

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: H9C75187114

Query= SEQ ID NO: 3

Length=2808

Sequences producing significant alignments:	Score (Bits)	E Value	Max Ident
Query_120568 SEQ ID NO: 1	4189	0.0	94%
Query_120570 SEQ ID NO: 4	4050	0.0	93%
Query_120569 SEQ ID NO: 2	4034	0.0	93%
Query_120571 SEQ ID NO: 5	3995	0.0	92%

ALIGNMENTS

>Query_120568 SEQ ID NO: 1

Length=2808

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

Query	1	ATGGCTTTCCTGTGGCTGCTGTCTTGTGGGCTCTGCTGGGCACCACTTTGGCCTGCTG	60
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Query	61	GTGCCCAGGGAGCTGTCTGGCAGC-AGCCCTGTGCTGGAGGAGACCCACCCTGCTCATCA	119
Sbjct	61	GTGCCTAGGGAGCTGTCTGG-GTCTAGCCCTGTGCTGGAGGAGACTCACCTGCCCATCA	119
Query	120	GCAGGGGGCTAGCAGGCCTGGCCCCAGGGATGCCCAGGCTCACCTGGGAGACCCAGGGC	179
Sbjct	120	GCAGGGGGCTAGCAGGCCTGGCCCCAGGGATGCTCAGGCCCACCCTGGCAGGCCCAGGGC	179
Query	180	TGTGCCCACTCAGTGTGATGTGCCCCCAACAGCAGGTTTGACTGTGCTCCTGACAAGGC	239
Sbjct	180	TGTGCCCACTCAGTGTGATGTGCCCCCAACAGCAGGTTTGACTGTGCCCCTGACAAGGC	239

Query	240	TATCACCCAGGAGCAGTGTGAGGCCAGGGGGTGCTGCTACATTCTGCTAAGCAGGGCCT	299
Sbjct	240	CATTACCCAGGAGCAGTGTGAGGCCAGGGGGCTGCTGCTACATTCCAGCTAAGCAGGGCCT	299
Query	300	GCAGGGGGCCCAGATGGGCCAGCCCTGGTGCTTCTTccccccTCTTATCCCAGCTATAA	359
Sbjct	300	GCAGGGGGCCCAGATGGGCCAGCCCTGGTGCTTCTTCCCCCCCAGCTATCCTAGCTATAA	359
Query	360	GCTGGAGAACCTGAGCAGCTCTGAGATGGGCTACACTGCCACCCTGACCAGGACCACTCC	419
Sbjct	360	ACTGGAGAACCTGAGCAGCTCTGAGATGGGCTATACTGCCACCCTGACTAGGACTACTCC	419
Query	420	CACCTTCTTTCCCAAGGATATTCTGACTCTGAGGCTGGATGTGATGATGGAGACTGAGAA	479
Sbjct	420	CACCTTTTTTCTAAGGATATCCTGACCCTGAGGCTGGATGTGATGATGGAGACTGAGAA	479
Query	480	CAGGCTGCACTTCACTATCAAGGACCCTGCCAATAGGAGGTATGAGGTGCCCCTGGAGAC	539
Sbjct	480	CAGGCTGCACTTCACTATTAAGGACCCTGCCAATAGGAGGTATGAAGTGCCTCTGGAGAC	539
Query	540	TCCTCATGTGCATAGCAGGGCCCCCTCTCCTCTGTATTCTGTGGAGTTCTCTGAGGAGCC	599
Sbjct	540	TCCTCATGTGCACTCTAGGGCCCCCAGCCCCCTGTATTCTGTGGAGTTCTCTGAGGAGCC	599
Query	600	CTTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTGCTGCTGAACACCACTGTGGC	659
Sbjct	600	CTTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTGCTGCTGAACACCACTGTGGC	659
Query	660	CCCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGAGCACTTCTCTGCCCAGCCAGTACAT	719
Sbjct	660	CCCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGAGCACCAGCCTGCCAGCCAGTACAT	719
Query	720	TACTGGGCTGGCTGAGCATCTGAGCCCCCTGATGCTGAGCACCTCTTGGACCAGGATCAC	779
Sbjct	720	CACTGGGCTGGCTGAGCATCTGAGCCCTCTGATGCTGAGCACCTCTTGGACCAGGATCAC	779
Query	780	CCTGTGGAACAGGGACCTGGCCCCCACTCCTGGGGCTAACCTGTATGGCTCTCACCCCTT	839
Sbjct	780	CCTGTGGAATAGGGATCTGGCCCCCACCCCTGGGGCTAATCTGTATGGCTCTCATCCCTT	839
Query	840	TTACCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTTCTGCTGAACAGCAATGC	899
Sbjct	840	TTACCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTTCTGCTGAACAGCAATGC	899
Query	900	TATGGATGTGGTGCTGCAGCCCTCTCCAGCCCTGTCTTGGAGGAGCACTGGGGGCATTCT	959
Sbjct	900	CATGGATGTGGTGCTGCAGCCCTCTCCTGCCCTGAGCTGGAGGAGCACTGGGGGCATCCT	959
Query	960	GGATGTGTACATTTTCTGGGGCCTGAACCCAAGTCTGTGGTGCAGCAGTACCTGGATGT	1019

