NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARi53H06

Lot# : 7675_B3Bd

Vector : pGCAP10

Gene	ZNF268	
RefSeq_mRNA	NM_003415.3	13390 bp

● Plasmid DNA purification

Date : 2023/03/27 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2023/03/28 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2023/03/28

DNA concentration (O.D.): 216 ng/ul

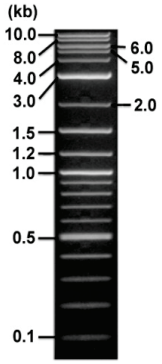
DNA	0.5 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.5 ul
Total	10 ul

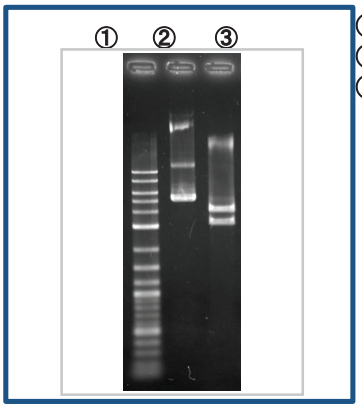
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 5.1, 0.3, 0.2 kb (unsure)

Erectrophoresis : 1% agarose gel, 1x TAE Buffer

Marker : 2-Log DNA Ladder (NEB#N3200L)





①:Marker
②:uncut
③:BamHI

● Confirmation of the sequence

Date : 2026/06/22

full sequence	ARi53H06hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/07/23

DNA (216 ng/ul)	78 ul
10x TE	67 ul
dH_2O	529 ul
Total	674 ul

● Shipping

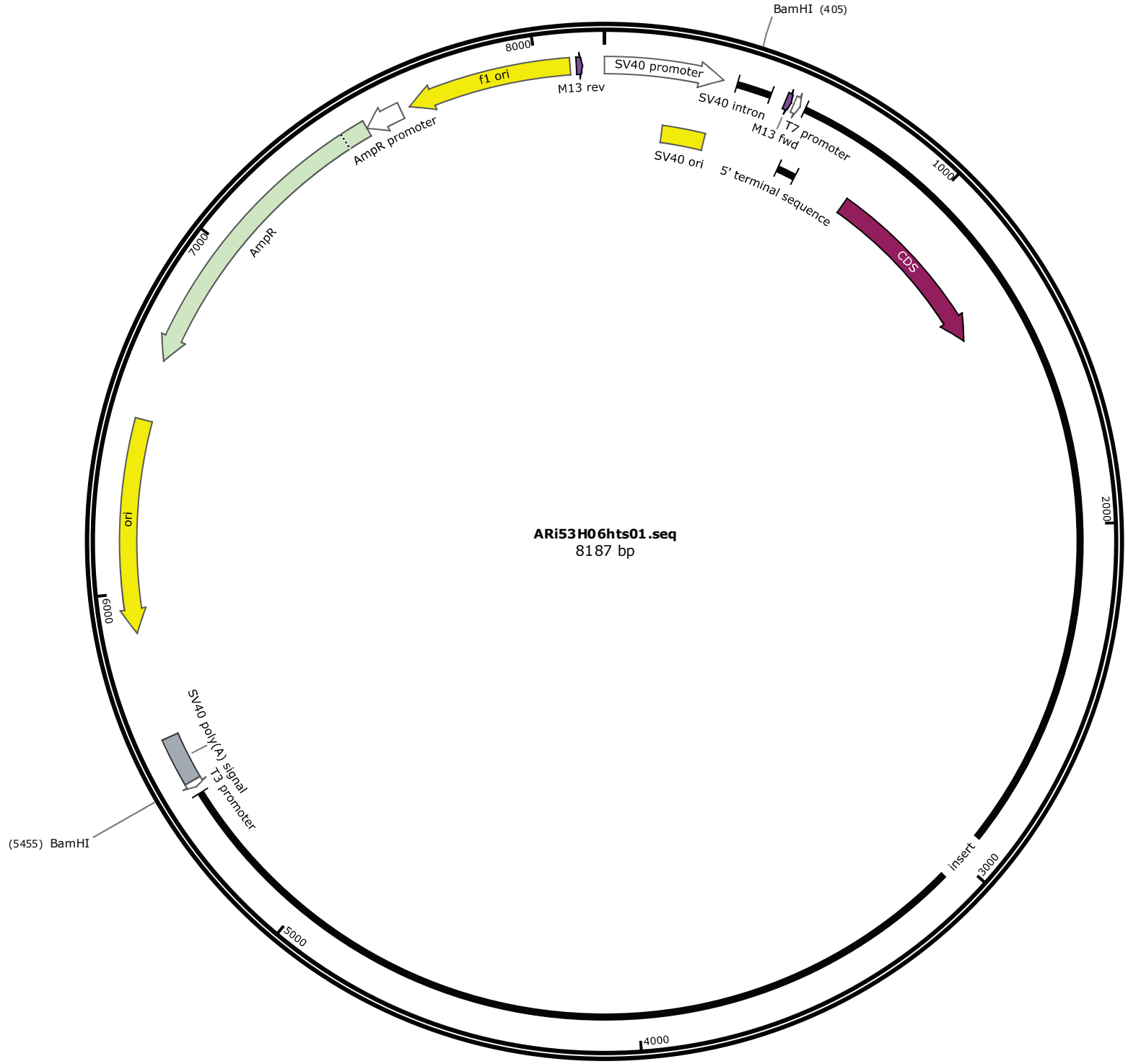
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY :

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'26.07.23
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http://dna.brc.riken.jp/index.html


BamHI (405)
8000
f1 ori
M13 rev
SV40 promoter
SV40 intron
M13 fwd
T7 promoter
1000
AmpR promoter
SV40 ori
5' terminal sequence
CDS
7000
AmpR
2000
ori
6000
SV40 poly(A) signal
T3 promoter
(5455) BamHI
insert
3000
5000
4000
ARi53H06hts01.seq
8187 bp

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_003415:Homo sapiens zinc finger protein...

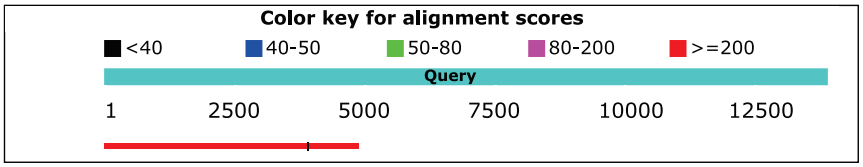
RID 3H74XWTV114 (Expires on 06-23 10:23 am)

Query ID	NM_152943.3	**Subject ID**	lcl|Query_3152731
Description	Homo sapiens zinc finger protein 268 (ZNF268), transcript variant 3, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	13496	**Subject Length**	8187
		Program	BLASTN 2.17.0+

ARi53H06hts01.seq

Graphic Summary

Distribution of the top 4 Blast Hits on 1 subject sequences



Dot Matrix View

Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
None provided	7035	10746	35%	0.0	99.84%	Query_3152731

Alignments

Sequence ID: Query_3152731 Length: 8187 Number of Matches: 4
Range 1: 568 to 4394

Score	Expect	Identities	Gaps	Strand	Frame
7035 bits(3809)	0.0()	3822/3828(99%)	1/3828(0%)	Plus/Plus	

Features:

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Query              10    GGCCGCCATTGTTCCGCGCCGATGGCGAGATCCTTGTTCCTCAGATAGCGTTCATCGCCC  69
Sbjct              568   ..............................................................  627

Query              70    GTCGTGGTCAACGGGCCAGCCGAGTCTGGAGTGGTTGCGAACCCTTCTGGCTGCAGATCT  129
Sbjct              628   ..............................................................  687

Query              130   GGAGGTGGAGGCAGTACCCTGGACTCTATTCTGCTGCCCCTTCAGGGTTTGGAGGAGCCG  189
Sbjct              688   ..............................................................  747

CDS:zinc finger prot  1                                                    M  A
Query              190   GAGCATCCCTCGCGTCCTGTCACTTCCAGCGAGGCACACAAAACTGACCGTAGGGATGGC  249
Sbjct              748   ..............................................................  807

