NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : ARe22H01
Vector : pKA1U5

Lot# : 7672_B0Kb

Gene	PRKCA	
RefSeq_mRNA	NM_002737.3	8964 bp

● Plasmid DNA purification

Date : 20.11.12 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 20.11.13 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 20.11.13

DNA concentration (O.D.): 321 ng/ul

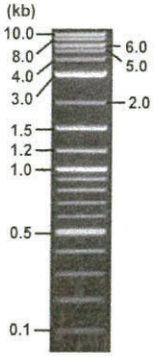
DNA	0.3 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.7 ul
Total	10 ul

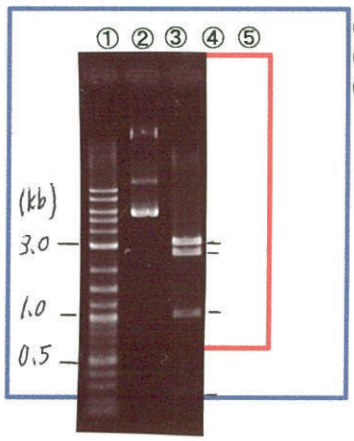
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.6, 1.0, 0.2 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 : 20.11.18

full sequence ARe22H01hts01.seq

検 '25.10.01 笹沼

● Adjust plasmid DNA solution to 25 ng/ul

Date : 20.11.20

DNA (321 ng/ul)	86.0 ul
10x TE	110.4 ul
dH_2O	907.8 ul
Total	1104.2 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