Sbjct	960	GGATGTGTACATCTTCCTGGGCCCTGAGCCCAAGTCTGTGGTCCAGCAGTATCTGGATGT	1019
Query	1020	GGTGGGCTACCCCTTCATGCCCCCTATTGGGGGCTGGGGTTTCACCTGTGCAGGTGGGG	1079
Sbjct	1020	GGTGGGCTACCCCTTTATGCCCCCTATTGGGGCCTGGGCTTCCACCTGTGCAGGTGGGG	1079
Query	1080	CTACAGCAGC-CTGCCATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCCCCATTTCC	1138
Sbjct	1080	GTATT-CTTCTACTGCTATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCTCACTTCC	1138
Query	1139	CCCTGGATGTGCAGTGGAATGACCTGGACTACATGGATAGCAGGAGGGATTTACCTTCA	1198
Sbjct	1139	CCCTGGATGTGCAGTGGAATGACCTGGACTATATGGACTCTAGGAGGGATTTACCTTCA	1198
Query	1199	ACAAGGATGGCTTCAGGGACTTTCTGCCATGGTGCAGGAGCTGCACCAGGGGGGCAGGA	1258
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Sbjct	1259	GGTACATGATGATTGTGGACCTGCCATCAGCAGCTCTGGCCCTGCTGGCAGCTATAGGC	1318
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Sbjct	1319	CCTATGATGAGGGCCTGAGGAGGGGGGTGTTTATCACTAATGAAACTGGGCAGCCCCTGA	1378
Query	1379	TTGGCAAGGTCTGGCCTGGCTCTACTGCCTTCCCTGATTTTACTAACCCCACTGCCCTGG	1438
Sbjct	1379	TTGGCAAGGTGTGGCCTGGCTCTACTGCCTTCCCTGACTTCACCAACCCCACTGCTCTGG	1438
Query	1439	CCTGGTGGGAGGACATGGTGGCTGAGTTCCATGATCAGGTGCCTTTTGATGGCATGTGGA	1498
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Query	1499	TTGATATGAATGAACCAAGCAACTTCATCAGAGGCTCTGAGGATGGCTGCCCCAACATG	1558
Sbjct	1499	TTGACATGAATGAGCCCAGCAACTTCATCAGGGGCTCTGAGGATGGGTGCCCCAATAATG	1558
Query	1559	AGCTGGAGAAcccccccTATGTGCCTGGGGTGGTGGGGGGCACTCTGCAGGCTGCCACCA	1618
Sbjct	1559	AGCTGGAGAACCCCCCTATGTGCCTGGGGTGGTGGGGGGCACCTGCAGGCTGCCACTA	1618
Query	1619	TTTGTGCTAGCAGCCACCAGTTCCTGAGCACCCACTACAATCTGCACAACCTGTATGGCC	1678
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Query	1679	TGACTGAAGCCATTGCCAGCCATAGGGCCCTGGTGAAGGCCAGGGGCACTAGGCCTTTTG	1738
Sbjct	1679	TGACTGAGGCCATTGCCAGCCACAGGGCCCTGGTGAAGGCCAGGGGCACTAGGCCCTTTG	1738

Query	1739	TGATCAGCAGGAGCACTTTTGGCTGGCCATGGCAGGTATGCTGGCCACTGGACTGGGGATG 	1798
Sbjct	1739	TGATCTCTAGAAGCACCTTTGCTGGCCATGGGAGGTATGCTGGCCACTGGACTGGGGATG	1798
Query	1799	TGTGGAGCAGCTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATTCTGCAGTTTAACCTGC 	1858
Sbjct	1799	TGTGGAGCTCTTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATCCTGCAGTTCAACCTGC	1858
Query	1859	TGGGGGTGCCCTGGTGGGGGCTGATGTGTGTGGCTTCCTGGGCAACACCTCTGAGGAGC 	1918
Sbjct	1859	TGGGGGTGCCCTGGTGGGGGCTGATGTGTGTGGCTTCCTGGGCAACACCTCTGAAGAGC	1918
Query	1919	TGTGTGTGAGGTGGACCCAGCTGGGGGCCTTTTATCCCTTCATGAGGAACCACAACAGCC 	1978
Sbjct	1919	TGTGTGTGAGGTGGACCCAGCTGGGGGCCTTCTACCCTTCATGAGGAACCACAACAGCC	1978
Query	1979	TGCTGAGCCTGCCTCAGGAGCCCTACTCTTTCTCTGAGCCTGCCCAGCAGGCCATGAGGA 	2038
Sbjct	1979	TGCTGAGCCTGCCTCAGGAGCCTTACTCTTTCTCTGAGCCTGCCCAGCAGGCCATGAGGA	2038
Query	2039	AGGCCCTGACCCTGAGGTATGCCCTGCTGCCCCACCTGTATACCCTGTTCCACCAGGCCC 	2098
Sbjct	2039	AGGCCCTGACCCTGAGGTATGCTCTGCTGCCCCACCTGTACACCCTGTTCCACCAGGCCC	2098
Query	2099	ATGTGGCTGGGGAGACTGTGGCCAGGCCCTGTTCTTGAGTTCCCCAAGGACAGCAGCA 	2158
Sbjct	2099	ATGTGGCTGGGGAGACTGTGGCCAGGCCCTGTTCTTGAGTTTCTTAAGGATAGCAGCA	2158
Query	2159	CCTGGACTGTGGATCATCAGCTGCTGTGGGGGGAGGCCCTGCTGATCACCCCTGTGCTGC 	2218
Sbjct	2159	CCTGGACTGTGGACCACCAGCTGCTGTGGGGGGAGGCCCTGCTGATTACCCCTGTGCTGC	2218
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Sbjct	2219	AGGCTGGCAAGGCTGAGGTGACTGGCTACTTCCCCCTGGGCACCTGGTATGACCTGCAGA	2278
Query	2279	CTGTGCCTGTGGAGGCTCTGGGCAGCCTGcccccccccTGCTGCTCCCAGGGAGCCTG 	2338
Sbjct	2279	CTGTGCCTGTGGAAGCCCTGGGCAGCCTGCCTCCCCCCTGCTGCCCCAGGGAGCCTG	2338
Query	2339	CCATCCA CTCTGAGGGCCAGTGGGTGACCCTGCCTGCTCCCCTGGACACCATCAATGTGC 	2398
Sbjct	2339	CCATCCA CTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTGGACACCATTAATGTGC	2398
Query	2399	ACCTGAGGGCTGGCTACATTATCCCCCTGCAGGGCCCAGGGCTGACTACCACTGAGAGCA 	2458
Sbjct	2399	ATCTGAGGGCTGGGTATATTATCCCCCTGCAGGGGCCTGGGCTGACTACCACTGAGAGCA	2458
Query	2459	GACAGCAGCCCATGGCTCTGGCTGTGGCCCTGACCAAggggggggaagctaggggggagc 	2518