CDS:zinc finger prot  3     T  R  V  R  T  A  S  I  W  V  P  P  L  Q  E  R  N  S  S  W
Query              250   CACCAGGGTCCGGACAGCTTCTATTTGGGTCCCACCTCTCCAAGAACGAAACAGTTCATG  309
Sbjct              808   ..............................................................  867

CDS:zinc finger prot  23    D  R  I  R  K  L  Q  G  Q  E  S  I  L  G  Q  G  T  P  G  L
Query              310   GGATAGGATCAGAAAGCTCCAAGGTCAGGAATCCATCTTGGGCCAAGGGACTCCTGGTCT  369
Sbjct              868   ..............................................................  927
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CDS:zinc finger prot  43     Q  P  L  P  G  T  P  R  Q  K  Q  K  S  R  R  I  E  K  V  L
Query                 370    GCAACCTCTCCCTGGAACACCCAGGCAGAAGCAGAAGAGTCGCAGAATAGAGAAAGTCCT  429
Sbjct                 928    ............................................................  987

CDS:zinc finger prot  63     E  W  L  F  I  S  Q  E  Q  P  K  I  T  K  S  W  G  P  L  S
Query                 430    AGAGTGGCTGTTTATTTCCCAAGAGCAGCCAAAAATCACCAAGTCCTGGGGACCTTTGTC  489
Sbjct                 988    ............................................................  1047

CDS:zinc finger prot  83     F  M  D  V  F  V  D  F  T  W  E  E  W  Q  L  L  D  P  A  Q
Query                 490    ATTCATGGATGTGTTTGTGGATTTTACCTGGGAGGAGTGGCAGCTGCTAGACCCAGCACA  549
Sbjct                 1048   ............................................................  1107

CDS:zinc finger prot  103    K  C  L  Y  R  S  V  M  L  E  N  Y  S  N  L  V  S  L  G  Y
Query                 550    GAAGTGCCTGTACAGGAGTGTGATGTTGGAGAACTATAGCAACCTGGTGTCCCTAGGGTA  609
Sbjct                 1108   ............................................................  1167

CDS:zinc finger prot  123    Q  H  T  K  P  D  I  I  F  K  L  E  Q  G  E  E  L  C  M  V
Query                 610    CCAACACACCAAACCTGATATCATCTTCAAGTTGGAACAAGGAGAAGAGCTGTGTATGGT  669
Sbjct                 1168   ............................................T...............  1227

CDS:zinc finger prot  143    Q  A  Q  V  P  N  Q  T  C  P  I  L  K  A  G  K  S  K  A  K
Query                 670    GCAGGCCCAAGTTCCAAATCAGACCTGTCCAATTTTGAAGGCTGGAAAGTCCAAAGCCAA  729
Sbjct                 1228   ............................................................  1287

CDS:zinc finger prot  163    V  L  A  G  L  V  S  G  E  G  L  L  C  A  S  K  M  T  P  C
Query                 730    GGTGCTGGCAGGTTTGGTGTCTGGTGAGGGCCTGCTCTGTGCTTCCAAGATGACGCCTTG  789
Sbjct                 1288   ..........................................A.................  1347

CDS:zinc finger prot  183    C  C  I  L  W  R  H  S  L  E  N
Query                 790    TTGCTGCATCCTCTGGAGACACAGTCTGGAAAATTGATGATCTTATGGATTGGCATCAGG  849
Sbjct                 1348   ............................................................  1407

Query                 850    AAAATAAAGACAAGCTGGGAAGTACGGCAAAAAGCTTTGAATGCACTACATTTGGAAAAC  909
Sbjct                 1408   ............................................................  1467

Query                 910    TATGTCTTCTTAGTACAAAGTATCTTTCAAGACAAAAACCTCATAAATGTGGCACGCATG  969
Sbjct                 1468   ............................................................  1527

Query                 970    GAAAGAGTTTGAAATATATAGATTTCACTAGTGATTATGCTAGAAATAATCCTAATGGGT  1029
Sbjct                 1528   ............................................................  1587

Query                 1030   TTCAGGTACATGGAAAATCATTCTTCCATTCTAAACATGAGCAAACTGTTATTGGAATAA  1089
Sbjct                 1588   ............................................................  1647