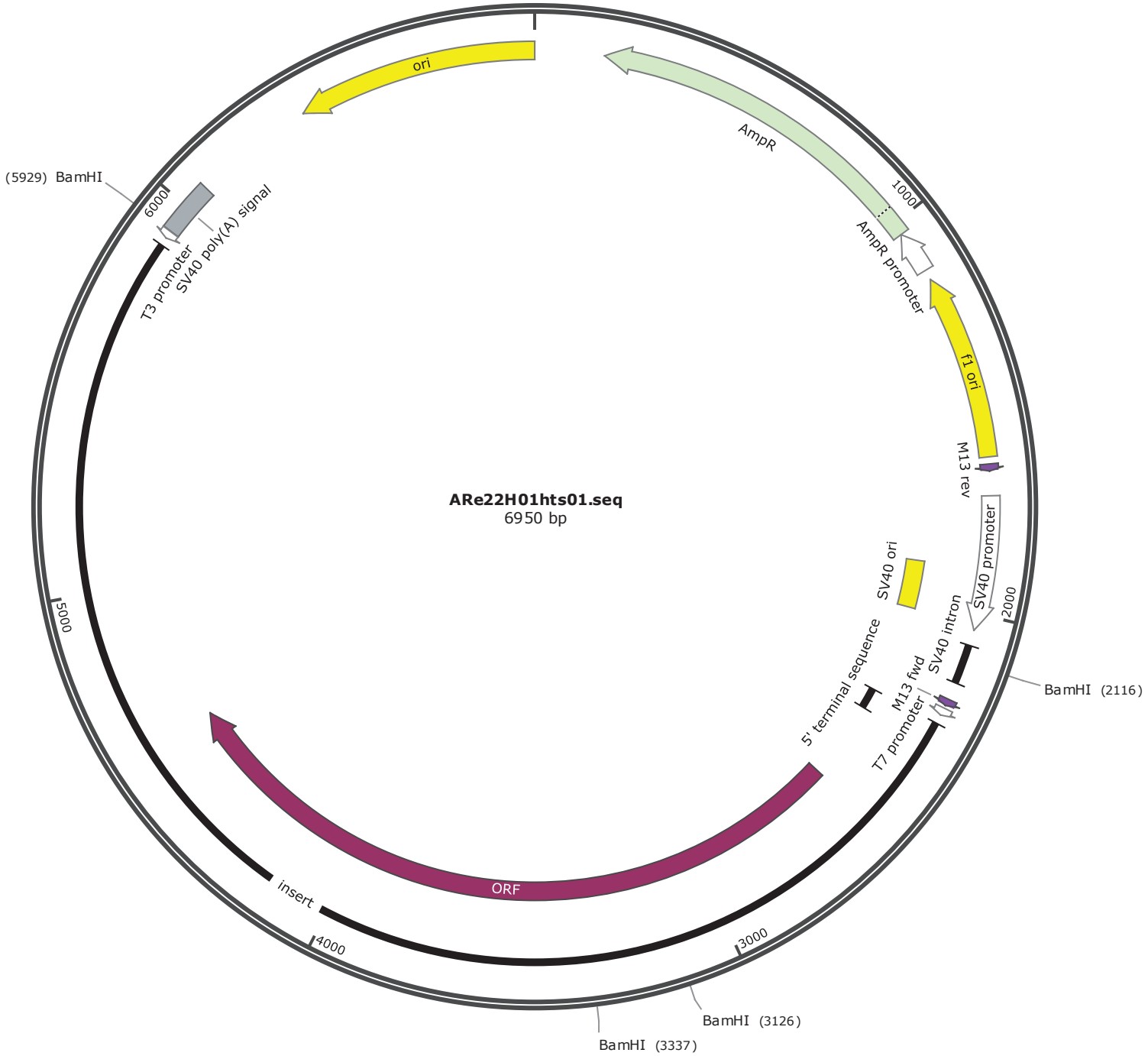
☐ ~~Conc. : ng/μl, Volume : μl~~

APPROVED BY :

確認 20.11.18 笹沼

検 '25.10.01 笹沼

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


ARe22H01hts01.seq
6950 bp
ori
AmpR
AmpR promoter
f1 ori
M13 rev
SV40 promoter
SV40 intron
M13 fwd
T7 promoter
5' terminal sequence
SV40 ori
ORF
insert
T3 promoter
SV40 poly(A) signal
(5929) BamHI
BamHI (2116)
BamHI (3126)
BamHI (3337)
1000
2000
3000
4000
5000
6000

BLAST Results

Questions/comments

Blast 2 sequences

Job title: ref|NM_002737.3|

RID DR45CK8F114 (Expires on 10-01 16:11 pm)

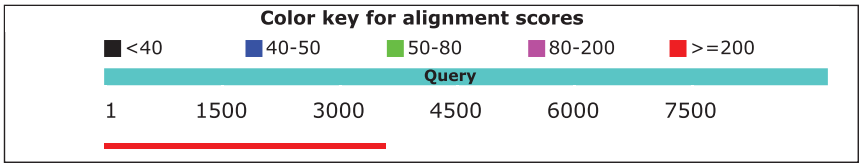
Query ID NM_002737.3
Description Homo sapiens protein kinase C alpha (PRKCA), mRNA
Molecule type nucleic acid
Query Length 8964

Subject ID lcl|Query_4786307
Description None
See details
Molecule type dna
Subject Length 6950
Program BLASTN 2.17.0+

ARe22H01hts01.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	6519	6519	39%	0.0	99.92%	Query_4786307

Alignments

Sequence ID: Query_4786307 Length: 6950 Number of Matches: 1
Range 1: 2330 to 5868

Score	Expect	Identities	Gaps	Strand	Frame
6519 bits(3530)	0.0()	3536/3539(99%)	0/3539(0%)	Plus/Plus	