Query	1	ATGGCTTTCTCTGTGGCTGCTGTCTTGTGGGCTCTGCTGGGACCACTTTGGCCTGCTG	60
Sbjct	1	ATGGCCTTCCTGTGGCTGCTGTCTTGCTGGGCTCTGCTGGGGACCACTTTGGCCTGCTG	60
Query	61	GTGCCCAGGGAGCTGTCTGGCAGCAGC-CCTGTGCTGGAGGAGACCCACCCTGCTCATCA	119
Sbjct	61	GTCCCCAGGGAGCTGTCTGGC-TCTTCTCCTGTCCTGGAGGAGACCCACCCTGCCCACCA	119
Query	120	GCAGGGGGCTAGCAGGCCTGGCCCCAGGGATGCCCAGGCTCACCTGGGAGACCCAGGGC	179
Sbjct	120	GCAGGGGGCTAGCAGGCCTGGCCCCAGGGATGCCCAGGCCACCTGGCAGGCCAGGGC	179
Query	180	TGTGCCCAGTCACTAGTGTGATGTGCCCCCAACAGCAGGTTTGACTGTGCTCCTGACAAGGC	239
Sbjct	180	TGTGCCCAGTCACTAGTGTGATGTGCCCCCAACAGCAGGTTTGACTGTGCCCCTGACAAGGC	239
Query	240	TATCACCCAGGAGCAGTGTGAGGCCAGGGGGTGCTGCTACATTCTGCTAAGCAGGGCCT	299
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[illegible]

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Query	1080	CTACAGCAGCACTGCCATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCCCATTTC	1139
Sbjct	1080	CTACAGCAGCACTGCCATCACCAGACAGGTGGTGGAGAACATGACCAGGGCCCATTTC	1139
Query	1140	CCTGGATGTGCAGTGGAAATGACCTGGACTACATGGATAGCAGGAGGGATTTCACCTTCAA	1199
Sbjct	1140	CCTGGATGTGCAGTGGAAATGACCTGGACTACATGGACAGCAGGAGGGACTTCACCTTTAA	1199
Query	1200	CAAGGATGGCTTCAGGGACTTTTCTGCCATGGTGCAGGAGCTGCACCAGGGGGGCAGGAG	1259
Sbjct	1200	CAAGGATGGCTTTAGGGACTTCCCTGCCATGGTGCAGGAGCTGCATCAGGGGGGCAGGAG	1259
Query	1260	GTATATGATGATTGTGGACCCTGCTATCAGCAGCTCTGGCCCTGCTGGCTCTTACAGGCC	1319
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Query	1320	CTATGATGAGGGCCTGAGGAGGGGGGTGTTTATCACTAATGAAACTGGCCAGCCTCTGAT	1379
Sbjct	1320	CTATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGCCAGCCCCTGAT	1379
Query	1380	TGGCAAGGTCTGGCCTGGCTCTACTGCCTTCCCTGATTTTACTAACCCCACTGCCCTGGC	1439
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Query	1440	CTGGTGGGAGGACATGGTGGCTGAGTTCCATGATCAGGTGCCTTTTGATGGCATGTGGAT	1499
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Query	1500	TGATATGAATGAACCAAGCAACTTCATCAGAGGCTCTGAGGATGGCTGCCCCAACAATGA	1559
Sbjct	1500	TGACATGAATGAGCCCAGCAATTTTCATCAGGGGCTCTGAGGATGGCTGCCCCAACAATGA	1559
Query	1560	GCTGGAGAAcccccccTATGTGCCTGGGGTGGTGGGGGGCACTCTGCAGGCTGCCACCAT	1619
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Query	1620	TTGTGCTAGCAGCCACCAGTTCCTGAGCACCCACTACAATCTGCACAACCTGTATGGCCT	1679
Sbjct	1620	CTGTGCCTCTAGCCACCAGTTCCTGAGCACCCACTATAACCTGCATAACCTGTATGGCCT	1679
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Query	1740	GATCAGCAGGAGCACTTTTGCTGGCCATGGCAGGTATGCTGGCCACTGGACTGGGGATGT	1799
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Query	1800	GTGGAGCAGCTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATTCTGCAGTTTAACTGCT	1859
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Query	1860	GGGGGTGCCCCTGGTGGGGGCTGATGTGTGTGGCTTCCTGGGCAACACCTCTGAGGAGCT	1919
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Query	1920	GTGTGTGAGGTGGACCCAGCTGGGGGCCTTTTATCCCTTCATGAGGAACCACAACAGCCT	1979
Sbjct	1920	GTGTGTGAGGTGGACTCAGCTGGGGGCCTTCTATCCCTTCATGAGGAACCACAACAGCCT	1979
Query	1980	GCTGAGCCTGCCTCAGGAGCCCTACTCTTTCTCTGAGCCTGCCCAGCAGGCCATGAGGAA	2039
Sbjct	1980	GCTGTCTCTGCCCCAGGAGCCCTACAGCTTCTCTGAGCCTGCTCAGCAGGCTATGAGGAA	2039
Query	2040	GGCCCTGACCCTGAGGTATGCCCTGCTGCCCCACCTGTATACCCTGTTCCACCAGGCCCA	2099
Sbjct	2040	GGCCCTGACCCTGAGGTATGCCCTGCTGCCCCATCTGTACACCCTGTTCCACCAGGCCCA	2099
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Query	2160	CTGGACTGTGGATCATCAGCTGCTGTGGGGGGAGGCCCTGCTGATCACCCCTGTGCTGCA	2219
Sbjct	2160	CTGGACTGTGGACCATCAGCTGCTGTGGGGGGAGGCTCTGCTGATTACCCCTGTGCTGCA	2219
Query	2220	GGCTGGCAAGGCTGAGGTCACTGGCTACTTCCCTCTGGGCACCTGGTATGACCTGCAGAC	2279
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Query	2280	TGTGCCTGTGGAGGCTCTGGGCAGCCTGccccccccccTGCTGCTCCAGGGAGCCTGC	2339
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Query	2340	CATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCTCCCCTGGACACCATCAATGTGCA	2399
Sbjct	2340	CATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCCTCTGGACACCATCAATGTGCA	2399
Query	2400	CCTGAGGGCTGGCTACATTATCCCCCTGCAGGGCCCAGGGCTGACTACCACTGAGAGCAG	2459
Sbjct	2400	CCTGAGGGCTGGCTATATCATCCCCCTGCAGGGCCCTGGGCTGACCACCACTGAGAGCAG	2459
Query	2460	ACAGCAGCCCATGGCTCTGGCTGTGGCCCTGACCAAggggggggaagctaggggggagct	2519
Sbjct	2460	GCAGCAGCCCATGGCCCTGGCTGTGGCCCTGACTAAGGGGGGGGAGGCCAGGGGGGAGCT	2519
Query	2520	gttctgggatgatggggagagcctggaggtgctggagaggggggCCTATACCCAGGTGAT	2579

