NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

Lot# : 7677_B5Hm

RIKEN Clone ID : RBd63G07

Vector : pGCAP10

Gene	IRAK1	
RefSeq_mRNA	NM_001569.4	3581 bp

● Plasmid DNA purification

Date : 2025/08/21 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2025/08/22 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/08/22

DNA concentration (O.D.): 121 ng/ul

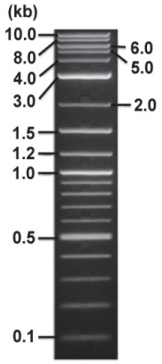
DNA	0.8 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.2 ul
Total	10 ul

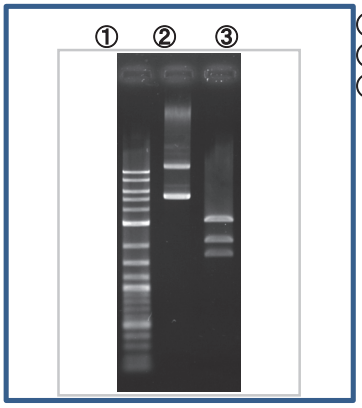
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.0, 1.7 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 : 2025/08/29

full sequence	RBd63G07hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/09/17

DNA (121 ng/ul)	80 ul
10x TE	39 ul
dH_2O	268 ul
Total	387 ul

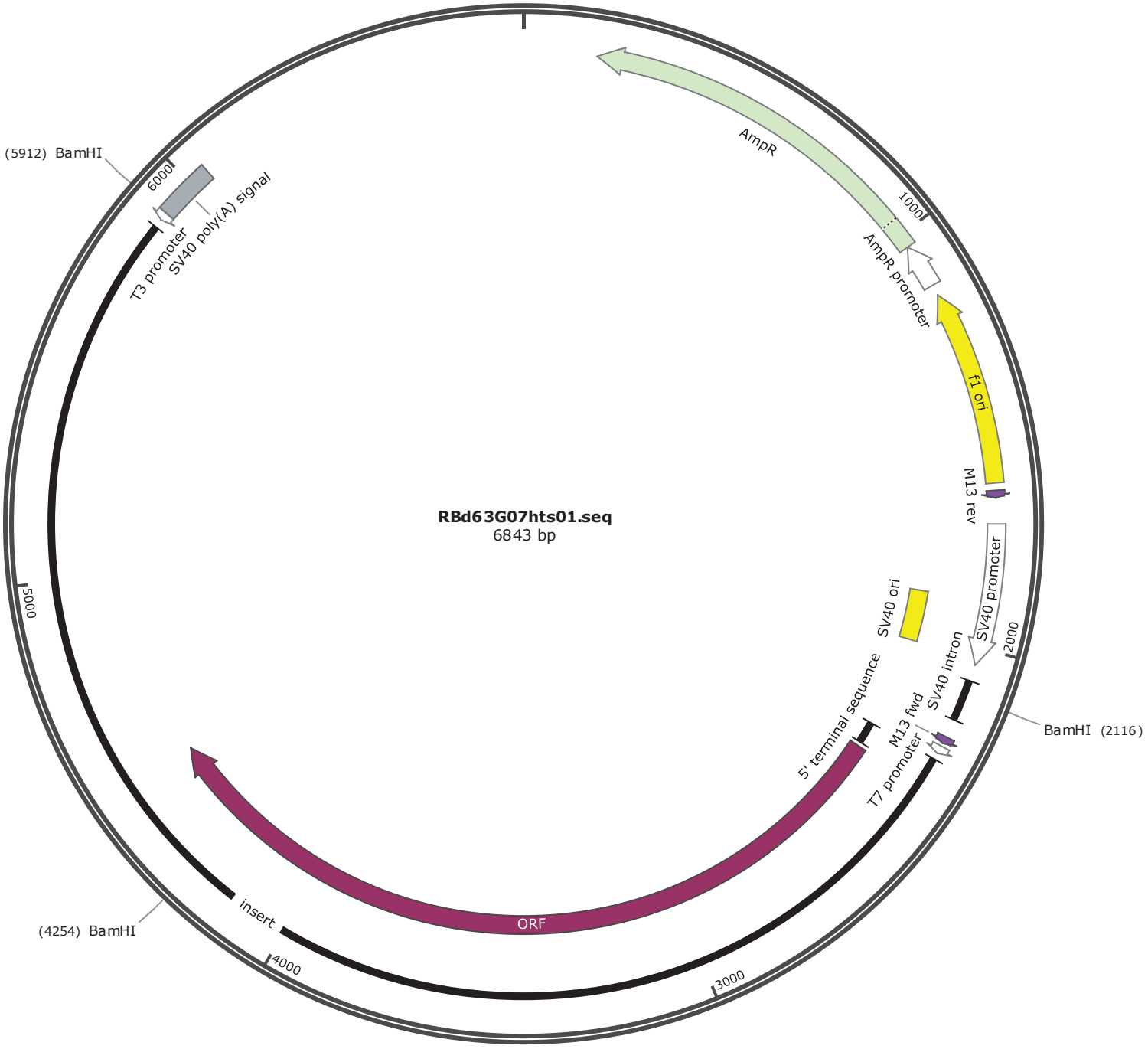
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '25.09.17 笹沼

