

BLASTN 2.14.1+

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: H9CFRBF4114

Query= SEQ ID NO: 5

Length=2808

Sequences producing significant alignments:	Score (Bits)	E Value	Max Ident
Query_34893 SEQ ID NO: 2	4117	0.0	93%
Query_34895 SEQ ID NO: 4	4056	0.0	93%
Query_34892 SEQ ID NO: 1	4012	0.0	92%
Query_34894 SEQ ID NO: 3	3995	0.0	92%

ALIGNMENTS

>Query_34893 SEQ ID NO: 2

Length=2808

Score = 4117 bits (2229), Expect = 0.0
Identities = 2619/2812 (93%), Gaps = 8/2812 (0%)
Strand=Plus/Plus

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Sbjct	1	ATGGCTTTCCTGTGGCTGCTGTCTTGCTGGGCCCTGCTGGGGACTACCTTTGGCCTGCTG	60
Query	61	GTGCCCAGGGAGCTGTCTGGGAGCAGCCCAGTGCTGGAGGAGACCCACCCTGCCCACCAG	120
Sbjct	61	GTGCCCAGGGAAGTGTCTGGCTCTAGCCCAGTGCTGGAGGAGACCCACCCTGCCCACCAG	120
Query	121	CAGGGGGCCAGCAGGCCTGGCCCTAGGGATGCCCAGGCCCCACCCTGGCAGGCCCAGGGCT	180
Sbjct	121	CAGGGGGCTTCTAGGCCTGGCCCCAGGGATGCCCAGGCCCCACCCTGGCAGGCCAAGGGCT	180
Query	181	GTGCCTACCCAGTGATGTGCCACCCAATTCTAGGTTTGACTGTGCTCCTGACAAGGCC	240
Sbjct	181	GTGCCCACCCAGTGATGTGCCCCCAACTCTAGATTTGATTGTGCCCCTGATAAGGCC	240

Query	241	ATCACTCAGGAGCAGTGTGAAGCTAGGGGGTGCTGCTACATCCCAGCCAAGCAGGGCCTG	300
Sbjct	241	ATCACCCAGGAGCAGTGTGAGGCTAGGGGCTGCTGCTACATCCCTGCTAAGCAGGGCCTG	300
Query	301	CAGGGGGCCCCAGATGGGCCAGCCCTGGTGCTTCTTcccccccAGCTA-CCCTAGCTACAA	359
Sbjct	301	CAGGGGGCTCAGATGGGCCAGCCCTGGTGCTTCTTCCCCCCCAGCTATCCCT-CTTACAA	359
Query	360	GCTGGAGAATCTGAGCAGCTCTGAGATGGGCTACACTGCTACCCTGACCAGGACCACTCC	419
Sbjct	360	GCTGGAGAATCTGAGCAGCTCTGAGATGGGCTACACTGCCACCCTGACCAGGACTACTCC	419
Query	420	TACCTTCTTCCCCAAGGACATCCTGACTCTGAGGCTGGATGTCATGATGGAGACTGAAAA	479
Sbjct	420	CACCTTCTTCCCCAAGGACATCCTGACCCTGAGGCTGGATGTGATGATGGAGACTGAGAA	479
Query	480	TAGGCTGCACTTCACCATCAAGGACCCTGCCAATAGGAGGTATGAGGTGCCTCTGGAGAC	539
Sbjct	480	CAGGCTGCATTTACCATCAAGGATCCTGCCAACAGGAGGTATGAGGTGCCTCTGGAGAC	539
Query	540	CCCCCATGTGCATAGCAGGGCTCCCAGCCCCCTGTATTCTGTGGAGTTCTCTGAGGAGCC	599
Sbjct	540	CCCCCATGTGCACAGCAGGGCTCCTTCTCCCCTGTACTCTGTGGAGTTCTCTGAGGAACC	599
Query	600	CTTTGGGGTCATTGTGAGGAGACAGCTGGATGGGAGGGTGCTGCTGAACACTACTGTGGC	659
Sbjct	600	CTTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTCCTGCTGAACACCACTGTGGC	659
Query	660	TCCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGTCTACCAGCCTGCCCAGCCAGTACAT	719
Sbjct	660	CCCCCTGTTCTTTGCTGATCAGTTCCTGCAGCTGTCCACTTCTCTGCCTAGCCAGTACAT	719
Query	720	CACTGGGCTGGCTGAGCATCTGAGCCCCCTGATGCTGAGCACCAGCTGGACCAGGATCAC	779
Sbjct	720	CACTGGGCTGGCTGAGCACCTGAGCCCTCTGATGCTGAGCACCTCTTGGACTAGGATCAC	779
Query	780	TCTGTGGAACAGGGATCTGGCCCCCACTCCTGGGGCCAACCTGTATGGGAGCCATCCCTT	839
Sbjct	780	CCTGTGGAACAGGGACCTGGCCCCCACCCTGGGGCCAACCTGTATGGCAGCCACCCCTT	839
Query	840	CTACCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTCTGCTGAACAGCAATGC	899
Sbjct	840	CTATCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTCTGCTGAATAGCAATGC	899
Query	900	CATGGATGTGGTGCTGCAGCCTAGCCCTGCCCTGAGCTGGAGGAGCACTGGGGGCATCCT	959
Sbjct	900	TATGGATGTGGTGCTGCAGCCCAGCCCTGCCCTGTCTTGGAGGAGCACTGGGGGCATCCT	959
Query	960	GGATGTCTACATCTTCCTGGGGCCTGAGCCCAAGTCTGTGGTGCAGCAGTATCTGGATGT	1019

