

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: H9BWDVXY114

Query= SEQ ID NO: 1

Length=2808

Sequences producing significant alignments:	Score (Bits)	E Value	Max Ident
Query_91029 SEQ ID NO: 3	4189	0.0	94%
Query_91030 SEQ ID NO: 4	4150	0.0	93%
Query_91028 SEQ ID NO: 2	4045	0.0	93%
Query_91031 SEQ ID NO: 5	4012	0.0	92%

ALIGNMENTS

>Query_91029 SEQ ID NO: 3

Length=2808

Score = 4189 bits (2268), Expect = 0.0
Identities = 2630/2810 (94%), Gaps = 4/2810 (0%)
Strand=Plus/Plus

Query	1	ATGGCTTTCCTGTGGCTGCTGAGCTGCTGGGCTCTGCTGGGCACCACTTTGGGCTGCTG	60
Sbjct	1	ATGGCTTTCCTGTGGCTGCTGTCTTGTGGGCTCTGCTGGGCACCACTTTGGCCTGCTG	60
Query	61	GTGCCTAGGGAGCTGTCTGG-GTCTAGCCCTGTGCTGGAGGAGACTCACCTGCCCATCA	119
Sbjct	61	GTGCCCAGGGAGCTGTCTGGCAGC-AGCCCTGTGCTGGAGGAGACCCACCCTGCTCATCA	119
Query	120	GCAGGGGGCTAGCAGGCCTGGCCCCAGGGATGCTCAGGCCCCACCCTGGCAGGCCCCAGGGC	179
Sbjct	120	GCAGGGGGCTAGCAGGCCTGGCCCCAGGGATGCCAGGCTCACCTGGGAGACCCAGGGC	179
Query	180	TGTGCCCACTCAGTGTGATGTGCCCCCAACAGCAGGTTTGACTGTGCCCCTGACAAGGC	239
Sbjct	180	TGTGCCCACTCAGTGTGATGTGCCCCCAACAGCAGGTTTGACTGTGCTCCTGACAAGGC	239

Query	240	CATTACCCAGGAGCAGTGTGAGGCCAGGGGCTGCTGCTACATTCCAGCTAAGCAGGGCCT	299
Sbjct	240	TATCACCCAGGAGCAGTGTGAGGCCAGGGGCTGCTGCTACATTCTGCTAAGCAGGGCCT	299
Query	300	GCAGGGGGCCCAGATGGGCCAGCCCTGGTGCTTCTTccccccAGCTATCCTAGCTATAA	359
Sbjct	300	GCAGGGGGCCCAGATGGGCCAGCCCTGGTGCTTCTTCCCCCCTCTTATCCCAGCTATAA	359
Query	360	ACTGGAGAACCTGAGCAGCTCTGAGATGGGCTATACTGCCACCCTGACTAGGACTACTCC	419
Sbjct	360	GCTGGAGAACCTGAGCAGCTCTGAGATGGGCTACACTGCCACCCTGACCAGGACCACTCC	419
Query	420	CACCTTTTTTCCTAAGGATATCCTGACCCTGAGGCTGGATGTGATGATGGAGACTGAGAA	479
Sbjct	420	CACCTTCTTCCCAAGGATATTCTGACTCTGAGGCTGGATGTGATGATGGAGACTGAGAA	479
Query	480	CAGGCTGCACTTCACTATTAAGGACCCTGCCAATAGGAGGTATGAAGTGCCTCTGGAGAC	539
Sbjct	480	CAGGCTGCACTTCACTATCAAGGACCCTGCCAATAGGAGGTATGAGGTGCCCCTGGAGAC	539
Query	540	TCCTCATGTGCACTCTAGGGCCCCCAGCCCCCTGTATTCTGTGGAGTTCTCTGAGGAGCC	599
Sbjct	540	TCCTCATGTGCATAGCAGGGCCCCCTTCTCCTCTGTATTCTGTGGAGTTCTCTGAGGAGCC	599
Query	600	CTTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTGCTGCTGAACACCACTGTGGC	659
Sbjct	600	CTTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTGCTGCTGAACACCACTGTGGC	659
Query	660	CCCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGAGCACCAAGCCTGCCCAGCCAGTACAT	719
Sbjct	660	CCCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGAGCACTTCTCTGCCAGCCAGTACAT	719
Query	720	CACTGGGCTGGCTGAGCATCTGAGCCCTCTGATGCTGAGCACCTCTTGGACCAGGATCAC	779
Sbjct	720	TACTGGGCTGGCTGAGCATCTGAGCCCCCTGATGCTGAGCACCTCTTGGACCAGGATCAC	779
Query	780	CCTGTGGAATAGGGATCTGGCCCCACCCCTGGGGCTAATCTGTATGGCTCTCATCCCTT	839
Sbjct	780	CCTGTGGAACAGGGACCTGGCCCCACTCCTGGGGCTAACCTGTATGGCTCTCACCCCTT	839
Query	840	TTACCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTTCTGCTGAACAGCAATGC	899
Sbjct	840	TTACCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTTCTGCTGAACAGCAATGC	899
Query	900	CATGGATGTGGTGCTGCAGCCCTCTCCTGCCCTGAGCTGGAGGAGCACTGGGGGCATCCT	959
Sbjct	900	TATGGATGTGGTGCTGCAGCCCTCTCCAGCCCTGTCTTGGAGGAGCACTGGGGGCATTCT	959
Query	960	GGATGTGTACATCTTCCTGGGGCCCTGAGCCCAAGTCTGTGGTCCAGCAGTATCTGGATGT	1019

