

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: H9C1NE5K114

Query= SEQ ID NO: 2

Length=2808

Sequences producing significant alignments:	Score (Bits)	E Value	Max Ident
Query_27809 SEQ ID NO: 5	4117	0.0	93%
Query_27806 SEQ ID NO: 1	4045	0.0	93%
Query_27807 SEQ ID NO: 3	4034	0.0	93%
Query_27808 SEQ ID NO: 4	4023	0.0	93%

ALIGNMENTS

>Query_27809 SEQ ID NO: 5

Length=2808

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

Query	1	ATGGCTTTCCTGTGGCTGCTGTCTTGCTGGGCCCTGCTGGGGACTACCTTTGGCCTGCTG	60
Sbjct	1	ATGGCCTTTCCTGTGGCTGCTGTCTTGCTGGGCCCTGCTGGGGACCACCTTTGGCCTGCTG	60
Query	61	GTGCCCAGGGAACTGTCTGGCTCTAGCCCAGTGCTGGAGGAGACCCACCCTGCCCACCAG	120
Sbjct	61	GTGCCCAGGGAGCTGTCTGGGAGCAGCCCAGTGCTGGAGGAGACCCACCCTGCCCACCAG	120
Query	121	CAGGGGGCTTCTAGGCCTGGCCCCAGGGATGCCCAGGCCCCACCCTGGCAGGCCAAGGGCT	180
Sbjct	121	CAGGGGGCCAGCAGGCCTGGCCCTAGGGATGCCCAGGCCCCACCCTGGCAGGCCAAGGGCT	180
Query	181	GTGCCCACCCAGTGATGTGCCCCCAACTCTAGATTTGATTGTGCCCCCTGATAAGGCC	240
Sbjct	181	GTGCCTACCCAGTGATGTGCCACCCAATTCTAGGTTTGACTGTGCTCCTGACAAGGCC	240

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

Sbjct	960	GGATGTCTACATCTTCCTGGGGCCTGAGCCCAAGTCTGTGGTGCAGCAGTATCTGGATGT	1019
Query	1020	GGTGGGCTACCCCTTCATGCCTCCCTACTGGGGCCTGGGCTTCCACCTGTGCAGGTGGGG	1079
Sbjct	1020	GGTGGGGTATCCCTTCATGCCCCCTACTGGGGCCTGGGCTTTCACCTGTGCAGGTGGGG	1079
Query	1080	CTACAGCTCTACTGCCATCACCAGGCAGGTGGTGGAGAATATGACCAGGGCCCACTTCCC	1139
Sbjct	1080	CTACAGCAGCACTGCCATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCCCACTTCCC	1139
Query	1140	CCTGGATGTGCAGTGGAATGACCTGGACTACATGGACTCTAGGAGGGACTTCACCTTCAA	1199
Sbjct	1140	TCTGGATGTGCAGTGGAATGACCTGGACTATATGGATTCTAGGAGAGACTTTACTTTTAA	1199
Query	1200	TAAGGATGGCTTCAGAGACTTCCCTGCCATGGTGCAGGAGCTGCATCAGGGGGGCAGGAG	1259
Sbjct	1200	CAAGGATGGCTTCAGGGATTTCCCTGCCATGGTGCAGGAGCTGCACCAGGGGGGCAGGAG	1259
Query	1260	GTACATGATGATTGTGGACCCTGCCATCAGCTCTTCTGGCCCTGCTGGCTCTTACAGGCC	1319
Sbjct	1260	GTACATGATGATTGTGGACCCTGCTATTAGCAGCTCTGGCCCTGCTGGGTCTTACAGGCC	1319
Query	1320	CTATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGGCAGCCCCTGAT	1379
Sbjct	1320	TTATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGCCAGCCCCTGAT	1379
Query	1380	TGGGAAGGTGTGGCCTGGCTCTACTGCCTTCCCTGACTTCACCAATCCTACTGCCCTGGC	1439
Sbjct	1380	TGGCAAGGTGTGGCCTGGCAGCACTGCCTTCCCTGACTTCACCAACCCCACTGCCCTGGC	1439
Query	1440	CTGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCCTTTGATGGCATGTGGAT	1499
Sbjct	1440	CTGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCCTTTGATGGGATGTGGAT	1499
Query	1500	TGACATGAATGAGCCCTCTAATTTTCATCAGGGGCTCTGAGGATGGCTGCCCCAACAATGA	1559
Sbjct	1500	TGACATGAATGAGCCCTCTAACTTCATCAGGGGGTCTGAGGATGGCTGCCCCAACAATGA	1559
Query	1560	GCTGGAGAAcccccccTATGTGCCTGGGGTGGTGGGGGGCACCCCTGCAGGCTGCCACCAT	1619
Sbjct	1560	GCTGGAGAACCCCCCTATGTGCCTGGGGTGGTGGGGGGCACTCTGCAGGCTGCCACTAT	1619
Query	1620	CTGTGCTAGCTCTCACCAGTTCCTGAGCACCCACTACAATCTGCATAACCTGTATGGCCT	1679
Sbjct	1620	CTGTGCTTCTTCTCACCAGTTTCTGAGCACCCACTATAATCTGCACAACCTGTATGGCCT	1679
Query	1680	GACTGAGGCCATTGCCAGCCACAGGGCCCTGGTGAAGGCTAGGGGCACCAGGCCCTTTGT	1739
Sbjct	1680	GACTGAGGCCATTGCCAGCCATAGGGCCCTGGTGAAGGCCAGGGGCACCAGGCCCTTTGT	1739

[illegible]

