

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)contig38887 (4320 letters)

Table with 4 columns: Sequences producing significant alignments:, Score (Bits), E Value, and sequence details. It lists 8 entries with scores ranging from 22 to 264 bits and E-values from 1E00 to 2E-73.

ALIGNMENTS

>Noname No definition line
Length=1635

Score = 264.1 bits (133), Expect = 2E-73
Identities = 429/527 (81), Gaps = 3/527 (1)
Strand = Plus/Minus

Table of sequence alignments between Query and Sbjct. It shows 8 pairs of aligned sequences with their respective start and end positions and scores.

```

Query 3847 GAACATAAACACAGGCTTGGACATGGGATGTATTTGAAGGTGTGATGATAACTAGTGGT 3906
          || || | || || | || | || | || | || | || | || | || | || | || |
Sbjct 299  GAGCAGAGAATACTGGCCTGGATATGGGAGACATTTGAAGGAGTGACAATAACGAGTGGT 240

Query 3907 TTTGGTGTTGGA---GAAGTGAATCTAAGGTTTTGTATGGTTGAATT 3950
          || || | || | | || | || | || | || | || | || | || | || |
Sbjct 239  TTTGGGGTGTATCAGAGGTGAATCTAAGATTTTGTATGTGCGAATT 193

```

Score = 69.9 bits (35), Expect = 6E-15  
Identities = 106/127 (83), Gaps = 2/127 (2)  
Strand = Plus/Minus

```

Query 2844 TCCAGCTCTATGTGGGAATGGAATTGCAGATTGCGGAATCTCGCTCATTTTACCACCATA 2903
          || || | || | || | || | || | || | || | || | || | || | || |
Sbjct 1314 TCCAGCTCGATGAGGGAATGGAATTGCTGATTCTGAAATCTCATCCATTATACCACCGTA 1255

Query 2904 AGGGTACATTTGAATATATGCCAA-TCCTACATCTTCTTCATATAACTTTTCCAAAAGTT 2962
          || || | || | || | || | || | || | || | || | || | || | || |
Sbjct 1254 AGGGTACAACACA-TACATCCCAACTCTACCTCTTCTTCATATAAATTTTCCAAAATTT 1196

Query 2963 TGACCAT 2969
          || || | || |
Sbjct 1195 TGACCAT 1189

```

Score = 40.1 bits (20), Expect = 6E-06  
Identities = 53/64 (83), Gaps = 0/64 (0)  
Strand = Plus/Minus

```

Query 3179 TATCCACTCTACCAAGAAAAATAGAAAAGAATGTAGCTTGTATTGTTGTCATATTCTTCC 3238
          || || | || | || | || | || | || | || | || | || | || | || |
Sbjct 967  TATCCACTCCACCAAGAAAAATGGAAGAGAAGTAACCATGTACTGTAGTCTTATTCTTCC 908

Query 3239 CATG 3242
          || |
Sbjct 907  CATG 904

```

Score = 32.2 bits (16), Expect = 1E-03  
Identities = 16/16 (100), Gaps = 0/16 (0)  
Strand = Plus/Minus

```

Query 3138 ACCCAACTCAGGAAAG 3153
          || || | || | || | || |
Sbjct 1008 ACCCAACTCAGGAAAG 993

```

Score = 22.3 bits (11), Expect = 1E00  
Identities = 11/11 (100), Gaps = 0/11 (0)  
Strand = Plus/Plus

```

Query 2206 ATGGAAGAAT 2216
          || || | || |
Sbjct 905  ATGGAAGAAT 915

```

Score = 22.3 bits (11), Expect = 1E00  
Identities = 11/11 (100), Gaps = 0/11 (0)

Strand = Plus/Minus

```
Query 1128 AGAAGATGGTT 1138
          |||
Sbjct 1060 AGAAGATGGTT 1050
```

Score = 22.3 bits (11), Expect = 1E00  
Identities = 11/11 (100), Gaps = 0/11 (0)  
Strand = Plus/Minus

```
Query 342 TTGAGAAAGCC 352
          |||
Sbjct 1147 TTGAGAAAGCC 1137
```

Score = 22.3 bits (11), Expect = 1E00  
Identities = 11/11 (100), Gaps = 0/11 (0)  
Strand = Plus/Minus

```
Query 1831 TGATTCTGAAA 1841
          |||
Sbjct 1287 TGATTCTGAAA 1277
```