Sbjct	960	GGATGTGTACATTTTCTGGGGCCTGAACCCAAGTCTGTGGTGCAGCAGTACCTGGATGT	1019
Query	1020	GGTGGGCTACCCCTTTATGCCCCCTATTGGGGCCTGGGCTTCCACCTGTGCAGGTGGGG	1079
Sbjct	1020	GGTGGGCTACCCCTTCATGCCCCCTATTGGGGGCTGGGGTTTCACCTGTGCAGGTGGGG	1079
Query	1080	GTATT-CTTCTACTGCTATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCTCACTTCC	1138
Sbjct	1080	CTACAGCAGC-ACTGCCATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCCCATTTC	1138
Query	1139	CCCTGGATGTGCAGTGGAATGACCTGGACTATATGGACTCTAGGAGGGATTTACCTTCA	1198
Sbjct	1139	CCCTGGATGTGCAGTGGAATGACCTGGACTACATGGATAGCAGGAGGGATTTACCTTCA	1198
Query	1199	ACAAGGATGGCTTCAGGGACTTCCCTGCTATGGTCCAGGAGCTGCATCAGGGGGGCAGGA	1258
Sbjct	1199	ACAAGGATGGCTTCAGGGACTTTCCTGCCATGGTGCAGGAGCTGCACCAGGGGGGCAGGA	1258
Query	1259	GGTACATGATGATTGTGGACCTGCCATCAGCAGCTCTGGCCCTGCTGGCAGCTATAGGC	1318
Sbjct	1259	GGTATATGATGATTGTGGACCTGCTATCAGCAGCTCTGGCCCTGCTGGCTCTTACAGGC	1318
Query	1319	CCTATGATGAGGGCCTGAGGAGGGGGGTGTTTATCACTAATGAAACTGGGCAGCCCCTGA	1378
Sbjct	1319	CCTATGATGAGGGCCTGAGGAGGGGGGTGTTTATCACTAATGAAACTGGCCAGCCTCTGA	1378
Query	1379	TTGGCAAGGTGTGGCCTGGCTCTACTGCCTTCCCTGACTTCACCAACCCCACTGCTCTGG	1438
Sbjct	1379	TTGGCAAGGTCTGGCCTGGCTCTACTGCCTTCCCTGATTTTACTAACCCCACTGCCCTGG	1438
Query	1439	CCTGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCTTTTGATGGCATGTGGA	1498
Sbjct	1439	CCTGGTGGGAGGACATGGTGGCTGAGTTCCATGATCAGGTGCCTTTTGATGGCATGTGGA	1498
Query	1499	TTGACATGAATGAGCCCAGCAACTTCATCAGGGGCTCTGAGGATGGGTGCCCCAATAATG	1558
Sbjct	1499	TTGATATGAATGAACCAAGCAACTTCATCAGAGGCTCTGAGGATGGCTGCCCCAACAATG	1558
Query	1559	AGCTGGAGAAcccccccTATGTGCCTGGGGTGGTGGGGGGCACCTGCAGGCTGCCACTA	1618
Sbjct	1559	AGCTGGAGAACCCCCCTATGTGCCTGGGGTGGTGGGGGGCACTCTGCAGGCTGCCACCA	1618
Query	1619	TTTGTGCCAGCTCTCACCAGTTCCTGAGCACCCACTACAACCTGCACAATCTGTATGGCC	1678
Sbjct	1619	TTTGTGCTAGCAGCCACCAGTTCCTGAGCACCCACTACAATCTGCACAACCTGTATGGCC	1678
Query	1679	TGACTGAGGCCATTGCCAGCCACAGGGCCCTGGTGAAGGCCAGGGGCACTAGGCCCTTTG	1738
Sbjct	1679	TGACTGAAGCCATTGCCAGCCATAGGGCCCTGGTGAAGGCCAGGGGCACTAGGCCCTTTG	1738

Query	1739	TGATCTCTAGAAGCACCTTTTGCTGGCCATGGGAGGTATGCTGGCCACTGGACTGGGGATG 	1798
Sbjct	1739	TGATCAGCAGGAGCACTTTTGTCTGGCCATGGCAGGTATGCTGGCCACTGGACTGGGGATG 	1798
Query	1799	TGTGGAGCTCTTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATCCTGCAGTTCAACCTGC 	1858
Sbjct	1799	TGTGGAGCAGCTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATTCTGCAGTTTAACCTGC 	1858
Query	1859	TGGGGGTGCCCTGCTGGGGGCTGATGTGTGTGGCTTCCTGGGCAACACCTCTGAAGAGC 	1918
Sbjct	1859	TGGGGGTGCCCTGCTGGGGGCTGATGTGTGTGGCTTCCTGGGCAACACCTCTGAGGAGC 	1918
Query	1919	TGTGTGTGAGGTGGACCCAGCTGGGGGCCTTCTACCCTTTCATGAGGAACCACAACAGCC 	1978
Sbjct	1919	TGTGTGTGAGGTGGACCCAGCTGGGGGCCTTTTATCCCTTCATGAGGAACCACAACAGCC 	1978
Query	1979	TGCTGAGCCTGCCTCAGGAGCCTTACTCTTTCTCTGAGCCTGCCAGCAGGCCATGAGGA 	2038
Sbjct	1979	TGCTGAGCCTGCCTCAGGAGCCTTACTCTTTCTCTGAGCCTGCCAGCAGGCCATGAGGA 	2038
Query	2039	AGGCCCTGACCCTGAGGTATGCTCTGCTGCCCCACCTGTACACCCTGTTCCACCAGGCCC 	2098
Sbjct	2039	AGGCCCTGACCCTGAGGTATGCCCTGCTGCCCCACCTGTATACCCTGTTCCACCAGGCCC 	2098
Query	2099	ATGTGGCTGGGGAGACTGTGGCCAGGCCCTGTTCTGGAGTTTCCTAAGGATAGCAGCA 	2158
Sbjct	2099	ATGTGGCTGGGGAGACTGTGGCCAGGCCCTGTTCTGGAGTTCCCCAAGGACAGCAGCA 	2158
Query	2159	CCTGGACTGTGGACCACCAGCTGCTGTGGGGGGAGGCCCTGCTGATTACCCCTGTGCTGC 	2218
Sbjct	2159	CCTGGACTGTGGATCATCAGCTGCTGTGGGGGGAGGCCCTGCTGATCACCCCTGTGCTGC 	2218
Query	2219	AGGCTGGCAAGGCTGAGGTGACTGGCTACTTCCCCCTGGGCACCTGGTATGACCTGCAGA 	2278
Sbjct	2219	AGGCTGGCAAGGCTGAGGTCACTGGCTACTTCCCTCTGGGCACCTGGTATGACCTGCAGA 	2278
Query	2279	CTGTGCCTGTGGAAGCCCTGGGCAGCCTGCCTccccccctGCTGCCCCCAGGGAGCCTG 	2338
Sbjct	2279	CTGTGCCTGTGGAGGCTCTGGGCAGCCTGCCCCCCCCCTGCTGCTCCCAGGGAGCCTG 	2338
Query	2339	CCATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTGGACACCATTAATGTGC 	2398
Sbjct	2339	CCATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCTCCCCCTGGACACCATCAATGTGC 	2398
Query	2399	ATCTGAGGGCTGGGTATATTATCCCCCTGCAGGGGCCCTGGGCTGACTACCACTGAGAGCA 	2458
Sbjct	2399	ACCTGAGGGCTGGCTACATTATCCCCCTGCAGGGGCCAGGGCTGACTACCACTGAGAGCA 	2458
Query	2459	GGCAGCAGCCTATGGCCCTGGCTGTGGCTCTGACTAAggggggggaggccaggggggagc 	2518