Sbjct	2520	GTTCTGGGATGATGGGGAGAGCCTGGAGGTGCTGGAGAGAGGGGGCCTACACCCAGGTGAT	2579
Query	2580	CTTCCTGGCTAGGAACAACACCATTGTCAATGAGCTGGTGAGGGTGACTTCTGAGGGGGC	2639
Sbjct	2580	CTTTCTGGCCAGGAACAACACCATTGTGAATGAGCTGGTGAGGGTGACTTCTGAGGGGGC	2639
Query	2640	TGGGCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCTCCCCAGCAGGTGCT	2699
Sbjct	2640	TGGCCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCCCCCAGCAGGTGCT	2699
Query	2700	GAGCAATGGGGTGCCTGTGAGCAACTTCACCTACAGCCCTGACACCAAGGTGCTGGACAT	2759
Sbjct	2700	GAGCAATGGGGTGCCTGTGTCTAACTTCACCTACAGCCCTGATACTAAGGTGCTGGATAT	2759
Query	2760	CTGTGTGTCTCTGCTGATGGGGGAGCAGTTCTGGTGAGCTGGTGCTGA	2808
Sbjct	2760	CTGTGTGAGCCTGCTGATGGGGGAGCAGTTTCTGGTGAGCTGGTGCTGA	2808

>Query_120569 SEQ ID NO: 2
Length=2808

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

Query	1	ATGGCTTTCTGTGGCTGCTGTCTTGTGGGCTCTGCTGGGCACCACTTTGGCCTGCTG	60
Sbjct	1	ATGGCTTTCTGTGGCTGCTGTCTTGTGGGCCCTGCTGGGGACTACCTTTGGCCTGCTG	60
Query	61	GTGCCCAGGGAGCTGTCTGGCAGCAGCCCTGTGCTGGAGGAGACCACTGCTCATCAG	120
Sbjct	61	GTGCCCAGGGAAGTGTCTGGCTCTAGCCCAGTGCTGGAGGAGACCACTGCCACCAAG	120
Query	121	CAGGGGGCTAGCAGGCCTGGCCCCAGGGATGCCCAGGCTCACCTGGGAGACCAAGGGCT	180
Sbjct	121	CAGGGGGCTTCTAGGCCTGGCCCCAGGGATGCCCAGGCCCACTGGCAGGCCAAGGGCT	180
Query	181	GTGCCCCACTCAGTGTGATGTGCCCCCAACAGCAGGTTTGACTGTGCTCCTGACAAGGCT	240
Sbjct	181	GTGCCCCACCAAGTGTGATGTGCCCCCAACTCTAGATTTGATTGTGCCCTGATAAGGCC	240
Query	241	ATCACCCAGGAGCAGTGTGAGGCCAGGGGGTGCTGCTACATTCTGCTAAGCAGGGCCTG	300
Sbjct	241	ATCACCCAGGAGCAGTGTGAGGCTAGGGGCTGCTGCTACATCCCTGCTAAGCAGGGCCTG	300
Query	301	CAGGGGGCCCCAGATGGGCCAGCCCTGGTGCTTCTTcccccccTCTTATCCCAGCTATAAG	360
Sbjct	301	CAGGGGGCTCAGATGGGCCAGCCCTGGTGCTTCTTCCCCCCCAGCTATCCCTCTTACAAG	360

