

Ago2 [NM_012154](#)

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R R V N R E I V E H M V Q H F K T Q I F
303 ggggatcggaagcccgtgtttgacggcaggaagaatctatacacagccatgccccttccg
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363 attgggagggacaaggtggagctggaggTcacgctgccaggagaaggcaaggatcgcatc
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543 cacttgccatccatgaggTtacacccccgtggccgctccttcttaccgctccgaaggc
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Q K R H H T R L F C T D K N E R V G K S
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3423 gtgataaatacagtacaatccttttccactgtttatgcttttaatagtagagaagaatata
3483 tatactcgtggttcagtaaaaaaaaaaaaaaaaaaaaaa 3520

New cloning using the template from Carl

pGEX-4T-1-hAgo2, done at 3.25.2011, Hank Qi

Vector : pGEX-4T-1, XhoI/NotI

Insert : Sall/NotI

clone 1, One C881T, non-sense mutation

all the other sequences are good with 4 sequencing primer-sequenced.

Sequencing results :

pGEX vector forward sequencing read 45-930

pGEX vector forward sequencing

NNNNNNNNNCCNNNNCCGGNTCTGGTTCGCCGT GGA TCC CCG GAA TTC CCG GGT CGA CTG GAC TAC TCGGGAGCC
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Sbjct	45	TACTCGGGAGCCGGCCCCGCACTTGACACCTCCTGCGCCGCGCCGCCATCCAAGGATAT	104
Query	129	GCCTTCAAGCCTCCACCTAGACCCGACTTTGGGACCTCCGGGAGAACAATCAAATTACAG	188
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Query	189	GCCAAATTTCTTTCGAAATGGACATCCCAAAATGACATCTATCATTATGAATTGGATATC	248
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Query	249	AAGCCAGAGAAGTGCCCGAGGAGAGTTAACAGGGAAATCGTGGAAACACATGGTCCAGCAC	308
Sbjct	225	AAGCCAGAGAAGTGCCCGAGGAGAGTTAACAGGGAAATCGTGGAAACACATGGTCCAGCAC	284
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Sbjct	345	ACAGCCATGCCCTTCCGATTGGGAGGACAAGTGGAGCTGGAGTCCAGTCCAGGA	404
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Sbjct	405	GAAGGCAAGGATCGCATCTTCAAGGTGTCCATCAAGTGGGTGTCTGCGTGAGCTTGCGAG	464
Query	489	GCGTTACACGATGCACTTTCAGGGCGGCTGCCAGCGTCCCTTTGAGACGATCCAGGCC	548
Sbjct	465	GCGTTACACGATGCACTTTCAGGGCGGCTGCCAGCGTCCCTTTGAGACGATCCAGGCC	524
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Sbjct	645	TTCCATCAGTCCGTCGGCCTTCTCTCTGGAATGATGCTGAATATTGATGTGTAGCA	704
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Sbjct	705	ACAGCGTTTACAAGGCACAGCCAGTAATCGAGTTTGTGTAAGTTTGGATTTTAAA	764
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Query 909 TGCAATGTGACCCGGCCGCCAGTCACCAAAACATTCCCGCTGCANCAGGAGAGCGGG 968
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Query 969 CAGANGNGGANTGCACGGTGGCCAGTATTTCAAGGACAGGCANNAGTTGGTTCTGCGC 1028
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Sbjct 945 CAGACGGTGGATGCACGGTGGCCAGTATTTCAAGGACAGGCACAAGTTGGTTCTGCGC 1004

Query 1029 TACCCCNCTCCCATGNTTANA-GTCGGannngagcagaaa 1070
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Sbjct 1005 TACCCCA-CCTCCCATGTTTACAAGTCGGACAGGAGCAGAAA 1046

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pgEX-Ago2-1-Ago2Seq1_B12.ab1

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Sbjct 567 CCCGTGGGCGCTCCTTCTCACCGCTCCGAAGGCTGCTCTAACCTCTTGGCGGGGGC 626

Query 90 CGAGAAGTGTGGTTTGGCTTCCATCAGTCCGTCGGCCTTCTCTGGAAAATGATGCTG 149
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Sbjct 627 CGAGAAGTGTGGTTTGGCTTCCATCAGTCCGTCGGCCTTCTCTGGAAAATGATGCTG 686

Query 150 AATATTGATGTGTCAGCAACAGCGTTTTTACAAGGCACAGCCAGTAATCGAGTTTGT 209
      |||
Sbjct 687 AATATTGATGTGTCAGCAACAGCGTTTTTACAAGGCACAGCCAGTAATCGAGTTTGT 746

Query 210 GAAGTTTGGATTTTAAAGTATTGAAGAACAACAAAAACCTCTGACAGATTCCCAAAG 269
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Sbjct 747 GAAGTTTGGATTTTAAAGTATTGAAGAACAACAAAAACCTCTGACAGATTCCCAAAG 806

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Query 570 TTAACGGACAATCAGACCTCAACCATGATCAGAGCGACTGCTAGGTCGGCGCCGATCGG 629
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Sbjct 1107 TTAACGGACAATCAGACCTCAACCATGATCAGAGCGACTGCTAGGTCGGCGCCGATCGG 1166

Query 630 CAAGAAGAGATTAGCAAATTTGATGCGAAGTGAAGTTTCAACACAGATCCATACGTCGGT 689
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Sbjct 1167 CAAGAAGAGATTAGCAAATTTGATGCGAAGTGAAGTTTCAACACAGATCCATACGTCGGT 1226

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Query 690 GAATTTGGAATCATGGTCAAAGATGAGATGACAGACGTGACTGGGCGGTGCTGCAGCCG 749
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Sbjct 1527 CANGGGGCGGACAGCGTGGAGCCC-ATGTTCCGGCACCTGAAGAACACGT-ATCGGGGCC 1584

Query 1048 TGCAGCTGG 1056
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pgEX-Ago2-1-Ago2Seq2_C12.ab1

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Query 92 GGGCGGGTGTGCAGCCGCCCTCCATCCTCTACGGGGGCAGGAATAAAGCTATTGCGGACC 151
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Query 152 CCTGTCCAGGGCGTCTGGGACATGCGGAACAAGCAGTTCCACACGGGCATCGAGATCAAG 211
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Query 212 GTGTGGGCCATTGCGTGTCTCGCCCCAGCGCCAGTGCACGGAAGTCCATCTGAAGTCC 271
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Sbjct 1449 TTCACAGAGCAGCTCAGAAAATCTCGAGAGACGCCGCATGCCCATCCAGGGCCAGCCG 1508

Query 332 TGCTTCTGCAAAATACGCGAGGGGGCGGACGCGTGGAGCCCATGTTCCGGCACCTGAAG 391
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 1509 TGCTTCTGCAAAATACGCGAGGGGGCGGACGCGTGGAGCCCATGTTCCGGCACCTGAAG 1568

Query 392 AACACGTATGCGGGCCTGCAGCTGGTGGTGCATCTGCCCGGCAAGACGCCCGTGTAC 451
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 1569 AACACGTATGCGGGCCTGCAGCTGGTGGTGCATCTGCCCGGCAAGACGCCCGTGTAC 1628

Query 452 GCCGAGTCAAGCGCGTGGGAGACACGGTGTGGGATGGCCACGCAGTGCCTGCAGATG 511
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Sbjct 1629 |||||
GCCGAGGTCAAGCGCGTGGGAGACCGGTGCTGGGGATGGCCACGCAGTGCCTGCAGATG 1688

Query 512 AAGAACGTGCAGAGGACCACGCCACAGACCCCTGTCCAACCTCTGCCTGAAGATCAACGTC 571
Sbjct 1689 AAGAACGTGCAGAGGACCACGCCACAGACCCCTGTCCAACCTCTGCCTGAAGATCAACGTC 1748

Query 572 AAGCTGGGAGGCGTGAACAACATCCTGCTGCCCCAGGGCAGGCCGCGGTGTTCCAGCAG 631
Sbjct 1749 AAGCTGGGAGGCGTGAACAACATCCTGCTGCCCCAGGGCAGGCCGCGGTGTTCCAGCAG 1808

Query 632 CCCGTCATCTTTCTGGGAGCAGACGTCACCTCAcccccccGCCGGGATGGGAAGAAGCCC 691
Sbjct 1809 CCCGTCATCTTTCTGGGAGCAGACGTCACCTCACCCCCCGCGGGATGGGAAGAAGCCC 1868

Query 692 TCCATTGCCCGCGTGGTGGGAGCAGATGGACGCCACCCCAATCGCTACTGCGCCACCGTG 751
Sbjct 1869 TCCATTGCCCGCGTGGTGGGAGCAGATGGACGCCACCCCAATCGCTACTGCGCCACCGTG 1928

Query 752 CGCGTGCAGCAGCACCAGGAGATCATAAAGACCTGGCCGCCATGGTCCGCGAGCTC 811
Sbjct 1929 CGCGTGCAGCAGCACCAGGAGATCATAAAGACCTGGCCGCCATGGTCCGCGAGCTC 1988

Query 812 CTCATCCAGTTTACAAGTCCACGCGCTTCAAGCCCACCCGCATCATTTCTACCGCGAC 871
Sbjct 1989 CTCATCCAGTTTACAAGTCCACGCGCTTCAAGCCCACCCGCATCATTTCTACCGCGAC 2048