Sbjct	2457	CAGGCAGCAGCCCATGGCCCTGGCTGTGGCTCTGACCAAGGGGGGGGAGGCCAGGGGGGA	2516
Query	2517	gctgttttgggatgatggggagagcctggaggtgctggagaggggggCCTACACTCAGGT	2576
Sbjct	2517	GCTGTTCTGGGATGATGGGGAGTCTCTGGAGGTGCTGGAGAGGGGGGCCTACACCCAGGT	2576
Query	2577	GATCTTCCTGGCCAGGAACAATACCATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGGG	2636
Sbjct	2577	GATCTTCTGGCCAGGAACAATACTATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGGG	2636
Query	2637	GGCTGGCCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGT	2696
Sbjct	2637	GGCTGGCCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGT	2696
Query	2697	GCTGAGCAATGGGGTGCCTGTGAGCAACTTCACCTATAGCCCTGATACCAAGGTGCTGGA	2756
Sbjct	2697	CCTGAGCAATGGGGTGCCTGTGAGCAACTTCACCTACTCTCTGACACCAAGGTGCTGGA	2756
Query	2757	TATTTGTGTGAGCCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808
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>Query_27806 SEQ ID NO: 1
Length=2808

Score = 4045 bits (2190), Expect = 0.0
Identities = 2603/2809 (93%), Gaps = 2/2809 (0%)
Strand=Plus/Plus

Query	1	ATGGCTTTCCTGTGGCTGCTGTCTTGCTGGGCCCTGCTGGGGACTACCTTTGGCCTGCTG	60
Sbjct	1	ATGGCTTTCCTGTGGCTGCTGAGCTGCTGGGCTCTGCTGGGCACCACCTTTGGGCTGCTG	60
Query	61	GTGCCCAGGGAACTGTCTGGCTCTAGCCCAGTGCTGGAGGAGACCCACCCTGCCCACCAG	120
Sbjct	61	GTGCCTAGGGAGCTGTCTGGGTCTAGCCCTGTGCTGGAGGAGACTCACCTGCCCATCAG	120
Query	121	CAGGGGGCTTCTAGGCCTGGCCCCAGGGATGCCCAGGCCCCACCCTGGCAGGCCAAGGGCT	180
Sbjct	121	CAGGGGGCTAGCAGGCCTGGCCCCAGGGATGCTCAGGCCCCACCCTGGCAGGCCAAGGGCT	180
Query	181	GTGCCCACCCAGTGATGTGCCCCCAACTCTAGATTTGATTGTGCCCCTGATAAGGCC	240
Sbjct	181	GTGCCCACCCAGTGATGTGCCCCCAACAGCAGGTTTGACTGTGCCCCTGACAAGGCC	240
Query	241	ATCACCCAGGAGCAGTGAGAGGCTAGGGGCTGCTGCTACATCCCTGCTAAGCAGGGCCTG	300
Sbjct	241	ATTACCCAGGAGCAGTGAGAGGCCAGGGGCTGCTGCTACATTCCAGCTAAGCAGGGCCTG	300

