG  441

Query  240  TGGGTTGAAGCCGGAGCTACCCTTGGAGAAGTTTATGATTGGGTTAATGAGAAAAATGAG  299
            |||||||||||||||||||||||||||||||||||||| ||||| | |||||||  ||||||
Sbjct  442  TGGGTTGAAGCCGGAGCTACCCTTGGAGAAGTTTATTATTGGATCAATGAGATGAATGAG  501

Query  300  AATCTTAGTTTGGGTGCTGGGTATTGCCCTACTGTTTGCGCAGCTGGACACTTTGGTGGA  359
            ||| |||||||   || |||||||||||||||||||| ||| || |||||||||| |||||
Sbjct  502  AATTTTAGTTTTCCTGGTGGGTATTGCCCTACTGTTGGCGTAGGTGGACACTTTAGTGGA  561

Query  360  GGAGGCTATGGACCATTGATGTGAAATTATGGCCTTGCGGCTGATAATATCGTTGATGCA  419
            ||||||||||| |||||||| |||||||||||||||||||||||||||| ||||||||
Sbjct  562  GGAGGCTATGGAGCATTGATGCGAAATTATGGCCTTGCGGCTGATAATATCATTGATGCA  621

Query  420  CACTTAGTCAACATTGATGGAAAAGTGCTAGATCGAAAAATATATGGGAGAAGATCTCTT  479
            |||||||||||  ||||||||||||| ||||||||||||  |  ||||||||||||||||
Sbjct  622  CACTTAGTCAATGTTGATGGAAAAGTTCTAGATCGAAAA-TCCATGGGAGAAGATCTATT  680
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Query  480  TTGGGCTATACGTTGTGGTGGAGGAGAAAGCTTCAGAATCATTGTAGCATGGAAAATTAG  539
            ||||||||||||| |||| |||||||||| |||  ||||||||| ||||||||||||| |
Sbjct  681  TTGGGCTATACGTGGTGGAGGAGGAGAAAACTTTGGAATCATTGCAGCATGGAAAATCAA  740

Query  540  ATTGGTTGCTGTCCCAACAAAGTCTACTATGTTTAGTGTTAAAAAGATCAAGGAGATACA  599
            | | |||| ||||||| ||||| ||||||| || ||||||||||||| || |||||||||
Sbjct  741  ACTTGTTGTTGTCCCATCAAAGGCTACTATATTCAGTGTTAAAAAGAACATGGAGATACA  800

Query  600  TGAGCTTGTGAAGTTAGTTAACAAGTGGCAAAA  632
            || |||||| |||||| ||||||| ||||||||
Sbjct  801  TGGGCTTGTCAAGTTATTTAACAAATGGCAAAA  833


 Score = 24.3 bits (12),  Expect = 5E-02
 Identities = 12/12 (100), Gaps = 0/12 (0)
 Strand = Plus/Plus

Query  353  TGGTGGAGGAGG  364
            ||||||||||||
Sbjct  693  TGGTGGAGGAGG  704


 Score = 22.3 bits (11),  Expect = 2E-01
 Identities = 11/11 (100), Gaps = 0/11 (0)
 Strand = Plus/Minus

Query  559  AAGTCTACTAT  569
            |||||||||||
Sbjct  395  AAGTCTACTAT  385


 Score = 22.3 bits (11),  Expect = 2E-01
 Identities = 11/11 (100), Gaps = 0/11 (0)
 Strand = Plus/Minus

Query  379   TGTGAAATTAT  389
             ||||||||||||
Sbjct  1407  TGTGAAATTAT  1397
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