Query 872 GGTGTCTCTGAAGGCAGTTCCAGCANN-TTCTCCACCAGAGTTGCTGGCCATCCGTGAG 930
Sbjct 2049 GGTGTCTCTGAAGGCAGTTCCAGCAGTTTCCACCAGAGTTGCTGGCCATCCGTGAG 2108

Query 931 GCCTGTATCAAGCTAGAAAAAGACTACCAGCCCGGGATCACCTTCATCGTGGNGCAGAAN 990
Sbjct 2109 GCCTGTATCAAGCTAGAAAAAGACTACCAGCCCGGGATCACCTTCATCGTGGTGCAGAAG 2168

Query 991 AGGCACCACACCCGGCTCTNCTGCACTGanan-ann-anCGGGNNGGAAA-GTGNANNN 1047
Sbjct 2169 AGGCACCACACCCGGCTCTTCTGCACTGACAAGAACGAGCGGGTTGGGAAAAGTGGAAAC 2228

Query 1048 -TTCCAGCAGGCACGACTGTGNNNNCGAAAAATCACCCNCCCCA 1090
Sbjct 2229 ATTCCAGCAGGCACGACTGTGGACACGAAAAATCACCCA-CCCCA 2271

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pgEX-Ago2-1-pGEX-3R_E05.ab1

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Query 57 TCAAGCAAAGTACATGGTGGCAGAGTGTCTTGGTGAACCTGGACCGCTTGGCCAGTGC 116
Sbjct 2621 TCAAGCAAAGTACATGGTGGCAGAGTGTCTTGGTGAACCTGGACCGCTTGGCCAGTGC 2562

Query 117 TTGGTGGTCTCGCCCGTTACTCTGCCAGAGGATGGCTTCCCTCAGCACTGTCTATGTTTC 176
Sbjct 2561 TTGGTGGTCTCGCCCGTTACTCTGCCAGAGGATGGCTTCCCTCAGCACTGTCTATGTTTC 2502

Query 177 CTTATCCACCAGGTTGTTACCTGGCCCGAAGGCCACAGGTGAGCGTAGTATGCTGGCGC 236

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Sbjct	2501	 CTTATCCACCAGGTGGTACCTGGCCCGGAAGGCCACCAGGTGAGCGTAGTATGCTGGCGC	2442
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Sbjct	2381	 CTGCAGCTCATCAGAGGAGAAACGATTGTCGTCCCAGAGGACGTGATAGTGCGAAGGCCT	2322
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Sbjct	2321	 GCTTGTCCCCTGGATGCCAGCGTGACTACACAGGTAGAAGTCGAACTCGGTGGGGTGGT	2262
Query	417	GATTTTCGTGTCCACAGTCGTGCCTGCTGGAATGTTTCCACTTTTCCCAACCCGCTCGTF	476
Sbjct	2261	 GATTTTCGTGTCCACAGTCGTGCCTGCTGGAATGTTTCCACTTTTCCCAACCCGCTCGTF	2202
Query	477	CTTGTCAAGTGCAGAAGAGCCGGGTGTGGTGCCTCTTCTGCACCAGATGAAGGTGATCCC	536
Sbjct	2201	 CTTGTCAAGTGCAGAAGAGCCGGGTGTGGTGCCTCTTCTGCACCAGATGAAGGTGATCCC	2142
Query	537	GGGCTGGTAGTCTTTTTCTAGCTTGATACAGGCCTCACGGATGGCCAGCAACTCGTGGTG	596
Sbjct	2141	 GGGCTGGTAGTCTTTTTCTAGCTTGATACAGGCCTCACGGATGGCCAGCAACTCGTGGTG	2082
Query	597	GAGAACCTGCTGGAAGTGGCCTTCAGAGACACCGTCGCGGTAGAAGATGATGCGGGTGGG	656
Sbjct	2081	 GAGAACCTGCTGGAAGTGGCCTTCAGAGACACCGTCGCGGTAGAAGATGATGCGGGTGGG	2022
Query	657	CTTGAAGCCGCTGGACTTGTAGAAGTGGATGAGGAGCTCGCGGACCATGGCGGCCAGGTC	716
Sbjct	2021	 CTTGAAGCCGCTGGACTTGTAGAAGTGGATGAGGAGCTCGCGGACCATGGCGGCCAGGTC	1962
Query	717	TTGTATGATCTCCTGCCGGTGTGCTGCACGCGCACGGTGGCGCAGTANCGATTGGGGTG	776
Sbjct	1961	 TTGTATGATCTCCTGCCGGTGTGCTGCACGCGCACGGTGGCGCAGTANCGATTGGGGTG	1902
Query	777	GGCGTCCATGCTGCCACCACGGCGGCAATGGANSGCTTCTTCCCATCCCCGGCggggggg	836
Sbjct	1901	 GGCGTCCATGCTGCCACCACGGCGGCAATGGANSGCTTCTTCCCATCCCCGGCGGGGGG	1842
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Sbjct	1841	 GTGAGTGACGTCTGCTCCCAGAAAGATGACGGGCTGTGGAACACCGCGGCCCTGCCCTG	1782
Query	897	GGGCAGCANN-TGTTGTTTCACGCCTCCCAGCTTGACGTTGANCTTCAGGCAGANNNTGGA	955
Sbjct	1781	 GGGCAGCAGGATGTTGTTTCACGCCTCCCAGCTTGACGTTGANCTTCAGGCAGAGGTTGGA	1722
Query	956	CAGGGTCTGNNGCGTGNNC-TCTGCACGTTCTTCANNTGCACGCACTNNNTGGC-ATCCC	1013
Sbjct	1721	 CAGGGTCTGTGGCGTGGTCTCTGCACGTTCTTCATCTGCACGCACTGCGTGGCCATCCC	1662
Query	1014	CAGCAC-GTNNNTCCN-CGNGCTTGACNTCGGCGTACANGGNGTNTTNNNGG-CAGGA	1070
Sbjct	1661	 CAGCACCGTG-TCTCCCACGCGCTTGACCTCGGCGTACACGGGCGTCTTGCCGGGCAGGA	1603
Query	1071	TGACC 1075 	
Sbjct	1602	TGACC 1598	

Home 3/25/11 12:21 PM
Comment: It is G in trace file

Home 3/25/11 12:22 PM
Comment: Seems like a G

pGEX-Ago2-2-pGEX5F_E10.ab1, 4T-3 SalI

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Query	63	TACTCGGGAGCCGGCCCGC	122
Sbjct	45	TACTCGGGAGCCGGCCCGC	104
Query	123	GCCTTCAAGCCTCCACCTAG	182
Sbjct	105	GCCTTCAAGCCTCCACCTAG	164
Query	183	GCCAAATTTCTCGAAATGG	242
Sbjct	165	GCCAAATTTCTCGAAATGG	224
Query	243	AAGCCAGAGAAGTGC	302
Sbjct	225	AAGCCAGAGAAGTGC	284
Query	303	TTTAAACACAGATCTTTGG	362
Sbjct	285	TTTAAACACAGATCTTTGG	344
Query	363	ACAGCCATGCCCTTCCGAT	422
Sbjct	345	ACAGCCATGCCCTTCCGAT	404
Query	423	GAAGGCAAGGATCGCATCT	482
Sbjct	405	GAAGGCAAGGATCGCATCT	464
Query	483	GCGTTACACGATGCACTTT	542
Sbjct	465	GCGTTACACGATGCACTTT	524
Query	543	CTGGACGTGGTCATGAGGCA	602
Sbjct	525	CTGGACGTGGTCATGAGGCA	584
Query	603	TTCACCGCTCCGAAGGCTG	662
Sbjct	585	TTCACCGCTCCGAAGGCTG	644
Query	663	TTCCATCAGTCCGTC	722
Sbjct	645	TTCCATCAGTCCGTC	704
Query	723	ACAGCGTTTTACAAGGCAC	782
Sbjct	705	ACAGCGTTTTACAAGGCAC	764
Query	783	AGTATTGAAGAACAACAAA	842
Sbjct	765	AGTATTGAAGAACAACAAA	824
Query	843	ATTAAGGTCTAAAGGTGGAG	902
Sbjct	825	ATTAAGGTCTAAAGGTGGAG	884
Query	903	TGCAATGTGACCCGCGCC	962
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Query   963   GCAGANNNGGAGTGCANGN-GGCCAGTATTCNNN--CNGGCACAAGTTNGTCTGNN 1019
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Sbjct   944   GCAGACGGTGGAGTGCACGGTGGCCAGTATTTCAAGGACAGGCACAAGTTGGTTCTGCG 1003

Query   1020  CTACCCCCACCTNCCNTGTTTACNAGT 1046
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Sbjct   1004  CTACCCCCACCTCCCATGTTTACAAGT 1030

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Query   35    TACACCCCGTGGGCGCTCCTCTTCCACCCGCTCCGAAGGCTGCTCTAACCCCTTGGC 94
|||||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Sbjct   561    TACACCCCGTGGGCGCTCCTCTTCCACCCGCTCCGAAGGCTGCTCTAACCCCTTGGC 620