Query	361	CTGGAGAACCTGAGCAGCTCTGAGATGGGCTACACTGCCACCCTGACCAGGACCACTCCC	420
Sbjct	361	CTGGAGAATCTGAGCAGCTCTGAGATGGGCTACACTGCCACCCTGACCAGGACTACTCCC	420
Query	421	ACCTTCTTTCCCAAGGATATTCTGACTCTGAGGCTGGATGTGATGATGGAGACTGAGAAC	480
Sbjct	421	ACCTTCTTCCCAAGGACATCCTGACCCTGAGGCTGGATGTGATGATGGAGACTGAGAAC	480
Query	481	AGGCTGCACTTCACTATCAAGGACCCTGCCAATAGGAGGTATGAGGTGCCCCTGGAGACT	540
Sbjct	481	AGGCTGCATTTCACCATCAAGGATCCTGCCAACAGGAGGTATGAGGTGCCTCTGGAGACC	540
Query	541	CCTCATGTGCATAGCAGGGCCCCCTTCTCCTCTGTATTCTGTGGAGTTCTCTGAGGAGCCC	600
Sbjct	541	CCCCATGTGCACAGCAGGGCTCCTTCTCCCCTGTACTCTGTGGAGTTCTCTGAGGAACCC	600
Query	601	TTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTGCTGCTGAACACCACTGTGGCC	660
Sbjct	601	TTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTCCTGCTGAACACCACTGTGGCC	660
Query	661	CCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGAGCACTTCTCTGCCCAGCCAGTACATT	720
Sbjct	661	CCCCTGTTCTTTGCTGATCAGTTCCTGCAGCTGTCCACTTCTCTGCCTAGCCAGTACATC	720
Query	721	ACTGGGCTGGCTGAGCATCTGAGCCCCCTGATGCTGAGCACCTCTTGGACCAGGATCACC	780
Sbjct	721	ACTGGGCTGGCTGAGCACCTGAGCCCCCTGATGCTGAGCACCTCTTGGACTAGGATCACC	780
Query	781	CTGTGGAACAGGGACCTGGCCCCCACTCCTGGGGCTAACCTGTATGGCTCTCACCCCTTT	840
Sbjct	781	CTGTGGAACAGGGACCTGGCCCCCACCCCTGGGGCCAACCTGTATGGCAGCCACCCCTTC	840
Query	841	TACCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTTCTGCTGAACAGCAATGCT	900
Sbjct	841	TATCTGGCCCTGGAGGATGGGGGCTCTGCCCATGGGGTGTTCTGCTGAATAGCAATGCT	900
Query	901	ATGGATGTGGTGCTGCAGCCCTCTCCAGCCCTGTCTTGGAGGAGCACTGGGGGCATTCTG	960
Sbjct	901	ATGGATGTGGTGCTGCAGCCCAGCCCTGCCCTGTCTTGGAGGAGCACTGGGGGCATCCTG	960
Query	961	GATGTGTACATTTTCCTGGGGCCTGAACCCAAGTCTGTGGTGCAGCAGTACCTGGATGTG	1020
Sbjct	961	GATGTGTACATTTTCCTGGGGCCTGAGCCCAAGTCTGTGGTGCAGCAGTACCTGGATGTG	1020
Query	1021	GTGGGCTACCCCTTCATGCCCCCTATTGGGGGCTGGGGTTTCACCTGTGCAGGTGGGGC	1080
Sbjct	1021	GTGGGCTACCCCTTCATGCCTCCCTACTGGGGCCTGGGCTTCCACCTGTGCAGGTGGGGC	1080
Query	1081	TACAGCAGCACTGCCATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCCCCATTTCCCC	1140

