NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARi60G09
Vector : pGCAP10

Lot# : 7675_B3Bd

Gene : ZNF185
RefSeq_mRNA : NM_001395254.1:4587 bp

● Plasmid DNA purification

Date : 23.03.22 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.03.23 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 23.03.23

DNA concentration (O.D.): 61 ng/ul

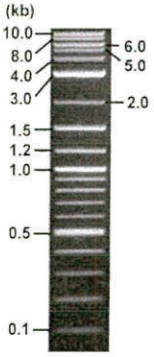
DNA	1.6 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	6.4 ul
Total	10 ul

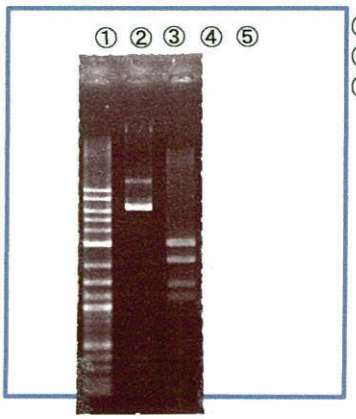
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.3, 1.4, 1.2 kb

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 : ARi60G09hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/07/23

DNA (61 ng/ul)	70	ul
10x TE	17	ul
dH_2O	84	ul
Total	171	ul

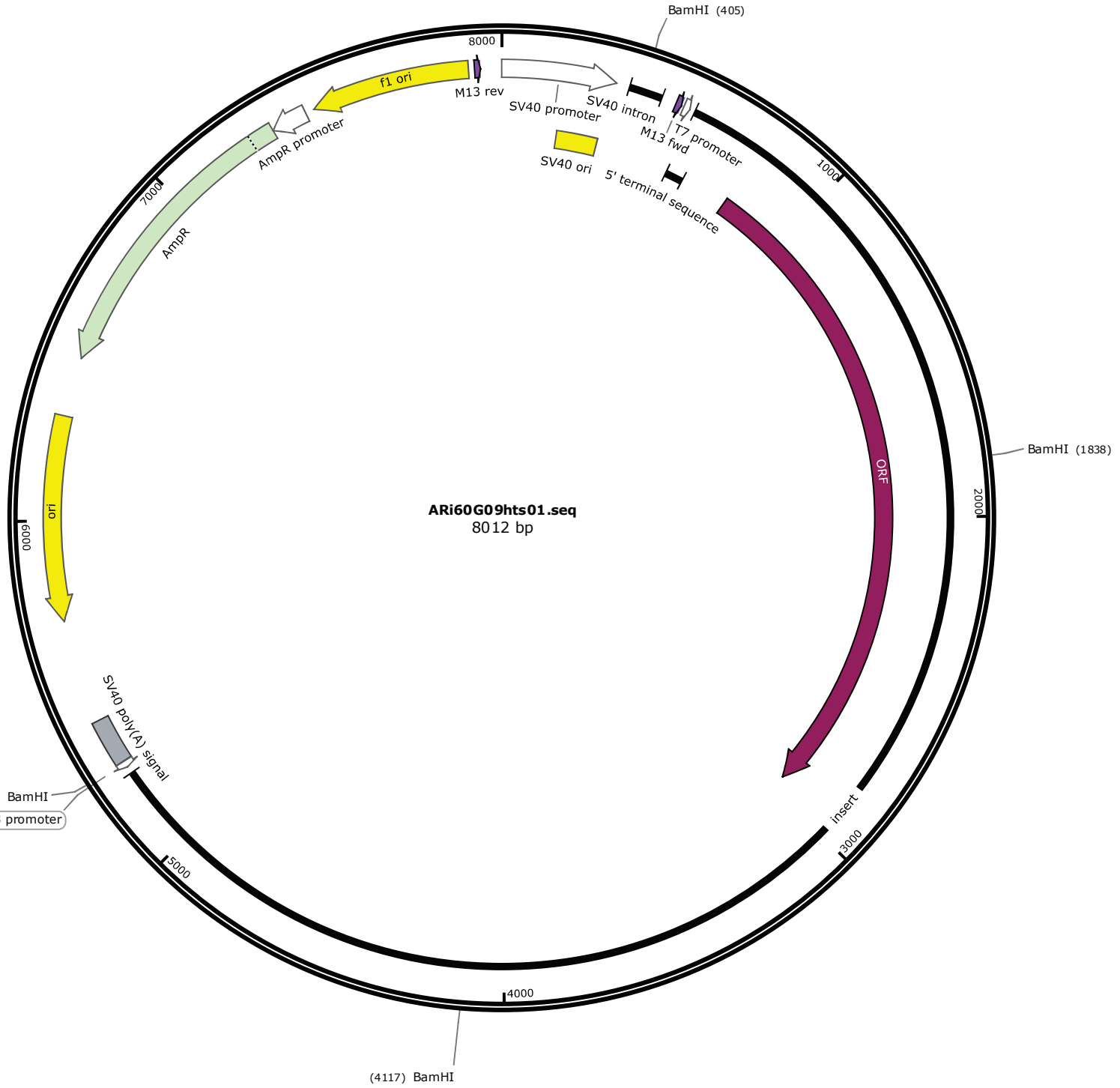
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '26.07.23 笹沼