Query   95    GGGGGCCGAGAAGTGTGGTTTGGCTTCCATCAGTCCGTCGGCCTTCTCTGGAAAATG 154
|||||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Sbjct   621    GGGGGCCGAGAAGTGTGGTTTGGCTTCCATCAGTCCGTCGGCCTTCTCTGGAAAATG 680

Query   155   ATGCTGAATATTGATGTGTGTCAGCAACAGCGTTTTACAAGGCACAGCCAGTAATCGAGTTT 214
|||||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Sbjct   681    ATGCTGAATATTGATGTGTGTCAGCAACAGCGTTTTACAAGGCACAGCCAGTAATCGAGTTT 740

Query   215   GTTGTGAAAGTTTGGATTTTAAAGTATTGAAGAACAACAATAAACCCTTGCAGATTTC 274
|||||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Sbjct   741    GTTGTGAAAGTTTGGATTTTAAAGTATTGAAGAACAACAATAAACCCTTGCAGATTTC 800

Query   275   CAAAGGTAAAGTTTACCAAGAAATTAAGGTCTAAAGTGGAGATAACGCACCTGTGGG 334
|||||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Sbjct   801    CAAAGGTAAAGTTTACCAAGAAATTAAGGTCTAAAGTGGAGATAACGCACCTGTGGG 860

Query   335   CAGATGAAGAGGAAGTACCCTGCTGCAATGTGACCCGGCGGCCAGTCACCAAACA 394
|||||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Sbjct   861    CAGATGAAGAGGAAGTACCCTGCTGCAATGTGACCCGGCGGCCAGTCACCAAACA 920

Query   395   TTCCCGCTGCAGCAGGAGAGCGGGCAGACGGTGGAGTGACCGTGGCCCAGTATTCAAG 454
|||||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Sbjct   921    TTCCCGCTGCAGCAGGAGAGCGGGCAGACGGTGGAGTGACCGTGGCCCAGTATTCAAG 980

Query   455   GACAGGCACAAGTTGGTCTGCGCTACCCCCACCTCCCATGTTTACAAGTCGGACAGGAG 514
|||||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Sbjct   981    GACAGGCACAAGTTGGTCTGCGCTACCCCCACCTCCCATGTTTACAAGTCGGACAGGAG 1040

Query   515   CAGAAACACACCTACCTTCCCTGGAGGCTGTAAACATTGTGGCAGGACAAAGATGTATT 574
|||||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Sbjct   1041  CAGAAACACACCTACCTTCCCTGGAGGCTGTAAACATTGTGGCAGGACAAAGATGTATT 1100

Query   575   AAAAAATTAAACGGACAATCAGACCTCAACCATGATCAGAGGACTGTAGGTCGGCGCCC 634
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Sbjct   1101  AAAAAATTAAACGGACAATCAGACCTCAACCATGATCAGAGGACTGTAGGTCGGCGCCC 1160

Query   635   GATCGGCAAGAAGAGATTAGCAAATTGATGCGAAGTCAAGTTTCAACACAGATCCATAC 694
|||||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Sbjct   1161  GATCGGCAAGAAGAGATTAGCAAATTGATGCGAAGTCAAGTTTCAACACAGATCCATAC 1220

Query   695   GTCCTGAATTTGGAATCATGGTCAAAGATGANATGACAGACGTGACTGGGCGGGTGCTG 754
|||||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Sbjct   1221  GTCCTGAATTTGGAATCATGGTCAAAGATGAGATGACAGACGTGACTGGGCGGGTGCTG 1280

Query   755   CAGCCGCCCTCCATCCTCTACGGGGCAGGAATAAAGCTATTGCGACCCCTGTCAGGGC 814

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Sbjct 1281   |||||||||||||||||||||||||||||||||||||||||||||||||||||| 1340
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Query 815    GTCTGGGACATGCGGAACAAGCAGTTCCACACGGGCATCGAGATCAANGTGTGGGCCATT 874
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1341   GTCTGGGACATGCGGAACAAGCAGTTCCACACGGGCATCGAGATCAAGGTGTGGGCCATT 1400
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Query 875    GCGTGTCTCGCCCCCAGCGCCAGTGCACGGAAAGTCCATCTGAAGTCTTCACAGAGCAG 934
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Query 995    ATACNCCNNGGGGGCGGACAGCNNNGANCC-ATGNTNCGGCNCCNNAAGAACAGTATGN 1053
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Sbjct 1520   ATACGCGCAGGGGGGCGGACAGCGTGGAGCCCATGTTCCGGCACCTGAAGAACAGTATGC 1579
              ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Query 1054   NGNCCGTCAGCTGGNGGNNNCATCCTGCCCNGNAAGa 1094
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Query 31     ATCNTACGTCCGTGAATTTGGAATCATGGTCAAAGATGAGATGACAGACGTGACTGGCC 90
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Query 91     GGGTGTGACAGCCGCCCTCCATCCTCTACGGGGGAGGAATAAAGCTATTGCGACCCCTG 150
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Sbjct 1513   TCTGCAAATACGCGCAGGGGGCGGACAGCGTGGAGCCCATGTTCCGGCACCTGAAGAACA 1572
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Query 391    CGTATGCGGGCCTGCAGCTGGTGGTGGTATCCTGCCCGCAAGACGCCCGTGTACGCCG 450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1573   CGTATGCGGGCCTGCAGCTGGTGGTGGTATCCTGCCCGCAAGACGCCCGTGTACGCCG 1632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Query 451    AGGTCAAGCGCTGGGAGACACGGTGGTGGTGGTGGGATGGCCACGCAGTGCCTGCAGATGAAGA 510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1633   AGGTCAAGCGCTGGGAGACACGGTGGTGGTGGTGGGATGGCCACGCAGTGCCTGCAGATGAAGA 1692
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Query 511    ACGTGCAGAGGACCACGCCACAGACCTGTCCAACCTCTGCCTGAAGATCAACGTCGAAAGC 570
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1693   ACGTGCAGAGGACCACGCCACAGACCTGTCCAACCTCTGCCTGAAGATCAACGTCGAAAGC 1752
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Query 571 TGGGAGCGGTGAACAACATCCTGCTGCCCCAGGGCAGGCCGCGGTGTTCCAGCAGCCCG 630
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Sbjct 1753 TGGGAGCGGTGAACAACATCCTGCTGCCCCAGGGCAGGCCGCGGTGTTCCAGCAGCCCG 1812

Query 631 TCATCTTTCTGGGAGCAGAGCTCACTCAcccccccGCCGGGATGGGAAGAAGCCCTCCA 690
          |||
Sbjct 1813 TCATCTTTCTGGGAGCAGAGCTCACTCACCCCCCGCGGGATGGGAAGAAGCCCTCCA 1872

Query 691 TTGCCGCGGTGGTGGGCAGCATGGACGCCACCCCAATCGCTACTGCGCCACCGTGCGCG 750
          |||
Sbjct 1873 TTGCCGCGGTGGTGGGCAGCATGGACGCCACCCCAATCGCTACTGCGCCACCGTGCGCG 1932

Query 751 TGCAGCAGCACCCGGCAGGAGATCATAACAAGACCTGNCCGCCATGGTCCGCGAGCTCCTCA 810
          |||
Sbjct 1933 TGCAGCAGCACCCGGCAGGAGATCATAACAAGACCTGGCCGCCATGGTCCGCGAGCTCCTCA 1992

Query 811 TCCAGTTCACAAAGTCCACGCGCTTCAAGCCCACCCGCATCATCTTCTACCGCAGCGGTG 870
          |||
Sbjct 1993 TCCAGTTCACAAAGTCCACGCGCTTCAAGCCCACCCGCATCATCTTCTACCGCAGCGGTG 2052

Query 871 TCTCTGAANGCCAGTTCACAGCANN-TTCTCCACCACGAGTTGCTGGCCATCTGTGANGCCT 929
          |||
Sbjct 2053 TCTCTGAAGCCAGTTCACAGCAGTTCTCCACCACGAGTTGCTGGCCATCCGTGAGGCCT 2112

Query 930 GTATCANGCTAGAAAAAGACTACCAGCCCGGGATCACCTTCATCGTGGTGCANAANAGGC 989
          |||
Sbjct 2113 GTATCAAGCTAGAAAAAGACTACCAGCCCGGGATCACCTTCATCGTGGTGCAGAAGAGGC 2172

Query 990 ACCACACCCGGCTCTTCTGCACTGANN-GAACGAGCCGGGNTGGGAAAAGTGNAAACATT 1048
          |||
Sbjct 2173 ACCACACCCGGCTCTTCTGCACTGACAAGAACGAGC-GGGTTGGGAAAAGTGGAAAACATT 2231

Query 1049 CCANCAGGNACGACTG 1064
          |||
Sbjct 2232 CCAGCAGGCACGACTG 2247

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pgEX-Ago2-2-pGEX-3R_F05.ab1

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NNNNNNNNNNNNNNNNNNNNCGCAGGAGATCGTCAGTCAGTCACGATGCGGCCGCTCAAGCAAAGTACATGGTGCCGAGAG
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Query 55 TCAAGCAAAGTACATGGTGGCGAGAGTGTCTTGGTGAACCTGGACCGCTTGGCCAGTGC 114
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Sbjct 2621 TCAAGCAAAGTACATGGTGGCGAGAGTGTCTTGGTGAACCTGGACCGCTTGGCCAGTGC 2562