Sbjct	2459	GACAGCAGCCCATGGCTCTGGCTGTGGCCCTGACCAAGGGGGGGGAAGCTAGGGGGGAGC	2518
Query	2519	tgttctgggatgatggggagagcctggaggtgctggagaggggggCCTACACCAGGTGA 	2578
Sbjct	2519	TGTTCTGGGATGATGGGGAGAGCCTGGAGGTGCTGGAGAGGGGGGCCTATAACCAGGTGA	2578
Query	2579	TTTTCTTGCCAGGAACAACACCATTTGTGAATGAGCTGGTGAGGGTGACCTCTGAGGGGG 	2638
Sbjct	2579	TCTTCCTGGCTAGGAACAACACCATTTGTCAATGAGCTGGTGAGGGTGACTTCTGAGGGGG	2638
Query	2639	CTGGCCTGCAGCTGCAGAAAGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGTGC 	2698
Sbjct	2639	CTGGGCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCTCCCCAGCAGGTGC	2698
Query	2699	TGAGCAATGGGGTGCCTGTGAGCAACTTCACCTACAGCCCTGACACCAAGGTGCTGGATA 	2758
Sbjct	2699	TGAGCAATGGGGTGCCTGTGAGCAACTTCACCTACAGCCCTGACACCAAGGTGCTGGACA	2758
Query	2759	TTTGTGTGAGCCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808
Sbjct	2759	TCTGTGTGTCTCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808

Score = 4150 bits (2247), Expect = 0.0
Identities = 2624/2811 (93%), Gaps = 6/2811 (0%)
Strand=Plus/Plus

Query	301	CAGGGGGCCCCAGATGGGCCAGCCCTGGTGCTTCTTcccccccAGCTATCCTAGCTATAAA	360
Sbjct	301	CAGGGGGCTCAGATGGGCCAGCCCTGGTGCTTCTTCCCCCTCTTATCCTAGCTATAAG	360
Query	361	CTGGAGAACCTGAGCAGCTCTGAGATGGGCTATACTGCCACCCTGACTAGGACTACTCCC	420
Sbjct	361	CTGGAGAACCTGAGCAGCTCTGAGATGGGGTACACTGCCACCCTGACCAGGACCACCCCC	420
Query	421	ACCTTTTTTTCCTAAGGATATCCTGACCCTGAGGCTGGATGTGATGATGGAGACTGAGAAC	480
Sbjct	421	ACTTTCCTCCCTAAGGACATCCTGACCCTGAGGCTGGATGTGATGATGGAGACTGAGAAT	480
Query	481	AGGCTGCACTTCACTATTAAGGACCCTGCCAATAGGAGGTATGAAGTGCCTCTGGAGACT	540
Sbjct	481	AGGCTGCACTTTACTATCAAGGACCCTGCCAACAGGAGGTATGAGGTGCCTCTGGAGACC	540
Query	541	CCTCATGTGCACTCTAGGGCCCCAGCCCCCTGTATTCTGTGGAGTTCTCTGAGGAGCCC	600
Sbjct	541	CCCCATGTGCATTCTAGGGCCCCAGCCCCCTGTACTCTGTGGAGTTCTCTGAGGAGCCC	600
Query	601	TTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTGCTGCTGAACACCACTGTGGCC	660
Sbjct	601	TTTGGGGTGATTGTGAGGAGACAGCTGGATGGCAGGGTCCTGCTGAACACCACTGTGGCT	660
Query	661	CCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGAGCACCAGCCTGCCCAGCCAGTACATC	720
Sbjct	661	CCCCTGTTTTTTGCTGACCAGTTCCTGCAGCTGAGCACCAGCCTGCCCAGCCAGTACATC	720
Query	721	ACTGGGCTGGCTGAGCATCTGAGCCCTCTGATGCTGAGCACCTCTTGGACCAGGATCACC	780
Sbjct	721	ACTGGGCTGGCTGAGCACCTGAGCCCCCTGATGCTGAGCACCAGCTGGACCAGGATCACC	780
Query	781	CTGTGGAATAGGGATCTGGCCCCACCCCTGGGGCTAATCTGTATGGCTCTCATCCCTTT	840
Sbjct	781	CTGTGGAACAGGGATCTGGCTCCTACCCCTGGGGCCAACCTGTATGGCTCTCACCCCTTT	840
Query	841	TACCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTTCTGCTGAACAGCAATGCC	900
Sbjct	841	TACCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTCTGCTGAACAGCAATGCT	900
Query	901	ATGGATGTGGTGCTGCAGCCCTCTCCTGCCCTGAGCTGGAGGAGCACTGGGGGCATCCTG	960
Sbjct	901	ATGGATGTGGTGCTGCAGCCCAGCCCTGCCCTGAGCTGGAGGTCTACTGGGGGCATCCTG	960
Query	961	GATGTGTACATCTTCCTGGGCCCTGAGCCCAAGTCTGTGGTCCAGCAGTATCTGGATGTG	1020
Sbjct	961	GATGTGTACATCTTTCTGGGGCCTGAGCCCAAGTCTGTGGTGCAGCAGTACCTGGATGTG	1020
Query	1021	GTGGGCTACCCCTTTATGCCCCCTATTGGGGCCTGGGCTTCCACCTGTGCAGGTGGGGG	1080