Query	301	CAGGGGGGCTCAGATGGGCCAGCCCTGGTGCTTCTTcccccccAGCTATCCCTCTTACAAG	360
Sbjct	301	CAGGGGGGCCAGATGGGCCAGCCCTGGTGCTTCTTCCCCCCCAGCTATCCTAGCTATAAA	360
Query	361	CTGGAGAATCTGAGCAGCTCTGAGATGGGCTACACTGCCACCCTGACCAGGACTACTCCC	420
Sbjct	361	CTGGAGAACCTGAGCAGCTCTGAGATGGGCTATACTGCCACCCTGACTAGGACTACTCCC	420
Query	421	ACCTTCTTCCCCAAGGACATCCTGACCCTGAGGCTGGATGTGATGATGGAGACTGAGAAC	480
Sbjct	421	ACCTTTTTTCTAAGGATATCCTGACCCTGAGGCTGGATGTGATGATGGAGACTGAGAAC	480
Query	481	AGGCTGCATTTTACCATCAAGGATCCTGCCAACAGGAGGTATGAGGTGCCTCTGGAGACC	540
Sbjct	481	AGGCTGCACTTCACTATTAAGGACCCTGCCAATAGGAGGTATGAAGTGCCTCTGGAGACT	540
Query	541	CCCCATGTGCACAGCAGGGCTCCTTCTCCCCTGTACTCTGTGGAGTTCTCTGAGGAACCC	600
Sbjct	541	CCTCATGTGCACTCTAGGGCCCCAGCCCCCTGTATTCTGTGGAGTTCTCTGAGGAGCCC	600
Query	601	TTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTCCTGCTGAACACCACTGTGGCC	660
Sbjct	601	TTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTGCTGCTGAACACCACTGTGGCC	660
Query	661	CCCCTGTTCTTTGCTGATCAGTTCCTGCAGCTGTCCACTTCTCTGCCTAGCCAGTACATC	720
Sbjct	661	CCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGAGCACCAGCCTGCCCAGCCAGTACATC	720
Query	721	ACTGGGCTGGCTGAGCACCTGAGCCCTCTGATGCTGAGCACCTCTTGGACTAGGATCACC	780
Sbjct	721	ACTGGGCTGGCTGAGCATCTGAGCCCTCTGATGCTGAGCACCTCTTGGACCAGGATCACC	780
Query	781	CTGTGGAACAGGGACCTGGCCCCACCCCTGGGGCCAACTGTATGGCAGCCACCCCTTC	840
Sbjct	781	CTGTGGAATAGGGATCTGGCCCCACCCCTGGGGCTAATCTGTATGGCTCTCATCCCTTT	840
Query	841	TATCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTCTGCTGAATAGCAATGCT	900
Sbjct	841	TACCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTTCTGCTGAACAGCAATGCC	900
Query	901	ATGGATGTGGTGCTGCAGCCCAGCCCTGCCCTGTCTTGGAGGAGCACTGGGGGCATCCTG	960
Sbjct	901	ATGGATGTGGTGCTGCAGCCCTCTCCTGCCCTGAGCTGGAGGAGCACTGGGGGCATCCTG	960
Query	961	GATGTGTACATTTTCTGGGGCCTGAGCCCAAGTCTGTGGTGCAGCAGTACCTGGATGTG	1020
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Sbjct	1021	GTGGGCTACCCCTTTATGCCCCCTATTGGGGCCTGGGCTTCCACCTGTGCAGGTGGGGG	1080
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Sbjct	1141	CTGGATGTGCAGTGGAATGACCTGGACTATATGGACTCTAGGAGGGATTTACCTTCAAC	1200
Query	1201	AAGGATGGCTTCAGAGACTTCCCTGCCATGGTGCAGGAGCTGCATCAGGGGGGCAGGAGG	1260
Sbjct	1201	AAGGATGGCTTCAGGGACTTCCCTGCTATGGTCCAGGAGCTGCATCAGGGGGGCAGGAGG	1260
Query	1261	TACATGATGATTGTGGACCCTGCCATCAGCTCTTCTGGCCCTGCTGGCTCTTACAGGCCC	1320
Sbjct	1261	TACATGATGATTGTGGACCCTGCCATCAGCAGCTCTGGCCCTGCTGGCAGCTATAGGCCC	1320
Query	1321	TATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGGCAGCCCCCTGATT	1380
Sbjct	1321	TATGATGAGGGCCTGAGGAGGGGGGTGTTTATCACTAATGAAACTGGGCAGCCCCCTGATT	1380
Query	1381	GGGAAGGTGTGGCCTGGCTCTACTGCCTTCCCTGACTTCACCAATCCTACTGCCCTGGCC	1440
Sbjct	1381	GGCAAGGTGTGGCCTGGCTCTACTGCCTTCCCTGACTTCACCAACCCCACTGCTCTGGCC	1440
Query	1441	TGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCCTTTGATGGCATGTGGATT	1500
Sbjct	1441	TGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCCTTTGATGGCATGTGGATT	1500
Query	1501	GACATGAATGAGCCCTCTAATTTTCATCAGGGGCTCTGAGGATGGCTGCCCCAACAATGAG	1560
Sbjct	1501	GACATGAATGAGCCCAGCAACTTCATCAGGGGCTCTGAGGATGGGTGCCCCAATAATGAG	1560
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Sbjct	1561	CTGGAGAACCCCCCTATGTGCCTGGGGTGGTGGGGGGCACCTGCAGGCTGCCACTATT	1620
Query	1621	TGTGCTAGCTCTCACCAGTTCCTGAGCACCCACTACAATCTGCATAACCTGTATGGCCTG	1680
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Query	1681	ACTGAGGCCATTGCCAGCCACAGGGCCCTGGTGAAGGCTAGGGGCACCAGGCCCTTTGTG	1740
Sbjct	1681	ACTGAGGCCATTGCCAGCCACAGGGCCCTGGTGAAGGCCAGGGGCACTAGGCCCTTTGTG	1740
Query	1741	ATTTCTAGGAGCACTTTTGTGGCCATGGCAGGTATGCTGGGCACTGGACTGGGGATGTG	1800
Sbjct	1741	ATCTCTAGAAGCACCTTTGTGGCCATGGGAGGTATGCTGGCCACTGGACTGGGGATGTG	1800