Query 115 TTGGTGGTCTCGCCCCTTACTCTGCCAGAGGTATGGCTTCCTTCAGCACTGTGATGTT 174
          |||
Sbjct 2561 TTGGTGGTCTCGCCCCTTACTCTGCCAGAGGTATGGCTTCCTTCAGCACTGTGATGTT 2502

Query 175 CTTATCCACAGGTGGTACCTGGCCCGGAAGGCCACAGGTGAGCGTAGTATGCTGGCGC 234
          |||
Sbjct 2501 CTTATCCACAGGTGGTACCTGGCCCGGAAGGCCACAGGTGAGCGTAGTATGCTGGCGC 2442

Query 235 TGGGATGGACACGGAGCGTGTGCAGCGCACGTAGGTGTGACACAGCTGGTAGGTTAGGAT 294
          |||
Sbjct 2441 TGGGATGGACACGGAGCGTGTGCAGCGCACGTAGGTGTGACACAGCTGGTAGGTTAGGAT 2382

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Query	295	CTGCAGCTCATCAGAGGAGAAACGATTGTCGTCCCAGAGGACGTGATAGTGCGAAGGCCT	354
Sbjct	2381	CTGCAGCTCATCAGAGGAGAAACGATTGTCGTCCCAGAGGACGTGATAGTGCGAAGGCCT	2322
Query	355	GCTTGTCCCCTGGATGCCAGCGTGACTACACAGGTAGAAGTCGAACTCGGTGGGGTGGGT	414
Sbjct	2321	GCTTGTCCCCTGGATGCCAGCGTGACTACACAGGTAGAAGTCGAACTCGGTGGGGTGGGT	2262
Query	415	GATTTTCGTGTCCACAGTCGTGCCTGCTGGAATGTTTCCACTTTTCCCAACCCGCTCGTT	474
Sbjct	2261	GATTTTCGTGTCCACAGTCGTGCCTGCTGGAATGTTTCCACTTTTCCCAACCCGCTCGTT	2202
Query	475	CTTGTCACTGCAGAAGAGCCGGGTGTGGTGCCTCTTCTGCACCACGATGAAGGTGATCCC	534
Sbjct	2201	CTTGTCACTGCAGAAGAGCCGGGTGTGGTGCCTCTTCTGCACCACGATGAAGGTGATCCC	2142
Query	535	GGGCTGGTAGTCTTTTCTAGCTTGATACAGGCCTCACGGATGCCAGCAACTCGTGGTG	594
Sbjct	2141	GGGCTGGTAGTCTTTTCTAGCTTGATACAGGCCTCACGGATGCCAGCAACTCGTGGTG	2082
Query	595	GAGAACCTGCTGGAAGTGGCCTTCAGAGACACCGTCGCGGTAGAAGATGATGCGGGTGGG	654
Sbjct	2081	GAGAACCTGCTGGAAGTGGCCTTCAGAGACACCGTCGCGGTAGAAGATGATGCGGGTGGG	2022
Query	655	CTTGAAGCGCGTGGACTTGTAGAAGTGGATGAGGAGCTCGCGGACCATGGCGGCCAGGTC	714
Sbjct	2021	CTTGAAGCGCGTGGACTTGTAGAAGTGGATGAGGAGCTCGCGGACCATGGCGGCCAGGTC	1962
Query	715	TTGTATGATCTCCTGCCGGTGTGCTGCACGCGCACGGTGGCGCAGTAGCGATTGGGGTG	774
Sbjct	1961	TTGTATGATCTCCTGCCGGTGTGCTGCACGCGCACGGTGGCGCAGTAGCGATTGGGGTG	1902
Query	775	GGCGTCCATGCTGCCACCACCGCGCAATGGAGGGCTTCTTCCCATCCCCGGCgggggg	834
Sbjct	1901	GGCGTCCATGCTGCCACCACCGCGCAATGGAGGGCTTCTTCCCATCCCCGGCgggggg	1842
Query	835	GTGAGTGACGTCTGCTCCAGAAAGATGACGGGTGCTGGAAACCCGGCGCCTGCCCTG	894
Sbjct	1841	GTGAGTGACGTCTGCTCCAGAAAGATGACGGGTGCTGGAAACCCGGCGCCTGCCCTG	1782
Query	895	GGGCGCANGATGTTGTTACCGCTCCCAGCTTGACGTTGATNNTTCAGGCANAGGTTGG	954
Sbjct	1781	GGGCGCANGATGTTGTTACCGCTCCCAGCTTGACGTTGATNNTTCAGGCANAGGTTGG	1723
Query	955	ACAGGGTCTGNGNCGNGTCTCNGCACGTTCTTCATCTGCACGCACTGNNNGNNCATC	1014
Sbjct	1722	ACAGGGTCTGNGNCGNGTCTCNGCACGTTCTTCATCTGCACGCACTGC-GTGGCCATC	1664
Query	1015	CCNCGCACNNNTCNCCNNGCTTGACCTCGGNGTANANGGNNGTCTTNNCGGGCA	1074
Sbjct	1663	CCNCGCACNNNTCNCCNNGCTTGACCTCGGNGTANANGGNNGTCTTNNCGGGCA	1606
Query	1075	GGATGAACCACCANCTGCAGGCCCGCATA 1106	
Sbjct	1605	GGATGA-CCACCACAGCTGCAGGCCCGCATA 1575	

pGEX-Ago2-3-pGEX5F_F10.ab1, 4T-1XhoI

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Query 71   TACTCGGGAGCGGGCCCGCACTTGCACCTCCTGCGCCGCGCCGCCATCCAAGGATAT  130
          |||
Sbjct 45   TACTCGGGAGCGGGCCCGCACTTGCACCTCCTGCGCCGCGCCGCCATCCAAGGATAT  104

Query 131  GCCTTCAAGCCTCCACCTAGACCCGACTTTGGGACCTCCGGGAGAACAAATCAAATTACAG  190
          |||
Sbjct 105  GCCTTCAAGCCTCCACCTAGACCCGACTTTGGGACCTCCGGGAGAACAAATCAAATTACAG  164

Query 191  GCCAATTTCTCGAAATGGACATCCCCAAAATTGACATCTATCATTATGAATTGGATATC  250
          |||
Sbjct 165  GCCAATTTCTCGAAATGGACATCCCCAAAATTGACATCTATCATTATGAATTGGATATC  224

Query 251  AAGCCAGAGAAGTGCCCGAGGAGAGTTAACAGGGAAATCGTGGAACACATGGTCCAGCAC  310
          |||
Sbjct 225  AAGCCAGAGAAGTGCCCGAGGAGAGTTAACAGGGAAATCGTGGAACACATGGTCCAGCAC  284

Query 311  TTTAAAACACAGATCTTTGGGGATCGGAAGCCCGTGTGTTGACGGCAGGAAGAATCTATAC  370
          |||
Sbjct 285  TTTAAAACACAGATCTTTGGGGATCGGAAGCCCGTGTGTTGACGGCAGGAAGAATCTATAC  344

Query 371  ACAGCCATGCCCTTCCGATTGGGAGGGACAAGGTGGAGCTGGAGTACGCTGCCAGGA  430
          |||
Sbjct 345  ACAGCCATGCCCTTCCGATTGGGAGGGACAAGGTGGAGCTGGAGTACGCTGCCAGGA  404

Query 431  GAAGGCAAGGATCGCATCTTCAAGGTGTCCATCAAGTGGGTGTCTGCGTGAGCTTGCAG  490
          |||
Sbjct 405  GAAGGCAAGGATCGCATCTTCAAGGTGTCCATCAAGTGGGTGTCTGCGTGAGCTTGCAG  464

Query 491  GCGTTACAGATGCACTTTTCAGGGCGGCTGCCAGCGTCCCTTTTGAGACGATCCAGGCC  550
          |||
Sbjct 465  GCGTTACAGATGCACTTTTCAGGGCGGCTGCCAGCGTCCCTTTTGAGACGATCCAGGCC  524

Query 551  CTGGACGTGGTTCATGAGGCACTTGCCATCCATGAGGTACACCCCGTGGGCGCTCCTTC  610
          |||
Sbjct 525  CTGGACGTGGTTCATGAGGCACTTGCCATCCATGAGGTACACCCCGTGGGCGCTCCTTC  584

Query 611  TTCACCGCTCCGAAGGCTGCTCTAACCCCTTTGGCGGGGGCCGAGAAGTGTGGTTTGGC  670
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Sbjct 585  TTCACCGCTCCGAAGGCTGCTCTAACCCCTTTGGCGGGGGCCGAGAAGTGTGGTTTGGC  644

Query 671  TTCCATCAGTCCGTCGGCCTTCTCTCTGAAAAATGATGCTGAATATTGATGTGTGAGCA  730
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Sbjct 645  TTCCATCAGTCCGTCGGCCTTCTCTCTGAAAAATGATGCTGAATATTGATGTGTGAGCA  704

Query 731  ACAGCGTTTACAAGGCACAGCCAGTAATCGAGTTTGTGTTGTGAAGTTTGGATTTTAAA  790
          |||
Sbjct 705  ACAGCGTTTACAAGGCACAGCCAGTAATCGAGTTTGTGTTGTGAAGTTTGGATTTTAAA  764