Sbjct	1021	GTGGGCTATCCTTTTATGCCCCCTATTGGGGCCTGGGCTTCCACCTGTGCAGGTGGGGC	1080
Query	1081	TA-TTCTTCTACTGCTATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCTCACTTCCC	1139
Sbjct	1081	TACAGCAGC-ACTGCCATCACCAGACAGGTGGTGGAGAACATGACCAGGGCCCACTTCCC	1139
Query	1140	CCTGGATGTGCAGTGGAATGACCTGGACTATATGGACTCTAGGAGGGATTTACCTTCAA	1199
Sbjct	1140	CCTGGATGTGCAGTGGAATGACCTGGACTACATGGACAGCAGGAGGGACTTCACCTTTAA	1199
Query	1200	CAAGGATGGCTTCAGGGACTTCCCTGCTATGGTCCAGGAGCTGCATCAGGGGGGCAGGAG	1259
Sbjct	1200	CAAGGATGGCTTTAGGGACTTCCCTGCCATGGTGCAGGAGCTGCATCAGGGGGGCAGGAG	1259
Query	1260	GTACATGATGATTGTGGACCCTGCCATCAGCAGCTCTGGCCCTGCTGGCAGC-TATAGGC	1318
Sbjct	1260	GTACATGATGATTGTGGACCCAGCCATCAGCAGCTCTGGGCCTGCTGG-GTCTTACAGGC	1318
Query	1319	CCTATGATGAGGGCCTGAGGAGGGGGGTGTTTATCACTAATGAAACTGGGCAGCCCCTGA	1378
Sbjct	1319	CCTATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGCCAGCCCCTGA	1378
Query	1379	TTGGCAAGGTGTGGCCTGGCTCTACTGCCTTCCCTGACTTCACCAACCCCACTGCTCTGG	1438
Sbjct	1379	TTGGCAAGGTGTGGCCTGGGAGCACTGCCTTCCCTGATTTTACCAACCCCACTGCCCTGG	1438
Query	1439	CCTGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCTTTTGATGGCATGTGGA	1498
Sbjct	1439	CCTGGTGGGAGGATATGGTGGCTGAGTTTCATGACCAGGTGCCTTTTGATGGCATGTGGA	1498
Query	1499	TTGACATGAATGAGCCCAGCAACTTCATCAGGGGCTCTGAGGATGGGTGCCCCAATAATG	1558
Sbjct	1499	TTGACATGAATGAGCCCAGCAATTCATCAGGGGCTCTGAGGATGGCTGCCCCAACAATG	1558
Query	1559	AGCTGGAGAAccccccTATGTGCCTGGGGTGGTGGGGGGCACCTGCAGGCTGCCACTA	1618
Sbjct	1559	AGCTGGAGAATCCTCCCTATGTGCCTGGGGTGGTGGGGGGCACCTGCAGGCTGCCACCA	1618
Query	1619	TTTGTGCCAGCT-CTCACCAGTTCCTGAGCACCCACTACAACCTGCACAATCTGTATGGC	1677
Sbjct	1619	TCTGTGCC-TCTAGCCACCAGTTCCTGAGCACCCACTATAACCTGCATAACCTGTATGGC	1677
Query	1678	CTGACTGAGGCCATTGCCAGCCACAGGGCCCTGGTGAAGGCCAGGGGCACTAGGCCCTTT	1737
Sbjct	1678	CTGACTGAGGCCATTGCCAGCCATAGAGCCCTGGTGAAGGCCAGAGGGACCAGGCCCTTT	1737
Query	1738	GTGATCTCTAGAAGCACCTTTGCTGGCCATGGGAGGTATGCTGGCCACTGGACTGGGGAT	1797
Sbjct	1738	GTGATCTCTAGGAGCACCTTTGCTGGCCATGGCAGGTATGCTGGCCACTGGACTGGGGAT	1797

Query	1798	GTGTGGAGCTCTTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATCCTGCAGTTCAACCTG	1857
Sbjct	1798	GTGTGGAGCTCTTGGGAGCAGCTGGCCAGCTCTGTGCCAGAGATCCTGCAGTTCAACCTG	1857
Query	1858	CTGGGGGTGCCCCCTGGTGGGGGCTGATGTGTGTGGCTTCCTGGGCAACACCTCTGAAGAG	1917
Sbjct	1858	CTGGGGGTGCCTCTGGTGGGGGCTGATGTGTGTGGCTTCCTGGGCAATACCTCTGAAGAG	1917
Query	1918	CTGTGTGTGAGGTGGACCCAGCTGGGGGCCTTCTACCCCTTTCATGAGGAACCACAACAGC	1977
Sbjct	1918	CTGTGTGTGAGGTGGACTCAGCTGGGGGCCTTCTATCCCTTCATGAGGAACCACAACAGC	1977
Query	1978	CTGCTGAGCCTGCCTCAGGAGCCTTACTCTTTCTCTGAGCCTGCCCAGCAGGCCATGAGG	2037
Sbjct	1978	CTGCTGTCTCTGCCCCAGGAGCCCTACAGCTTCTCTGAGCCTGCTCAGCAGGCTATGAGG	2037
Query	2038	AAGGCCCTGACCCTGAGGTATGCTCTGCTGCCCCACCTGTACACCCTGTTCCACCAGGCC	2097
Sbjct	2038	AAGGCCCTGACCCTGAGGTATGCCCTGCTGCCCCATCTGTACACCCTGTTCCACCAGGCC	2097
Query	2098	CATGTGGCTGGGGAGACTGTGGCCAGGCCCTGTTTCCTGGAGTTTCCTAAGGATAGCAGC	2157
Sbjct	2098	CATGTGGCTGGGGAGACTGTGGCCAGGCCCTGTTTCTGGAGTTTCCCAAGGACAGCAGC	2157
Query	2158	ACCTGGACTGTGGACCACCAGCTGCTGTGGGGGGAGGCCCTGCTGATTACCCCTGTGCTG	2217
Sbjct	2158	ACCTGGACTGTGGACCATCAGCTGCTGTGGGGGGAGGCTCTGCTGATTACCCCTGTGCTG	2217
Query	2218	CAGGCTGGCAAGGCTGAGGTGACTGGCTACTTCCCCCTGGGCACTTGGTATGACCTGCAG	2277
Sbjct	2218	CAGGCTGGCAAGGCTGAGGTGACTGGGTACTTCCCCCTGGGGACTTGGTATGACCTGCAG	2277
Query	2278	ACTGTGCCTGTGGAAGCCCTGGGCAGCCTGCCTccccccTGCTGCCCCCAGGGAGCCT	2337
Sbjct	2278	ACTGTGCCTGTGGAAGCTCTGGGCAGCCTGCCCCACCCCTGCTGCCCCTAGGGAGCCT	2337
Query	2338	GCCATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTGGACACCATTAATGTG	2397
Sbjct	2338	GCCATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTCTGGACACCATCAATGTG	2397
Query	2398	CATCTGAGGGCTGGGTATATTATCCCCCTGCAGGGGCCTGGGCTGACTACCACTGAGAGC	2457
Sbjct	2398	CACCTGAGGGCTGGCTATATCATCCCCCTGCAGGGCCCTGGGCTGACCACCACTGAGAGC	2457
Query	2458	AGGCAGCAGCCTATGGCCCTGGCTGTGGCTCTGACTAAGgggggggaggccaggggggag	2517
Sbjct	2458	AGGCAGCAGCCCATGGCCCTGGCTGTGGCCCTGACTAAGGGGGGGGAGGCCAGGGGGGAG	2517
Query	2518	ctgttctgggatgatggggagagcctggaggtgctggagaggggggCCTACACCCAGGTG	2577