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


RBd63G07hts01.seq
6843 bp
(5912) BamHI
6000
T3 promoter
SV40 poly(A) signal
AmpR
1000
AmpR promoter
f1 ori
M13 rev
SV40 promoter
2000
BamHI (2116)
SV40 intron
M13 fwd
T7 promoter
SV40 ori
5' terminal sequence
ORF
insert
(4254) BamHI
3000
4000
5000

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_001569:Homo sapiens interleukin 1 receptor...

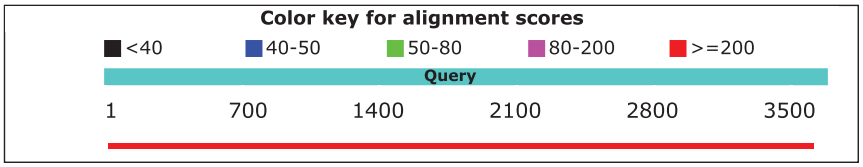
RID B2K718EE114 (Expires on 08-30 14:46 pm)

Query ID	NM_001569.4	**Subject ID**	lcl|Query_4474821
Description	Homo sapiens interleukin 1 receptor associated kinase 1 (IRAK1), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	3581	**Subject Length**	6843
		Program	BLASTN 2.17.0+

RBd63G07hts01.seq

Graphic Summary

Distribution of the top 1 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	6560	6560	99%	0.0	99.92%	Query_4474821

Alignments

Sequence ID: Query_4474821 Length: 6843 Number of Matches: 1
Range 1: 2279 to 5839

Score	Expect	Identities	Gaps	Strand	Frame
6560 bits(3552)	0.0()	3558/3561(99%)	0/3561(0%)	Plus/Plus	