Sbjct	960	GGATGTGTACATTTTCCTGGGGCCTGAGCCCAAGTCTGTGGTGCAGCAGTACCTGGATGT	1019
Query	1020	GGTGGGGTATCCCTTCATGCCCCCTACTGGGGCCTGGGCTTTCACCTGTGCAGGTGGGG	1079
Sbjct	1020	GGTGGGCTACCCCTTCATGCCTCCCTACTGGGGCCTGGGCTTCCACCTGTGCAGGTGGGG	1079
Query	1080	CTACAGCAGCACTGCCATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCCCACTTCCC	1139
Sbjct	1080	CTACAGCTCTACTGCCATCACCAGGCAGGTGGTGGAGAAATATGACCAGGGCCCACTTCCC	1139
Query	1140	TCTGGATGTGCAGTGGAATGACCTGGACTATATGGATTCTAGGAGAGACTTTACTTTTAA	1199
Sbjct	1140	CCTGGATGTGCAGTGGAATGACCTGGACTACATGGACTCTAGGAGGGACTTCACCTTCAA	1199
Query	1200	CAAGGATGGCTTCAGGGATTTCCCTGCCATGGTGCAGGAGCTGCACCAGGGGGGCAGGAG	1259
Sbjct	1200	TAAGGATGGCTTCAGAGACTTCCCTGCCATGGTGCAGGAGCTGCATCAGGGGGGCAGGAG	1259
Query	1260	GTACATGATGATTGTGGACCCTGCTATTAGCAGCTCTGGCCCTGCTGGGTCTTACAGGCC	1319
Sbjct	1260	GTACATGATGATTGTGGACCCTGCCATCAGCTCTTCTGGCCCTGCTGGCTCTTACAGGCC	1319
Query	1320	TTATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGCCAGCCCCTGAT	1379
Sbjct	1320	CTATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGGCAGCCCCTGAT	1379
Query	1380	TGGCAAGGTGTGGCCTGGCAGCACTGCCTTCCCTGACTTCACCAACCCCACTGCCCTGGC	1439
Sbjct	1380	TGGGAAGGTGTGGCCTGGCTCTACTGCCTTCCCTGACTTCACCAATCCTACTGCCCTGGC	1439
Query	1440	CTGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCCTTTGATGGGATGTGGAT	1499
Sbjct	1440	CTGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCCTTTGATGGCATGTGGAT	1499
Query	1500	TGACATGAATGAGCCCTCTAACTTCATCAGGGGGTCTGAGGATGGCTGCCCCAACCAATGA	1559
Sbjct	1500	TGACATGAATGAGCCCTCTAATTTTCATCAGGGGCTCTGAGGATGGCTGCCCCAACCAATGA	1559
Query	1560	GCTGGAGAAcccccccTATGTGCCTGGGGTGGTGGGGGGCACTCTGCAGGCTGCCACTAT	1619
Sbjct	1560	GCTGGAGAACCCCCCTATGTGCCTGGGGTGGTGGGGGGCACCTGCAGGCTGCCACCAT	1619
Query	1620	CTGTGCTTCTTCTCACCAGTTTCTGAGCACCCACTATAATCTGCACAACCTGTATGGCCT	1679
Sbjct	1620	CTGTGCTAGCTCTCACCAGTTCCTGAGCACCCACTACAATCTGCATAACCTGTATGGCCT	1679
Query	1680	GACTGAGGCCATTGCCAGCCATAGGGCCCTGGTGAAGGCCAGGGGCACAGGCCCTTTGT	1739
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[illegible]

Sbjct	2457	TAGGCAGCAGCCCATGGCCCTGGCTGTGGCCCTGACCAAGGGGGGGGAGGCTAGGGGGGA	2516
Query	2517	gctgttctgggatgatggggagtctctggaggtgctggagaggggggCCTACACCCAGGT	2576
Sbjct	2517	GCTGTTTTGGGATGATGGGGAGAGCCTGGAGGTGCTGGAGAGGGGGGCCTACACTCAGGT	2576
Query	2577	GATCTTTCTGGCCAGGAACAATACTATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGGG	2636
Sbjct	2577	GATCTTCCTGGCCAGGAACAATACCATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGGG	2636
Query	2637	GGCTGGCCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGT	2696
Sbjct	2637	GGCTGGCCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGT	2696
Query	2697	CCTGAGCAATGGGGTGCCTGTGAGCAACTTCACCTACTCTCCTGACACCAAGGTGCTGGA	2756
Sbjct	2697	GCTGAGCAATGGGGTGCCTGTGAGCAACTTCACCTATAGCCCTGATACCAAGGTGCTGGA	2756
Query	2757	CATTTGTGTGTCTCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808
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>Query_34895 SEQ ID NO: 4
Length=2808

Score = 4056 bits (2196), Expect = 0.0
Identities = 2605/2809 (93%), Gaps = 2/2809 (0%)
Strand=Plus/Plus