Query	1801	TGG-TCTAGCTGGGAGCAGCTGGCTTCTTCTGTGCCTGAGATCCTGCAGTTCAACCTGCT 	1859
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Query	1860	GGGGGTGCCTCTGGTGGGGGCTGATGTGTGTGGGTTCTGGGCAACACTTCTGAGGAGCT 	1919
Sbjct	1860	GGGGGTGCCCCTGGTGGGGGCTGATGTGTGTGGCTTCTGGGCAACACCTCTGAAGAGCT	1919
Query	1920	GTGTGTGAGGTGGACCCAGCTGGGGGCCTTCTACCCTTTCATGAGGAACCACAACAGCCT 	1979
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Query	1980	GCTGAGCCTGCCCCAGGAGCCCTACAGCTTCTCTGAGCCTGCCAGCAGGCCATGAGGAA 	2039
Sbjct	1980	GCTGAGCCTGCCTCAGGAGCCTTACTCTTCTCTGAGCCTGCCAGCAGGCCATGAGGAA	2039
Query	2040	GGCCCTGACCCTGAGGTATGCCCTGCTGCCCCACCTGTACACCCTGTTCCACCAGGCCCA 	2099
Sbjct	2040	GGCCCTGACCCTGAGGTATGCTCTGCTGCCCCACCTGTACACCCTGTTCCACCAGGCCCA	2099
Query	2100	TGTGGCTGGGGAGACTGTGGCTAGGCCTCTGTTCTGGAGTTCCCCAAGGACTCTAGCAC 	2159
Sbjct	2100	TGTGGCTGGGGAGACTGTGGCCAGGCCCTGTTCTGGAGTTTCTTAAGGATAGCAGCAC	2159
Query	2160	CTGGACTGTGGACCACCAGCTGCTGTGGGGGGAGGCCCTGCTGATCACTCCTGTGCTGCA 	2219
Sbjct	2160	CTGGACTGTGGACCACCAGCTGCTGTGGGGGGAGGCCCTGCTGATTACCCCTGTGCTGCA	2219
Query	2220	GGCTGGGAAGGCTGAGGTGACTGGCTATTTCCCCCTGGGCACCTGGTATGACCTGCAGAC 	2279
Sbjct	2220	GGCTGGCAAGGCTGAGGTGACTGGCTACTTCCCCCTGGGCACTTGGTATGACCTGCAGAC	2279
Query	2280	TGTGCCTGTGGAGGCCCTGGGGAGCCTGccccccccccTGCTGCCCCCAGGGAGCCTGC 	2339
Sbjct	2280	TGTGCCTGTGGAAGCCCTGGGCAGCCTGCCTCCCCCCCCTGCTGCCCCCAGGGAGCCTGC	2339
Query	2340	CATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTCTGGATACCATCAATGTGCA 	2399
Sbjct	2340	CATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCCTGGACACCATTAATGTGCA	2399
Query	2400	CCTGAGGGCTGGCTACATCATTCCCCTGCAGGGCCCTGGCCTGACCACTACTGAGTCTAG 	2459
Sbjct	2400	TCTGAGGGCTGGGTATATTATCCCCCTGCAGGGGCCTGGGCTGACTACCACTGAGAGCAG	2459
Query	2460	GCAGCAGCCCATGGCCCTGGCTGTGGCCCTGACCAAggggggggaggctagggggggagct 	2519
Sbjct	2460	GCAGCAGCCTATGGCCCTGGCTGTGGCTCTGACTAAGGGGGGGGAGGCCAGGGGGGAGCT	2519
Query	2520	gttttgggatgatggggagagcctggaggtgctggagaggggggCCTACACTCAGGTGAT 	2579

Sbjct	2520	GTTCTGGGATGATGGGGAGAGCCTGGAGGTGCTGGAGAGGGGGGCCTACACCCAGGTGAT	2579
Query	2580	CTTCCTGGCCAGGAACAATACCATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGGGGGC	2639
Sbjct	2580	TTTCCTGGCCAGGAACAACACCATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGGGGGC	2639
Query	2640	TGGCCTGCAGCTGCAGAAAGGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGTGCT	2699
Sbjct	2640	TGGCCTGCAGCTGCAGAAAGGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGTGCT	2699
Query	2700	GAGCAATGGGGTGCCTGTGAGCAACTTCACCTATAGCCCTGATACCAAGGTGCTGGATAT	2759
Sbjct	2700	GAGCAATGGGGTGCCTGTGAGCAACTTCACCTACAGCCCTGACACCAAGGTGCTGGATAT	2759
Query	2760	TTGTGTGAGCCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808
Sbjct	2760	TTGTGTGAGCCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808

>Query_27807 SEQ ID NO: 3
Length=2808

Score = 4034 bits (2184), Expect = 0.0
Identities = 2600/2808 (93%), Gaps = 0/2808 (0%)
Strand=Plus/Plus

Query	1	ATGGCTTTCTGTGGCTGCTGTCTTGCTGGGCCCTGCTGGGGACTACCTTTGGCCTGCTG	60
Sbjct	1	ATGGCTTTCTGTGGCTGCTGTCTTGTTGGGCTCTGCTGGGCACCACTTTGGCCTGCTG	60
Query	61	GTGCCCAGGGAACTGTCTGGCTCTAGCCCAGTGCTGGAGGAGACCCACCTGCCACCAG	120
Sbjct	61	GTGCCCAGGGAGCTGTCTGGCAGCAGCCCTGTGCTGGAGGAGACCCACCTGCTCATCAG	120
Query	121	CAGGGGGCTTCTAGGCCTGGCCCCAGGGATGCCCAGGCCACCCCTGGCAGGCCAAGGGCT	180
Sbjct	121	CAGGGGGCTAGCAGGCCTGGCCCCAGGGATGCCCAGGCTCACCTGGGAGACCCAGGGCT	180
Query	181	GTGCCCACCCAGTGTGATGTGCCCCCAACTCTAGATTTGATTGTGCCCCTGATAAGGCC	240
Sbjct	181	GTGCCCCTCAGTGTGATGTGCCCCCAACAGCAGGTTTGACTGTGCTCCTGACAAGGCT	240
Query	241	ATCACCCAGGAGCAGTGTGAGGCTAGGGGCTGCTGCTACATCCCTGCTAAGCAGGGCCTG	300
Sbjct	241	ATCACCCAGGAGCAGTGTGAGGCCAGGGGGTGCTGCTACATTCCTGCTAAGCAGGGCCTG	300
Query	301	CAGGGGGCTCAGATGGGCCAGCCCTGGTGCTTCTTccccccAGCTATCCCTCTTACAAG	360
Sbjct	301	CAGGGGGCCCAGATGGGCCAGCCCTGGTGCTTCTTCCCCCCTCTTATCCCAGCTATAAG	360