Features:

```
Query              21   ggccggcccaggcccgcgcccgccgcggccctgagaggccccggcaggtcccggcccggc  80
Sbjct              2279 ............................................................  2338

CDS:interleukin-1 re 1                M  A  G  G  P  G  P  G  E  P  A  A  P  G  A  Q  H
Query              81   ggcggcagccatggccgggggccgggcccgggggagcccgcagcccccggcgcccAGCA  140
Sbjct              2339 ............................................................  2398

CDS:interleukin-1 re 18     F  L  Y  E  V  P  P  W  V  M  C  R  F  Y  K  V  M  D  A  L
Query              141  CTTCTTGTACGAGGTGCCGCCCTGGGTCATGTGCCGCTTCTACAAAGTGATGGACGCCCT  200
Sbjct              2399 ............................................................  2458

CDS:interleukin-1 re 38     E  P  A  D  W  C  Q  F  A  A  L  I  V  R  D  Q  T  E  L  R
Query              201  GGAGCCCGCCGACTGGTGCCAGTTCGCCGCCCTGATCGTGCGCGACCAGACCGAGCTGCG  260
Sbjct              2459 ............................................................  2518

CDS:interleukin-1 re 58     L  C  E  R  S  G  Q  R  T  A  S  V  L  W  P  W  I  N  R  N
Query              261  GCTGTGCGAGCGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAA  320
Sbjct              2519 ............................................................  2578

CDS:interleukin-1 re 78     A  R  V  A  D  L  V  H  I  L  T  H  L  Q  L  L  R  A  R  D
Query              321  CGCCCGTGTGGCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGA  380
Sbjct              2579 ............................................................  2638
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CDS:interleukin-1 re  98    I  I  T  A  W  H  P  P  A  P  L  P  S  P  G  T  T  A  P  R
Query                 381   CATCATCACAGCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGCCCCGAG  440
Sbjct                 2639  ............................................................  2698

CDS:interleukin-1 re  118   P  S  S  I  P  A  P  A  E  A  E  A  W  S  P  R  K  L  P  S
Query                 441   GCCCAGCAGCATCCCTGCACCCGCCGAGGCCGAGGCCTGGAGCCCCCGGAAGTTGCCATC  500
Sbjct                 2699  ............................................................  2758

CDS:interleukin-1 re  138   S  A  S  T  F  L  S  P  A  F  P  G  S  Q  T  H  S  G  P  E
Query                 501   CTCAGCCTCCACCTTCCTCTCCCCAGCTTTTCCAGGCTCCCAGACCCATTCAGGGCCTGA  560
Sbjct                 2759  ............................................................  2818

CDS:interleukin-1 re  158   L  G  L  V  P  S  P  A  S  L  W  P  P  P  P  P  S  P  A  P  S
Query                 561   GCTCGGCCTGGTCCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCAGCCCCTTC  620   573 C>T
Sbjct                 2819  ............T...............................................  2878

CDS:interleukin-1 re  178   S  T  K  P  G  P  E  S  S  V  S  L  L  Q  G  A  R  P  F  P
Query                 621   TTCTACCAAGCCAGGCCCAGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGCCCCTTTCC  680   677 T>C (F196S)
Sbjct                 2879  ............................................C...............  2938

CDS:interleukin-1 re  198   F  C  W  P  L  C  E  I  S  R  G  T  H  N  F  S  E  E  L  K
Query                 681   GTTTTGCTGGCCCCTCTGTGAGATTTCCCGGGGCACCCACAACTTCTCGGAGGAGCTCAA  740
Sbjct                 2939  ............................................................  2998

CDS:interleukin-1 re  218   I  G  E  G  G  F  G  C  V  Y  R  A  V  M  R  N  T  V  Y  A
Query                 741   GATCGGGGAGGGTGGCTTTGGGTGCGTGTACCGGGCGGTGATGAGGAACACGGTGTATGC  800
Sbjct                 2999  ............................................................  3058

CDS:interleukin-1 re  238   V  K  R  L  K  E  N  A  D  L  E  W  T  A  V  K  Q  S  F  L
Query                 801   TGTGAAGAGGCTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAGAGCTTCCT  860
Sbjct                 3059  ............................................................  3118

CDS:interleukin-1 re  258   T  E  V  E  Q  L  S  R  F  R  H  P  N  I  V  D  F  A  G  Y
Query                 861   GACCGAGGTGGAGCAGCTGTCCAGGTTTCGTCACCCAAACATTGTGGACTTTGCTGGCTA  920
Sbjct                 3119  ............................................................  3178

CDS:interleukin-1 re  278   C  A  Q  N  G  F  Y  C  L  V  Y  G  F  L  P  N  G  S  L  E
Query                 921   CTGTGCTCAGAACGGCTTCTACTGCCTGGTGTACGGCTTCCTGCCCAACGGCTCCCTGGA  980
Sbjct                 3179  ............................................................  3238

CDS:interleukin-1 re  298   D  R  L  H  C  Q  T  Q  A  C  P  P  L  S  W  P  Q  R  L  D
Query                 981   GGACCGTCTCCACTGCCAGACCCAGGCCTGCCCACCTCTCTCCTGGCCTCAGCGACTGGA  1040
Sbjct                 3239  ............................................................  3298