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
7000
AmpR
ORF
BamHI (1838)
2000
ARi60G09hts01.seq
8012 bp
ori
6000
SV40 poly(A) signal
(5280) BamHI
T3 promoter
insert
3000
5000
4000
(4117) BamHI

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_007150:Homo sapiens zinc finger protein...

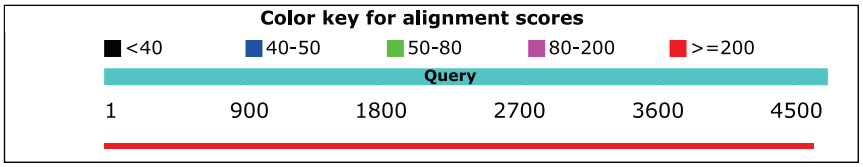
RID 3HD15S59114 (Expires on 06-23 12:03 pm)

Query ID	NM_001395254.1	**Subject ID**	lcl|Query_2086657
Description	Homo sapiens zinc finger protein 185 with LIM domain (ZNF185), transcript variant 11, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	4587	**Subject Length**	8012
		Program	BLASTN 2.17.0+

ARi60G09hts01.seq

Graphic Summary

Distribution of the top 3 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	8455	9000	100%	0.0	99.93%	Query_2086657

Alignments

Sequence ID: Query_2086657 Length: 8012 Number of Matches: 3
Range 1: 568 to 5154

Score	Expect	Identities	Gaps	Strand	Frame
8455 bits(4578)	0.0()	4584/4587(99%)	0/4587(0%)	Plus/Plus	

Features:

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Query              1    AGtccgcgcctcctcgcctccctgcgcgctccccgctgtgcaccgcgccccgcgccccgc  60
Sbjct            568    ............................................................  627

Query             61    gcctgcctccccggcccggcccggcccggcccgggcgccgtccacccgagggagcccgcgc  120
Sbjct            628    ............................................................  687

Query            121    ccTGCGACTGCCCGACCCTCCACCCGCCCCACGAGCCGGGCACCGGTGCCAGAAGCCCTG  180
Sbjct            688    ............................................................  747

CDS:zinc finger prot  1                                          M  S  I  S  A  L  G  G
Query            181    CTGAATCAAGTGAGAGGAGAGCTGCGGAGCAATCACCATGAGTATCTCAGCTCTTGGAGG  240
Sbjct            748    .........C.....A............................................  807

CDS:zinc finger prot  9      R  T  K  G  K  P  L  P  P  G  E  E  E  R  N  N  V  L  K  Q
Query            241    CCGCACCAAAGGGAAGCCTCTGCCACCAGGCGAGGAGGAGCGCAATAACGTTCTCAAGCA  300
Sbjct            808    ..A.........................................................  867