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Query	61	GTGCCCAGGGAGCTGTCTGGGAGCAGC-CCAGTGCTGGAGGAGACCCACCCTGCCCACCA	119
Sbjct	61	GTCCCCAGGGAGCTGTCTGG-CTCTTCTCCTGTCTGGAGGAGACCCACCCTGCCCACCA	119
Query	120	GCAGGGGGCCAGCAGGCCTGGCCCTAGGGATGCCCAGGCCCCACCCTGGCAGGCCCAGGGC	179
Sbjct	120	GCAGGGGGCTAGCAGGCCTGGCCCCAGGGATGCCCAGGCCCCACCCTGGCAGGCCCAGGGC	179
Query	180	TGTGCCTACCCAGTGTGATGTGCCACCCAATTCTAGGTTTGACTGTGCTCCTGACAAGGC	239
Sbjct	180	TGTGCCACCCAGTGTGATGTGCCTCCCAACAGCAGGTTTGACTGTGCCCTGACAAGGC	239
Query	240	CATCACTCAGGAGCAGTGTGAAGCTAGGGGGTGCTGCTACATCCCAGCCAAGCAGGGCCT	299
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Sbjct	300	GCAGGGGGCTCAGATGGGCCAGCCCTGGTGCTTCTTTCCCCCTCTTATCCTAGCTATAA	359
Query	360	GCTGGAGAATCTGAGCAGCTCTGAGATGGGCTACACTGCTACCCTGACCAGGACCACTCC	419
Sbjct	360	GCTGGAGAACCTGAGCAGCTCTGAGATGGGGTACACTGCCACCCTGACCAGGACCACCCC	419
Query	420	TACCTTCTTCCCCAAGGACATCCTGACTCTGAGGCTGGATGTCATGATGGAGACTGAAAA	479
Sbjct	420	CACCTTCTTCCCTAAGGACATCCTGACCCTGAGGCTGGATGTGATGATGGAGACTGAGAA	479
Query	480	TAGGCTGCACTTCACCATCAAGGACCCTGCCAATAGGAGGTATGAGGTGCCTCTGGAGAC	539
Sbjct	480	TAGGCTGCACTTTACTATCAAGGACCCTGCCAACAGGAGGTATGAGGTGCCTCTGGAGAC	539
Query	540	CCCCCATGTGCATAGCAGGGCTCCCAGCCCCCTGTATTCTGTGGAGTTCTCTGAGGAGCC	599
Sbjct	540	CCCCCATGTGCATTCTAGGGCCCCCAGCCCCCTGTACTCTGTGGAGTTCTCTGAGGAGCC	599
Query	600	CTTTGGGGTCATTGTGAGGAGACAGCTGGATGGGAGGGTGCTGCTGAACACTACTGTGGC	659
Sbjct	600	CTTTGGGGTGATTGTGAGGAGACAGCTGGATGGCAGGGTCCTGCTGAACACCACTGTGGC	659
Query	660	TCCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGTCTACCAGCCTGCCCAGCCAGTACAT	719
Sbjct	660	TCCCCTGTTTTTTGCTGACCAGTTCCTGCAGCTGAGCACCAGCCTGCCCAGCCAGTACAT	719
Query	720	CACTGGGCTGGCTGAGCATCTGAGCCCCCTGATGCTGAGCACCAGCTGGACCAGGATCAC	779
Sbjct	720	CACTGGGCTGGCTGAGCACCTGAGCCCCCTGATGCTGAGCACCAGCTGGACCAGGATCAC	779
Query	780	TCTGTGGAACAGGGATCTGGCCCCCACTCCTGGGGCCAACCTGTATGGGAGCCATCCCTT	839
Sbjct	780	CCTGTGGAACAGGGATCTGGCTCCTACCCCTGGGGCCAACCTGTATGGCTCTCACCCCTT	839
Query	840	CTACCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTCTCTGCTGAACAGCAATGC	899
Sbjct	840	TTACCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTCTCTGCTGAACAGCAATGC	899
Query	900	CATGGATGTGGTGCTGCAGCCTAGCCCTGCCCTGAGCTGGAGGAGCACTGGGGGCATCCT	959
Sbjct	900	TATGGATGTGGTGCTGCAGCCCAGCCCTGCCCTGAGCTGGAGGTCTACTGGGGGCATCCT	959
Query	960	GGATGTCTACATCTTCTGGGGCCTGAGCCCAAGTCTGTGGTGCAGCAGTATCTGGATGT	1019
Sbjct	960	GGATGTGTACATCTTTCTGGGGCCTGAGCCCAAGTCTGTGGTGCAGCAGTACCTGGATGT	1019
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Sbjct	1020	GGTGGGCTATCCTTTTATGCCCCCTATTGGGGCCTGGGCTTCCACCTGTGCAGGTGGGG	1079
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Sbjct	1080	CTACAGCAGCACTGCCATCACCAGACAGGTGGTGGAGAACATGACCAGGGCCCACTTCCC	1139
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Query	1200	CAAGGATGGCTTCAGGGATTTCCCTGCCATGGTGCAGGAGCTGCACCAGGGGGGCAGGAG	1259
Sbjct	1200	CAAGGATGGCTTTAGGGACTTCCCTGCCATGGTGCAGGAGCTGCATCAGGGGGGCAGGAG	1259
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Sbjct	1320	CTATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGCCAGCCCCTGAT	1379
Query	1380	TGGCAAGGTGTGGCCTGGCAGCACTGCCTTCCCTGACTTCACCAACCCCACTGCCCTGGC	1439
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Query	1440	CTGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCCTTTGATGGGATGTGGAT	1499
Sbjct	1440	CTGGTGGGAGGATATGGTGGCTGAGTTTCATGACCAGGTGCCCTTTGATGGCATGTGGAT	1499
Query	1500	TGACATGAATGAGCCCTCTAACTTCATCAGGGGGTCTGAGGATGGCTGCCCCAACAATGA	1559
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Query	1680	GACTGAGGCCATTGCCAGCCATAGGGCCCTGGTGAAGGCCAGGGGCACCAGGCCCTTTGT	1739
Sbjct	1680	GACTGAGGCCATTGCCAGCCATAGAGCCCTGGTGAAGGCCAGAGGGACCAGGCCCTTTGT	1739
Query	1740	GATCAGCAGGTCTACCTTTGCTGGCCATGGCAGGTATGCTGGCCACTGGACTGGGGATGT	1799
Sbjct	1740	GATCTCTAGGAGCACCTTTGCTGGCCATGGCAGGTATGCTGGCCACTGGACTGGGGATGT	1799