Query	361	CTGGAGAATCTGAGCAGCTCTGAGATGGGCTACACTGCCACCCTGACCAGGACTACTCCC	420
Sbjct	361	CTGGAGAACCTGAGCAGCTCTGAGATGGGCTACACTGCCACCCTGACCAGGACCACTCCC	420
Query	421	ACCTTCTTCCCCAAGGACATCCTGACCCTGAGGCTGGATGTGATGATGGAGACTGAGAAC	480
Sbjct	421	ACCTTCTTCCCCAAGGATATTCTGACTCTGAGGCTGGATGTGATGATGGAGACTGAGAAC	480
Query	481	AGGCTGCATTTACCATCAAGGATCCTGCCAACAGGAGGTATGAGGTGCCTCTGGAGACC	540
Sbjct	481	AGGCTGCACTTCACTATCAAGGACCCTGCCAATAGGAGGTATGAGGTGCCCCTGGAGACT	540
Query	541	CCCCATGTGCACAGCAGGGCTCCTTCTCCCCTGTACTCTGTGGAGTTCTCTGAGGAACCC	600
Sbjct	541	CCTCATGTGCATAGCAGGGCCCCTTCTCCTCTGTATTCTGTGGAGTTCTCTGAGGAGCCC	600
Query	601	TTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTCCTGCTGAACACCACTGTGGCC	660
Sbjct	601	TTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTGCTGCTGAACACCACTGTGGCC	660
Query	661	CCCCTGTTCTTTGCTGATCAGTTCCTGCAGCTGTCCACTTCTCTGCCTAGCCAGTACATC	720
Sbjct	661	CCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGAGCACTTCTCTGCCCAGCCAGTACATT	720
Query	721	ACTGGGCTGGCTGAGCACCTGAGCCCTCTGATGCTGAGCACCTCTTGGACTAGGATCACC	780
Sbjct	721	ACTGGGCTGGCTGAGCATCTGAGCCCCCTGATGCTGAGCACCTCTTGGACCAGGATCACC	780
Query	781	CTGTGGAACAGGGACCTGGCCCCCACCCTGGGGCCAACCTGTATGGCAGCCACCCCTTC	840
Sbjct	781	CTGTGGAACAGGGACCTGGCCCCCACTCCTGGGGCTAACCTGTATGGCTCTCACCCCTTT	840
Query	841	TATCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTCTGCTGAATAGCAATGCT	900
Sbjct	841	TACCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTCTGCTGAACAGCAATGCT	900
Query	901	ATGGATGTGGTGCTGCAGCCCAGCCCTGCCCTGTCTTGAGGAGCACTGGGGGCATCCTG	960
Sbjct	901	ATGGATGTGGTGCTGCAGCCCTCTCCAGCCCTGTCTTGAGGAGCACTGGGGGCATTCTG	960
Query	961	GATGTGTACATTTTCTGGGGCCTGAGCCCAAGTCTGTGGTGCAGCAGTACCTGGATGTG	1020
Sbjct	961	GATGTGTACATTTTCTGGGGCCTGAACCCAAGTCTGTGGTGCAGCAGTACCTGGATGTG	1020
Query	1021	GTGGGCTACCCCTTCATGCCTCCCTACTGGGGCCTGGGCTTCCACCTGTGCAGGTGGGGC	1080
Sbjct	1021	GTGGGCTACCCCTTCATGCCCCCTATTGGGGGCTGGGGTTTCACCTGTGCAGGTGGGGC	1080
Query	1081	TACAGCTCTACTGCCATCACCAGGCAGGTGGTGGAGAATATGACCAGGGCCCCACTTCCCC	1140

Sbjct	1081	TACAGCAGCACTGCCATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCCCCATTTCCCC	1140
Query	1141	CTGGATGTGCAGTGGAATGACCTGGACTACATGGACTCTAGGAGGGACTTCACCTTCAAT	1200
Sbjct	1141	CTGGATGTGCAGTGGAATGACCTGGACTACATGGATAGCAGGAGGGATTTACCTTCAAC	1200
Query	1201	AAGGATGGCTTCAGAGACTTCCCTGCCATGGTGCAGGAGCTGCATCAGGGGGGCAGGAGG	1260
Sbjct	1201	AAGGATGGCTTCAGGGACTTTCCTGCCATGGTGCAGGAGCTGCACCAGGGGGGCAGGAGG	1260
Query	1261	TACATGATGATTGTGGACCCTGCCATCAGCTCTTCTGGCCCTGCTGGCTCTTACAGGCCC	1320
Sbjct	1261	TATATGATGATTGTGGACCCTGCTATCAGCAGCTCTGGCCCTGCTGGCTCTTACAGGCCC	1320
Query	1321	TATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGGCAGCCCCTGATT	1380
Sbjct	1321	TATGATGAGGGCCTGAGGAGGGGGGTGTTTATCACTAATGAAACTGGCCAGCCTCTGATT	1380
Query	1381	GGGAAGGTGTGGCCTGGCTCTACTGCCTTCCCTGACTTCACCAATCCTACTGCCCTGGCC	1440
Sbjct	1381	GGCAAGGTCTGGCCTGGCTCTACTGCCTTCCCTGATTTTACTAACCCCACTGCCCTGGCC	1440
Query	1441	TGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCCTTTGATGGCATGTGGATT	1500
Sbjct	1441	TGGTGGGAGGACATGGTGGCTGAGTTCCATGATCAGGTGCCTTTTATGGCATGTGGATT	1500
Query	1501	GACATGAATGAGCCCTCTAATTTTCATCAGGGGCTCTGAGGATGGCTGCCCCAACAATGAG	1560
Sbjct	1501	GATATGAATGAACCAAGCAACTTCATCAGAGGCTCTGAGGATGGCTGCCCCAACAATGAG	1560
Query	1561	CTGGAGAAcccccccTATGTGCCTGGGGTGGTGGGGGGCACCTGCAGGCTGCCACCATC	1620
Sbjct	1561	CTGGAGAACCCCCCTATGTGCCTGGGGTGGTGGGGGGCACTCTGCAGGCTGCCACCATT	1620
Query	1621	TGTGCTAGCTCTCACCAGTTCCTGAGCACCCACTACAATCTGCATAACCTGTATGGCCTG	1680
Sbjct	1621	TGTGCTAGCAGCCACCAGTTCCTGAGCACCCACTACAATCTGCACAACCTGTATGGCCTG	1680
Query	1681	ACTGAGGCCATTGCCAGCCACAGGGCCCTGGTGAAGGCTAGGGGCACCAGGCCCTTTGTG	1740
Sbjct	1681	ACTGAAGCCATTGCCAGCCATAGGGCCCTGGTGAAGGCCAGGGGCACTAGGCCTTTTGTG	1740
Query	1741	ATTTCTAGGAGCACTTTTGCTGGCCATGGCAGGTATGCTGGGCACTGGACTGGGGATGTG	1800
Sbjct	1741	ATCAGCAGGAGCACTTTTGCTGGCCATGGCAGGTATGCTGGCCACTGGACTGGGGATGTG	1800
Query	1801	TGGTCTAGCTGGGAGCAGCTGGCTTCTTCTGTGCCTGAGATCCTGCAGTTCAACCTGCTG	1860
Sbjct	1801	TGGAGCAGCTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATTCTGCAGTTTAACCTGCTG	1860