Features:

```
Query   1     GTCAGTGAGCCTGGGGCCAGCGGGCGAGCCAGCGgctccggctcccgctcccgctccgcg  60
Sbjct   2330  ............................................................  2389

Query   61    cagcaccagcccgactctccccggcccccgccgcgccccctcgccgcgacctcggccacc  120
Sbjct   2390  ............................................................  2449

Query   121   ggcccgcgccccgcgcccggggtcgccccgagcccgcacctctcccccgccgcccccgcc  180
Sbjct   2450  ............................................................  2509

Query   181   cacccggccctccgcggccgcagctccccgGCGGAGGCAAGAGGTGGTTgggggggACCA  240
Sbjct   2510  ............................................................  2569

CDS:protein kinase C  1    M  A  D  V  F  P  G  N  D  S  T  A  S  Q  D  V  A  N  R  F
Query   241   TGGCTGACGTTTTCCCGGGCAACGACTCCACGGCGTCTCAGGACGTGGCCAACCGCTTCG  300
Sbjct   2570  ............................................................  2629

CDS:protein kinase C  21   A  R  K  G  A  L  R  Q  K  N  V  H  E  V  K  D  H  K  F  I
Query   301   CCCGCAAAGGGGCGCTGAGGCAGAAGAACGTGCACGAGGTGAAGGACCACAAATTCATCG  360
Sbjct   2630  ............................................................  2689

CDS:protein kinase C  41   A  R  F  F  K  Q  P  T  F  C  S  H  C  T  D  F  I  W  G  F
Query   361   CGCGCTTCTTCAAGCAGCCCACCTTCTGCAGCCACTGCACCGACTTCATCTGGGGGTTTG  420
Sbjct   2690  ............................................................  2749
```

```
CDS:protein kinase C  61    G  K  Q  G  F  Q  C  Q  V  C  C  F  V  V  H  K  R  C  H  E
Query                 421   GGAAACAAGGCTTCCAGTGCCAAGTTTGCTGTTTTGTGGTCCACAAGAGGTGCCATGAAT  480
Sbjct                 2750  ............................................................  2809

CDS:protein kinase C  81    F  V  T  F  S  C  P  G  A  D  K  G  P  D  T  D  D  P  R  S
Query                 481   TTGTTACTTTTTCTTGTCCGGGTGCGGATAAGGGACCCGACACTGATGACCCCAGGAGCA  540
Sbjct                 2810  ............................................................  2869

CDS:protein kinase C  101   K  H  K  F  K  I  H  T  Y  G  S  P  T  F  C  D  H  C  G  S
Query                 541   AGCACAAGTTCAAAATCCACACTTACGGAAGCCCCACCTTCTGCGATCACTGTGGGTCAC  600
Sbjct                 2870  ............................................................  2929

CDS:protein kinase C  121   L  L  Y  G  L  I  H  Q  G  M  K  C  D  T  C  D  M  N  V  H
Query                 601   TGCTCTATGGACTTATCCATCAAGGGATGAAATGTGACACCTGCGATATGAACGTTCACA  660
Sbjct                 2930  ............................................................  2989

CDS:protein kinase C  141   K  Q  C  V  I  N  V  P  S  L  C  G  M  D  H  T  E  K  R  G
Query                 661   AGCAATGCGTCATCAATGTCCCCAGCCTCTGCGGAATGGATCACACTGAGAAGAGGGGGC  720