CDS:zinc finger prot  29     M  K  V  R  T  T  L  K  G  D  K  S  W  I  T  K  Q  D  E  S
Query            301    GATGAAAGTGCGAACCACGCTGAAGGGGGACAAGAGCTGGATTACCAAGCAGGATGAATC  360
Sbjct            868    ............................................................  927
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243 G>A (R9H)

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CDS:zinc finger prot  49    E G R T I E L P S G R S R A T S F S S A
Query                 361   GGAGGGTCGCACCATAGAGCTGCCCTCAGGCCGGAGTCGCGCCACATCCTTTTCATCAGC  420
Sbjct                 928   ............................................................  987

CDS:zinc finger prot  69    G E V P K P R P P S T R A P T G Y I I R
Query                 421   TGGGGAGGTTCCGAAGCCTAGGCCTCCGAGCACAAGGGCTCCCACTGGCTACATCATCCG  480
Sbjct                 988   ............................................................  1047

CDS:zinc finger prot  89    G V F T K P I D S S S Q P Q Q Q F P K A
Query                 481   GGGAGTGTTCACCAAGCCCATAGACAGCTCTTCCCAGCCCCAGCAGCAGTTCCCCAAGGC  540
Sbjct                 1048  ............................................................  1107

CDS:zinc finger prot  109   N G T P K S A A S L V R T A N A G P P R
Query                 541   CAACGGGACTCCAAAAAGTGCTGCCAGTCTGGTGAGAACAGCTAACGCTGGTCCTCCCCG  600
Sbjct                 1108  ............................................................  1167

CDS:zinc finger prot  129   P S S S G Y K M T T E D Y K K L A P Y N
Query                 601   CCCCTCCTCCTCTGGCTACAAGATGACCACTGAGGATTACAAGAAGCTGGCACCCTACAA  660
Sbjct                 1168  ............................................................  1227

CDS:zinc finger prot  149   I R R S S T S G D T E E E E E E E V V P
Query                 661   TATCAGGCGCAGCTCTACATCAGGGGACACCgaggaggaggaggaggaggaggTGGTGCC  720
Sbjct                 1228  ............................................................  1287

CDS:zinc finger prot  169   F S S D E Q K R R S E A A S G V L R R T
Query                 721   ATTCTCCTCAGATGAACAGAAACGGAGGTCAGAGGCTGCAAGCGGTGTTCTGAGGAGGAC  780
Sbjct                 1288  ............................................................  1347

CDS:zinc finger prot  189   A P R E H S Y V L S A A K K S T G S P T
Query                 781   AGCTCCCCGGGAGCACTCCTACGTCCTGTCAGCGGCCAAGAAGAGCACTGGCAGTCCTAC  840
Sbjct                 1348  ............................................................  1407

CDS:zinc finger prot  209   Q E T Q A P F I A K R V E V V E E D G P
Query                 841   CCAGGAGACACAGGCACCGTTTATCGCGAAGAGGGTGGAGGTGGTGGAAGAGGACGGGCC  900
Sbjct                 1408  ............................................................  1467

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Query                 901   TTCTGAGAAGAGCCAGGACCCACCTGCTCTGGCAAGATCCACTCCTGGCTCAAACAGTGC  960
Sbjct                 1468  ............................................................  1527

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Query                 961   GGATGGAGGCAGGACCAAAGCGTCTCGGGCAATTTGGATCGAGTGCCTGCCAAGTATGCC  1020
Sbjct                 1528  ............................................................  1587

CDS:zinc finger prot  269   S P A G S Q E L S S R G E E I V R L Q I
Query                 1021  TAGCCCCGCTGGGAGCCAGGAGCTCAGCTCAAGAGGTGAGGAAATTGTCCGCCTGCAGAT  1080
Sbjct                 1588  ............................................................  1647