Sbjct	2518	CTGTTCTGGGATGATGGGGAGAGCCTGGAGGTGCTGGAGAGAGGGGCCTACACCCAGGTG	2577
Query	2578	ATTTTCCTGGCCAGGAACAACACCATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGGGG	2637
Sbjct	2578	ATCTTTCTGGCCAGGAACAACACCATTGTGAATGAGCTGGTGAGGGTGACTTCTGAGGGG	2637
Query	2638	GCTGGCCTGCAGCTGCAGAAAGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGTG	2697
Sbjct	2638	GCTGGCCTGCAGCTGCAGAAAGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGTG	2697
Query	2698	CTGAGCAATGGGGTGCCTGTGAGCAACTTCACCTACAGCCCTGACACCAAGGTGCTGGAT	2757
Sbjct	2698	CTGAGCAATGGGGTGCCTGTGTCTAACTTCACCTACAGCCCTGATACTAAGGTGCTGGAT	2757
Query	2758	ATTTGTGTGAGCCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808
Sbjct	2758	ATCTGTGTGAGCCTGCTGATGGGGGAGCAGTTTCTGGTGAGCTGGTGCTGA	2808

>Query_91028 SEQ ID NO: 2
Length=2808

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

Query	1	ATGGCTTTCCTGTGGCTGCTGAGCTGCTGGGCTCTGCTGGGCACCACTTTGGGCTGCTG	60
Sbjct	1	ATGGCTTTCCTGTGGCTGCTGTCTTGCTGGGCCCTGCTGGGGACTACCTTTGGCCTGCTG	60
Query	61	GTGCCTAGGGAGCTGTCTGGGTCTAGCCCTGTGCTGGAGGAGACTACCCCTGCCATCAG	120
Sbjct	61	GTGCCCAGGGAAGTGTCTGGCTCTAGCCCAGTGCTGGAGGAGACCCACCCCTGCCACCAAG	120
Query	121	CAGGGGGCTAGCAGGCCTGGCCCCAGGGATGCTCAGGCCCCACCCTGGCAGGCCCAGGGCT	180
Sbjct	121	CAGGGGGCTTCTAGGCCTGGCCCCAGGGATGCCAGGCCCCACCCTGGCAGGCCAAGGGCT	180
Query	181	GTGCCCCACCAAGTGTGATGTGCCCCCAACAGCAGGTTTGACTGTGCCCTGACAAGGCC	240
Sbjct	181	GTGCCCCACCAAGTGTGATGTGCCCCCAACTCTAGATTTGATTGTGCCCTGATAAGGCC	240
Query	241	ATTACCCAGGAGCAGTGTGAGGCCAGGGGCTGCTGCTACATTCCAGCTAAGCAGGGCCTG	300
Sbjct	241	ATCACCCAGGAGCAGTGTGAGGCTAGGGGCTGCTGCTACATCCCTGCTAAGCAGGGCCTG	300
Query	301	CAGGGGGCCCCAGATGGGCCAGCCCTGGTGCTTCTTcccccccAGCTATCCTAGCTATAAA	360
Sbjct	301	CAGGGGGCTCAGATGGGCCAGCCCTGGTGCTTCTTCCCCCCCAGCTATCCCTCTTACAAG	360

Query	361	CTGGAGAACCTGAGCAGCTCTGAGATGGGCTATACTGCCACCCTGACTAGGACTACTCCC	420
Sbjct	361	CTGGAGAATCTGAGCAGCTCTGAGATGGGCTACACTGCCACCCTGACCAGGACTACTCCC	420
Query	421	ACCTTTTTTTCCTAAGGATATCCTGACCCTGAGGCTGGATGTGATGATGGAGACTGAGAAC	480
Sbjct	421	ACCTTCTTCCCCAAGGACATCCTGACCCTGAGGCTGGATGTGATGATGGAGACTGAGAAC	480
Query	481	AGGCTGCACTTCACTATTAAGGACCCTGCCAATAGGAGGTATGAAGTGCCTCTGGAGACT	540
Sbjct	481	AGGCTGCATTTCACCATCAAGGATCCTGCCAACAGGAGGTATGAGGTGCCTCTGGAGACC	540
Query	541	CCTCATGTGCACTCTAGGGCCCCCAGCCCCCTGTATTCTGTGGAGTTCTCTGAGGAGCCC	600
Sbjct	541	CCCCATGTGCACAGCAGGGCTCCTTCTCCCCTGTACTCTGTGGAGTTCTCTGAGGAACCC	600
Query	601	TTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTGCTGCTGAACACCACTGTGGCC	660
Sbjct	601	TTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTCCTGCTGAACACCACTGTGGCC	660
Query	661	CCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGAGCACCAGCCTGCCCAGCCAGTACATC	720
Sbjct	661	CCCCTGTTCTTTGCTGATCAGTTCCTGCAGCTGTCCACTTCTCTGCCTAGCCAGTACATC	720
Query	721	ACTGGGCTGGCTGAGCATCTGAGCCCTCTGATGCTGAGCACCTCTTGACCAGGATCACC	780
Sbjct	721	ACTGGGCTGGCTGAGCACCTGAGCCCTCTGATGCTGAGCACCTCTTGAGTAGGATCACC	780
Query	781	CTGTGGAATAGGGATCTGGCCCCCACCCTGGGGCTAATCTGTATGGCTCTCATCCCTTT	840
Sbjct	781	CTGTGGAACAGGGACCTGGCCCCCACCCTGGGGCCAACCTGTATGGCAGCCACCCTTC	840
Query	841	TACCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTTCTGCTGAACAGCAATGCC	900
Sbjct	841	TATCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTCTGCTGAATAGCAATGCT	900
Query	901	ATGGATGTGGTGCTGCAGCCCTCTCCTGCCCTGAGCTGGAGGAGCACTGGGGGCATCCTG	960
Sbjct	901	ATGGATGTGGTGCTGCAGCCCAGCCCTGCCCTGTCTTGAGGAGCACTGGGGGCATCCTG	960
Query	961	GATGTGTACATCTTCCTGGGGCCTGAGCCCCAAGTCTGTGGTCCAGCAGTATCTGGATGTG	1020
Sbjct	961	GATGTGTACATTTTCCTGGGGCCTGAGCCCCAAGTCTGTGGTGCAGCAGTACCTGGATGTG	1020
Query	1021	GTGGGCTACCCCTTTATGCCCCCTATTGGGGCCTGGGCTTCCACCTGTGCAGGTGGGGG	1080
Sbjct	1021	GTGGGCTACCCCTTCATGCCTCCCTACTGGGGCCTGGGCTTCCACCTGTGCAGGTGGGGC	1080
Query	1081	TATTCTTCTACTGCTATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCTCACTTCCCC	1140