CDS:interleukin-1 re  318   I  L  L  G  T  A  R  A  I  Q  F  L  H  Q  D  S  P  S  L  I
Query                 1041  CATCCTTCTGGGTACAGCCCGGGCAATTCAGTTTCTACATCAGGACAGCCCCAGCCTCAT  1100
Sbjct                 3299  ............................................................  3358

CDS:interleukin-1 re  338   H  G  D  I  K  S  S  N  V  L  L  D  E  R  L  T  P  K  L  G
Query                 1101  CCATGGAGACATCAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCCAAGCTGGG  1160
Sbjct                 3359  ............................................................  3418

CDS:interleukin-1 re  358   D  F  G  L  A  R  F  S  R  F  A  G  S  S  P  S  Q  S  S  M
Query                 1161  AGACTTTGGCCTGGCCCGGTTCAGCCGCTTTGCCGGGTCCAGCCCCAGCCAGAGCAGCAT  1220
Sbjct                 3419  ............................................................  3478

CDS:interleukin-1 re  378   V  A  R  T  Q  T  V  R  G  T  L  A  Y  L  P  E  E  Y  I  K
Query                 1221  GGTGGCCCGGACACAGACAGTGCGGGGCACCCTGGCCTACCTGCCCGAGGAGTACATCAA  1280
Sbjct                 3479  ............................................................  3538
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CDS:interleukin-1 re  398   T  G  R  L  A  V  D  T  D  T  F  S  F  G  V  V  V  L  E  T
Query                 1281  GACGGGAAGGCTGGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTGCTAGAGAC  1340
Sbjct                 3539  ............................................................  3598

CDS:interleukin-1 re  418   L  A  G  Q  R  A  V  K  T  H  G  A  R  T  K  Y  L  K  D  L
Query                 1341  CTTGGCTGGTCAGAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTGAAAGACCT  1400
Sbjct                 3599  ............................................................  3658

CDS:interleukin-1 re  438   V  E  E  E  A  E  E  A  G  V  A  L  R  S  T  Q  S  T  L  Q
Query                 1401  GGTGGAAGAGGAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAGCACACTGCA  1460
Sbjct                 3659  ............................................................  3718

CDS:interleukin-1 re  458   A  G  L  A  A  D  A  W  A  A  P  I  A  M  Q  I  Y  K  K  H
Query                 1461  AGCAGGTCTGGCTGCAGATGCCTGGGCTGCTCCCATCGCCATGCAGATCTACAAGAAGCA  1520
Sbjct                 3719  ............................................................  3778

CDS:interleukin-1 re  478   L  D  P  R  P  G  P  C  P  P  E  L  G  L  G  L  G  Q  L  A
Query                 1521  CCTGGACCCCAggcccgggccctgcccacctgagctgggcctgggcctgggccagctggc  1580
Sbjct                 3779  ............................................................  3838

CDS:interleukin-1 re  498   C  C  C  L  H  R  R  A  K  R  R  P  P  M  T  Q  V  Y  E  R
Query                 1581  ctgctgctgcctgcaccgccgggccAAAAGGAGGCCTCCTATGACCCAGGTGTACGAGAG  1640
Sbjct                 3839  ............................................................  3898

CDS:interleukin-1 re  518   L  E  K  L  Q  A  V  V  A  G  V  P  G  H  S  E  A  A  S  C
Query                 1641  GCTAGAGAAGCTGCAGGCAGTGGTGGCGGGGGTGCCCGGGCATTCGGAGGCCGCCAGCTG  1700   1685 C>T (S532L)
Sbjct                 3899  ..........................................T.................  3958

CDS:interleukin-1 re  538   I  P  P  S  P  Q  E  N  S  Y  V  S  S  T  G  R  A  H  S  G
Query                 1701  CATCCCCCCTTCCCCGCAGGAGAACTCCTACGTGTCCAGCACTGGCAGAGCCCACAGTGG  1760
Sbjct                 3959  ............................................................  4018

CDS:interleukin-1 re  558   A  A  P  W  Q  P  L  A  A  P  S  G  A  S  A  Q  A  A  E  Q
Query                 1761  GGCTGCTCCATGGCAGCCCCTGGCAGCGCCATCAGGAGCCAGTGCCCAGGCAGCAGAGCA  1820
Sbjct                 4019  ............................................................  4078

CDS:interleukin-1 re  578   L  Q  R  G  P  N  Q  P  V  E  S  D  E  S  L  G  G  L  S  A
Query                 1821  GCTGCAGAGAGGCCCCAACCAGCCCGTGGAGAGTGACGAGAGCCTAGGCGGCCTCTCTGC  1880
Sbjct                 4079  ............................................................  4138

CDS:interleukin-1 re  598   A  L  R  S  W  H  L  T  P  S  C  P  L  D  P  A  P  L  R  E
Query                 1881  TGCCCTGCGCTCCTGGCACTTGACTCCAAGCTGCCCTCTGGACCCAGCACCCCTCAGGGA  1940
Sbjct                 4139  ............................................................  4198

CDS:interleukin-1 re  618   A  G  C  P  Q  G  D  T  A  G  E  S  S  W  G  S  G  P  G  S
Query                 1941  GGCCGGCTGTCCTCAGGGGGACACGGCAGGAGAATCGAGCTGGGGGAGTGGCCCAGGATC  2000
Sbjct                 4199  ............................................................  4258

CDS:interleukin-1 re  638   R  P  T  A  V  E  G  L  A  L  G  S  S  A  S  S  S  S  E  P