CDS:zinc finger prot  289   L T P R A G L R L V A P D V E G M R S S
Query                 1081  CCTGACACCCAGGGCAGGACTCCGCCTGGTGGCCCCAGACGTGGAAGGCATGAGGTCTTC  1140
Sbjct                 1648  ............................................................  1707

CDS:zinc finger prot  309   P G N K D K E A P C S R E L Q R D L A G
Query                 1141  CCCAGGCAACAAAGACAAGGAGGCCCCCTGCTCCAGAGAGCTCCAGAGGGACTTGGCTGG  1200
Sbjct                 1708  ............................................................  1767

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Query                 1201  TGAGGAGGCTTTCAGGGCCCCCAACACAGATGCTGCAAGGTCAAGTGCACAGTTGAGTGA  1260
Sbjct                 1768  ............................................................  1827
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CDS:zinc finger prot  349   G N V G S G A T G S R P E G L A A V D I
Query                 1261  TGGCAATGTGGGATCCGGAGCCACGGGCTCCCGGCCTGAAGGCTTGGCTGCAGTAGACAT  1320
Sbjct                 1828  ............................................................  1887

CDS:zinc finger prot  369   G S E R G R L C A A A S F A S F L E D Q
Query                 1321  CGGCTCCGAGAGAGGAAGGCTGTGTGCAGCTGCTAGCTTTGCCTCTTTCCTGGAAGACCA  1380
Sbjct                 1888  ............................................................  1947

CDS:zinc finger prot  389   D G H S A N S Q S C K P R P A A I S S S
Query                 1381  GGATGGGCACAGTGCCAACTCTCAGTCCTGCAAGCCTAGACCAGCAGCCATCAGCTCCAG  1440
Sbjct                 1948  ............................................................  2007

CDS:zinc finger prot  409   A T S V S A V P A D R K S N S T A A Q E
Query                 1441  TGCCACTTCAGTCTCTGCTGTCCCTGCTGATAGGAAGAGCAACAGCACAGCAGCCCAGGA  1500
Sbjct                 2008  ............................................................  2067

CDS:zinc finger prot  429   D A K A D P K G A L A D Y E G K D V A T
Query                 1501  GGATGCAAAGGCAGACCCAAAGGGGGCCTTGGCTGATTATGAGGGGAAGGATGTGGCCAC  1560
Sbjct                 2068  ............................................................  2127

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Query                 1561  CAGGGTCGGAGAGGCCTGGCAGGAGAGGCCTGGAGCTCCAAGAGGTGGCCAAGGAGACCC  1620
Sbjct                 2128  ............................................................  2187

CDS:zinc finger prot  469   A V P A Q Q P A D P S T P E R Q S S P S
Query                 1621  AGCTGTACCCGCTCAGCAACCTGCAGATCCCAGCACCCCAGAGCGGCAGAGCAGCCCCAG  1680
Sbjct                 2188  ............................................................  2247

CDS:zinc finger prot  489   G S E Q L V R R E S C G S S V L T D F E
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Sbjct                 2248  ............................................................  2307

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Query                 1741  GGGGAAGGATGTGGCCACCAAGGTCGGAGAGGCCTGGCAGGACAGGCCTGGAGCCCCAAG  1800
Sbjct                 2308  ............................................................  2367

CDS:zinc finger prot  529   G G Q G D P A V P T Q Q P A D P S T P E
Query                 1801  AGGTGGCCAAGGAGACCCAGCTGTACCCACTCAGCAACCTGCAGATCCCAGTACCCCAGA  1860
Sbjct                 2368  ............................................................  2427

CDS:zinc finger prot  549   Q Q N S P S G S E Q F V R R E S C T S R
Query                 1861  ACAGCAGAACAGCCCCAGCGGATCTGAGCAATTCGTCAGACGAGAGAGCTGCACCAGCAG  1920
Sbjct                 2428  ............................................................  2487