Sbjct	1081	TACAGCTCTACTGCCATCACCAGGCAGGTGGTGGAGAATATGACCAGGGCCCCACTTCCCC	1140
Query	1141	CTGGATGTGCAGTGGAATGACCTGGACTACATGGATAGCAGGAGGGATTTACCTTCAAC	1200
Sbjct	1141	CTGGATGTGCAGTGGAATGACCTGGACTACATGGACTCTAGGAGGGACTTCACCTTCAAT	1200
Query	1201	AAGGATGGCTTCAGGGACTTTCCTGCCATGGTGCAGGAGCTGCACCAGGGGGGCAGGAGG	1260
Sbjct	1201	AAGGATGGCTTCAGAGACTTCCCTGCCATGGTGCAGGAGCTGCATCAGGGGGGCAGGAGG	1260
Query	1261	TATATGATGATTGTGGACCCTGCTATCAGCAGCTCTGGCCCTGCTGGCTCTTACAGGCCC	1320
Sbjct	1261	TACATGATGATTGTGGACCCTGCCATCAGCTCTTCTGGCCCTGCTGGCTCTTACAGGCCC	1320
Query	1321	TATGATGAGGGCCTGAGGAGGGGGGTGTTTATCACTAATGAAACTGGCCAGCCTCTGATT	1380
Sbjct	1321	TATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGGCAGCCCCTGATT	1380
Query	1381	GGCAAGGTCTGGCCTGGCTCTACTGCCTTCCCTGATTTTACTAACCCCCACTGCCCTGGCC	1440
Sbjct	1381	GGGAAGGTGTGGCCTGGCTCTACTGCCTTCCCTGACTTCACCAATCCTACTGCCCTGGCC	1440
Query	1441	TGGTGGGAGGACATGGTGGCTGAGTTCCATGATCAGGTGCCTTTTGATGGCATGTGGATT	1500
Sbjct	1441	TGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCTTTTGATGGCATGTGGATT	1500
Query	1501	GATATGAATGAACCAAGCAACTTCATCAGAGGCTCTGAGGATGGCTGCCCCAACAATGAG	1560
Sbjct	1501	GACATGAATGAGCCCTCTAATTTTCATCAGGGGCTCTGAGGATGGCTGCCCCAACAATGAG	1560
Query	1561	CTGGAGAAcccccccTATGTGCCTGGGGTGGTGGGGGGCACTCTGCAGGCTGCCACCATT	1620
Sbjct	1561	CTGGAGAACCCCCCTATGTGCCTGGGGTGGTGGGGGGCACCTGCAGGCTGCCACCATC	1620
Query	1621	TGTGCTAGCAGCCACCAGTTCCTGAGCACCCACTACAATCTGCACAACCTGTATGGCCTG	1680
Sbjct	1621	TGTGCTAGCTCTCACCAGTTCCTGAGCACCCACTACAATCTGCATAACCTGTATGGCCTG	1680
Query	1681	ACTGAAGCCATTGCCAGCCATAGGGCCCTGGTGAAGGCCAGGGGCACTAGGCCTTTTG TG	1740
Sbjct	1681	ACTGAGGCCATTGCCAGCCACAGGGCCCTGGTGAAGGCTAGGGGCACCAGGCCCTTTTG TG	1740
Query	1741	ATCAGCAGGAGCACTTTTGCTGGCCATGGCAGGTATGCTGGCCACTGGACTGGGGATGTG	1800
Sbjct	1741	ATTTCTAGGAGCACTTTTGCTGGCCATGGCAGGTATGCTGGGCACTGGACTGGGGATGTG	1800
Query	1801	TGGAGCAGCTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATTCTGCAGTTTAACCTGCTG	1860
Sbjct	1801	TGGTCTAGCTGGGAGCAGCTGGCTTCTTCTGTGCCTGAGATCCTGCAGTTCAACCTGCTG	1860

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

>Query_120571 SEQ ID NO: 5
Length=2808

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

Query	1	ATGGCTTTCTGTGGCTGCTGTCTTGTGGCTCTGCTGGGCACCACTTTGGCCTGCTG	60
Sbjct	1	ATGGCCTTTCTGTGGCTGCTGTCTTGTGGCCCTGCTGGGGACCACTTTGGCCTGCTG	60
Query	61	GTGCCCAGGGAGCTGTCTGGCAGCAGCCCTGTGCTGGAGGAGACCCACCCTGCTCATCAG	120
Sbjct	61	GTGCCCAGGGAGCTGTCTGGGAGCAGCCAGTGTGCTGGAGGAGACCCACCCTGCCACCAG	120
Query	121	CAGGGGGCTAGCAGGCCTGGCCCCAGGGATGCCCAGGCTCACCTGGGAGACCCAGGGCT	180
Sbjct	121	CAGGGGGCCAGCAGGCCTGGCCCTAGGGATGCCCAGGCCCCACCTGGCAGGCCAGGGCT	180
Query	181	GTGCCCCTCAGTGTGATGTGCCCCCAACAGCAGGTTTGACTGTGCTCCTGACAAGGCT	240
Sbjct	181	GTGCCTACCCAGTGTGATGTGCCACCCAATTCTAGGTTTGACTGTGCTCCTGACAAGGCC	240
Query	241	ATCACCCAGGAGCAGTGTGAGGCCAGGGGGTGCTGCTACATTCCTGCTAAGCAGGGCCTG	300
Sbjct	241	ATCACTCAGGAGCAGTGTGAAGCTAGGGGGTGCTGCTACATCCCAGCCAAGCAGGGCCTG	300
Query	301	CAGGGGGCCCCAGATGGGCCAGCCCTGGTGCTTCTTccccccTCTTATCCCAGCTATAAG	360
Sbjct	301	CAGGGGGCCCCAGATGGGCCAGCCCTGGTGCTTCTTCCCCCAGCTACCCTAGCTACAAG	360
Query	361	CTGGAGAACCTGAGCAGCTCTGAGATGGGCTACACTGCCACCCTGACCAGGACCACTCCC	420
Sbjct	361	CTGGAGAATCTGAGCAGCTCTGAGATGGGCTACACTGCTACCCTGACCAGGACCACTCCT	420