Sbjct                 2990  ............................................................  3049

CDS:protein kinase C  161   R  I  Y  L  K  A  F  V  A  D  F  K  L  H  V  T  V  R  D  A
Query                 721   GGATTTACCTAAAGGCTGAGGTTGCTGATGAAAAGCTCCATGTCACAGTACGAGATGCAA  780
Sbjct                 3050  ............................................................  3109

CDS:protein kinase C  181   K  N  L  I  P  M  D  P  N  G  L  S  D  P  Y  V  K  L  K  L
Query                 781   AAAATCTAATCCCTATGGATCCAAACGGGCTTTCAGATCCTTATGTGAAGCTGAAACTTA  840
Sbjct                 3110  ............................................................  3169

CDS:protein kinase C  201   I  P  D  P  K  N  E  S  K  Q  K  T  K  T  I  R  S  T  L  N
Query                 841   TTCCTGATCCCAAGAATGAAAGCAAGCAAAAAACCAAAACCATCCGCTCCACACTAAATC  900
Sbjct                 3170  ............................................................  3229

CDS:protein kinase C  221   P  Q  W  N  E  S  F  T  F  K  L  K  P  S  D  K  D  R  R  L
Query                 901   CGCAGTGGAATGAGTCCTTTACATTCAAATTGAAACCTTCAGACAAAGACCGACGACTGT  960
Sbjct                 3230  ............................................................  3289

CDS:protein kinase C  241   S  V  E  I  W  D  W  D  R  T  T  R  N  D  F  M  G  S  L  S
Query                 961   CTGTAGAAATCTGGGACTGGGATCGAACAACAAGGAATGACTTCATGGGATCCCTTTCCT  1020
Sbjct                 3290  ............................................................  3349

CDS:protein kinase C  261   F  G  V  S  E  L  M  K  M  P  A  S  G  W  Y  K  L  L  N  Q
Query                 1021  TTGGAGTTTCGGAGCTGATGAAGATGCCGGCCAGTGGATGGTACAAGTTGCTTAACCAAG  1080
Sbjct                 3350  ..........................................A.............  3409

CDS:protein kinase C  281   F  E  G  E  Y  Y  N  V  P  I  P  E  G  D  E  E  G  N  M  E
Query                 1081  AAGAAGGTGAGTACTACAACGTACCCATTCCGGAAGGGGACGAGGAAGGAAACATGGAAC  1140
Sbjct                 3410  ............................................................  3469

CDS:protein kinase C  301   L  R  Q  K  F  E  K  A  K  L  G  P  A  G  N  K  V  I  S  P
Query                 1141  TCAGGCAGAAATTCGAGAAAGCCAAACTTGGCCCTGCTGGCAACAAAGTCATCAGTCCCT  1200
Sbjct                 3470  ............................................................  3529

CDS:protein kinase C  321   S  E  D  R  K  Q  P  S  N  N  L  D  R  V  K  L  T  D  F  N
Query                 1201  CTGAAGACAGGAAACAACCTTCCAACAACCTTGACCGAGTGAAACTCACGGACTTCAATT  1260
Sbjct                 3530  ............................................................  3589

CDS:protein kinase C  341   F  L  M  V  L  G  K  G  S  F  G  K  V  M  L  A  D  R  K  G
Query                 1261  TCCTCATGGTGTTGGGAAAGGGGAGTTTTGGAAAGGTGATGCTTGCCGACAGGAAGGGCA  1320
```