Query	1800	GTGGTCTTCTTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATCCTGCAGTTCAACCTGCT	1859
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Query	1860	GGGGGTGCCTCTGGTGGGGGCTGATGTGTGTGGCTTTCTGGGCAACACCTCTGAGGAGCT	1919
Sbjct	1860	GGGGGTGCCTCTGGTGGGGGCTGATGTGTGTGGCTTCCTGGGCAATACCTCTGAAGAGCT	1919
Query	1920	GTGTGTGAGGTGGACCCAGCTGGGGGCCTTTTACCCCTTCATGAGGAACCACAATAGCCT	1979
Sbjct	1920	GTGTGTGAGGTGGACTCAGCTGGGGGCCTTCTATCCCTTCATGAGGAACCACAACAGCCT	1979
Query	1980	GCTGAGCCTGCCCCAGGAGCCTTACTCTTTCTCTGAGCCTGCCCAGCAGGCCATGAGGAA	2039
Sbjct	1980	GCTGTCTCTGCCCCAGGAGCCCTACAGCTTCTCTGAGCCTGCTCAGCAGGCTATGAGGAA	2039
Query	2040	GGCCCTGACTCTGAGGTATGCCCTGCTGCCCCATCTGTATACCCTGTTTCACCAGGCCCA	2099
Sbjct	2040	GGCCCTGACCCTGAGGTATGCCCTGCTGCCCCATCTGTACACCCTGTTCCACCAGGCCCA	2099
Query	2100	TGTGGCTGGGGAGACTGTGGCTAGGCCTCTGTTTCTGGAGTTCCCTAAGGACTCTAGCAC	2159
Sbjct	2100	TGTGGCTGGGGAGACTGTGGCCAGGCCCTGTTTCTGGAGTTTCCCAAGGACAGCAGCAC	2159
Query	2160	CTGGACTGTGGACCACCAGCTGCTGTGGGGGGAGGCCCTGCTGATCACCCCTGTGCTGCA	2219
Sbjct	2160	CTGGACTGTGGACCATCAGCTGCTGTGGGGGGAGGCTCTGCTGATTACCCCTGTGCTGCA	2219
Query	2220	GGCTGGCAAGGCTGAGGTGACTGGCTACTTCCCCCTGGGCACCTGGTATGACCTGCAGAC	2279
Sbjct	2220	GGCTGGCAAGGCTGAGGTGACTGGGTACTTCCCCCTGGGGACTTGGTATGACCTGCAGAC	2279
Query	2280	TGTGCCTGTGGAGGCCCTGGGGAGCCTGCCTcccccccccTGCTGCCCCCAGGGAGCCTGC	2339
Sbjct	2280	TGTGCCTGTGGAAGCTCTGGGCAGCCTGCCCCACCCCTGCTGCCCCTAGGGAGCCTGC	2339
Query	2340	CATTCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTCTGGACACCATCAATGTGCA	2399
Sbjct	2340	CATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTCTGGACACCATCAATGTGCA	2399
Query	2400	CCTGAGGGCTGGGTACATCATCCCCCTGCAGGGCCCTGGCCTGACCACCACTGAGAGCAG	2459
Sbjct	2400	CCTGAGGGCTGGCTATATCATCCCCCTGCAGGGCCCTGGGCTGACCACCACTGAGAGCAG	2459
Query	2460	GCAGCAGCCCATGGCCCTGGCTGTGGCTCTGACCAAggggggggagggccaggggggagct	2519
Sbjct	2460	GCAGCAGCCCATGGCCCTGGCTGTGGCCCTGACTAAGGGGGGGGAGGCCAGGGGGGAGCT	2519
Query	2520	gttctgggatgatggggaggtctctggaggtgctggagaggggggCCTACACCCAGGTGAT	2579

Sbjct	2520	GTTCTGGGATGATGGGGAGAGCCTGGAGGTGCTGGAGAGAGGGGCCTACACCCAGGTGAT	2579
Query	2580	CTTTCTGGCCAGGAACAATACTATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGGGGGC	2639
Sbjct	2580	CTTTCTGGCCAGGAACAACACCATTGTGAATGAGCTGGTGAGGGTGACTTCTGAGGGGGC	2639
Query	2640	TGGCCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGTCCT	2699
Sbjct	2640	TGGCCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGTGCT	2699
Query	2700	GAGCAATGGGGTGCCTGTGAGCAACTTCACCTACTCTCCTGACACCAAGGTGCTGGACAT	2759
Sbjct	2700	GAGCAATGGGGTGCCTGTGTCTAACTTCACCTACAGCCCTGATACTAAGGTGCTGGATAT	2759
Query	2760	TTGTGTGTCTCTGCTGATGGGGGAGCAGTTCTGGTGAGCTGGTGCTGA	2808
Sbjct	2760	CTGTGTGAGCCTGCTGATGGGGGAGCAGTTTCTGGTGAGCTGGTGCTGA	2808

>Query_34892 SEQ ID NO: 1
Length=2808

Score = 4012 bits (2172), Expect = 0.0
Identities = 2601/2813 (92%), Gaps = 10/2813 (0%)
Strand=Plus/Plus

Query	1	ATGGCCTTTCTGTGGCTGCTGTCTGCTGGGCCCTGCTGGGGACCACCTTTGGCCTGCTG	60
Sbjct	1	ATGGCTTTCTGTGGCTGCTGAGCTGCTGGGCTCTGCTGGGCACCACCTTTGGGCTGCTG	60
Query	61	GTGCCCAGGGAGCTGTCTGGGAGCAGCCCAGTGCTGGAGGAGACCCACCCTGCCACCAG	120
Sbjct	61	GTGCCTAGGGAGCTGTCTGGGTCTAGCCCTGTGCTGGAGGAGACTCACCTGCCCATCAG	120
Query	121	CAGGGGGCCAGCAGGCCTGGCCCTAGGGATGCCCAGGCCCCACCCTGGCAGGCCCAGGGCT	180
Sbjct	121	CAGGGGGCTAGCAGGCCTGGCCCCAGGGATGCTCAGGCCCCACCCTGGCAGGCCCAGGGCT	180
Query	181	GTGCCTACCCAGTGTGATGTGCCACCCAATTCTAGGTTTGACTGTGCTCCTGACAAGGCC	240
Sbjct	181	GTGCCCACCCAGTGTGATGTGCCCCCAACAGCAGGTTTGACTGTGCCCCCTGACAAGGCC	240
Query	241	ATCACTCAGGAGCAGTGTGAAGCTAGGGGGTGCTGCTACATCCCAGCCAAGCAGGGCCTG	300
Sbjct	241	ATTACCCAGGAGCAGTGTGAGGCCAGGGGCTGCTGCTACATTCCAGCTAAGCAGGGCCTG	300
Query	301	CAGGGGGCCCCAGATGGGCCAGCCCTGGTGCTTCTTcccccccAGCTACCCTAGCTACAAG	360
Sbjct	301	CAGGGGGCCCCAGATGGGCCAGCCCTGGTGCTTCTTCCCCCCCAGCTATCCTAGCTATAAA	360