Query	1861	GGGGTGCCTCTGGTGGGGGCTGATGTGTGTGGGTTCTGGGCAACACTTCTGAGGAGCTG	1920
Sbjct	1861	GGGGTGCCCTGGTGGGGGCTGATGTGTGTGGCTTCTGGGCAACACCTCTGAGGAGCTG	1920
Query	1921	TGTGTGAGGTGGACCCAGCTGGGGGCCTTCTACCCCTTTCATGAGGAACCACAACAGCCTG	1980
Sbjct	1921	TGTGTGAGGTGGACCCAGCTGGGGGCCTTTTATCCCTTCATGAGGAACCACAACAGCCTG	1980
Query	1981	CTGAGCCTGCCCCAGGAGCCCTACAGCTTCTCTGAGCCTGCCAGCAGGCCATGAGGAAG	2040
Sbjct	1981	CTGAGCCTGCCTCAGGAGCCCTACTCTTTCTCTGAGCCTGCCAGCAGGCCATGAGGAAG	2040
Query	2041	GCCCTGACCCTGAGGTATGCCCTGCTGCCCCACCTGTACACCCTGTTCCACCAGGCCCAT	2100
Sbjct	2041	GCCCTGACCCTGAGGTATGCCCTGCTGCCCCACCTGTATACCCTGTTCCACCAGGCCCAT	2100
Query	2101	GTGGCTGGGGAGACTGTGGCTAGGCCTCTGTTCTGGAGTTCCCCAAGGACTCTAGCACC	2160
Sbjct	2101	GTGGCTGGGGAGACTGTGGCCAGGCCCTGTTCTGGAGTTCCCCAAGGACAGCAGCACC	2160
Query	2161	TGGACTGTGGACCACCAGCTGCTGTGGGGGGAGGCCCTGCTGATCACTCCTGTGCTGCAG	2220
Sbjct	2161	TGGACTGTGGATCATCAGCTGCTGTGGGGGGAGGCCCTGCTGATCACCCCTGTGCTGCAG	2220
Query	2221	GCTGGGAAGGCTGAGGTGACTGGCTATTTCCCCCTGGGCACCTGGTATGACCTGCAGACT	2280
Sbjct	2221	GCTGGCAAGGCTGAGGTCACTGGCTACTTCCCTCTGGGCACCTGGTATGACCTGCAGACT	2280
Query	2281	GTGCCTGTGGAGGCCCTGGGGAGCCTGccccccccccTGCTGCCCCCAGGGAGCCTGCC	2340
Sbjct	2281	GTGCCTGTGGAGGCTCTGGGCAGCCTGCCCCCCCCCTGCTGCTCCAGGGAGCCTGCC	2340
Query	2341	ATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTGGATAACCATCAATGTGCAC	2400
Sbjct	2341	ATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCTCCCTGGACACCATCAATGTGCAC	2400
Query	2401	CTGAGGGCTGGCTACATCATTTCCCCTGCAGGGCCCTGGCCTGACCACTACTGAGTCTAGG	2460
Sbjct	2401	CTGAGGGCTGGCTACATTATCCCCCTGCAGGGCCAGGGCTGACTACCACTGAGAGCAGA	2460
Query	2461	CAGCAGCCCATGGCCCTGGCTGTGGCCCTGACCAAggggggggaggctaggggggagctg	2520
Sbjct	2461	CAGCAGCCCATGGCTCTGGCTGTGGCCCTGACCAAGGGGGGGGAAGCTAGGGGGGAGCTG	2520
Query	2521	ttttgggatgatggggagagcctggaggtgctggagagggggCCTACACTCAGGTGATC	2580
Sbjct	2521	TTCTGGGATGATGGGGAGAGCCTGGAGGTGCTGGAGAGGGGGCCTATACCCAGGTGATC	2580
Query	2581	TTCTGGCCAGGAACAATACCATTTGTGAATGAGCTGGTGAGGGTGACCTCTGAGGGGGCT	2640

Sbjct	2581	TTCCTGGCTAGGAACAACACCATTTGTCAATGAGCTGGTGAGGGTGACTTCTGAGGGGGCT	2640
Query	2641	GGCCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGTGCTG	2700
Sbjct	2641	GGGCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCTCCCCAGCAGGTGCTG	2700
Query	2701	AGCAATGGGGTGCCTGTGAGCAACTTCACCTATAGCCCTGATACCAAGGTGCTGGATATT	2760
Sbjct	2701	AGCAATGGGGTGCCTGTGAGCAACTTCACCTACAGCCCTGACACCAAGGTGCTGGACATC	2760
Query	2761	TGTGTGAGCCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808
Sbjct	2761	TGTGTGTCTCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808