1070 G>A

```
Sbjct                 3590  ............................................................  3649

CDS:protein kinase C  361   T  E  E  L  Y  A  I  K  I  L  K  K  D  V  V  I  Q  D  D  D
Query                 1321  CAGAAGAACTGTATGCAATCAAAATCCTGAAGAAGGATGTGGTGATTCAGGATGATGACG  1380
Sbjct                 3650  ............................................................  3709

CDS:protein kinase C  381   V  E  C  T  M  V  E  K  R  V  L  A  L  L  D  K  P  P  F  L
Query                 1381  TGGAGTGCACCATGGTAGAAAAGCGAGTCTTGGCCCTGCTTGACAAACCCCCGTTCTTGA  1440
Sbjct                 3710  ............................................................  3769

CDS:protein kinase C  401   T  Q  L  H  S  C  F  Q  T  V  D  R  L  Y  F  V  M  E  Y  V
Query                 1441  CGCAGCTGCACTCCTGCTTCCAGACAGTGGATCGGCTGTACTTCGTCATGGAATATGTCA  1500
Sbjct                 3770  ............................................................  3829

CDS:protein kinase C  421   N  G  G  D  L  M  Y  H  I  Q  Q  V  G  K  F  K  E  P  Q  A
Query                 1501  ACGGTGGGGACCTCATGTACCACATTCAGCAAGTAGGAAAATTTAAGGAACCACAAGCAG  1560
Sbjct                 3830  ............................................................  3889

CDS:protein kinase C  441   V  F  Y  A  A  E  I  S  I  G  L  F  F  L  H  K  R  G  I  I
Query                 1561  TATTCTATGCGGCAGAGATTTCCATCGGATTGTTCTTTCTTCATAAAAGAGGAATCATTT  1620
Sbjct                 3890  ............................................................  3949

CDS:protein kinase C  461   Y  R  D  L  K  L  D  N  V  M  L  D  S  E  G  H  I  K  I  A
Query                 1621  ATAGGGATCTGAAGTTAGATAACGTCATGTTGGATTCAGAAGGACATATCAAAATTGCTG  1680
Sbjct                 3950  ............................................................  4009

CDS:protein kinase C  481   D  F  G  M  C  K  E  H  M  M  D  G  V  T  T  R  T  F  C  G
Query                 1681  ACTTTGGGATGTGCAAGGAACACATGATGGATGGAGTCACGACCAGGACCTTCTGTGGGA  1740
Sbjct                 4010  ............................................................  4069

CDS:protein kinase C  501   T  P  D  Y  I  A  P  E  I  I  A  Y  Q  P  Y  G  K  S  V  D
Query                 1741  CTCCAGATTATATCGCCCCAGAGATAATCGCTTATCAGCCGTATGGAAAATCTGTGGACT  1800
Sbjct                 4070  ............................................................  4129

CDS:protein kinase C  521   W  W  A  Y  G  V  L  L  Y  E  M  L  A  G  Q  P  P  F  D  G
Query                 1801  GGTGGGCCTATGGCGTCCTGTTGTATGAAATGCTTGCCGGGCAGCCTCCATTTGATGGTG  1860
Sbjct                 4130  ............................................................  4189

CDS:protein kinase C  541   E  D  E  D  E  L  F  Q  S  I  M  E  H  N  V  S  Y  P  K  S
Query                 1861  AAGATGAAGACGAGCTATTTCAGTCTATCATGGAGCACAACGTTTCCTATCCAAAATCCT  1920
Sbjct                 4190  ............................................................  4249

CDS:protein kinase C  561   L  S  K  E  A  V  S  V  C  K  G  L  M  T  K  H  P  A  K  R
Query                 1921  TGTCCAAGGAGGCTGTTTCTGTCTGCAAAGGACTGATGACCAAACACCCAGCCAAGCGGC  1980
Sbjct                 4250  .....................A.....................................  4309

CDS:protein kinase C  581   L  G  C  G  P  E  G  E  R  D  V  R  E  H  A  F  F  R  R  I
Query                 1981  TGGGCTGTGGGCCTGAGGGGGAGAGGGACGTGAGAGAGCATGCCTTCTTCCGGAGGATCG  2040
Sbjct                 4310  ............................................................  4369

CDS:protein kinase C  601   D  W  E  K  L  E  N  R  E  I  Q  P  P  F  K  P  K  V  C  G
Query                 2041  ACTGGGAAAAACTGGAGAACAGGGAGATCCAGCCACCATTCAAGCCCAAAGTGTGTGGCA  2100
Sbjct                 4370  ............................................................  4429

CDS:protein kinase C  621   K  G  A  E  N  F  D  K  F  F  T  R  G  Q  P  V  L  T  P  P
Query                 2101  AAGGAGCAGAGAACTTTGACAAGTTCTTCACACGAGGACAGCCCGTCTTAACACCACCTG  2160
Sbjct                 4430  ............................................................  4489

CDS:protein kinase C  641   D  Q  L  V  I  A  N  I  D  Q  S  D  F  E  G  F  S  Y  V  N
```