Query                 1090   AATACTGTGAAAGTATTGAATCTGGAAAAACCGTCAATAAGAAATCGCAACTTATGTGCC  1149
Sbjct                 1648   ............................................................  1707

Query                 1150   AACAAATGTATATGGGCGAAAAACCCTTTGGATGCAGCTGTTGTGAGAAAGCCTTCAGCA  1209
Sbjct                 1708   ............................................................  1767

Query                 1210   GCAAGTCATACCTTCTAGTGCATCAGCAAACTCATGCCGAAGAGAAACCCTATGGTTGTA  1269
Sbjct                 1768   ............................................................  1827

Query                 1270   ATGAATGTGGGAAAGACTTCAGTAGTAAATCATACCTCATTGTACATCAGAGAATTCATA  1329
Sbjct                 1828   ............................................................  1887

Query                 1330   CAGGAGAGAAACTACATGAATGCAGTGAATGCAGGAAAACATTCAGTTTCCATTCACAGC  1389
Sbjct                 1888   ............................................................  1947

Query                 1390   TTGTTATACATCAGAGAATTCACACAGGTGAGAATCCCTATGAGTGCTGTGAATGTGGGA  1449
Sbjct                 1948   ............................................................  2007

Query                 1450   AAGTCTTCAGTAGGAAAGACCAGCTTGTTTCACACCAGAAAACTCATTCAGGACAGAAAC  1509
Sbjct                 2008   ............................................................  2067

Query                 1510   CATATGTGTGTAATGAATGTGGGAAAGCTTTTGGTTTAAAATCACAGCTCATTATACATG  1569
Sbjct                 2068   ............................................................  2127

Query                 1570   AAAGAATTCATACAGGAGAGAAACCATATGAATGCAATGAATGTCAGAAAGCCTTTAATA  1629
Sbjct                 2128   ............................................................  2187

Query                 1630   CAAAGTCAAACCTTATGGTACATCAGAGAACCCATACAGGGGAGAAACCTTATGTTTGTA  1689
Sbjct                 2188   ............................................................  2247

Query                 1690   GTGATTGTGGAAAAGCCTTTACATTCAAGTCACAGCTCATTGTACATCAGGGGATTCACA  1749
Sbjct                 2248   ............................................................  2307

Query                 1750   CAGGAGTAAAGCCCTATGGGTGTATTCAGTGTGGTAAAGGATTCAGTTTGAAATCACAGC  1809
Sbjct                 2308   ............................................................  2367

Query                 1810   TCATTGTACATCAGAGAAGTCACACAGGAATGAAACCTTATGTATGCAATGAATGTGGCA  1869
Sbjct                 2368   ............................................................  2427

Query                 1870   AAGCCTTCAGGAGCAAGTCATACCTTATTATACATACAAGGACTCATACAGGAGAAAAAC  1929
Sbjct                 2428   ............................................................  2487

Query                 1930   TCCATGAATGCAACAATTGTGGGAAAGCCTTCAGTTTTAAATCACAGCTCATTATACATC  1989
Sbjct                 2488   ............................................................  2547

Query                 1990   AGAGGATTCATACAGGAGAGAACCCCTATGAATGCCATGAATGTGGGAAAGCCTTCAGTC  2049
Sbjct                 2548   ............................................................  2607

Query                 2050   GGAAATACCAGCTTATTTCACACCAGAGAACTCATGCAGGAGAGAAGCCTTATGAATGCA  2109
Sbjct                 2608   ............................................................  2667

Query                 2110   CCGACTGTGGAAAGGCTTTTGGTTTAAAGTCACAGCTTATTATACACCAGAGAACTCATA  2169
Sbjct                 2668   ............................................................  2727

Query                 2170   CAGGGGAGAAACCATTTGAATGTAGTGAGTGTCAGAAAGCCTTTAATACAAAGTCAAACC  2229
Sbjct                 2728   ............................................................  2787

Query                 2230   TGATTGTACATCAGAGAACTCATACAGGAGAGAAACCCTATAGTTGTAATGAATGTGGAA  2289
Sbjct                 2788   ............................................................  2847