Sbjct	1081	TACAGCTCTACTGCCATCACCAGGCAGGTGGTGGAGAATATGACCAGGGGCCCACTTCCCC	1140
Query	1141	CTGGATGTGCAGTGGAATGACCTGGACTATATGGACTCTAGGAGGGATTTACCTTCAAC	1200
Sbjct	1141	CTGGATGTGCAGTGGAATGACCTGGACTACATGGACTCTAGGAGGGACTTCACCTTCAAT	1200
Query	1201	AAGGATGGCTTCAGGGACTTCCCTGCTATGGTCCAGGAGCTGCATCAGGGGGGCAGGAGG	1260
Sbjct	1201	AAGGATGGCTTCAGAGACTTCCCTGCCATGGTGCAGGAGCTGCATCAGGGGGGCAGGAGG	1260
Query	1261	TACATGATGATTGTGGACCCTGCCATCAGCAGCTCTGGCCCTGCTGGCAGCTATAGGCCC	1320
Sbjct	1261	TACATGATGATTGTGGACCCTGCCATCAGCTCTTCTGGCCCTGCTGGCTCTTACAGGCCC	1320
Query	1321	TATGATGAGGGCCTGAGGAGGGGGGTGTTTATCACTAATGAAACTGGGCAGCCCCTGATT	1380
Sbjct	1321	TATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGGCAGCCCCTGATT	1380
Query	1381	GGCAAGGTGTGGCCTGGCTCTACTGCCTTCCCTGACTTCACCAACCCCCACTGCTCTGGCC	1440
Sbjct	1381	GGGAAGGTGTGGCCTGGCTCTACTGCCTTCCCTGACTTCACCAATCCTACTGCCCTGGCC	1440
Query	1441	TGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCTTTTGATGGCATGTGGATT	1500
Sbjct	1441	TGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCTTTTGATGGCATGTGGATT	1500
Query	1501	GACATGAATGAGCCCAGCAACTTCATCAGGGGCTCTGAGGATGGGTGCCCCAATAATGAG	1560
Sbjct	1501	GACATGAATGAGCCCTCTAATTTTCATCAGGGGCTCTGAGGATGGCTGCCCCAACAATGAG	1560
Query	1561	CTGGAGAAcccccccTATGTGCCTGGGGTGGTGGGGGGCACCTGCAGGCTGCCACTATT	1620
Sbjct	1561	CTGGAGAACCCCCCTATGTGCCTGGGGTGGTGGGGGGCACCTGCAGGCTGCCACCATC	1620
Query	1621	TGTGCCAGCTCTCACCAGTTCCTGAGCACCCACTACAACCTGCACAATCTGTATGGCCTG	1680
Sbjct	1621	TGTGCTAGCTCTCACCAGTTCCTGAGCACCCACTACAATCTGCATAACCTGTATGGCCTG	1680
Query	1681	ACTGAGGCCATTGCCAGCCACAGGGCCCTGGTGAAGGCCAGGGGCACTAGGCCCTTTGTG	1740
Sbjct	1681	ACTGAGGCCATTGCCAGCCACAGGGCCCTGGTGAAGGCTAGGGGCACCAGGCCCTTTGTG	1740
Query	1741	ATCTCTAGAAGCACCTTTGCTGGCCATGGGAGGTATGCTGGCCACTGGACTGGGGATGTG	1800
Sbjct	1741	ATTTCTAGGAGCACTTTTGCTGGCCATGGCAGGTATGCTGGGCACTGGACTGGGGATGTG	1800
Query	1801	TGGAGCT-CTTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATCCTGCAGTTCAACCTGCT	1859
Sbjct	1801	TGG-TCTAGCTGGGAGCAGCTGGCTTCTTCTGTGCCTGAGATCCTGCAGTTCAACCTGCT	1859

