

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)contig28261 (2145 letters)

Table with 4 columns: Sequences producing significant alignments:, Score (Bits), E Value, and sequence details. It lists 8 entries, all with 'No definition line' and scores ranging from 22 to 1420 bits.

ALIGNMENTS

>Noname No definition line
Length=1635

Score = 1419.9 bits (716), Expect = 0E00
Identities = 1176/1326 (89), Gaps = 5/1326 (0)
Strand = Plus/Minus

Table of sequence alignments between Query and Sbjct. It shows 10 pairs of aligned sequences with their respective start and end positions and scores.

Query	1242	CATATAATTTTTCCAAAATTTTGACAAACGCAGATTCTGGAATTGGTTTCTTAACGTAGT	1301
Sbjct	1216	CATATAATTTTTCCAAAATTTTGACCATTGCAGTTTCAGGTATTAGTTTCTTAACATAGT	1157
Query	1302	CTAACTTAATCTTTAAAGAACCG--TTCTGCCAGCTGATCTATCAAGCAAATTTCCCTT	1359
Sbjct	1156	CTAACTTAA--TTGAGAAAGCCGCTCTCTCCAGCTGATCTATCAAGCAAATTTCCCTT	1099
Query	1360	ATTTAAATATCAGTGCCGTAATTTACAACACCGCTATAAAAAGATGATAATATCAATCTA	1419
Sbjct	1098	TTTTAAATTAGCAGTGTTGTAATTTACAACACCACTGTAGAAGATGGTTGTATCAATCCA	1039
Query	1420	GCTCAATTGTTTGAATCTGTTTTTTTAATACCCAACCTCAGGAAAACCTTTATTCATCAA	1479
Sbjct	1038	GCTCAATTCTTTGCAATCAGTTTTTTTAATACCCAACCTCAGGAAAGCTCTTGTTTCATCAA	979
Query	1480	GTCGACTAGACTATCCACTCCACCAAGGAAAACCTGAAGAGAAGTAAGTGTATTGTTGT	1539
Sbjct	978	GTCAACTAGACTATCCACTCCACCAAGAAAAATGGAAGAGAAGTAACCATGTACTGTAGT	919
Query	1540	CTTATTCTTCCCATGATTATTTGTAATATTCCTAGTTATGAAGTGAGTCATGAGTAATAA	1599
Sbjct	918	CTTATTCTTCCCATGATTATCTGTAATATTCCTAGTTCTGAAGTGAGTCGTGAGCATTAA	859
Query	1600	ATCTTTGTCATACTTGTAAGCAATATTTTGCCATTTGTTAACTAACTTGACAAGCTCATG	1659
Sbjct	858	ATCTTTGTCATACTTGTAAGCAATATTTTGCCATTTGTTAAATAACTTGACAAGCCCATG	799
Query	1660	TATCTCCATGATCTTTTTAACTAAACATAGTAGACTTTGTTGGGACAGCAACCAGTCT	1719
Sbjct	798	TATCTCCATGTTCTTTTTAACTGAATATAGTAGCCTTTGATGGGACAACAACAAGTTT	739
Query	1720	AATTTTCCATGCTACAATGATTCCGAAGCTTTCTCCTCCACCACCGTATAGCCCCAAA	1779
Sbjct	738	GATTTTCCATGCTGCAATGATTCCAAAGTTTTCTCCTCCTCCACCACGTATAGCCCCAAA	679
Query	1780	GAGATCTTCCCCATAGATTTTCGATCTAGCACTTTTGCATCAACGTTGACTAAGTGTGC	1839
Sbjct	678	TAGATCTTCTCCCATGGATTTTCGATCTAGAACTTTTCCATCAACATTGACTAAGTGTGC	619
Query	1840	ATCAACGATATTATCAGCCGCGAGGCCATAATTTGCATCAATGGTCCATATCCTCCTCC	1899
Sbjct	618	ATCAATGATATTATCAGCCGCAAGGCCATAATTTGCATCAATGCTCCATAGCCTCCTCC	559
Query	1900	ACCAAAGTGTCCAGCTGCGCTAACAGTAGGGCAATACCCAGCAGCCAAACTAAGATTCTC	1959
Sbjct	558	ACTAAAGTGTCCACCTACGCCAACAGTAGGGCAATACCCACCAGGAAAACCTAAAATTCTC	499
Query	1960	ATTTTTCTCATTAACCAATAATAAACTTCTCCAAGGGTAGCTCCGGCTTCAACCCTTGC	2019
Sbjct	498	ATTCATCTCATTGATCCAATAATAAACTTCTCCAAGGGTAGCTCCGGCTTCAACCACGC	439
Query	2020	GATTTGGCTATGAACATCTATGTTGATTGAATGCATGTTTCTCAAGTCTACTATAACAAA	2079
Sbjct	438	AGTTTGGCTATGAATATCTACTTTGACCGTATGCATGTTTCTCAAGTCTACTATAGCAA	379
Query	2080	TGGGACTTGAGATATGTAGGACATGTCTTCAGAATCATGACCACCGCTTCGAGTTCGAAT	2139
Sbjct	378	TGGGACTTGAGATATGTAGGACAAACCTCAGCATCATGGCCACCGCTTCGAGTTCGAAT	319

Query 2140 TTGCAA 2145  
          |||||  
Sbjct 318 CTGCAA 313

Score = 26.3 bits (13), Expect = 4E-02  
Identities = 13/13 (100), Gaps = 0/13 (0)  
Strand = Plus/Minus

Query 1891 TCCTCCTCCACCA 1903  
          |||||||  
Sbjct 705 TCCTCCTCCACCA 693

Score = 22.3 bits (11), Expect = 7E-01  
Identities = 11/11 (100), Gaps = 0/11 (0)  
Strand = Plus/Plus

Query 1688 ATAGTAGACTT 1698  
          |||||||  
Sbjct 385 ATAGTAGACTT 395

Score = 22.3 bits (11), Expect = 7E-01  
Identities = 11/11 (100), Gaps = 0/11 (0)  
Strand = Plus/Plus

Query 1404 TGATAATATCA 1414  
          |||||||  
Sbjct 603 TGATAATATCA 613

Score = 22.3 bits (11), Expect = 7E-01  
Identities = 11/11 (100), Gaps = 0/11 (0)  
Strand = Plus/Plus

Query 801 AAGATCTATTT 811  
          |||||||  
Sbjct 671 AAGATCTATTT 681

Score = 22.3 bits (11), Expect = 7E-01  
Identities = 11/11 (100), Gaps = 0/11 (0)  
Strand = Plus/Minus

Query 1144 TCCAGCTCAAT 1154  
          |||||||  
Sbjct 1042 TCCAGCTCAAT 1032

Score = 22.3 bits (11), Expect = 7E-01  
Identities = 11/11 (100), Gaps = 0/11 (0)  
Strand = Plus/Minus

Query 441 ATCTATCAAGC 451  
          |||||||  
Sbjct 1120 ATCTATCAAGC 1110

Score = 22.3 bits (11), Expect = 7E-01  
Identities = 11/11 (100), Gaps = 0/11 (0)  
Strand = Plus/Plus

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Query  909  GTCAAAATTTT  919
        |||
Sbjct  1192  GTCAAAATTTT  1202
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