NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBdS081A22
Vector : pGCAP10
Lot# : 6608_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.): 368 ng/ul

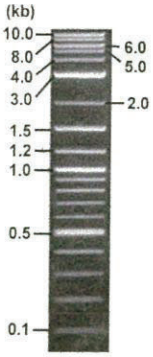
DNA	0.3 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.7 ul
Total	10 ul

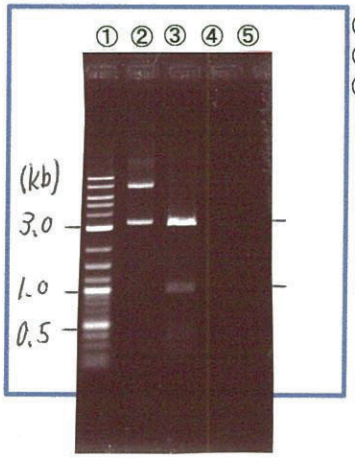
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 1.0, 0.3, 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 RBdS081A22hts01.seq

検 '25.10.01 笹沼

● Adjust plasmid DNA solution to 25 ng/ul

Date : 20.11.20

DNA (368 ng/ul)	86.0 ul
10x TE	126.5 ul
dH_2O	1053.4 ul
Total	1265.9 ul

● Shipping

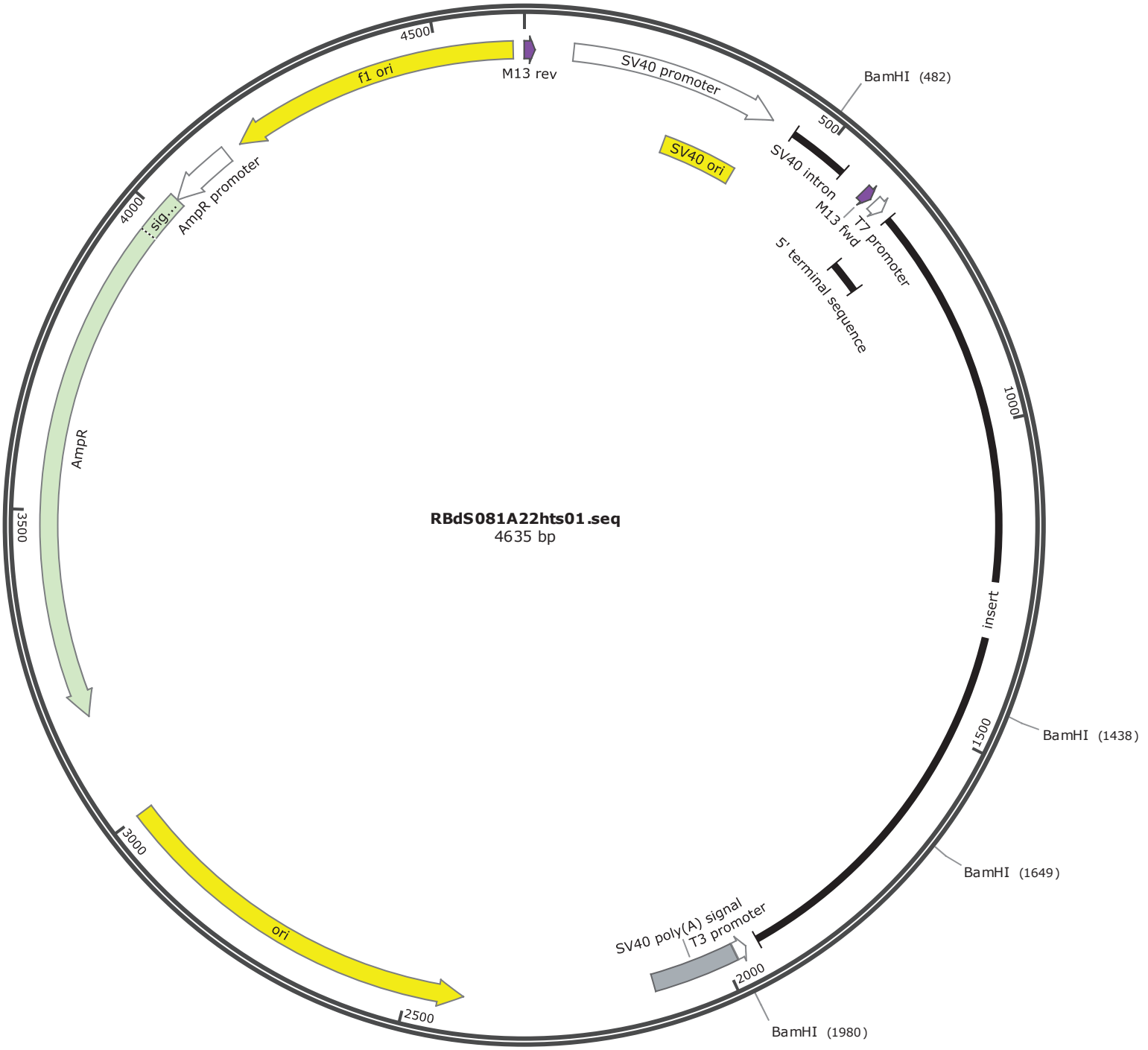
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ ~~Conc. : ng/μl, Volume : μl~~

APPROVED BY :

確認 20.11.18 笹沼

検 '25.10.01 笹沼


RBdS081A22hts01.seq
4635 bp
4500
f1 ori
M13 rev
SV40 promoter
BamHI (482)
500
SV40 ori
SV40 intron
M13 fwd
T7 promoter
5' terminal sequence
1000
insert
1500
BamHI (1438)
BamHI (1649)
SV40 poly(A) signal
T3 promoter
2000
BamHI (1980)
2500
ori
3000
3500
AmpR
...sig...
AmpR promoter
4000

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_008037:Mus musculus fos-like antigen 2...