Query	361	CTGGAGAATCTGAGCAGCTCTGAGATGGGCTACACTGCTACCCTGACCAGGACCACTCCT	420
Sbjct	361	CTGGAGAACCTGAGCAGCTCTGAGATGGGCTATACTGCCACCCTGACTAGGACTACTCCC	420
Query	421	ACCTTCTTCCCCAAGGACATCCTGACTCTGAGGCTGGATGTCATGATGGAGACTGAAAAT	480
Sbjct	421	ACCTTTTTTCTTAAGGATATCCTGACCCTGAGGCTGGATGTGATGATGGAGACTGAGAAC	480
Query	481	AGGCTGCACTTCACCATCAAGGACCCTGCCAATAGGAGGTATGAGGTGCCTCTGGAGACC	540
Sbjct	481	AGGCTGCACTTCACTATTAAGGACCCTGCCAATAGGAGGTATGAAGTGCCTCTGGAGACT	540
Query	541	CCCCATGTGCATAGCAGGGCTCCCAGCCCCCTGTATTCTGTGGAGTTCTCTGAGGAGCCC	600
Sbjct	541	CCTCATGTGCACTCTAGGGCCCCAGCCCCCTGTATTCTGTGGAGTTCTCTGAGGAGCCC	600
Query	601	TTTGGGGTCATTGTGAGGAGACAGCTGGATGGGAGGGTGCTGCTGAACACTACTGTGGCT	660
Sbjct	601	TTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTGCTGCTGAACACCACTGTGGCC	660
Query	661	CCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGTCTACCAGCCTGCCCAGCCAGTACATC	720
Sbjct	661	CCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGAGCACCAGCCTGCCCAGCCAGTACATC	720
Query	721	ACTGGGCTGGCTGAGCATCTGAGCCCCCTGATGCTGAGCACCAGCTGGACCAGGATCACT	780
Sbjct	721	ACTGGGCTGGCTGAGCATCTGAGCCCTCTGATGCTGAGCACCTCTTGACCAGGATCACC	780
Query	781	CTGTGGAACAGGGATCTGGCCCCACTCCTGGGGCCAACCTGTATGGGAGCCATCCCTTC	840
Sbjct	781	CTGTGGAATAGGGATCTGGCCCCACCCCTGGGGCTAATCTGTATGGCTCTCATCCCTTT	840
Query	841	TACCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTCTGCTGAACAGCAATGCC	900
Sbjct	841	TACCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTTCTGCTGAACAGCAATGCC	900
Query	901	ATGGATGTGGTGCTGCAGCCTAGCCCTGCCCTGAGCTGGAGGAGCACTGGGGGCATCCTG	960
Sbjct	901	ATGGATGTGGTGCTGCAGCCCTCTCCTGCCCTGAGCTGGAGGAGCACTGGGGGCATCCTG	960
Query	961	GATGTCTACATCTTCCTGGGGCCTGAGCCCAAGTCTGTGGTGCAGCAGTATCTGGATGTG	1020
Sbjct	961	GATGTGTACATCTTCCTGGGGCCTGAGCCCAAGTCTGTGGTCCAGCAGTATCTGGATGTG	1020
Query	1021	GTGGGGTATCCCTTCATGCCCCCTACTGGGGCCTGGGCTTTCACCTGTGCAGGTGGGGC	1080
Sbjct	1021	GTGGGCTACCCCTTTATGCCCCCTATTGGGGCCTGGGCTTCACCTGTGCAGGTGGGGG	1080
Query	1081	TACAGCAGC-ACTGCCATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCCCACTTCCC	1139

Sbjct	1081	TA-TTCTTCTACTGCTATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCTCACTTCCC	1139
Query	1140	TCTGGATGTGCAGTGGAATGACCTGGACTATATGGATTCTAGGAGAGACTTTACTTTTAA	1199
Sbjct	1140	CCTGGATGTGCAGTGGAATGACCTGGACTATATGGACTCTAGGAGGGATTTCACCTTCAA	1199
Query	1200	CAAGGATGGCTTCAGGGATTTCCCTGCCATGGTGCAGGAGCTGCACCAGGGGGGCAGGAG	1259
Sbjct	1200	CAAGGATGGCTTCAGGGACTTCCCTGCTATGGTCCAGGAGCTGCATCAGGGGGGCAGGAG	1259
Query	1260	GTACATGATGATTGTGGACCCTGCTATTAGCAGCTCTGGCCCTGCTGG-GTCTTACAGGC	1318
Sbjct	1260	GTACATGATGATTGTGGACCCTGCCATCAGCAGCTCTGGCCCTGCTGGCAGC-TATAGGC	1318
Query	1319	CTTATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGCCAGCCCCTGA	1378
Sbjct	1319	CCTATGATGAGGGCCTGAGGAGGGGGGTGTTTATCACTAATGAAACTGGGCAGCCCCTGA	1378
Query	1379	TTGGCAAGGTGTGGCCTGGCAGCACTGCCTTCCCTGACTTCACCAACCCCCACTGCCCTGG	1438
Sbjct	1379	TTGGCAAGGTGTGGCCTGGCTCTACTGCCTTCCCTGACTTCACCAACCCCCACTGCTCTGG	1438
Query	1439	CCTGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCCTTTGATGGGATGTGGA	1498
Sbjct	1439	CCTGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCTTTTATGGCATGTGGA	1498
Query	1499	TTGACATGAATGAGCCCTCTAACTTCATCAGGGGGTCTGAGGATGGCTGCCCCAACAATG	1558
Sbjct	1499	TTGACATGAATGAGCCAGCAACTTCATCAGGGGGTCTGAGGATGGGTGCCCCAATAATG	1558
Query	1559	AGCTGGAGAAcccccccTATGTGCCTGGGGTGGTGGGGGGCACTCTGCAGGCTGCCACTA	1618
Sbjct	1559	AGCTGGAGAACCCCCCTATGTGCCTGGGGTGGTGGGGGGCACCTGCAGGCTGCCACTA	1618
Query	1619	TCTGTGCTTCTTCTCACCAGTTTCTGAGCACCCACTATAATCTGCACAACCTGTATGGCC	1678
Sbjct	1619	TTTGTGCCAGCTCTCACCAGTTCCTGAGCACCCACTACAACCTGCACAATCTGTATGGCC	1678
Query	1679	TGACTGAGGCCATTGCCAGCCATAGGGCCCTGGTGAAGGCCAGGGGCACCAGGCCCTTTG	1738
Sbjct	1679	TGACTGAGGCCATTGCCAGCCACAGGGCCCTGGTGAAGGCCAGGGGCACCTAGGCCCTTTG	1738
Query	1739	TGATC---AGCAGGTCTACCTTTGCTGGCCATGGCAGGTATGCTGGCCACTGGACTGGGG	1795
Sbjct	1739	TGATCTCTAG-AAG-C-ACCTTTGCTGGCCATGGGAGGTATGCTGGCCACTGGACTGGGG	1795
Query	1796	ATGTGTGGTCTTCTTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATCCTGCAGTTCAACC	1855
Sbjct	1796	ATGTGTGGAGCTCTTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATCCTGCAGTTCAACC	1855

Query	1856	TGCTGGGGGTGCCTCTGGTGGGGGCTGATGTGTGTGGCTTTCTGGGCAACACCTCTGAGG	1915
Sbjct	1856	TGCTGGGGGTGCCCCTGGTGGGGGCTGATGTGTGTGGCTTCCTGGGCAACACCTCTGAAG	1915
Query	1916	AGCTGTGTGTGAGGTGGACCCAGCTGGGGGCCCTTTTACCCCTTCATGAGGAACCACAATA	1975
Sbjct	1916	AGCTGTGTGTGAGGTGGACCCAGCTGGGGGCCCTTCTACCCCTTCATGAGGAACCACAACA	1975
Query	1976	GCCTGCTGAGCCTGCCCCAGGAGCCTTACTCTTTCTCTGAGCCTGCCCAGCAGGCCATGA	2035
Sbjct	1976	GCCTGCTGAGCCTGCCTCAGGAGCCTTACTCTTTCTCTGAGCCTGCCCAGCAGGCCATGA	2035
Query	2036	GGAAGGCCCTGACTCTGAGGTATGCCCTGCTGCCCCATCTGTATACCCTGTTTCACCAGG	2095
Sbjct	2036	GGAAGGCCCTGACCCTGAGGTATGCTCTGCTGCCCCACCTGTACACCCTGTTCCACCAGG	2095
Query	2096	CCCATGTGGCTGGGGAGACTGTGGCTAGGCCTCTGTTTCTGGAGTTCCTAAGGACTCTA	2155
Sbjct	2096	CCCATGTGGCTGGGGAGACTGTGGCCAGGCCCTGTTCTGAGTTCCTAAGGATAGCA	2155
Query	2156	GCACCTGGACTGTGGACCACCAGCTGCTGTGGGGGGAGGCCCTGCTGATCACCCCTGTGC	2215
Sbjct	2156	GCACCTGGACTGTGGACCACCAGCTGCTGTGGGGGGAGGCCCTGCTGATTACCCTGTGC	2215
Query	2216	TGCAGGCTGGCAAGGCTGAGGTGACTGGCTACTTCCCCCTGGGCACCTGGTATGACCTGC	2275
Sbjct	2216	TGCAGGCTGGCAAGGCTGAGGTGACTGGCTACTTCCCCCTGGGCACTTGGTATGACCTGC	2275
Query	2276	AGACTGTGCCTGTGGAGGCCCTGGGGAGCCTGCCTccccccctTGCTGCCCCCAGGGAGC	2335
Sbjct	2276	AGACTGTGCCTGTGGAAGCCCTGGGCAGCCTGCCTCCCCCCTGCTGCCCCCAGGGAGC	2335
Query	2336	CTGCCATTCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTCTGGACACCATCAATG	2395
Sbjct	2336	CTGCCATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCCTGGACACCATTAATG	2395
Query	2396	TGCACCTGAGGGCTGGGTACATCATCCCCCTGCAGGGCCCTGGCCTGACCACCACTGAGA	2455
Sbjct	2396	TGCATCTGAGGGCTGGGTATATTATCCCCCTGCAGGGGCTGGGCTGACTACCACTGAGA	2455
Query	2456	GCAGGCAGCAGCCCATGGCCCTGGCTGTGGCTCTGACCAAggggggggaggccagggggg	2515
Sbjct	2456	GCAGGCAGCAGCCTATGGCCCTGGCTGTGGCTCTGACTAAGGGGGGGGAGGCCAGGGGGG	2515
Query	2516	agctgttctgggatgatggggagtctctggaggtgctggagaggggggCCTACACCCAGG	2575
Sbjct	2516	AGCTGTTCTGGGATGATGGGGAGAGCCTGGAGGTGCTGGAGAGGGGGGCTACACCCAGG	2575
Query	2576	TGATCTTTCTGGCCAGGAACAATACTATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGG	2635

Sbjct	2576	TGATTTTCCTGGCCAGGAACAACACCATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGG	2635
Query	2636	GGGCTGGCCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGG	2695
Sbjct	2636	GGGCTGGCCTGCAGCTGCAGAAAGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGG	2695
Query	2696	TCCTGAGCAATGGGGTGCCTGTGAGCAACTTCACCTACTCTCCTGACACCAAGGTGCTGG	2755
Sbjct	2696	TGCTGAGCAATGGGGTGCCTGTGAGCAACTTCACCTACAGCCCTGACACCAAGGTGCTGG	2755
Query	2756	ACATTTGTGTGTCTCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808
Sbjct	2756	ATATTTGTGTGAGCCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808