Query 791  AGTATTGAAGAACAACAAAAACCTCTGACAGATTCCCAAAGGTAAGTTTACCAAAGAA  850
          |||
Sbjct 765  AGTATTGAAGAACAACAAAAACCTCTGACAGATTCCCAAAGGTAAGTTTACCAAAGAA  824

Query 851  ATTAAGGTCTAANNN-GGAGANAACGCACTGTGGGCAGATGAAGAGGAAGTACCCTGTC  909
          |||
Sbjct 825  ATTAAGGTCTAAGGTGGAGATAACGCACTGTGGGCAGATGAAGAGGAAGTACCCTGTC  884

Query 910  TGCAATGTGACCCGCGCCCGCCAGTACCACAAACATTCCCGCTGCANCNNN-AGCGGG  968
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Sbjct 885  TGCAATGTGACCCGCGCCCGCCAGTACCACAAACATTCCCGCTGCAGCAGGAGAGCGGG  944

Query 969  CANANGNNGNAGTGCACGNG-GGCCAGTNNTTTCNNGN-CNGNNNCNAGTTGGTTCTGC  1026
          |||
Sbjct 945  CAGACGGTGGAGTGC-ACGGTGGCCAGTA-TTCAAGGACAGGCACAAGTTGGTTCTGC  1002

Query 1027 NNCTACCCCCACCNNCCATGTTT  1050
          |||
Sbjct 1003 G-CTACCCCC-ACCTCCCATGTTT  1024
  
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pGEX-Ago2-3-pGEX-3R_G05.ab1
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Query	56	TCAAGCAAAGTACATGGTGCAGAGTGTCTTGGTGAACCTGGACCGCTTGGCCAGTGC	115
Sbjct	2621	TCAAGCAAAGTACATGGTGCAGAGTGTCTTGGTGAACCTGGACCGCTTGGCCAGTGC	2562
Query	116	TTGGTGGTCTCGCCCGTTACTCTGCCAGAGGTATGGCTTCCCTCAGCACTGTCTATGTT	175
Sbjct	2561	TTGGTGGTCTCGCCCGTTACTCTGCCAGAGGTATGGCTTCCCTCAGCACTGTCTATGTT	2502
Query	176	CTTATCCACCAGGTGGTACCTGGCCCGAAGGCCACAGGTGAGCGTAGTATGCTGGCGC	235
Sbjct	2501	CTTATCCACCAGGTGGTACCTGGCCCGAAGGCCACAGGTGAGCGTAGTATGCTGGCGC	2442
Query	236	TGGGATGGACACGGAGCGTGTGCAGCGCACGTAGGTGTGACACAGCTGGTAGGTTAGGAT	295
Sbjct	2441	TGGGATGGACACGGAGCGTGTGCAGCGCACGTAGGTGTGACACAGCTGGTAGGTTAGGAT	2382
Query	296	CTGCAGCTCATCAGAGGAGAAACGATTGTCGTCCCAGAGGACGTGATAGTGCAGAGCCCT	355
Sbjct	2381	CTGCAGCTCATCAGAGGAGAAACGATTGTCGTCCCAGAGGACGTGATAGTGCAGAGCCCT	2322
Query	356	GCTTGTCCCTGGATGCCAGCGTACTACACAGGTAGAAGTCGAACTCGGTGGGGTGGGT	415
Sbjct	2321	GCTTGTCCCTGGATGCCAGCGTACTACACAGGTAGAAGTCGAACTCGGTGGGGTGGGT	2262
Query	416	GATTTTCGTGTCCACAGTCTGCTGCTGGAATGTTTCCACTTTTCCCAACCCGCTCGTT	475
Sbjct	2261	GATTTTCGTGTCCACAGTCTGCTGCTGGAATGTTTCCACTTTTCCCAACCCGCTCGTT	2202
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Sbjct	2201	CTTGTAGTGCAGAAAGCCGGGTGTGGTGCCTCTTCTGCACCAGATGAAGGTGATCCC	2142
Query	536	GGGCTGGTAGTCTTTTTCTAGCTTGATACAGGCCTCACGATGGCCAGCAACTCGTGGT	595
Sbjct	2141	GGGCTGGTAGTCTTTTTCTAGCTTGATACAGGCCTCACGATGGCCAGCAACTCGTGGT	2082
Query	596	GAGAACCTGCTGGAAGTGGCCTTCCAGAGACACCGTTCGCGGTAGAAGATGATGCGGGTGGG	655
Sbjct	2081	GAGAACCTGCTGGAAGTGGCCTTCCAGAGACACCGTTCGCGGTAGAAGATGATGCGGGTGGG	2022
Query	656	CTTGAAGCGCGTGGACTTGTAGAAGTGGATGAGGAGCTCGCGGACCATGGCGGCCAGGTC	715
Sbjct	2021	CTTGAAGCGCGTGGACTTGTAGAAGTGGATGAGGAGCTCGCGGACCATGGCGGCCAGGTC	1962
Query	716	TTGTATGATCTCCTGCCGGTGTGCTGCACGCGCACGGTGGCGCAGTAGCGATTGGGGTG	775
Sbjct	1961	TTGTATGATCTCCTGCCGGTGTGCTGCACGCGCACGGTGGCGCAGTAGCGATTGGGGTG	1902
Query	776	GGCGTCCATGCTGCCACACCGCGGCAATGGAGGGCTTCTTCCATCCCCGGCgggggg	835
Sbjct	1901	GGCGTCCATGCTGCCACACCGCGGCAATGGAGGGCTTCTTCCATCCCCGGCGGGGGG	1842
Query	836	GTGAGTGACGTCTGCTCCCAGAAAGATGACGGGCTGCTGGAAACACCGCGGCTGCCCTG	895
Sbjct	1841	GTGAGTGACGTCTGCTCCCAGAAAGATGACGGGCTGCTGGAAACACCGCGGCTGCCCTG	1782

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Query 896 GGGCAGCANN-TGTTGTTTCAGGCCTCCCAGCTTGACGTTGANNTTCNAGGNAGANGTTGG 954
          |||      |||      |||      |||      |||      |||      |||      |||      |||
Sbjct 1781 GGGCAGCAGGATGTTGTTTCAGGCCTCCCAGCTTGACGTTGATCTTC-AGGCAGAGGTTGG 1723

Query 955 ACAGGGTCTGTGGCGTGGTCCTNNTGCACGTTCTTCATCTGCACGCACTGCGTGGNCATC 1014
          |||      |||      |||      |||      |||      |||      |||      |||      |||
Sbjct 1722 ACAGGGTCTGTGGCGTGGTCCTC-TGCACGTTCTTCATCTGCACGCACTGCGTGGCCATC 1664

Query 1015 CCCAGCANCCTGTNNCCACNCGCTTGAACNTCGNCGNACANGGNCGTCTTGNNGGGCAG 1074
          |||      |||      |||      |||      |||      |||      |||      |||      |||
Sbjct 1663 CCCAGCACCCTGTCTCCACGCGCTTGACC-TCGGCGTACACGGGCGTCTTGCCGGGCAG 1605

Query 1075 GATGA 1079
          |||
Sbjct 1604 GATGA 1600

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Vector: pGEX-4T-3, Sall and NotI
 Insert: Sall and NotI
 Clone 4 is chosen, Framing is perfect.

pGEX vector 5' forward primer: read: to 824

pGEX-Ago2-4-pGEX5F_G10.ab1, 4T-3 Sall

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NNNNNNNNNNNNNNNNCTCGNCTGTTCCGCGT GGA TCC CCG AAT TCC CGG ATC GAC TACTCGGGAGCCGGCCCCCG
ACTTGACCTCTCGGCCGCGCCCCCATCCAAGGATATGCCTTCAAGCTCCACCTAGACCCGACTTTGGGACCTCCG
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ANN

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Query 61 TACTCGGGAGCCGGCCCCGCACTTGACCTCTCGCGCCGCCCCCATCCAAGGATAT 120
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Sbjct 45 TACTCGGGAGCCGGCCCCGCACTTGACCTCTCGCGCCGCCCCCATCCAAGGATAT 104

Query 121 GCCTTCAAGCCTCCACCTAGACCCGACTTTGGGACCTCCGGGAGAACATCAAATTACAG 180
          |||      |||      |||      |||      |||      |||      |||      |||      |||
Sbjct 105 GCCTTCAAGCCTCCACCTAGACCCGACTTTGGGACCTCCGGGAGAACATCAAATTACAG 164

Query 181 GCCAATTTCTTCGAAATGGACATCCCCAAATTGACATCTATCATTATGAATTGGATATC 240
          |||      |||      |||      |||      |||      |||      |||      |||      |||
Sbjct 165 GCCAATTTCTTCGAAATGGACATCCCCAAATTGACATCTATCATTATGAATTGGATATC 224

Query 241 AAGCCAGAGAAGTGCAGGAGAGTTAACAGGGAATCGTGAACACATGGTCCAGCAC 300
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Sbjct 225 AAGCCAGAGAAGTGCAGGAGAGTTAACAGGGAATCGTGAACACATGGTCCAGCAC 284

