

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)contig31598 (4721 letters)

Sequences producing significant alignments:		Score (Bits)	E Value
Noname	No definition line	2546	0E00
Noname	No definition line	26	9E-02
Noname	No definition line	24	4E-01
Noname	No definition line	24	4E-01
Noname	No definition line	24	4E-01
Noname	No definition line	22	1E00

ALIGNMENTS

>Noname No definition line
Length=1635

Score = 2545.8 bits (1284), Expect = 0E00
Identities = 1293/1296 (100), Gaps = 0/1296 (0)
Strand = Plus/Minus

Query	54	TGGAATTGCTGATTCTGAAATCTCATCCATTATACCACCGTAAGGGTACAACACATACAT	113
Sbjct	1296	TGGAATTGCTGATTCTGAAATCTCATCCATTATACCACCGTAAGGGTACAACACATACAT	1237
Query	114	CCCAACTCCTACCTCTTCTTCATATAATTTTTCCAAAATTTTGACCATTGCAGTTTCAGG	173
Sbjct	1236	CCCAACTCCTACCTCTTCTTCATATAATTTTTCCAAAATTTTGACCATTGCAGTTTCAGG	1177
Query	174	TATTAGTTTCTTAACATAGTCTAACTTAATTGAGAAAGCCGTCTTCTTCCCAGCTGATCT	233
Sbjct	1176	TATTAGTTTCTTAACATAGTCTAACTTAATTGAGAAAGCCGTCTTCTTCCCAGCTGATCT	1117
Query	234	ATCAAGCAAAATTTCCTTTTTAAAATTAGCAGTGTTGTAATTTACAACACCACTGTAGAA	293
Sbjct	1116	ATCAAGCAAAATTTCCTTTTTAAAATTAGCAGTGTTGTAATTTACAACACCACTGTAGAA	1057
Query	294	GATGGTTGTATCAATCCAGCTCAATTCTTTGCAATCAGTTTTTTTAATACCCAACCTCAGG	353
Sbjct	1056	GATGGTTGTATCAATCCAGCTCAATTCTTTGCAATCAGTTTTTTTAATACCCAACCTCAGG	997
Query	354	AAAGCTCTTGTTTCATCAAGTCAACTAGACTATCCACTCCACCAAGAAAAATGGAAGAGAA	413
Sbjct	996	AAAGCTCTTGTTTCATCAAGTCAACTAGACTATCCACTCCACCAAGAAAAATGGAAGAGAA	937
Query	414	GTAACCATGTACTGTAGTCTTATTCTTCCCATGATTATCTGTAATATTCCTAGTTCTGAA	473
Sbjct	936	GTAACCATGTACTGTAGTCTTATTCTTCCCATGATTATCTGTAATATTCCTAGTTCTGAA	877
Query	474	GTGAGTCGTGAGCATTAAATCTTTGTCATACTTGTAAGCAATATTTTGCCATTTGTTAAA	533