Score = 3995 bits (2163), Expect = 0.0
Identities = 2596/2811 (92%), Gaps = 6/2811 (0%)
Strand=Plus/Plus

Query	421	ACCTTCTTTCCCAAGGACATCCTGACTCTGAGGCTGGATGTGATGATGGAGACTGAAAAAT	480
Sbjct	421	ACCTTCTTTCCCAAGGATATTCTGACTCTGAGGCTGGATGTGATGATGGAGACTGAGAAC	480
Query	481	AGGCTGCACTTCACCATCAAGGACCCTGCCAATAGGAGGTATGAGGTGCCTCTGGAGACC	540
Sbjct	481	AGGCTGCACTTCACTATCAAGGACCCTGCCAATAGGAGGTATGAGGTGCCCCCTGGAGACT	540
Query	541	CCCCATGTGCATAGCAGGGCTCCCAGC-CCCCTGTATTCTGTGGAGTTCTCTGAGGAGCC	599
Sbjct	541	CCTCATGTGCATAGCAGGGC-CCCTTCTCCTCTGTATTCTGTGGAGTTCTCTGAGGAGCC	599
Query	600	CTTTGGGGTCATTGTGAGGAGACAGCTGGATGGGAGGGTGCTGCTGAACACTACTGTGGC	659
Sbjct	600	CTTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTGCTGCTGAACACCACTGTGGC	659
Query	660	TCCCCGTTCCTTTGCTGACCAGTTCCTGCAGCTGTCTACCAGCCTGCCCAGCCAGTACAT	719
Sbjct	660	CCCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGAGCACTTCTCTGCCCAGCCAGTACAT	719
Query	720	CACTGGGCTGGCTGAGCATCTGAGCCCCCTGATGCTGAGCACCAGCTGGACCAGGATCAC	779
Sbjct	720	TACTGGGCTGGCTGAGCATCTGAGCCCCCTGATGCTGAGCACCTCTTGACCAGGATCAC	779
Query	780	TCTGTGGAACAGGGATCTGGCCCCCACTCCTGGGGCCAACCTGTATGGGAGCCATCCCTT	839
Sbjct	780	CCTGTGGAACAGGGACCTGGCCCCCACTCCTGGGGCTAACCTGTATGGCTCTCACCCCTT	839
Query	840	CTACCTGGCCCTGGAGGATGGGGCTCTGCCCATGGGGTGTTCTGCTGAACAGCAATGC	899
Sbjct	840	TTACCTGGCCCTGGAGGATGGGGCTCTGCCCATGGGGTGTTCTGCTGAACAGCAATGC	899
Query	900	CATGGATGTGGTGCTGCAGCCTAGCCCTGCCCTGAGCTGGAGGAGCACTGGGGGCATCCT	959
Sbjct	900	TATGGATGTGGTGCTGCAGCCCTCTCAGCCCTGTCTTGAGGAGCACTGGGGGCATTCT	959
Query	960	GGATGTCTACATCTTCCTGGGGCCTGAGCCCAAGTCTGTGGTGCAGCAGTATCTGGATGT	1019
Sbjct	960	GGATGTGTACATTTTCCTGGGGCCTGAACCAAGTCTGTGGTGCAGCAGTACCTGGATGT	1019
Query	1020	GGTGGGGTATCCCTTCATGCCCCCTACTGGGGCTGGGCTTTCACCTGTGCAGGTGGGG	1079
Sbjct	1020	GGTGGGCTACCCCTTCATGCCCCCTATTGGGGCTGGGGTTTCACCTGTGCAGGTGGGG	1079
Query	1080	CTACAGCAGCACTGCCATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCCCACTTCCC	1139
Sbjct	1080	CTACAGCAGCACTGCCATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCCCACTTCCC	1139
Query	1140	TCTGGATGTGCAGTGGAATGACCTGGACTATATGGATTCTAGGAGAGACTTTACTTTTAA	1199

Sbjct	1140	CCTGGATGTGCAGTGGAATGACCTGGACTACATGGATAGCAGGAGGGATTTCACCTTCAA	1199
Query	1200	CAAGGATGGCTTCAGGGATTTCCCTGCCATGGTGCAGGAGCTGCACCAGGGGGGCAGGAG	1259
Sbjct	1200	CAAGGATGGCTTCAGGGACTTTCCCTGCCATGGTGCAGGAGCTGCACCAGGGGGGCAGGAG	1259
Query	1260	GTACATGATGATTGTGGACCCTGCTATTAGCAGCTCTGGCCCTGCTGGGTCTTACAGGCC	1319
Sbjct	1260	GTATATGATGATTGTGGACCCTGCTATCAGCAGCTCTGGCCCTGCTGGGTCTTACAGGCC	1319
Query	1320	TTATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGCCAGCCCCTGAT	1379
Sbjct	1320	CTATGATGAGGGCCTGAGGAGGGGGGTGTTTATCACTAATGAAACTGGCCAGCCTCTGAT	1379
Query	1380	TGGCAAGGTGTGGCCTGGCAGCACTGCCTTCCCTGACTTCACCAACCCCACTGCCCTGGC	1439
Sbjct	1380	TGGCAAGGTCTGGCCTGGCTCTACTGCCTTCCCTGATTTTACTAACCCCACTGCCCTGGC	1439
Query	1440	CTGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCCTTTGATGGGATGTGGAT	1499
Sbjct	1440	CTGGTGGGAGGACATGGTGGCTGAGTTCCATGATCAGGTGCCCTTTGATGGCATGTGGAT	1499
Query	1500	TGACATGAATGAGCCCTCTAACTTCATCAGGGGGTCTGAGGATGGCTGCCCCAACAATGA	1559
Sbjct	1500	TGATATGAATGAACCAAGCAACTTCATCAGAGGCTCTGAGGATGGCTGCCCCAACAATGA	1559
Query	1560	GCTGGAGAAccccccTATGTGCCTGGGGTGGTGGGGGGCACTCTGCAGGCTGCCACTAT	1619
Sbjct	1560	GCTGGAGAACCCCCCTATGTGCCTGGGGTGGTGGGGGGCACTCTGCAGGCTGCCACCAT	1619
Query	1620	CTGTGCTT-CTTCTCACCAGTTTCTGAGCACCCACTATAATCTGCACAACCTGTATGGCC	1678
Sbjct	1620	TTGTGCTAGCAGC-CACCAGTTCCTGAGCACCCACTACAATCTGCACAACCTGTATGGCC	1678
Query	1679	TGACTGAGGCCATTGCCAGCCATAGGGCCCTGGTGAAGGCCAGGGGCACCAGGCCCTTTG	1738
Sbjct	1679	TGACTGAAGCCATTGCCAGCCATAGGGCCCTGGTGAAGGCCAGGGGCACCAGGCCCTTTG	1738
Query	1739	TGATCAGCAGGTCTACCTTTGCTGGCCATGGCAGGTATGCTGGCCACTGGACTGGGGATG	1798
Sbjct	1739	TGATCAGCAGGAGCACTTTTGCTGGCCATGGCAGGTATGCTGGCCACTGGACTGGGGATG	1798
Query	1799	TGTGGT-CTTCTTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATCCTGCAGTTCAACCTG	1857
Sbjct	1799	TGTGGAGCAGC-TGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATTCTGCAGTTTAACTG	1857
Query	1858	CTGGGGGTGCCTCTGGTGGGGGCTGATGTGTGTGGCTTTCTGGGCAACACCTCTGAGGAG	1917
Sbjct	1858	CTGGGGGTGCCCCCTGGTGGGGGCTGATGTGTGTGGCTTCTGGGCAACACCTCTGAGGAG	1917