Query 301 TTTAAACACAGATCTTTGGGGATCGGAAGCCCGTGTGACGCGAGGAAGAAATCTATAC 360
          |||      |||      |||      |||      |||      |||      |||      |||      |||
Sbjct 285 TTTAAACACAGATCTTTGGGGATCGGAAGCCCGTGTGACGCGAGGAAGAAATCTATAC 344

Query 361 ACAGCCATGCCCTTCCGATTGGGAGGACAAAGTGGAGCTGGAGTACGCTGCCAGGA 420
          |||      |||      |||      |||      |||      |||      |||      |||      |||
Sbjct 345 ACAGCCATGCCCTTCCGATTGGGAGGACAAAGTGGAGCTGGAGTACGCTGCCAGGA 404

Query 421 GAAGGCAAGGATCGCATCTTCAAGGTGTCCATCAAGTGGGTGTCCGTGAGCTTGCAG 480
          |||      |||      |||      |||      |||      |||      |||      |||      |||
Sbjct 405 GAAGGCAAGGATCGCATCTTCAAGGTGTCCATCAAGTGGGTGTCCGTGAGCTTGCAG 464

Query 481 GCGTTACACGATGCACTTTCAAGGCGGCTGCCAGCGTCCCTTTTGGAGACGATCCAGGCC 540
          |||      |||      |||      |||      |||      |||      |||      |||      |||

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Sbjct 465  GCCTTACACGATGCACCTTTCAGGGCGGCTGCCAGCGTCCTCTTTGAGACGATCCAGGCC 524
Query 541  CTGGACGTGGTCATGAGGCACTTGCCATCCATGAGGTACACCCCGTGGGCGCTCCTTC 600
          |||
Sbjct 525  CTGGACGTGGTCATGAGGCACTTGCCATCCATGAGGTACACCCCGTGGGCGCTCCTTC 584
Query 601  TTCACCGCTCCGAAGGTGCTCTAACCCCTTTGGCGGGGCGGAGAAAGTGTGGTTTGGC 660
          |||
Sbjct 585  TTCACCGCTCCGAAGGTGCTCTAACCCCTTTGGCGGGGCGGAGAAAGTGTGGTTTGGC 644
Query 661  TTCATCAGTCCGTCGGCCCTCTCTCTGGAAAATGATGCTGAATATTGATGTGTACGA 720
          |||
Sbjct 645  TTCATCAGTCCGTCGGCCCTCTCTCTGGAAAATGATGCTGAATATTGATGTGTACGA 704
Query 721  ACACGGCTTTTACAAGGCACAGCCAGTAATCGAGTTTGTGGTGAAGTTTGGATTTTAAA 780
          |||
Sbjct 705  ACACGGCTTTTACAAGGCACAGCCAGTAATCGAGTTTGTGGTGAAGTTTGGATTTTAAA 764
Query 781  AGTATTGAAGAACAACAAAAACCTCTGACAGATTCCCAAAGGGTAAAGTTTACCAAAGAA 840
          |||
Sbjct 765  AGTATTGAAGAACAACAAAAACCTCTGACAGATTCCCAAAGGGTAAAGTTTACCAAAGAA 824
Query 841  ATTAAGGTCTAAAGGTGGAGATAACGCACTGTGGGCAGATGAAAGGAAGTACCGTCTC 900
          |||
Sbjct 825  ATTAAGGTCTAAAGGTGGAGATAACGCACTGTGGGCAGATGAAAGGAAGTACCGCTC 884
          |||
Query 901  TGCAATGTGACCCGGCGCCCGCCAGTCCAAAACATTCGCCGTGCAGCAGNNAGANCGG 960
          |||
Sbjct 885  TGCAATGTGACCCGGCGCCCGCCAGTCCAAAACATTCGCCGTGCAGCAGG-AGAGCGG 943
Query 961  GCANANNGNGANTGCANNGNGNCCANTATTTANGGACAGGCACAAGTTGGTTCTGCM 1020
          |||
Sbjct 944  GCAGACGGTGGAGTGCACGGTGGCCAGTATTTCAAGGCAGGCACAAGTTGGTTCTGCG 1003
Query 1021 CTACCCCNACCCNCCNNTGTTTACAAGTC 1048
          |||
Sbjct 1004 CTACCCCNACCCNCCNNTGTTTACAAGTC 1031

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Home 3/26/11 9:44 PM
Comment: It is G in the
Home 3/26/11 9:44 PM
Comment: Doesn't change the coding

Ago2 Sequence primer 1: read: 567 to 1466

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pGEX-Ago2-4-Ago2-seq1_A03.ab1
NNNNNNNNNNNNNNNCCNCCGTTGGGCGCTCCTTCTTCCACCGCTCCGAAGGCTGCTCTAACCCCTCTTG
GCGGGGCGGAGAAAGTGTGGTTTGGCTTCCATCAGTCCGTCGGCCCTTCTCTGGAAAATGATGCTGAATATTGATGTG
TCAGCAACAGCGTTTTACAAGGCACAGCCAGTAATCGAGTTTGTGGTGAAGTTTGGATTTTAAAAGTATTGAAGAACA
ACAAAAACCTCTGACAGATTCCCAAAGGGTAAAGTTTACCAAAGAAATTAAGGCTCAAAGGTGGAGATAACGCACTGTG
GGCAGATGAAGAGGAAGTACCGTGTCTGCAATGTGACCAGGCGCCCGCCAGTCCAAAACATTCCGCTGCAGCAGGAG
AGCGGGCAGACGGTGGAGTGCACGGTGGCCAGTATTTCAAGGACAGGCACAAGTTGGTTCTGCGTACCACCCAGTCCTC
ATGTTTACAAGTCCGACAGGAGCAGAAACACACCTACCTTCCCTGGAGGTCTGTAAACATTGTTGGCAGGACAAAGATGTA
TTAAAAAATTAACGGACAATCAGACTCAACCATGATCAGAGCGACTGCTAGGTCCGCGCCGATCCGCAAGAAGAGATT
AGCAAAATGATGCGAAGTGAAGTTTCAACACAGATCCATACGTCCTGTAATTTGGAATCATGTTCAAAGATGAGATGAC
AGACGTGACTGGGCGGTGCTGACCGCCCTCCATCCTTACGGGGGAGGAATAAAGCTATTGCGACCCCTGTCCAGG
GCGTCTGGGACATGCGGAACAAGCAGTTCACACGGGCATCAGATCAAGGTTGGGCCATTCGCTCCGCCCCAG
CGCCAGTGCACGGAAGTCCATCTGAAGTCTTACAGAGCAGCTCAGAAAGATCTCGAGAGACGCGCGCATGCCATCC
AGGGCAGCCGTCTCTGCAANTACGCGNNNGGGGCGGANAGCCTNNNCCCATGNTNCGGCACCTGAAAGAACAGTATG
CGGNNGCAGCNGGTNGNNGNCATCNNNCNANANGCCGNNACNCNAGNCAANNNNNNGGNNANNNNCTGG
GGANGNNNNNNNNNNGCANATGAANAANNNTNNCN
Query 29   CCGTGGGCGCTCCTTCTTCCCGCTCCGAAGGCTGCTCTAACCCCTTTGGCGGGGC 88
          |||
Sbjct 567  CCCGTGGGCGCTCCTTCTTCCCGCTCCGAAGGCTGCTCTAACCCCTTTGGCGGGGC 626
Query 89   CGAGAAGTGTGGTTTGGCTTCCATCAGTCCGTCGGCCTTCTCTCTGGAAAATGATGCTG 148
          |||
Sbjct 627  CGAGAAGTGTGGTTTGGCTTCCATCAGTCCGTCGGCCTTCTCTCTGGAAAATGATGCTG 686
Query 149  AATATTGATGTGTCAGCAACAGCGTTTTTACAAGGCACAGCCAGTAATCGAGTTTGGTTGT 208
          |||
Sbjct 687  AATATTGATGTGTCAGCAACAGCGTTTTTACAAGGCACAGCCAGTAATCGAGTTTGGTTGT 746
Query 209  GAAGTTTGGATTTTAAAAGTATTGAAGAACAACAAAAACCTCTGACAGATTCCCAAAGG 268
          |||
Sbjct 747  GAAGTTTGGATTTTAAAAGTATTGAAGAACAACAAAAACCTCTGACAGATTCCCAAAGG 806
Query 269  GTAAAGTTTACCAAAGAAATTAAGGCTCAAAGGTGGAGATAACGCACTGTGGGCAGATG 328