Sbjct	876	 GTGAGTCGTGAGCATTAAATCTTTGTCATACTTGTAAGCAATATTTTGCCATTTGTTAAA	817
Query	534	TAACCTTGACAAGCCCATGTATCTCCATGTTCTTTTTAACACTGAATATAGTAGCCTTTGA	593
Sbjct	816	 TAACCTTGACAAGCCCATGTATCTCCATGTTCTTTTTAACACTGAATATAGTAGCCTTTGA	757
Query	594	TGGGACAACAACAAGTTTGATTTTCCATGCTGCAATGATTCCAAAGTTTCTCCTCCTCC	653
Sbjct	756	 TGGGACAACAACAAGTTTGATTTTCCATGCTGCAATGATTCCAAAGTTTCTCCTCCTCC	697
Query	654	ACCACGTATAGCCCAAAATAGATCTTCTCCCATGGATTTTCGATCTAGAACTTTTCCATC	713
Sbjct	696	 ACCACGTATAGCCCAAAATAGATCTTCTCCCATGGATTTTCGATCTAGAACTTTTCCATC	637
Query	714	AACATTGACTAAGTGTGCATCAATGATATTATCAGCCGCAAGGCCATAATTTGCGATCAA	773
Sbjct	636	 AACATTGACTAAGTGTGCATCAATGATATTATCAGCCGCAAGGCCATAATTTGCGATCAA	577
Query	774	TGCTCCATAGCCTCCTCCACTAAAGTGTCCACCTACGCCAACAGTAGGGCAATACCCACC	833
Sbjct	576	 TGCTCCATAGCCTCCTCCACTAAAGTGTCCACCTACGCCAACAGTAGGGCAATACCCACC	517
Query	834	AGGAAAACAAAATTCTCATTTCATCTCATTTGATCCAATAATAAACTTCTCCAAGGGTAGC	893
Sbjct	516	 AGGAAAACAAAATTCTCATTTCATCTCATTTGATCCAATAATAAACTTCTCCAAGGGTAGC	457
Query	894	TCCGGCTTCAACCCACGCAGTTTGGCTATGAATATCTACTTTGACCGTATGCATGTTTCT	953
Sbjct	456	 TCCGGCTTCAACCCACGCAGTTTGGCTATGAATATCTACTTTGACCGTATGCATGTTTCT	397
Query	954	CAAGTCTACTATAGCAAATGGGACTTGAGATATGTAGGACAAACCCTCAGCATCATGGCC	1013
Sbjct	396	 CAAGTCTACTATAGCAAATGGGACTTGAGATATGTAGGACAAACCCTCAGCATCATGGCC	337
Query	1014	ACCGCTTCGAGTTTGAATCTGCAAACCAACTTTCTTGGAGCAGAGAATACTGGCCTGGAT	1073
Sbjct	336	 ACCGCTTCGAGTTTGAATCTGCAAACCAACTTTCTTGGAGCAGAGAATACTGGCCTGGAT	277
Query	1074	ATGGGAGACATTTGAAGGAGTGACAATAACGAGTGGTTTTGGGGTTGTATCAGAGGTGAA	1133
Sbjct	276	 ATGGGAGACATTTGAAGGAGTGACAATAACGAGTGGTTTTGGGGTTGTATCAGAGGTGAA	217
Query	1134	TCTAAGATTTTGTATTGTGCAATTCAGGACAGACATATAACAATTGGTCGTGTTGAGTGTA	1193
Sbjct	216	 TCTAAGATTTTGTATTGTGCAATTCAGGACAGACATATAACAATTGGTCGTGTTGAGTGTA	157
Query	1194	TATGAATTTTGGATTTGCTGGATTGTTAGGAATATATCCGAGAAGCATTTAAGGAAGTT	1253
Sbjct	156	 TATGAATTTTGGATTTGCTGGATTGTTAGGAATATATCCGAGAAGCATTTAAGGAAGTT	97
Query	1254	TTCTTGAGGATTAGCTATTGAAATTTGGATATTGAATGAGAGAAAGAAAAATATTATTTT	1313
Sbjct	96	 TTCTTGAGGATTAGCTAATGAAATTTGGATATTGAATGAGAGAAAGAAAAATATTATTTT	37
Query	1314	GCAAACAAACCAAAGGAGAATGTTGAGCAATTCAT	1349
Sbjct	36	 GCAAACAAACCAAAGGAAAATGCTGAGCAATTCAT	1

Score = 26.3 bits (13), Expect = 9E-02
Identities = 13/13 (100), Gaps = 0/13 (0)
Strand = Plus/Plus

```
Query 2859 TGGAAAAATTATA 2871
          |||
Sbjct 1202 TGGAAAAATTATA 1214
```

Score = 24.3 bits (12), Expect = 4E-01
Identities = 12/12 (100), Gaps = 0/12 (0)
Strand = Plus/Plus

```
Query 1222 GGAATATATTCC 1233
          |||
Sbjct 117  GGAATATATTCC 128
```

Score = 24.3 bits (12), Expect = 4E-01
Identities = 12/12 (100), Gaps = 0/12 (0)
Strand = Plus/Minus

```
Query 2515 ATATGGGAGACA 2526
          |||
Sbjct 278  ATATGGGAGACA 267
```

Score = 24.3 bits (12), Expect = 4E-01
Identities = 12/12 (100), Gaps = 0/12 (0)
Strand = Plus/Plus

```
Query 3865 AATTTTAGTTTT 3876
          |||
Sbjct 502  AATTTTAGTTTT 513
```

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

```
Query 3682 GCTACTATATT 3692
          |||
Sbjct 763  GCTACTATATT 773
```