Query	1918	CTGTGTGTGAGGTGGACCCAGCTGGGGGCCTTTTACCCCTTCATGAGGAACCACAATAGC	1977
Sbjct	1918	CTGTGTGTGAGGTGGACCCAGCTGGGGGCCTTTTATCCCTTCATGAGGAACCACAACAGC	1977
Query	1978	CTGCTGAGCCTGCCCCAGGAGCCTTACTCTTTCTCTGAGCCTGCCCAGCAGGCCATGAGG	2037
Sbjct	1978	CTGCTGAGCCTGCCTCAGGAGCCCTACTCTTTCTCTGAGCCTGCCCAGCAGGCCATGAGG	2037
Query	2038	AAGGCCCTGACTCTGAGGTATGCCCTGCTGCCCCATCTGTATACCCTGTTTCACCAGGCC	2097
Sbjct	2038	AAGGCCCTGACCCTGAGGTATGCCCTGCTGCCCCACCTGTATACCCTGTTCCACCAGGCC	2097
Query	2098	CATGTGGCTGGGGAGACTGTGGCTAGGCCTCTGTTTCTGGAGTTCCCTAAGGACTCTAGC	2157
Sbjct	2098	CATGTGGCTGGGGAGACTGTGGCCAGGCCCTGTTCTGAGTTCCCCAAGGACAGCAGC	2157
Query	2158	ACCTGGACTGTGGACCACCAGCTGCTGTGGGGGGAGGCCCTGCTGATCACCCCTGTGCTG	2217
Sbjct	2158	ACCTGGACTGTGGATCATCAGCTGCTGTGGGGGGAGGCCCTGCTGATCACCCCTGTGCTG	2217
Query	2218	CAGGCTGGCAAGGCTGAGGTGACTGGCTACTTCCCCCTGGGCACCTGGTATGACCTGCAG	2277
Sbjct	2218	CAGGCTGGCAAGGCTGAGGTCACTGGCTACTTCCCTCTGGGCACCTGGTATGACCTGCAG	2277
Query	2278	ACTGTGCCTGTGGAGGCCCTGGGGAGCCTGCCTccccccTGCTGCCCCAGGGAGCCT	2337
Sbjct	2278	ACTGTGCCTGTGGAGGCTCTGGGCAGCCTGCCCCCCCCCTGCTGCTCCCAGGGAGCCT	2337
Query	2338	GCCATTCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCTCTGGACACCATCAATGTG	2397
Sbjct	2338	GCCATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCTCCCCTGGACACCATCAATGTG	2397
Query	2398	CACCTGAGGGCTGGGTACATCATCCCCCTGCAGGGCCCTGGCCTGACCACCACTGAGAGC	2457
Sbjct	2398	CACCTGAGGGCTGGCTACATTATCCCCCTGCAGGGCCCAGGGCTGACTACCACTGAGAGC	2457
Query	2458	AGGCAGCAGCCCATGGCCCTGGCTGTGGCTCTGACCAAggggggggaggccaggggggag	2517
Sbjct	2458	AGACAGCAGCCCATGGCTCTGGCTGTGGCCCTGACCAAGGGGGGGGAAGCTAGGGGGGAG	2517
Query	2518	ctgttctgggatgatggggagtctctggaggtgctggagaggggggCCTACACCCAGGTG	2577
Sbjct	2518	CTGTTCTGGGATGATGGGGAGAGCCTGGAGGTGCTGGAGAGGGGGGCCTATACCCAGGTG	2577
Query	2578	ATCTTTCTGGCCAGGAACAATACTATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGGGG	2637
Sbjct	2578	ATCTTCCTGGCTAGGAACAACACCATTGTCAATGAGCTGGTGAGGGTGACTTCTGAGGGG	2637
Query	2638	GCTGGCCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGTC	2697

Sbjct	2638	GCTGGGCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCTCCCCAGCAGGTG	2697
Query	2698	CTGAGCAATGGGGTGCCTGTGAGCAACTTCACCTACTCTCCTGACACCAAGGTGCTGGAC	2757
Sbjct	2698	CTGAGCAATGGGGTGCCTGTGAGCAACTTCACCTACAGCCCTGACACCAAGGTGCTGGAC	2757
Query	2758	ATTTGTGTGTCTCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808
Sbjct	2758	ATCTGTGTGTCTCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808