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Sbjct	1213	ATCCATACGTCCGTGAATTTGGAATCATGGTCAAAGATGAGATGACAGACGTGACTGGGC	1272
Query	88	GGGTGCTGCAGCCGCCCTCCATCCTCTACGGGGCAGGAATAAAGCTATTGCGACCCCTG	147
Sbjct	1273	GGGTGCTGCAGCCGCCCTCCATCCTCTACGGGGCAGGAATAAAGCTATTGCGACCCCTG	1332
Query	148	TCCAGGCGCTCTGGGACATGCGGAACAAGCAGTTCCACACGGGCATCGAGATCAAGGTGT	207
Sbjct	1333	TCCAGGCGCTCTGGGACATGCGGAACAAGCAGTTCCACACGGGCATCGAGATCAAGGTGT	1392
Query	208	GGGCCATTGCGTGTTCGCCCCCGAGCGCCAGTGACCGGAAGTCCATCTGAAGTCCTTCA	267
Sbjct	1393	GGGCCATTGCGTGTTCGCCCCCGAGCGCCAGTGACCGGAAGTCCATCTGAAGTCCTTCA	1452
Query	268	CAGAGCAGCTCAGAAAGATCTCGAGAGACGCCGGCATGCCCATCCAGGGCCAGCCGTGCT	327
Sbjct	1453	CAGAGCAGCTCAGAAAGATCTCGAGAGACGCCGGCATGCCCATCCAGGGCCAGCCGTGCT	1512
Query	328	TCTGCAAAATACGCGCAGGGGGCGGACAGCGTGGAGCCCATGTTCCGGCACCTGAAGAACA	387
Sbjct	1513	TCTGCAAAATACGCGCAGGGGGCGGACAGCGTGGAGCCCATGTTCCGGCACCTGAAGAACA	1572
Query	388	CGTATGCGGGCTGCAGTGGTGGTGGTTCATCCTGCCCGGCAAGACGCCCGTGTACGCCG	447
Sbjct	1573	CGTATGCGGGCTGCAGTGGTGGTGGTTCATCCTGCCCGGCAAGACGCCCGTGTACGCCG	1632
Query	448	AGGTCAAGCGCGTGGGAGACACGGTGTGGGATGGCCACGCAGTCCGTGCAGATGAAGA	507
Sbjct	1633	AGGTCAAGCGCGTGGGAGACACGGTGTGGGATGGCCACGCAGTCCGTGCAGATGAAGA	1692
Query	508	ACGTGCAGAGGACCACGCCACAGACCTGTCCAACCTCTGCCTGAAGATCAACGTCAAGC	567
Sbjct	1693	ACGTGCAGAGGACCACGCCACAGACCTGTCCAACCTCTGCCTGAAGATCAACGTCAAGC	1752
Query	568	TGGGAGCGCTGAACAACATCCTGCTGCCCGAGGGCAGCCCGCGGTTCAGCAGCCCG	627
Sbjct	1753	TGGGAGCGCTGAACAACATCCTGCTGCCCGAGGGCAGCCCGCGGTTCAGCAGCCCG	1812
Query	628	TCATCTTTCTGGGAGCAGACGTCACTCAccccccGCCGGGATGGGAAGCCCTCCA	687
Sbjct	1813	TCATCTTTCTGGGAGCAGACGTCACTCAccccccGCCGGGATGGGAAGCCCTCCA	1872
Query	688	TTGCCGCCGTGGTGGGCAGCATGGACGCCACCCCAATCGCTACTGCGCCACCGTGC	747
Sbjct	1873	TTGCCGCCGTGGTGGGCAGCATGGACGCCACCCCAATCGCTACTGCGCCACCGTGC	1932
Query	748	TGCAGCAGCACCAGGAGATCATAACAAGACCTGGCCGCCATGGTCCGCGAGCTCCTCA	807
Sbjct	1933	TGCAGCAGCACCAGGAGATCATAACAAGACCTGGCCGCCATGGTCCGCGAGCTCCTCA	1992
Query	808	TCCAGTTCTACAAGTCCACGCGCTTCAAGCCACCCGCATCATCTTCTACCGCAGCGGTG	867
Sbjct	1993	TCCAGTTCTACAAGTCCACGCGCTTCAAGCCACCCGCATCATCTTCTACCGCAGCGGTG	2052
Query	868	TCTCTGAAGCCAGTTCACGNN-TTCTCCACCAGAGTTGCTGGCCATCCGTGAGGCCT	926
Sbjct	2053	TCTCTGAAGCCAGTTCACGNN-TTCTCCACCAGAGTTGCTGGCCATCCGTGAGGCCT	2112
Query	927	GTATCAAGCTAGAAAAGACTACCAGCCCGGATCACCTTCATCGTGGTGCANAANAGGC	986
Sbjct	2113	GTATCAAGCTAGAAAAGACTACCAGCCCGGATCACCTTCATCGTGGTGCANAANAGGC	2172
Query	987	ACCACACCCGGCTCTNCTGCACTGACAAGAACGAGCGGTTGGGAAAAGNNNAACATTN	1046
Sbjct	2173	ACCACACCCGGCTCTNCTGCACTGACAAGAACGAGCGGTTGGGAAAAGTGGAAACATTC	2232
Query	1047	CAGCAGGCAGACTGNTGGNCAGAAAATCACCC-CNCC-CNNGANTTCGACTNCTAC	1102
Sbjct	2233	CAGCAGGCAGACTG-TGGACAGAAAATCACCCACCCACC-GAGTTCGACTTCTAC	2288

Ago2 sequence primer 3: read: 1810-2577

pGEX-Ago2-4-Ago2-seq3_C03 . ab1
 NNNNNNNNNNNNNNNNNNNNNNNCAGCCNGTCATCTTTCTGGGAGCAGACGTCACTCAcccccccGCCGGGGATGGGAAGAAG
 AAGCCCTCCATTCGCCCGGTGGGGCAGCATGGACGCCACCCCAATCGCTACTGCGCCACCCTGCGCGTGCAGCAGCA
 CCGGACAGGAGATCATAAAGACTGGCCGCGCATGGTCCGCGAGCTCCTCATCCAGTTCTACAAGTCCACGCGCTTAAGC
 CCACCAGCATCATCTTACCGCGACGGTGTCTCTGAAGGCCAGTTCAGCAGGTTCTCCACCACAGTTGCTGGCCATC
 CGTAGGCCCTGTATCAAGTAGAAAAGACTACCAGCCGGGATCACCTTCATCGTGGTGCAGAAGAGGCACCACCCG
 GCTCTTCTGACTGACAAGAACGAGCGGGTGGGAAAAGTGGAAACATTCCAGCAGGCACGACTGGGACACGAAATCA
 CCCACCCACCGAGTTCGACTTCTACTGTGTAGTACAGCTGGCATCCAGGGGACAAGCAGGCTTCGCACTATCACGTC
 CTCTGGGACGAACTCTCTCTGATGAGCTGCAGTCTAACCTACCAGCTGTGTACACCTACGTCGGCTGCAC
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 GTTCACCAAGACACTCTGTGACCAATGTAATTGCTTGAGCGGCCGCATCGTGACTGACTGACGATCTGCTCGCGCTT
 TCGGTGATGACGGTGAACAACTTCTGACACATGCACTCCCGGAGACGGTACAGCTTGTCTGAAGCGGATGCCGGGAGC
 AGACAAGCCCGTCAGNGCGTCAAGCGGGTGGGGGCGTCCGAGGCGCAGCATTGACCCAGTCNCCGTANCATAGCCN
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 NNACGTCCNNGNNANTTTTCGNNAANGCCNNNNNNCCNNNNNNNNNNNTTNCANNANNNNNNANNNNNNNTCANN
 NNNNNANNAACNNNNNNNNNNNNN

Query	24	CAGCCNGTCATCTTTCTGGGAGCAGACGTCACTCA	cccccccGCCGGGGATGGGAAGAAG	83
Sbjct	1806	CAGCCCCTCATCTTTCTGGGAGCAGACGTCACTCA	CCCCCCCCGCGGGATGGGAAGAAG	1865
Query	84	CCCTCCATTGCCCGCGTGGTGGGCAGCATGGACGCC	ACCCCAATCGCTACTGCGCCACC	143
Sbjct	1866	CCCTCCATTGCCCGCGTGGTGGGCAGCATGGACGCC	ACCCCAATCGCTACTGCGCCACC	1925
Query	144	GTGCGCGTGCAGCAGCACCCGACGAGATCATA	AAGACCTGGCCGCCATGGTCCGCGAG	203
Sbjct	1926	GTGCGCGTGCAGCAGCACCCGACGAGATCATA	AAGACCTGGCCGCCATGGTCCGCGAG	1985
Query	204	CTCCTCATCCAGTTCACAAGTCCACGCGCTTCA	AGCCACCCGCATCATCTTCTACCGC	263
Sbjct	1986	CTCCTCATCCAGTTCACAAGTCCACGCGCTTCA	AGCCACCCGCATCATCTTCTACCGC	2045
Query	264	GACGGTGTCTCTGAAGGCCAGTTCACAGCAGTTC	CCACCACGAGTTGCTGGCCATCCGT	323
Sbjct	2046	GACGGTGTCTCTGAAGGCCAGTTCACAGCAGTTC	CCACCACGAGTTGCTGGCCATCCGT	2105
Query	324	GAGGCCGTATCAAGCTAGAAAAGACTACCAGCCGG	GATCACCTTCATCGTGGTGAG	383
Sbjct	2106	GAGGCCGTATCAAGCTAGAAAAGACTACCAGCCGG	GATCACCTTCATCGTGGTGAG	2165
Query	384	AAGAGGCACACACCCGGCTTCTGCACTGACA	AAGACGAGCGGGTGGGAAAAGTGA	443
Sbjct	2166	AAGAGGCACACACCCGGCTTCTGCACTGACA	AAGACGAGCGGGTGGGAAAAGTGA	2225
Query	444	AACATTCAGCAGGACGACTGTGGACACGAAAA	TACCCACCCACCAGTTGCACTTC	503
Sbjct	2226	AACATTCAGCAGGACGACTGTGGACACGAAAA	TACCCACCCACCAGTTGCACTTC	2285
Query	504	TACCTGTGTAGTCAAGTCCGCTGGCATCCAGGGG	AAGCAGGCTTCGCACTATCACGTCCTC	563
Sbjct	2286	TACCTGTGTAGTCAAGTCCGCTGGCATCCAGGGG	AAGCAGGCTTCGCACTATCACGTCCTC	2345
Query	564	TGGGACGACAATCGTTTCTCTGTATGAGCTGC	AGATCCTAACCTACCAGCTGTGTCAC	623
Sbjct	2346	TGGGACGACAATCGTTTCTCTGTATGAGCTGC	AGATCCTAACCTACCAGCTGTGTCAC	2405
Query	624	ACCTACGTGCGCTGCACACGCTCCGTGTCCAT	CCCAGCGCCAGCATACTACGCTCACCTG	683
Sbjct	2406	ACCTACGTGCGCTGCACACGCTCCGTGTCCAT	CCCAGCGCCAGCATACTACGCTCACCTG	2465
Query	684	GTGGCCTTCGGGCCAGGTACACCTGGTGGATA	AAGGAACATGACAGTGTGAAGGAAGC	743
Sbjct	2466	GTGGCCTTCGGGCCAGGTACACCTGGTGGATA	AAGGAACATGACAGTGTGAAGGAAGC	2525
Query	744	CATACCTCTGGGCAGAGTAACGGGGCAGACC	ACCAAGCACTGGCCAA gCGG CCAGGTT	803
Sbjct	2526	CATACCTCTGGGCAGAGTAACGGGGCAGACC	ACCAAGCACTGGCCAA gCGG TCCAGGTT	2585
Query	804	CACCAAGACACTCTGTGCACCATGTACTTTGCT	TGA 839	