Query                 2290   AAGCCTTTACGTTCAAATCACAGCTCATTGTACATAAAGGAGTGCACACTGGAGTAAAAC  2349
Sbjct                 2848   ............................................................  2907

Query                 2350   CCTATGGATGCAGTCAATGTGCAAAAACCTTTAGTTTGAAGTCCCAGCTCATTGTACATC  2409
Sbjct                 2908   ............................................................  2967

Query                 2410   AGAGAAGTCACACAGGAGTAAAACCATATGGATGCAGTGAGTGTGGGAAAGCCTTCAGGA  2469
Sbjct                 2968   ............................................................  3027

Query                 2470   GCAAGTCATACCTTATTATACATATGAGAACTCATACAGGAGAGAAACCACATGAGTGCA  2529
Sbjct                 3028   ............................................................  3087

Query                 2530   GGGAATGCGGGAAATCCTTTAGTTTCAATTCACAACTCATTGTGCATCAGAGAATTCACA  2589
Sbjct                 3088   ............................................................  3147
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665 A>T (M141L)

784 G>A

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Query  2590  CAGGAGAAAATCCCTATGAATGCAGTGAATGTGGGAAAGCCTTTAATAGGAAAGACCAGC  2649
Sbjct  3148  ............................................................  3207

Query  2650  TCATTTCACATCAGCGAACTCATGCAGGGGAAAAGCCTTATGGGTGCAGTGAATGTGGGA  2709
Sbjct  3208  ............................................................  3267

Query  2710  AAGCTTTTAGCAGCAAGTCATACCTAATTATACACATGAGAACTCATTCAGGTGAAAAAC  2769
Sbjct  3268  ............................................................  3327

Query  2770  CATATGAATGTAATGAATGTGGGAAAGCCTTCATTTGGAAATCACTACTCATTGTACATG  2829
Sbjct  3328  ............................................................  3387

Query  2830  AGCGAACTCATGCAGGGGTCAACCCTTATAAATGCAGTCAATGTGAGAAATCCTTCAGTG  2889
Sbjct  3388  ............................................................  3447

Query  2890  GGAAATTACGCCTTCTTGTACACCAGAGAATGCACACAAGAGAGAAACCATATGAATGCA  2949
Sbjct  3448  ..........................................C.................  3507

Query  2950  GTGAGTGTGGAAAAGCCTTCATTAGGAATTCTCAACTCATTGTACATCAAAGAACTCATT  3009
Sbjct  3508  ............................................................  3567

Query  3010  CAGGAGAGAAACCCTATGGGTGCAATGAATGTGGGAAAACCTTCTCTCAAAAATCAATTC  3069
Sbjct  3568  ............................................................  3627

Query  3070  TCAGTGCACATCAGAGAACACATACAGGAGAGAAGCCTTGTAAGTGCACTGAATGTGGGA  3129
Sbjct  3628  ............................................................  3687

Query  3130  AAGCCTTTTGTTGGAAGTCACAGCTCATTATGCATCAGAGAACTCATGTAGATGACAAAC  3189
Sbjct  3688  ............................................................  3747

Query  3190  ATTGATAATTTTACGAAACTCTGAAAAGTGGATTCACAAGAGATAGAAACAATCATATAT  3249
Sbjct  3748  ............................................................  3807

Query  3250  AAAGAGAAACTCTGTAAGTGGAATCATCTTGTCATCTTCCAGAAAACTCATACTGAATAG  3309
Sbjct  3808  ............................................................  3867

Query  3310  AAACTTTATGAATGCACAGCATATGGAAAGGCATCCACAGAAAGCTGTTCTTTACATGCA  3369
Sbjct  3868  -...........................................................  3926

Query  3370  AAAAGATAGTAGACAATACACAGGAAAACTGAATTTAGTAACCACTCTGAAAATTTTTAG  3429
Sbjct  3927  ............................................................  3986

Query  3430  CAGCAAGTCATACCttttttttAAAAAGTTCATACAGGTGAGGAACCATGTTAAACGTTGT  3489
Sbjct  3987  ............................................................  4046

Query  3490  AAAGTCATTTTACTAAAATAAGATTCACAAAGAGGAAACTTCATGAACCAGATGAATATA  3549
Sbjct  4047  ..............C.............................................  4106