Query	1860	GGGGGTGCCCCTGGTGGGGGCTGATGTGTGTGGCTTCCTGGGCAACACCTCTGAAGAGCT	1919
Sbjct	1860	GGGGGTGCCTCTGGTGGGGGCTGATGTGTGTGGGTTCTGGGCAACACTTCTGAGGAGCT	1919
Query	1920	GTGTGTGAGGTGGACCCAGCTGGGGGCCCTTCTACCCTTTCATGAGGAACCACAACAGCCT	1979
Sbjct	1920	GTGTGTGAGGTGGACCCAGCTGGGGGCCCTTCTACCCTTTCATGAGGAACCACAACAGCCT	1979
Query	1980	GCTGAGCCTGCCTCAGGAGCCTTACTCTTTCTCTGAGCCTGCCCAGCAGGCCATGAGGAA	2039
Sbjct	1980	GCTGAGCCTGCCCCAGGAGCCCTACAGCTTCTCTGAGCCTGCCCAGCAGGCCATGAGGAA	2039
Query	2040	GGCCCTGACCCTGAGGTATGCTCTGCTGCCCCACCTGTACACCCTGTTCCACCAGGCCCA	2099
Sbjct	2040	GGCCCTGACCCTGAGGTATGCCCTGCTGCCCCACCTGTACACCCTGTTCCACCAGGCCCA	2099
Query	2100	TGTGGCTGGGGAGACTGTGGCCAGGCCCTGTTCTGGAGTTTCCTAAGGATAGCAGCAC	2159
Sbjct	2100	TGTGGCTGGGGAGACTGTGGCTAGGCCTCTGTTCTGGAGTTCCCCAAGGACTCTAGCAC	2159
Query	2160	CTGGACTGTGGACCACCAGCTGCTGTGGGGGGAGGCCCTGCTGATTACCCCTGTGCTGCA	2219
Sbjct	2160	CTGGACTGTGGACCACCAGCTGCTGTGGGGGGAGGCCCTGCTGATCACTCCTGTGCTGCA	2219
Query	2220	GGCTGGCAAGGCTGAGGTGACTGGCTACTTCCCCCTGGGCACTTGGTATGACCTGCAGAC	2279
Sbjct	2220	GGCTGGGAAGGCTGAGGTGACTGGCTATTTCCCCCTGGGCACCTGGTATGACCTGCAGAC	2279
Query	2280	TGTGCCTGTGGAAGCCCTGGGCAGCCTGCCTccccccctTGCTGCCCCCAGGGAGCCTGC	2339
Sbjct	2280	TGTGCCTGTGGAGGCCCTGGGGAGCCTGCCCCCCCCCTGCTGCCCCCAGGGAGCCTGC	2339
Query	2340	CATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTGGACACCATTAATGTGCA	2399
Sbjct	2340	CATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTCTGGATAACCATCAATGTGCA	2399
Query	2400	TCTGAGGGCTGGGTATATTATCCCCCTGCAGGGGCCTGGGCTGACTACCACTGAGAGCAG	2459
Sbjct	2400	CCTGAGGGCTGGCTACATCATTTCCCCTGCAGGGCCCTGGCCTGACCACTACTGAGTCTAG	2459
Query	2460	GCAGCAGCCTATGGCCCTGGCTGTGGCTCTGACTAAggggggggaggccaggggggagct	2519
Sbjct	2460	GCAGCAGCCCATGGCCCTGGCTGTGGCCCTGACCAAGGGGGGGGAGGCTAGGGGGGAGCT	2519
Query	2520	gttctgggatgatggggagagcctggaggtgctggagaggggggCCTACACCCAGGTGAT	2579
Sbjct	2520	GTTTTGGGATGATGGGGAGAGCCTGGAGGTGCTGGAGAGGGGGGCCTACACTCAGGTGAT	2579
Query	2580	TTTCCTGGCCAGGAACAACACCATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGGGGGC	2639

Sbjct	2580	CTTCCTGGCCAGGAACAATACCATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGGGGGC	2639
Query	2640	TGGCCTGCAGCTGCAGAAAGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGTGCT	2699
Sbjct	2640	TGGCCTGCAGCTGCAGAAAGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGTGCT	2699
Query	2700	GAGCAATGGGGTGCCTGTGAGCAACTTCACCTACAGCCCTGACACCAAGGTGCTGGATAT	2759
Sbjct	2700	GAGCAATGGGGTGCCTGTGAGCAACTTCACCTATAGCCCTGATACCAAGGTGCTGGATAT	2759
Query	2760	TTGTGTGAGCCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808
Sbjct	2760	TTGTGTGAGCCTGCTGATGGGGGAGCAGTTCCTGGTGAGCTGGTGCTGA	2808

>Query_91031 SEQ ID NO: 5
Length=2808

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

Query	1	ATGGCTTTCTGTGGCTGCTGAGCTGCTGGGCTCTGCTGGGCACCACTTTGGGCTGCTG	60
Sbjct	1	ATGGCCTTTCTGTGGCTGCTGTCCTGCTGGGCCCTGCTGGGGACCACTTTGGCCTGCTG	60
Query	61	GTGCCTAGGGAGCTGTCTGGGTCTAGCCCTGTGCTGGAGGAGACTCACCTGCCCATCAG	120
Sbjct	61	GTGCCCAGGGAGCTGTCTGGGAGCAGCCAGTGCTGGAGGAGACCACTGCCACCAAG	120
Query	121	CAGGGGGCTAGCAGGCCTGGCCCCAGGGATGCTCAGGCCCCACCTGGCAGGCCCCAGGGCT	180
Sbjct	121	CAGGGGGCCAGCAGGCCTGGCCCTAGGGATGCCCAGGCCCCACCTGGCAGGCCCCAGGGCT	180
Query	181	GTGCCCACCCAGTGTGATGTGCCCCCAACAGCAGGTTTGACTGTGCCCCCTGACAAGGCC	240
Sbjct	181	GTGCCTACCCAGTGTGATGTGCCACCCAATTCTAGGTTTGACTGTGCTCCTGACAAGGCC	240
Query	241	ATTACCCAGGAGCAGTGTGAGGCCAGGGGCTGCTGCTACATTCCAGCTAAGCAGGGCCTG	300
Sbjct	241	ATCACTCAGGAGCAGTGTGAAGCTAGGGGGTGCTGCTACATCCCAGCCAAGCAGGGCCTG	300
Query	301	CAGGGGGCCCCAGATGGGCCAGCCCTGGTGCTTCTTcccccccAGCTATCCTAGCTATAAA	360
Sbjct	301	CAGGGGGCCCCAGATGGGCCAGCCCTGGTGCTTCTTCCCCCCCAGCTACCCTAGCTACAAG	360
Query	361	CTGGAGAACCTGAGCAGCTCTGAGATGGGCTATACTGCCACCCTGACTAGGACTACTCCC	420
Sbjct	361	CTGGAGAATCTGAGCAGCTCTGAGATGGGCTACACTGCTACCCTGACCAGGACCACTCCT	420

[illegible]