CDS:zinc finger prot  569   V R S P S S C M V T V T V T A T S E Q P
Query                 1921  GGTGAGGAGCCCCTCGAGCTGCATGGTCACTGTTACTGTCACTGCCACATCTGAGCAGCC  1980
Sbjct                 2488  ............................................................  2547

CDS:zinc finger prot  589   H I Y I P A P A S E L D S S S T T K G I
Query                 1981  TCACATTTATATTCCAGCCCCCGCAAGTGAATTGGACTCCAGCTCTACCACCAAAGGGAT  2040
Sbjct                 2548  ............................................................  2607

CDS:zinc finger prot  609   L F V K E Y V N A S E V S S G K P V S A
Query                 2041  TCTCTTCGTGAAGGAGTACGTGAATGCTAGTGAAGTGTCTTCTGGGAAGCCAGTATCTGC  2100
Sbjct                 2608  ............................................................  2667

CDS:zinc finger prot  629   R Y S N V S S I E D S F A M E K K P P C
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Sbjct                 2668  ..........................................................  2727

CDS:zinc finger prot  649     G  S  T  P  Y  S  E  R  T  T  G  G  I  C  T  Y  C  N  R  E
Query                 2161  TGGCAGCACTCCATACTCTGAGAGGACAACTGGAGGGATCTGTACTTACTGCAACCGTGA  2220
Sbjct                 2728  ..........................................................  2787

CDS:zinc finger prot  669     I  R  D  C  P  K  I  T  L  E  H  L  G  I  C  C  H  E  Y  C
Query                 2221  GATCCGAGACTGTCCAAAGATTACCCTAGAACATCTTGGTATCTGCTGCCATGAATATTG  2280
Sbjct                 2788  ..........................................................  2847

CDS:zinc finger prot  689     F  K  C  G  I  C  S  K  P  M  G  D  L  L  D  Q  I  F  I  H
Query                 2281  CTTTAAGTGTGGGATTTGCAGTAAACCGATGGGCGATCTCCTGGATCAGATCTTCATTCA  2340
Sbjct                 2848  ..........................................................  2907

CDS:zinc finger prot  709     R  D  T  I  H  C  G  K  C  Y  E  K  L  F
Query                 2341  CCGTGACACCATTCACTGTGGGAAATGCTATGAGAAGCTCTTCTAGCGACCCCCCACCGC  2400
Sbjct                 2908  ..........................................................  2967

Query                 2401  CAGGCTGATCAGAAGCTGATGACTCGTGGACAAATTTGGCTGTCCCCAGTTTTGCCCCAA  2460
Sbjct                 2968  ..........................................................  3027

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Sbjct                 3028  ..........................................................  3087

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Sbjct                 3088  ..........................................................  3147

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Sbjct                 3148  ..........................................................  3207

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Sbjct                 3208  ..........................................................  3267

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Sbjct                 3268  ..........................................................  3327

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Sbjct                 3328  ..........................................................  3387

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Sbjct                 3448  ..........................................................  3507

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Sbjct                 3508  ..........................................................  3567

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Sbjct                 3568  ..........................................................  3627

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Sbjct                 3628  ..........................................................  3687

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Sbjct                 3688  ..........................................................  3747

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Sbjct                 3748  ..........................................................  3807
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Query                 3301  CATCTTAGACATGAGGATATTGGAACTCAGAGAGGTGGCTATTGCATTGCGCAGAACGCT  3360
Sbjct                 3868  ..........................................................  3927

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Sbjct                 3928  ..........................................................  3987

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Sbjct                 3988  ..........................................................  4047

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Query                 3841  GGGCAGATGTAAGCCTGTCCATGCAGTCAGCCGATCCTCTGCTCAGGTTCAGCTGGACTC  3900
Sbjct                 4408  ..........................................................  4467

Query                 3901  TGCCATCTGTGGGCCCAGCATCACTCTGTAAGTTCCTTGAAAGGAAGAACAACCTTAGAG  3960
Sbjct                 4468  ..........................................................  4527