Query	421	ACCTTCTTTCCCAAGGATATTCTGACTCTGAGGCTGGATGTGATGATGGAGACTGAGAAC	480
Sbjct	421	ACCTTCTTCCCAAGGACATCCTGACTCTGAGGCTGGATGTCATGATGGAGACTGAAAAT	480
Query	481	AGGCTGCACTTCACTATCAAGGACCCTGCCAATAGGAGGTATGAGGTGCCCCCTGGAGACT	540
Sbjct	481	AGGCTGCACTTCACCATCAAGGACCCTGCCAATAGGAGGTATGAGGTGCTCTGGAGACC	540
Query	541	CCTCATGTGCATAGCAGGGC-CCCTTCTCCTCTGTATTCTGTGGAGTTCTCTGAGGAGCC	599
Sbjct	541	CCCCATGTGCATAGCAGGGCTCCCAGC-CCCCTGTATTCTGTGGAGTTCTCTGAGGAGCC	599
Query	600	CTTTGGGGTGATTGTGAGGAGGCAGCTGGATGGCAGGGTGCTGCTGAACACCACTGTGGC	659
Sbjct	600	CTTTGGGGTCATTGTGAGGAGACAGCTGGATGGGAGGGTGCTGCTGAACACTACTGTGGC	659
Query	660	CCCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGAGCACTTCTCTGCCCAGCCAGTACAT	719
Sbjct	660	TCCCCCTGTTCTTTGCTGACCAGTTCCTGCAGCTGTCTACCAGCCTGCCCAGCCAGTACAT	719
Query	720	TACTGGGCTGGCTGAGCATCTGAGCCCCCTGATGCTGAGCACCTCTTGACCAGGATCAC	779
Sbjct	720	CACTGGGCTGGCTGAGCATCTGAGCCCCCTGATGCTGAGCACCAGCTGGACCAGGATCAC	779
Query	780	CCTGTGGAACAGGGACCTGGCCCCCACTCCTGGGGCTAACCTGTATGGCTCTCACCCCTT	839
Sbjct	780	TCTGTGGAACAGGGATCTGGCCCCCACTCCTGGGGCCAACCTGTATGGGAGCCATCCCTT	839
Query	840	TTACCTGGCCCTGGAGGATGGGGCTCTGCCCATGGGGTGTTTCTGCTGAACAGCAATGC	899
Sbjct	840	CTACCTGGCCCTGGAGGATGGGGCTCTGCCCATGGGGTGTTCTGCTGAACAGCAATGC	899
Query	900	TATGGATGTGGTGCTGCAGCCCTCTCCAGCCCTGTCTTGAGGAGCACTGGGGGCATTCT	959
Sbjct	900	CATGGATGTGGTGCTGCAGCCTAGCCCTGCCCTGAGCTGGAGGAGCACTGGGGGCATCCT	959
Query	960	GGATGTGTACATTTTCTGGGGCCTGAACCCAAGTCTGTGGTGCAGCAGTACCTGGATGT	1019
Sbjct	960	GGATGTCTACATCTTCTGGGGCCTGAGCCCAAGTCTGTGGTGCAGCAGTATCTGGATGT	1019
Query	1020	GGTGGGCTACCCCTTCATGCCCCCTATTGGGGGCTGGGGTTTCACCTGTGCAGGTGGGG	1079
Sbjct	1020	GGTGGGGTATCCCTTCATGCCCCCTACTGGGGCCTGGGCTTTCACCTGTGCAGGTGGGG	1079
Query	1080	CTACAGCAGCACTGCCATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCCCCATTTCCC	1139
Sbjct	1080	CTACAGCAGCACTGCCATCACCAGGCAGGTGGTGGAGAACATGACCAGGGCCCCACTTCCC	1139
Query	1140	CCTGGATGTGCAGTGGAATGACCTGGACTACATGGATAGCAGGAGGGATTTCACCTTCAA	1199

Sbjct	1140	TCTGGATGTGCAGTGGAATGACCTGGACTATATGGATTCTAGGAGAGACTTTACTTTTAA	1199
Query	1200	CAAGGATGGCTTCAGGGACTTTCTGCCATGGTGCAGGAGCTGCACCAGGGGGGCAGGAG	1259
Sbjct	1200	CAAGGATGGCTTCAGGGATTTCCCTGCCATGGTGCAGGAGCTGCACCAGGGGGGCAGGAG	1259
Query	1260	GTATATGATGATTGTGGACCCTGCTATCAGCAGCTCTGGCCCTGCTGGCTCTTACAGGCC	1319
Sbjct	1260	GTACATGATGATTGTGGACCCTGCTATTAGCAGCTCTGGCCCTGCTGGGTCTTACAGGCC	1319
Query	1320	CTATGATGAGGGCCTGAGGAGGGGGGTGTTTATCACTAATGAAACTGGCCAGCCTCTGAT	1379
Sbjct	1320	TTATGATGAGGGCCTGAGGAGGGGGGTGTTTCATCACCAATGAGACTGGCCAGCCCCTGAT	1379
Query	1380	TGGCAAGGTCTGGCCTGGCTCTACTGCCTTCCCTGATTTTACTAACCCCACTGCCCTGGC	1439
Sbjct	1380	TGGCAAGGTGTGGCCTGGCAGCACTGCCTTCCCTGACTTCACCAACCCCACTGCCCTGGC	1439
Query	1440	CTGGTGGGAGGACATGGTGGCTGAGTTCCATGATCAGGTGCCTTTTGATGGCATGTGGAT	1499
Sbjct	1440	CTGGTGGGAGGACATGGTGGCTGAGTTCCATGACCAGGTGCCCTTTGATGGGATGTGGAT	1499
Query	1500	TGATATGAATGAACCAAGCAACTTCATCAGAGGCTCTGAGGATGGCTGCCCCAACAATGA	1559
Sbjct	1500	TGACATGAATGAGCCCTCTAACTTCATCAGGGGGTCTGAGGATGGCTGCCCCAACAATGA	1559
Query	1560	GCTGGAGAAccccccTATGTGCCTGGGGTGGTGGGGGGCACTCTGCAGGCTGCCACCAT	1619
Sbjct	1560	GCTGGAGAAACCCCCCTATGTGCCTGGGGTGGTGGGGGGCACTCTGCAGGCTGCCACTAT	1619
Query	1620	TTGTGCTAGCAGC-CACCAGTTCCTGAGCACCCACTACAATCTGCACAACCTGTATGGCC	1678
Sbjct	1620	CTGTGCTT-CTTCTCACCAGTTTCTGAGCACCCACTATAATCTGCACAACCTGTATGGCC	1678
Query	1679	TGACTGAAGCCATTGCCAGCCATAGGGCCCTGGTGAAGGCCAGGGGCACTAGGCCTTTTG	1738
Sbjct	1679	TGACTGAGGCCATTGCCAGCCATAGGGCCCTGGTGAAGGCCAGGGGCACCAGGCCCTTTG	1738
Query	1739	TGATCAGCAGGAGCACTTTTGCTGGCCATGGCAGGTATGCTGGCCACTGGACTGGGGATG	1798
Sbjct	1739	TGATCAGCAGGTCTACCTTTGCTGGCCATGGCAGGTATGCTGGCCACTGGACTGGGGATG	1798
Query	1799	TGTGGAGCAGC-TGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATTCTGCAGTTTAACCTG	1857
Sbjct	1799	TGTGGT-CTTCTGGGAGCAGCTGGCCAGCTCTGTGCCTGAGATCTGCAGTTCAACCTG	1857
Query	1858	CTGGGGGTGCCCCTGGTGGGGGCTGATGTGTGTGGCTTCTGGGCAACACCTCTGAGGAG	1917
Sbjct	1858	CTGGGGGTGCCTCTGGTGGGGGCTGATGTGTGTGGCTTCTGGGCAACACCTCTGAGGAG	1917