Sbjct 2586 CACCAAGACACTCTGCGCACCATGTACTTTGCTTGA 2621

pGEX-Ago2-4-pGEX3R_D03.ab1

NNNNNNNNNNNNNNNAACNCGCGAGGACAGATCGTCAGTCACTGCGGCGCTCAAGCAAAGTACATGGTGACAG
AGTGTCTTGGTGAACCTGGGCGCCTTGGCCAGTGTCTGGTGTCTCGCCGTTACTCTGCCAGAGGTATGGCTTCCTT
CAGCACTGTATGTTCCCTATCCACCAGGTGGTACCTGGCCCGAAAGGCCACCAGGTGAGCGTAGTATGCTGGCGCTGGG
ATGGACACGGAGCGTGTGACGCGACGTAGGTGTGACACAGCTGGTAGGTTAGGATCTGCAGCTCATCAGAGGAGAAACG
ATTGTGCTCCAGAGGACGTAGTGTGCGAAGGCTGCTTGTCCCTGGATGCCAGCGTGACTACACAGGTAGAAAGTCGA
ACTCGGTGGGTGGGTGATTTTCGTGTCCACAGTCTGCTGCTGGAATGTTCCACTTTTCCCAACCCGCTCGTTCTTG
TCAGTGAGAAGAGCCGGGTGTGGTGCCTCTTCTGCACCACGATGAAGGTGATCCCGGGCTGGTAGTCTTTTTCTAGCTT
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NNCCNNCNCNTCNCNCCNNGNNNATTTGCNNANNNGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAATNTTNNGN
ANNNNNNNN

Query 57 TCAAGCAAAGTACATGGTGC CAGAGTGTCTTGGTGAACCTGC CCGCCTTGGCCAGTGC 116
Sbjct 2621 TCAAGCAAAGTACATGGTGCAGAGTGTCTTGGTGAACCTGGACCGCCTTGGCCAGTGC 2562
Query 117 TTGGTGGTCTCGCCCGTTACTCTGCCAGAGGTATGGCTTCCTTCAGCACTGTATGTTTC 176
Sbjct 2561 TTGGTGGTCTCGCCCGTTACTCTGCCAGAGGTATGGCTTCCTTCAGCACTGTATGTTTC 2502
Query 177 CTTATCCACCAGGTGGTACCTGGCCCGAAGGCCACCAGGTGAGCGTAGTATGCTGGCGC 236
Sbjct 2501 CTTATCCACCAGGTGGTACCTGGCCCGAAGGCCACCAGGTGAGCGTAGTATGCTGGCGC 2442
Query 237 TGGGATGGACACGGAGCGTGTGCAGCGCACGTAGGTGTGACACAGCTGGTAGGTAGGAT 296
Sbjct 2441 TGGGATGGACACGGAGCGTGTGCAGCGCACGTAGGTGTGACACAGCTGGTAGGTAGGAT 2382
Query 297 CTGCAGCTCATCAGAGGAGAAACGATTGTCGTCCAGAGGACGTGATAGTGCAAGGCCT 356
Sbjct 2381 CTGCAGCTCATCAGAGGAGAAACGATTGTCGTCCAGAGGACGTGATAGTGCAAGGCCT 2322
Query 357 GCTTGTCCCTGGATGCCAGCGTGACTACACAGGTAGAAGTCGAACTCGGTGGGGTGGGT 416
Sbjct 2321 GCTTGTCCCTGGATGCCAGCGTGACTACACAGGTAGAAGTCGAACTCGGTGGGGTGGGT 2262
Query 417 GATTTTCGTGTCCACAGTCTGCTGCTGGAATGTTTCCACTTTTCCCAACCCGCTCGTT 476
Sbjct 2261 GATTTTCGTGTCCACAGTCTGCTGCTGGAATGTTTCCACTTTTCCCAACCCGCTCGTT 2202
Query 477 CTTGTGAGTGCAGAAGAGCCGGGTGTGGTGCCTCTTCTGCACCACGATGAAGGTGATCCC 536
Sbjct 2201 CTTGTGAGTGCAGAAGAGCCGGGTGTGGTGCCTCTTCTGCACCACGATGAAGGTGATCCC 2142
Query 537 GGGCTGGTAGTCTTTTTCTAGCTTGATACAGGCTCACGGATGGCCAGCAACTCGTGGTG 596
Sbjct 2141 GGGCTGGTAGTCTTTTTCTAGCTTGATACAGGCTCACGGATGGCCAGCAACTCGTGGTG 2082
Query 597 GAGAACCTGCTGGAACCTGGCCTTCAGAGACACCGTCGCGGTANAAGATGATGCGGGTGGG 656
Sbjct 2081 GAGAACCTGCTGGAACCTGGCCTTCAGAGACACCGTCGCGGTANAAGATGATGCGGGTGGG 2022
Query 657 CTTGAAGCGCTGGACTTGTAGAAGTGGATGAGGAGCTCGCGGACCATGGCGGCCAGGTC 716
Sbjct 2021 CTTGAAGCGCTGGACTTGTAGAAGTGGATGAGGAGCTCGCGGACCATGGCGGCCAGGTC 1962
Query 717 TTGTATGATCTCCTGCCGGTGTGCTGCACGCGCACGGTGGCGCANTANCGATTGGGGTG 776
Sbjct 1961 TTGTATGATCTCCTGCCGGTGTGCTGCACGCGCACGGTGGCGCANTANCGATTGGGGTG 1902
Query 777 GCGTCCATGCTGCCACACCGCGGCAATGGANGGCTTCTTCCATCCCCGGCGgggggg 836
Sbjct 1901 GCGTCCATGCTGCCACACCGCGGCAATGGANGGCTTCTTCCATCCCCGGCGGGGGG 1842
Query 837 TGAGTGACGTCTGCTCCAGAAAGATGACGGGCTGCTGGAACACCGGGGCTGCGCCTG 896

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Sbjct 1841 |||||
GTGAGTGACGTCTGCTCCCAGAAAGATGACGGGCTGCTGGAACACCGGGGCTGCCCTG 1782

Query 897 GGGCAGCANN-TGTTGTTACAGCCTCCCAGCTTGACGTTGATCTTCNNTTGA 954
||||| |||||

Sbjct 1781 GGGCAGCAGGATGTTGTTACAGCCTCCCAGCTTGACGTTGATCTTCAGGCAGAGTTGA 1722

Query 955 CAGGGTCTGTGGCGTGGNCTCTGCNCGTTCTTCATCTGCACGCACTGCGTGNN-ATCCC 1013
||||| |||||

Sbjct 1721 CAGGGTCTGTGGCGTGGTCTCTGCACGTTCTTCATCTGCACGCACTGCGTGGCCATCCC 1662

Query 1014 CAGCACCGTGTNNNCNACNCGCTTGACCTNNTTGTANNNGGNGTNTTGNNGGNAGGAT 1072
||||| |||||

Sbjct 1661 CAGCACCGTGTCTCCCACGCGCTTGACCTCGGCGTACACGGGCGTCTTGCCGGGCAGGAT 1602

Query 1073 GANNACCANNGCTGCAGNCC-GCATA 1099
|| ||| ||||| |||||

Sbjct 1601 GACCACCACCAGCTGCAGGCCCGCATA 1574

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