

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)contig73347 (1106 letters)

Table with 4 columns: Sequences producing significant alignments, Score (Bits), and E Value. It lists five noname entries with scores ranging from 22 to 811 and E values from 3E-01 to 0E00.

ALIGNMENTS

>Noname No definition line Length=1635

Score = 811.3 bits (409), Expect = 0E00
Identities = 721/825 (87), Gaps = 0/825 (0)
Strand = Plus/Minus

Table of sequence alignments between Query and Sbjct. It shows multiple alignment blocks with sequence coordinates and vertical bar indicators for matches.

```

Sbjct 1215 ATATAATTTTCCAAAATTTTGACCATTGCAGTTTCAGGTATTAGTTTCTTAACATAGTC 1156
Query 761 TAACTTAATCTTGAAAGCACCGTTCTGCCAGCTGATCTAACAAGCGAAATTTGGTTATTT 820
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 1155 TAACTTAATTTGAGAAAGCCGTCCTTCTCCAGCTGATCTATCAAGCAAATTTCTTTTTT 1096
Query 821 AAAATTATCAGTGCCGTAATTTACAACACCGCTATAGAAGATGATAGTATCAATCCAGCT 880
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 1095 AAAATTAGCAGTGTTGTAATTTACAACACCACTGTAGAAGATGGTTGTATCAATCCAGCT 1036
Query 881 CAATTGTTTGCAATCTATTTTTTTAATACCAAACCTCAGGAAAACCTCTTGTTTCATTAAGTC 940
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 1035 CAATTCCTTTGCAATCAGTTTTTTTTAATACCAAACCTCAGGAAAAGCTCTTGTTTCATCAAGTC 976
Query 941 GACTAGACTATCCACTCCACCAAGGAAAACCTAAAGAGAAGTAAGTGTGTATTGTTGTCTT 1000
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 975 AACTAGACTATCCACTCCACCAAGAAAATGGAAGAGAAGTAACCATGTACTGTAGTCTT 916
Query 1001 ATTCTTCCCTTGATTATCTGTAATATTCCTAGTTATGAAGTGAGTCATGAGTAATAAATC 1060
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 915 ATTCTTCCCATGATTATCTGTAATATTCCTAGTTCTGAAGTGAGTCGTGAGCATTAAATC 856
Query 1061 TATGTCATACTTGTAAGAAATATTTTGCCACTTGTAACTAACTT 1105
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 855 TTTGTCATACTTGTAAGCAATATTTTGCCATTTGTAAATAACTT 811

```

Score = 24.3 bits (12), Expect = 9E-02
Identities = 12/12 (100), Gaps = 0/12 (0)
Strand = Plus/Minus

```

Query 963 AGGAAAACCTAAA 974
          ||| | | | | | | | | | | |
Sbjct 516 AGGAAAACCTAAA 505

```

Score = 22.3 bits (11), Expect = 3E-01
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Minus

```

Query 468 TTGAGATATGT 478
          ||| | | | | | | | | | | |
Sbjct 372 TTGAGATATGT 362

```

Score = 22.3 bits (11), Expect = 3E-01
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Plus

```

Query 260 AAGATCTATTT 270
          ||| | | | | | | | | | | |
Sbjct 671 AAGATCTATTT 681

```

Score = 22.3 bits (11), Expect = 3E-01
Identities = 11/11 (100), Gaps = 0/11 (0)
Strand = Plus/Plus

```

Query 368 GTCAAAATTTT 378
          ||| | | | | | | | | | | |

```

Sbjct 1192 GTCAAAATTTT 1202