Query                 2001  CCGGCCCACAGCCGTGGAAGGACTGGCCCTTGGCAGCTCTGCATCATCGTCGTCAGAGCC  2060
Sbjct                 4259  ............................................................  4318

CDS:interleukin-1 re  658   P  Q  I  I  I  N  P  A  R  Q  K  M  V  Q  K  L  A  L  Y  E
Query                 2061  ACCGCAGATTATCATCAACCCTGCCCGACAGAAGATGGTCCAGAAGCTGGCCCTGTACGA  2120
Sbjct                 4319  ............................................................  4378

CDS:interleukin-1 re  678   D  G  A  L  D  S  L  Q  L  L  S  S  S  S  L  P  G  L  G  L
Query                 2121  GGATGGGGCCCTGGACAGCCTGCAGCTGCTGTCGTCCAGCTCCCTCCCAGGCTTGGGCCT  2180
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Sbjct                4379 ..................................................  4438

CDS:interleukin-1 re  698     E  Q  D  R  Q  G  P  E  E  S  D  E  F  Q  S
Query                2181 GGAACAGGACAGGCAGGGGCCCGAAGAAAGTGATGAATTTCAGAGCTGATGTGTTCACCT  2240
Sbjct                4439 ..................................................  4498

Query                2241 GGGCAGATCCCCCAAATCCGGAAGTCAAAGTTCTCATGGTCAGAAGTTCTCATGGTGCAC  2300
Sbjct                4499 ..................................................  4558

Query                2301 GAGTCCTCAGCACTCTGCCGGCAGTGGGGGTGGGGGCCCATGCCCGCGGGGGAGAGAAGG  2360
Sbjct                4559 ..................................................  4618

Query                2361 AGGTGGCCCTGCTGTTCTAGGCTCTGTGGGCATAGGCAGGCAGAGTGGAACCCTGCCTCC  2420
Sbjct                4619 ..................................................  4678

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Sbjct                4679 ..................................................  4738

Query                2481 GGGAGGCTGCTGGCTGCACAGACCCGTGAGGGGAGGAGAGGGGCTGCTGTGCAGGGGTGT  2540
Sbjct                4739 ..................................................  4798

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Sbjct                4799 ..................................................  4858

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Sbjct                4859 ..................................................  4918

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Sbjct                4919 ..................................................  4978

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Sbjct                4979 ..................................................  5038

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Sbjct                5039 ..................................................  5098

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Sbjct                5099 ..................................................  5158

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Sbjct                5159 ..................................................  5218

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Sbjct                5219 ..................................................  5278

Query                3021 GTAAGTCTCATGGTTCAGTCCTAGCAAGAAGCGAGAATTCTGAGATCCTCCAGAAAGTCG  3080
Sbjct                5279 ..................................................  5338

Query                3081 AGCAGCACCCACCTCCAACCTCGGGCCAGTGTCTTCAGGCTTTACTGGGGACCTGCGAGC  3140
Sbjct                5339 ..................................................  5398

Query                3141 TGGCCTAATGTGGTGGCCTGCAAGCCAGGCCATCCCTGGGCGCCACAGACGAGCTCCGAG  3200
Sbjct                5399 ..................................................  5458

Query                3201 CCAGGTCAGGCTTCGGAGGCCACAAGCTCAGCCTCAGGCCCAGGCACTGATTGTGGCAGA  3260
Sbjct                5459 ..................................................  5518

Query                3261 GGGGCCACTACCCAAGGTCTAGCTAGGCCCAAGACCTAGTTACCCAGACAGTGAGAAGCC  3320
Sbjct                5519 ..................................................  5578

Query                3321 CCTGGAAGGCAGAAAAGTTGGGAGCATGGCAGACAGGGAAGGGAAACATTTTCAGGGAAA  3380
Sbjct                5579 ..................................................  5638

Query                3381 AGACATGTATCACATGTCTTCAGAAGCAAGTCAGGTTTCATGTAACCGAGTGTCCTCTTG  3440
Sbjct                5639 ..................................................  5698

Query                3441 CGTGTCCAAAAGTAGCCCAGGGCTGTAGCACAGGCTTCACAGTGATTTTGTGTTCAGCCG  3500
Sbjct                5699 ..................................................  5758

Query                3501 TGAGTCACACTACATGCCCCCGTGAAGCTGGGCATTGGTGACGTCCAGGTTGTCCTTGAG  3560
Sbjct                5759 ..................................................  5818

Query                3561 TAATAAAAACGTATGTTGCAA  3581
Sbjct                5819 .....................  5839
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