>Query_27808 SEQ ID NO: 4
Length=2808

Score = 4023 bits (2178), Expect = 0.0
Identities = 2600/2810 (93%), Gaps = 4/2810 (0%)
Strand=Plus/Plus

Query	1	ATGGCTTTCTGTGGCTGCTGTCTTGCTGGGCCCTGCTGGGGACTACCTTTGGCCTGCTG	60
Sbjct	1	ATGGCCTTCTGTGGCTGCTGTCTTGCTGGGCTCTGCTGGGGACCACCTTTGGCCTGCTG	60
Query	61	GTGCCCAGGGAACTGTCTGGCTCTAGCCCAGTGCTGGAGGAGACCCACCCTGCCCACCAG	120
Sbjct	61	GTCCCCAGGGAGCTGTCTGGCTCTTCTCCTGTCTGGAGGAGACCCACCCTGCCCACCAG	120
Query	121	CAGGGGGCTTCTAGGCCTGGCCCCAGGGATGCCCAGGCCACCCTGGCAGGCCAAGGGCT	180
Sbjct	121	CAGGGGGCTAGCAGGCCTGGCCCCAGGGATGCCCAGGCCACCCTGGCAGGCCAAGGGCT	180
Query	181	GTGCCCACCCAGTGTGATGTGCCCCCAACTCTAGATTTGATTGTGCCCCTGATAAGGCC	240
Sbjct	181	GTGCCCACCCAGTGTGATGTGCCTCCCAACAGCAGGTTTACTGTGCCCCTGACAAGGCC	240
Query	241	ATCACCCAGGAGCAGTGTGAGGCTAGGGGCTGCTGCTACATCCCTGCTAAGCAGGGCCTG	300
Sbjct	241	ATCACCCAGGAGCAGTGTGAGGCCAGGGGCTGCTGCTATATCCCTGCCAAGCAGGGCCTG	300
Query	301	CAGGGGGCTCAGATGGGCCAGCCCTGGTGCTTCTTccccccAGCTATCCCTCTTACAAG	360
Sbjct	301	CAGGGGGCTCAGATGGGCCAGCCCTGGTGCTTCTTTCCCCCTCTTATCCTAGCTATAAG	360
Query	361	CTGGAGAATCTGAGCAGCTCTGAGATGGGCTACACTGCCACCCTGACCAGGACTACTCCC	420
Sbjct	361	CTGGAGAACCTGAGCAGCTCTGAGATGGGGTACACTGCCACCCTGACCAGGACCACCCCC	420

[illegible]

Sbjct	1141	CTGGATGTGCAGTGGGAATGACCTGGACTACATGGACAGCAGGAGGGACTTCACCTTTAAC	1200
Query	1201	AAGGATGGCTTCAGAGACTTCCCTGCCATGGTGCAGGAGCTGCATCAGGGGGGCAGGAGG	1260
Sbjct	1201	AAGGATGGCTTTAGGGACTTCCCTGCCATGGTGCAGGAGCTGCATCAGGGGGGCAGGAGG	1260
Query	1261	TACATGATGATTGTGGACCCCTGCCATCAGCTCTTCTGGCCCTGCTGGCTCTTACAGGCCC	1320
Sbjct	1261	TACATGATGATTGTGGACCCAGCCATCAGCAGCTCTGGGCCTGCTGGGTCTTACAGGCCC	1320
Query	1321	TATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGGCAGCCCCTGATT	1380
Sbjct	1321	TATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGCCAGCCCCTGATT	1380
Query	1381	GGGAAGGTGTGGCCTGGCTCTACTGCCTTCCCTGACTTCACCAATCCTACTGCCCTGGCC	1440
Sbjct	1381	GGCAAGGTGTGGCCTGGGAGCACTGCCTTCCCTGATTTTACCAACCCCACTGCCCTGGCC	1440
Query	1441	TGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCCTTTGATGGCATGTGGATT	1500
Sbjct	1441	TGGTGGGAGGATATGGTGGCTGAGTTTCATGACCAGGTGCCCTTTGATGGCATGTGGATT	1500
Query	1501	GACATGAATGAGCCCTCTAATTTTCATCAGGGGCTCTGAGGATGGCTGCCCCAACAATGAG	1560
Sbjct	1501	GACATGAATGAGCCCAGCAATTTTCATCAGGGGCTCTGAGGATGGCTGCCCCAACAATGAG	1560
Query	1561	CTGGAGAAcccccccTATGTGCCTGGGGTGGTGGGGGGCACCCCTGCAGGCTGCCACCATC	1620
Sbjct	1561	CTGGAGAATCCTCCCTATGTGCCTGGGGTGGTGGGGGGCACCCCTGCAGGCTGCCACCATC	1620
Query	1621	TGTGC-TAGCTCTCACCAGTTCCTGAGCACCCACTACAATCTGCATAACCTGTATGGCCT	1679
Sbjct	1621	TGTGCCTCTAGC-CACCAGTTCCTGAGCACCCACTATAACCTGCATAACCTGTATGGCCT	1679
Query	1680	GACTGAGGCCATTGCCAGCCACAGGGCCCTGGTGAAGGCTAGGGGCACCAGGCCCTTTGT	1739
Sbjct	1680	GACTGAGGCCATTGCCAGCCATAGAGCCCTGGTGAAGGCCAGAGGGACCAGGCCCTTTGT	1739
Query	1740	GATTTCTAGGAGCACTTTTGCTGGCCATGGCAGGTATGCTGGGCACTGGACTGGGGATGT	1799
Sbjct	1740	GATCTCTAGGAGCACCTTTTGCTGGCCATGGCAGGTATGCTGGCCACTGGACTGGGGATGT	1799
Query	1800	GTGG-TCTAGCTGGGAGCAGCTGGCTTCTTCTGTGCCTGAGATCCTGCAGTTCAACCTGC	1858
Sbjct	1800	GTGGAGCT-CTTGGGAGCAGCTGGCCAGCTCTGTGCCAGAGATCCTGCAGTTCAACCTGC	1858
Query	1859	TGGGGGTGCCTCTGGTGGGGGCTGATGTGTGTGGGTTCTGGGCAACACTTCTGAGGAGC	1918
Sbjct	1859	TGGGGGTGCCTCTGGTGGGGGCTGATGTGTGTGGCTTCTGGGCAATACCTCTGAAGAGC	1918