Query  3550  GAATAGACTTCTTTGAAATTCATAGTTTACAGAATTTTAATGAGAGAAATTATTGAGCTA  3609
Sbjct  4107  ............................................................  4166

Query  3610  ATGAATGGCAGAATTAACAAAATTACAAACATTTTATGTATCGGAAGCATATACCTTGGA  3669
Sbjct  4167  ............................................................  4226

Query  3670  GGGACCATGCTATAAGGGAAAGTGTAAATCTAGAAATGAGAAACCCCTAGGGAAAAAATA  3729
Sbjct  4227  ..............G.............................................  4286

Query  3730  TATATAGGAGTGAACATCTTATGAATGTACCAAATAAACCACAGCTGGACTGTTAACCTC  3789

Sbjct  4287  ............................................................  4346

Query  3790  ACCTTAGAAGCTTCATTCTaaaaaaaaaaaaaaaaaaaaaaaaaaaaa  3837
Sbjct  4347  ..............................................  4394
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Range 2: 4389 to 5328

Score	Expect	Identities	Gaps	Strand	Frame
1698 bits(919)	0.0()	933/940(99%)	0/940(0%)	Plus/Plus	

Features:

```
Query  3809  aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaCCAACCTGTTATTATATCTTAATATTAATTT  3868
Sbjct  4389  ..............................A..........A...................  4448

Query  3869  TGAAGAATTATTTCTTTTAGGAATCATTTTAAGAAATTTTATTCCAGGTGTTCCAAAATT  3928
Sbjct  4449  ..............C.............................................  4508

Query  3929  TCAGGAAAAGGTTTGAGAAAATTCTCAATTATAAATAATAAGATACAGATTATTTCATTG  3988
Sbjct  4509  ............................................................  4568

Query  3989  TACAAGTGAATCTAGTAAGGAGGTTAAGAATAAGAAATAACATCCCAGAGCCTACAGGGA  4048
Sbjct  4569  ............................................................  4628

Query  4049  TATTTAGATATCTTCCTATGTGTACTACATAATATGAATTTTGCAGTTTGGCATTTTACT  4108
Sbjct  4629  ............................................................  4688

Query  4109  TGCGAATGCCATATGTGAGACAAAAATCATCTTCCAGAGATTTCAGTATCTCTGATACTG  4168
Sbjct  4689  ..T.........................................................  4748

Query  4169  ACAATATCTCTGATATGACAATATCATCTTCCAGAGATTTCTACTCTGCATACCAACATT  4228
Sbjct  4749  ............................................................  4808

Query  4229  GTTTCTTTGTGTCTTACCAAATGCAACTTGTTACTAGAATATGACTTACTAAAAATGCAT  4288
Sbjct  4809  ..........................................T.................  4868

Query  4289  TTCCACACTGCAAACATTTTTTAGGGCTATCTTCTGCCCTTTGGAAGCAGTCTTGGCAGC  4348
Sbjct  4869  ............................................................  4928

Query  4349  AACCTCTTTAGTAATCAATATAAGGCACACTTCATGTGTTTGTGTAGCCTGGAATCTATT  4408
Sbjct  4929  ............................................................  4988

Query  4409  CTACCTTCACAGGTTAGAACATCTTGATTTCCTCTTAACGAAACATTCCCTAACGGTGTA  4468
Sbjct  4989  ............................................................  5048

Query  4469  TGTAGTCATGAGGGAACCACCATTCAAGATGCCCTGCTCAGGACTTGGCATGAGCACTAT  4528
Sbjct  5049  ............................................................  5108

Query  4529  GGTCAGCTGAGGCTCAGAACTGTACATTGTTAATGGGTTTTTCAAGTTCAGAAAAGCAAC  4588
Sbjct  5109  ............................................................  5168

Query  4589  ATGAGCTTTTGTTCTGTGGTAGCATGTTGATGTAATAAGTAGCTATTTCAATAGAGGTTC  4648
Sbjct  5169  ..............A.............................................  5228

Query  4649  CCAGAACAGCTTTTGTTACTGTCATTTTCTTAACTTTGTTCACTTGTCTTTTATTTTGAG  4708
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