Query                 3961  TATTTCTGATACAAAATGAGGGCCTCTGCTCTTGATTTAATTATAAAATGTCTACGTCTT  4020
Sbjct                 4528  ..........................................................  4587

Query                 4021  TCTCCAGTTTCTGAGCCCTATGCACATTGGCTTGTGGGCTTGTTCTTCCTGCCAAATGAT  4080
Sbjct                 4588  ..........................................................  4647

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Sbjct                 4648  ..........................................................  4707

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Sbjct                 4708  ..........................................................  4767

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Sbjct                 4768  ..........................................................  4827

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Sbjct                 4828  ..........................................................  4887

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Sbjct                 4888  ..........................................................  4947

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Sbjct  4948  ..................................................  5007

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Sbjct  5068  ..................................................  5127

Query  4561  AATTATAATAAATGGTAAGATATCACA  4587
Sbjct  5128  .........................  5154
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Range 2: 2096 to 2293

Score	Expect	Identities	Gaps	Strand	Frame
272 bits(147)	3e-75()	181/198(91%)	0/198(0%)	Plus/Plus	

Features:

```
CDS:zinc finger prot  504   L  T  D  F  E  G  K  D  V  A  T  K  V  G  E  A  W  Q  D  R
Query                 1727  TTGACTGATTTTGAGGGGAAGGATGTGGCCACCAAGGTCGGAGAGGCCTGGCAGGACAGG  1786
Sbjct                 2096  ...G......A.....................G.....................G...  2155

CDS:zinc finger prot  524   P  G  A  P  R  G  G  Q  G  D  P  A  V  P  T  Q  Q  P  A  D
Query                 1787  CCTGGAGCCCCAAGAGGTGGCCAAGGAGACCCAGCTGTACCCACTCAGCAACCTGCAGAT  1846
Sbjct                 2156  .........T.....................................G.....................  2215

CDS:zinc finger prot  544   P  S  T  P  E  Q  Q  N  S  P  S  G  S  E  Q  F  V  R  R  E
Query                 1847  CCCAGTACCCCAGAACAGCAGAACAGCCCCAGCGGATCTGAGCAATTCGTCAGACGAGAG  1906
Sbjct                 2216  .....C.........G.G.....G.....................C.T.............  2275

CDS:zinc finger prot  564   S  C  T  S  R  V
Query                 1907  AGCTGCACCAGCAGGGTG  1924
Sbjct                 2276  ..T..TGG......C...  2293
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Range 3: 2294 to 2491

Score	Expect	Identities	Gaps	Strand	Frame
272 bits(147)	3e-75()	181/198(91%)	0/198(0%)	Plus/Plus	

Features:

```
CDS:zinc finger prot  438   L  A  D  Y  E  G  K  D  V  A  T  R  V  G  E  A  W  Q  E  R
Query                 1529  TTGGCTGATTATGAGGGGAAGGATGTGGCCACCAGGGTCGGAGAGGCCTGGCAGGAGAGG  1588
Sbjct                 2294  ...A......T.....................A.....................C...  2353

CDS:zinc finger prot  458   P  G  A  P  R  G  G  Q  G  D  P  A  V  P  A  Q  Q  P  A  D
Query                 1589  CCTGGAGCTCCAAGAGGTGGCCAAGGAGACCCAGCTGTACCCGCTCAGCAACCTGCAGAT  1648
Sbjct                 2354  .........C.....................................A.....................  2413

CDS:zinc finger prot  478   P  S  T  P  E  R  Q  S  S  P  S  G  S  E  Q  L  V  R  R  E
Query                 1649  CCCAGCACCCCAGAGCGGCAGAGCAGCCCCAGCGGATCTGAGCAACTTGTCAGACGAGAG  1708

Sbjct                 2414  .....T.........A.A.....A.....................T.C.............  2473

CDS:zinc finger prot  498   S  C  G  S  S  V
Query                 1709  AGTTGTGGCAGCAGCGTG  1726
Sbjct                 2474  ..C..CAC......G...  2491
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