Query	1919	TGTGTGTGAGGTGGACCCAGCTGGGGGCCTTCTACCCCTTTCATGAGGAACCACAACAGCC	1978
Sbjct	1919	TGTGTGTGAGGTGGACTCAGCTGGGGGCCTTCTATCCCTTCATGAGGAACCACAACAGCC	1978
Query	1979	TGCTGAGCCTGCCCCAGGAGCCCTACAGCTTCTCTGAGCCTGCCCAGCAGGCCATGAGGA	2038
Sbjct	1979	TGCTGTCTCTGCCCCAGGAGCCCTACAGCTTCTCTGAGCCTGCTCAGCAGGCTATGAGGA	2038
Query	2039	AGGCCCTGACCCTGAGGTATGCCCTGCTGCCCCACCTGTACACCCTGTTCCACCAGGCCC	2098
Sbjct	2039	AGGCCCTGACCCTGAGGTATGCCCTGCTGCCCCATCTGTACACCCTGTTCCACCAGGCCC	2098
Query	2099	ATGTGGCTGGGGAGACTGTGGCTAGGCCTCTGTTCTGGAGTTCCCCAAGGACTCTAGCA	2158
Sbjct	2099	ATGTGGCTGGGGAGACTGTGGCCAGGCCCTGTTTCTGGAGTTTCCAAGGACAGCAGCA	2158
Query	2159	CCTGGACTGTGGACCACCAGCTGCTGTGGGGGGAGGCCCTGCTGATCACTCCTGTGCTGC	2218
Sbjct	2159	CCTGGACTGTGGACCATCAGCTGCTGTGGGGGGAGGCTCTGCTGATTACCCCTGTGCTGC	2218
Query	2219	AGGCTGGGAAGGCTGAGGTGACTGGCTATTTCCCCCTGGGCACCTGGTATGACCTGCAGA	2278
Sbjct	2219	AGGCTGGCAAGGCTGAGGTGACTGGGTACTTCCCCCTGGGGACTTGGTATGACCTGCAGA	2278
Query	2279	CTGTGCCTGTGGAGGCCCTGGGGAGCCTGccccccccccTGCTGCCCCCAGGGAGCCTG	2338
Sbjct	2279	CTGTGCCTGTGGAAGCTCTGGGCAGCCTGCCCCACCCCTGCTGCCCCCTAGGGAGCCTG	2338
Query	2339	CCATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTCTGGATAACCATCAATGTGC	2398
Sbjct	2339	CCATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTCTGGACACCATCAATGTGC	2398
Query	2399	ACCTGAGGGCTGGCTACATCATTCCCCTGCAGGGCCCTGGCCTGACCACTACTGAGTCTA	2458
Sbjct	2399	ACCTGAGGGCTGGCTATATCATCCCCTGCAGGGCCCTGGGCTGACCACCACTGAGAGCA	2458
Query	2459	GGCAGCAGCCCATGGCCCTGGCTGTGGCCCTGACCAAggggggggaggctaggggggagc	2518
Sbjct	2459	GGCAGCAGCCCATGGCCCTGGCTGTGGCCCTGACTAAGGGGGGGGAGGCCAGGGGGGAGC	2518
Query	2519	tgttttgggatgatggggagagcctggaggtgctggagaggggggCCTACACTCAGGTGA	2578
Sbjct	2519	TGTTCTGGGATGATGGGGAGAGCCTGGAGGTGCTGGAGAGAGGGGCCTACACCCAGGTGA	2578
Query	2579	TCTTCCTGGCCAGGAACAATACCATTTGTGAATGAGCTGGTGAGGGTGACCTCTGAGGGGG	2638
Sbjct	2579	TCTTTCTGGCCAGGAACAACACCATTTGTGAATGAGCTGGTGAGGGTGACTTCTGAGGGGG	2638
Query	2639	CTGGCCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGTGC	2698

Sbjct	2639	CTGGCCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGTGC	2698
Query	2699	TGAGCAATGGGGTGCCTGTGAGCAACTTCACCTATAGCCCTGATACCAAGGTGCTGGATA	2758
Sbjct	2699	TGAGCAATGGGGTGCCTGTGTCTAACTTCACCTACAGCCCTGATACTAAGGTGCTGGATA	2758
Query	2759	TTTGTGTGAGCCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808
Sbjct	2759	TCTGTGTGAGCCTGCTGATGGGGGAGCAGTTTCTGGTGAGCTGGTGCTGA	2808