1941 G>A (V568I)

```
Query          2161  ATCAGCTGGTTATTGCTAACATAGACCAGTCTGATTTTGAAGGGTTCTCGTATGTCAACC  2220
Sbjct          4490  ..............................................................  4549

CDS:protein kinase C  661  P  Q  F  V  H  P  I  L  Q  S  A  V
Query          2221  CCCAGTTTGTGCACCCCATCTTACAGAGTGCAGTATGAAACTCACCAGCGAGAACAAACA  2280
Sbjct          4550  ..............................................................  4609

Query          2281  CCTCCCCAGCCCCCAGCCCTCCCCGCAGTGGGAAGTGAATCCTTAACCCTAAAATTTTAA  2340
Sbjct          4610  ..............................................................  4669

Query          2341  GGCCACGGCCTTGTGTCTGATTCCATATGGAGGCCTGAAAATTGTAGGGTTATTAGTCCA  2400
Sbjct          4670  ..............................................................  4729

Query          2401  AATGTGATCAACTGTTCAGGGTCTCTCTCTTACAACCAAGAACATTATCTTAGTGGAAGA  2460
Sbjct          4730  ..............................................................  4789

Query          2461  TGGTACGTCATGCTCAGTGTCCAGTTTAATTCTGTAGAAGTTACGTCTGGCTCTAGGTTA  2520
Sbjct          4790  ..............................................................  4849

Query          2521  ACCCTTCCTAGAAAGCAAGCAGACTGTTGCCCCATTTTGGGTACAATTTGATATACTTTC  2580
Sbjct          4850  ..............................................................  4909

Query          2581  CATACCCTCCATCTGTGGATTTTTCAGCATTGGAATCCCCCAACCAGAGATGTTAAAGTG  2640
Sbjct          4910  ..............................................................  4969

Query          2641  AGCCTGTCCCAGGAAACATCTCCACCCAAGACGTCTTTGGAATCCAAGAACAGGAAGCCA  2700
Sbjct          4970  ..............................................................  5029

Query          2701  AGAGAGTGAGCAGGGAGGGATTGGGGGTGGGGGAGGCCTCAAAATACCGACTGCGTCCAT  2760
Sbjct          5030  ..............................................................  5089

Query          2761  TCTCTGCCTCCATGGAAACAGCCCCTAGAATCTGAAAGGCCGGGATAAACCTAATCACTG  2820
Sbjct          5090  ..............................................................  5149

Query          2821  TTCCCAAACATTGACAAATCCTAACCCAACCATGGTCCAGCAGTTACCAGTTTAAACaaa  2880
Sbjct          5150  ..............................................................  5209

Query          2881  aaaaCCTCAGATGAGTGTTGGGTGAATCTGTCATCTGGTACCCTCCTTGGTTGATAACTG  2940
Sbjct          5210  ..............................................................  5269

Query          2941  TCTTGATACTTTTCATTCTTTGTAAGAGGCCAAATCGTCTAAGGACGTTGCTGAACAAGC  3000
Sbjct          5270  ..............................................................  5329

Query          3001  GTGTGAAATCATTTCAGATCAAGGATAAGCCAGTGTGTACATATGTTCATTTTAATCTCT  3060
Sbjct          5330  ..............................................................  5389

Query          3061  GGGAGATTATTTTTCCATCCAGGGTGCCATCAGTAATCATGCCACTACTCACCAGTGTTG  3120
Sbjct          5390  ..............................................................  5449

Query          3121  TTCACCAACACCCACCCCCACACACACCAACATTTTGCTGCCTACCTTGTTATCCTTCTC  3180
Sbjct          5450  ...G..........................................................  5509

Query          3181  AAGAAGCTGAAGTGTACGCCCTCTCCCCTTTTGTGCTTATTTATTTAATAGGCTGCAGTG  3240
Sbjct          5510  ..............................................................  5569

Query          3241  TCGCTTATGAAAGTACGATGTACAGTAACTTAATGGAAGTGCTGACTCTAGCATCAGCCT  3300
Sbjct          5570  ..............................................................  5629

Query          3301  CTACCGATTGATTTTCCTCCCTTCTCTAGCCCTGGATGTCCACTTAGGGATAAAAAGAAT  3360
```

```
Sbjct          5630  ..............................................................  5689

Query          3361  ATGGTTTTGGTTCCCATTTCTAGTTCACGTTGAATGACAGGCCTGGAGCTGTAGAATCAG  3420
Sbjct          5690  ..............................................................  5749

Query          3421  GAAACCCGGATGCCTAACAGCTCAAAGATGTTTTGTTAATAGAAGGATTTTAATACGTTT  3480
Sbjct          5750  ..............................................................  5809

Query          3481  TGCAAATGCATCATGCAATGAATTTTGCATGTTTATAATAAACCTTAATAACAAGTGAA  3539
Sbjct          5810  ..............................................................  5868
```

BLAST is a registered trademark of the National Library of Medicine

検
'25.09.30
笹沼