Query	1918	CTGTGTGTGAGGTGGACCCAGCTGGGGGCCTTTTATCCCTTCATGAGGAACCACAACAGC	1977
Sbjct	1918	CTGTGTGTGAGGTGGACCCAGCTGGGGGCCTTTTACCCCTTCATGAGGAACCACAATAGC	1977
Query	1978	CTGCTGAGCCTGCCTCAGGAGCCCTACTCTTTCTCTGAGCCTGCCCAGCAGGCCATGAGG	2037
Sbjct	1978	CTGCTGAGCCTGCCCCAGGAGCCTTACTCTTTCTCTGAGCCTGCCCAGCAGGCCATGAGG	2037
Query	2038	AAGGCCCTGACCCTGAGGTATGCCCTGCTGCCCCACCTGTATACCCTGTTCCACCAGGCC	2097
Sbjct	2038	AAGGCCCTGACTCTGAGGTATGCCCTGCTGCCCCATCTGTATACCCTGTTTCACCAGGCC	2097
Query	2098	CATGTGGCTGGGGAGACTGTGGCCAGGCCCTGTTCTGGAGTTCCCCAAGGACAGCAGC	2157
Sbjct	2098	CATGTGGCTGGGGAGACTGTGGCTAGGCCTCTGTTTCTGGAGTTCCCTAAGGACTCTAGC	2157
Query	2158	ACCTGGACTGTGGATCATCAGCTGCTGTGGGGGAGGCCCTGCTGATCACCCCTGTGCTG	2217
Sbjct	2158	ACCTGGACTGTGGACCACCAGCTGCTGTGGGGGAGGCCCTGCTGATCACCCCTGTGCTG	2217
Query	2218	CAGGCTGGCAAGGCTGAGGTCACTGGCTACTTCCCTCTGGGCACCTGGTATGACCTGCAG	2277
Sbjct	2218	CAGGCTGGCAAGGCTGAGGTGACTGGCTACTTCCCCCTGGGCACCTGGTATGACCTGCAG	2277
Query	2278	ACTGTGCCTGTGGAGGCTCTGGGCAGCCTGccccccccccTGCTGCTCCCAGGGAGCCT	2337
Sbjct	2278	ACTGTGCCTGTGGAGGCCCTGGGGAGCCTGCCTCCCCCCCCCTGCTGCCCCAGGGAGCCT	2337
Query	2338	GCCATCCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCTCCCCTGGACACCATCAATGTG	2397
Sbjct	2338	GCCATTCACTCTGAGGGCCAGTGGGTGACCCTGCCTGCCCCTCTGGACACCATCAATGTG	2397
Query	2398	CACCTGAGGGCTGGCTACATTATCCCCCTGCAGGGCCCAGGGCTGACTACCACTGAGAGC	2457
Sbjct	2398	CACCTGAGGGCTGGGTACATCATCCCCCTGCAGGGCCCTGGCCTGACCACCACTGAGAGC	2457
Query	2458	AGACAGCAGCCCATGGCTCTGGCTGTGGCCCTGACCAAggggggggaagctaggggggag	2517
Sbjct	2458	AGGCAGCAGCCCATGGCCCTGGCTGTGGCTCTGACCAAGGGGGGGGAGGCCAGGGGGGAG	2517
Query	2518	ctgttctgggatgatggggagagcctggaggtgctggagaggggggCCTATACCCAGGTG	2577
Sbjct	2518	CTGTTCTGGGATGATGGGGAGTCTCTGGAGGTGCTGGAGAGGGGGGCCTACACCCAGGTG	2577
Query	2578	ATCTTCCTGGCTAGGAACAACACCATTGTCAATGAGCTGGTGAGGGTGACTTCTGAGGGG	2637
Sbjct	2578	ATCTTTCTGGCCAGGAACAATACTATTGTGAATGAGCTGGTGAGGGTGACCTCTGAGGGG	2637
Query	2638	GCTGGGCTGCAGCTGCAGAAGGTGACTGTGCTGGGGGTGGCCACTGCTCCCCAGCAGGTG	2697

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