Sbjct	1140	TCTGGATGTGCAGTGGAATGACCTGGACTATATGGATTCTAGGAGAGACTTTACTTTTAA	1199
Query	1200	CAAGGATGGCTTCAGGGACTTCCCTGCTATGGTCCAGGAGCTGCATCAGGGGGGCAGGAG	1259
Sbjct	1200	CAAGGATGGCTTCAGGGATTTCCCTGCCATGGTGCAGGAGCTGCACCAGGGGGGCAGGAG	1259
Query	1260	GTACATGATGATTGTGGACCCTGCCATCAGCAGCTCTGGCCCTGCTGGCAGC-TATAGGC	1318
Sbjct	1260	GTACATGATGATTGTGGACCCTGCTATTAGCAGCTCTGGCCCTGCTGG-GTCTTACAGGC	1318
Query	1319	CCTATGATGAGGGCCTGAGGAGGGGGGTGTTTATCACTAATGAAACTGGGCAGCCCCTGA	1378
Sbjct	1319	CTTATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGCCAGCCCCTGA	1378
Query	1379	TTGGCAAGGTGTGGCCTGGCTCTACTGCCTTCCCTGACTTCACCAACCCCACTGCTCTGG	1438
Sbjct	1379	TTGGCAAGGTGTGGCCTGGCAGCACTGCCTTCCCTGACTTCACCAACCCCACTGCCCTGG	1438
Query	1439	CCTGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCTTTTGATGGCATGTGGA	1498
Sbjct	1439	CCTGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCCTTTGATGGGATGTGGA	1498
Query	1499	TTGACATGAATGAGCCCAGCAACTTCATCAGGGGCTCTGAGGATGGGTGCCCAATAATG	1558
Sbjct	1499	TTGACATGAATGAGCCCTCTAACTTCATCAGGGGGTCTGAGGATGGCTGCCCAACAATG	1558
Query	1559	AGCTGGAGAAcccccccTATGTGCCTGGGGTGGTGGGGGGCACCCCTGCAGGCTGCCACTA	1618
Sbjct	1559	AGCTGGAGAACCCCCCTATGTGCCTGGGGTGGTGGGGGGCACTCTGCAGGCTGCCACTA	1618
Query	1619	TTTGTGCCAGCTCTCACCAGTTCCTGAGCACCCACTACAACCTGCACAATCTGTATGGCC	1678
Sbjct	1619	TCTGTGCTTCTTCTCACCAGTTTCTGAGCACCCACTATAATCTGCACAACCTGTATGGCC	1678
Query	1679	TGACTGAGGCCATTGCCAGCCACAGGGCCCTGGTGAAGGCCAGGGGCACTAGGCCCTTTG	1738
Sbjct	1679	TGACTGAGGCCATTGCCAGCCATAGGGCCCTGGTGAAGGCCAGGGGCACTAGGCCCTTTG	1738
Query	1739	TGATCTCTAG-AAG-C-ACCTTTGCTGGCCATGGGAGGTATGCTGGCCACTGGACTGGGG	1795
Sbjct	1739	TGATC---AGCAGGTCTACCTTTGCTGGCCATGGCAGGTATGCTGGCCACTGGACTGGGG	1795
Query	1796	ATGTGTGGAGCTCTTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATCCTGCAGTTCAACC	1855
Sbjct	1796	ATGTGTGGTCTTCTTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATCCTGCAGTTCAACC	1855
Query	1856	TGCTGGGGGTGCCCTGGTGGGGGCTGATGTGTGTGGCTTCTGGGCAACACCTCTGAAG	1915
Sbjct	1856	TGCTGGGGGTGCCTCTGGTGGGGGCTGATGTGTGTGGCTTCTGGGCAACACCTCTGAGG	1915

Query	1916	AGCTGTGTGTGAGGTGGACCCAGCTGGGGGCCTTCTACCCTTTTCATGAGGAACCAACA 	1975
Sbjct	1916	AGCTGTGTGTGAGGTGGACCCAGCTGGGGGCCTTTTACCCCTTCATGAGGAACCAATA	1975
Query	1976	GCCTGCTGAGCCTGCCTCAGGAGCCTTACTCTTTCTCTGAGCCTGCCCAGCAGGCCATGA 	2035
Sbjct	1976	GCCTGCTGAGCCTGCCCCAGGAGCCTTACTCTTTCTCTGAGCCTGCCCAGCAGGCCATGA	2035
Query	2036	GGAAGGCCCTGACCCTGAGGTATGCTCTGCTGCCCCACCTGTACACCCTGTTCCACCAGG 	2095
Sbjct	2036	GGAAGGCCCTGACTCTGAGGTATGCCCTGCTGCCCCATCTGTATACCCTGTTTCACCAGG	2095
Query	2096	CCCATGTGGCTGGGGAGACTGTGGCCAGGCCCTGTTCTTGAGTTTCCTAAGGATAGCA 	2155
Sbjct	2096	CCCATGTGGCTGGGGAGACTGTGGCTAGGCCTCTGTTTCTTGAGTTCCCTAAGGACTCTA	2155
Query	2156	GCACCTGGACTGTGGACCACCAGCTGCTGTGGGGGGAGGCCCTGCTGATTACCCCTGTGC 	2215
Sbjct	2156	GCACCTGGACTGTGGACCACCAGCTGCTGTGGGGGGAGGCCCTGCTGATCACCCCTGTGC	2215
Query	2216	TGCAGGCTGGCAAGGCTGAGGTGACTGGCTACTTCCCCTGGGCACTTGGTATGACCTGC 	2275
Sbjct	2216	TGCAGGCTGGCAAGGCTGAGGTGACTGGCTACTTCCCCTGGGCACTTGGTATGACCTGC	2275
Query	2276	AGACTGTGCCTGTGGAAGCCCTGGGCAGCCTGCCTcccccccTGCTGCCCCAGGGAGC 	2335
Sbjct	2276	AGACTGTGCCTGTGGAGGCCCTGGGGAGCCTGCCTCCCCCCTGCTGCCCCAGGGAGC	2335
Query	2336	CTGCCATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTGGACACCATTAATG 	2395
Sbjct	2336	CTGCCATTCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTGGACACCATCAATG	2395
Query	2396	TGCATCTGAGGGCTGGGTATATTATCCCCCTGCAGGGGCCCTGGGCTGACTACCACTGAGA 	2455
Sbjct	2396	TGCACCTGAGGGCTGGGTACATCATCCCCCTGCAGGGCCCTGGCCTGACCACCACTGAGA	2455
Query	2456	GCAGGCAGCAGCCTATGGCCCTGGCTGTGGCTCTGACTAAggggggggaggccagggggg 	2515
Sbjct	2456	GCAGGCAGCAGCCCATGGCCCTGGCTGTGGCTCTGACCAAGGGGGGGGAGGCCAGGGGGG	2515
Query	2516	agctgttctgggatgatggggagagcctggaggtgctggagaggggggCCTACACCCAGG 	2575
Sbjct	2516	AGCTGTTCTGGGATGATGGGGAGTCTCTGGAGGTGCTGGAGAGGGGGGCTACACCCAGG	2575
Query	2576	TGATTTTCCTGGCCAGGAACAACACCATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGG 	2635
Sbjct	2576	TGATCTTTCTGGCCAGGAACAATACTATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGG	2635
Query	2636	GGGCTGGCCTGCAGCTGCAGAAAGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGG 	2695

[illegible]