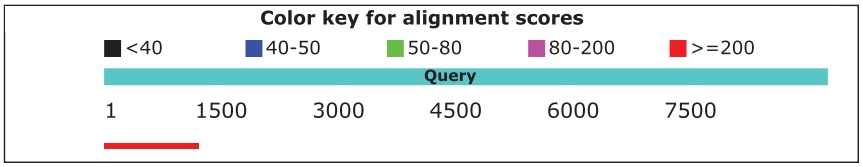
RID DTB6CWF9114 (Expires on 10-02 12:23 pm)

Query ID	NM_002737.3	**Subject ID**	lcl|Query_7299399
Description	Homo sapiens protein kinase C alpha (PRKCA), mRNA	**Description**	None
Molecule type	nucleic acid		See details
Query Length	8964	**Molecule type**	dna
		Subject Length	4635
		Program	BLASTN 2.17.0+

RB d S081A22hts01.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	2132	2132	13%	0.0	100.00%	Query_7299399

Alignments

Sequence ID: Query_7299399 Length: 4635 Number of Matches: 1
Range 1: 645 to 1798

Score	Expect	Identities	Gaps	Strand	Frame
2132 bits(1154)	0.0()	1154/1154(100%)	0/1154(0%)	Plus/Plus	

Features:

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Query              4    AGTGAGCCTGGGGCCAGCGGGCGAGCCAGCGgctccggctcccgctcccgctccgcgcag  63
Sbjct              645  ............................................................  704

Query              64   caccagcccgactctccccggcccccgccgcgccccctcgccgcgacctcggccaccggc  123
Sbjct              705  ............................................................  764

Query              124  ccgcgccccgcgcccggggtcgccccgagcccgcacctctcccccgccgcccccgcccac  183
Sbjct              765  ............................................................  824

CDS:protein kinase C  1                                                        M
Query              184  ccggccctccgcggccgcagctccccgGCGGAGGCAAGAGGTGGTTgggggggACCATGG  243
Sbjct              825  ............................................................  884

CDS:protein kinase C  2    A  D  V  F  P  G  N  D  S  T  A  S  Q  D  V  A  N  R  F  A
Query              244  CTGACGTTTTCCCGGGCAACGACTCCACGGCGTCTCAGGACGTGGCCAACCGCTTCGCCC  303
Sbjct              885  ............................................................  944

CDS:protein kinase C  22   R  K  G  A  L  R  Q  K  N  V  H  E  V  K  D  H  K  F  I  A
Query              304  GCAAAGGGGCGCTGAGGCAGAAGAACGTGCACGAGGTGAAGGACCACAAATTCATCGCGC  363
Sbjct              945  ............................................................  1004

CDS:protein kinase C  42   R  F  F  K  Q  P  T  F  C  S  H  C  T  D  F  I  W  G  F  G
Query              364  GCTTCTTCAAGCAGCCCACCTTCTGCAGCCACTGCACCGACTTCATCTGGGGGTTTGGGA  423
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Sbjct                1005  ..........................................................  1064

CDS:protein kinase C   62   K  Q  G  F  Q  C  Q  V  C  C  F  V  V  H  K  R  C  H  E  F
Query                424   AACAAGGCTTCCAGTGCCAAGTTTGCTGTTTTGTGGTCCACAAGAGGTGCCATGAATTTG  483
Sbjct                1065  ..........................................................  1124

CDS:protein kinase C   82   V  T  F  S  C  P  G  A  D  K  G  P  D  T  D  D  P  R  S  K
Query                484   TTACTTTTTCTTGTCCGGGTGCGGATAAGGGACCCGACACTGATGACCCCAGGAGCAAGC  543
Sbjct                1125  ..........................................................  1184

CDS:protein kinase C   102  H  K  F  K  I  H  T  Y  G  S  P  T  F  C  D  H  C  G  S  L
Query                544   ACAAGTTCAAAATCCACACTTACGGAAGCCCCACCTTCTGCGATCACTGTGGGTCACTGC  603
Sbjct                1185  ..........................................................  1244

CDS:protein kinase C   122  L  Y  G  L  I  H  Q  G  M  K  C  D  T  C  D  M  N  V  H  K
Query                604   TCTATGGACTTATCCATCAAGGGATGAAAATGTGACACCTGCGATATGAACGTTCACAAGC  663
Sbjct                1245  ..........................................................  1304

CDS:protein kinase C   142  Q  C  V  I  N  V  P  S  L  C  G  M  D  H  T  E  K  R  G  R
Query                664   AATGCGTCATCAATGTCCCCAGCCTCTGCGGAATGGATCACACTGAGAAGAGGGGGCGGA  723
Sbjct                1305  ..........................................................  1364

CDS:protein kinase C   162  I  Y  L  K  A  E  V  A  D  E  K  L  H  V  T  V  R  D  A  K
Query                724   TTTACCTAAAGGCTGAGGTTGCTGATGAAAAGCTCCATGTCACAGTACGAGATGCAAAAA  783
Sbjct                1365  ..........................................................  1424

CDS:protein kinase C   182  N  L  I  P  M  D  P  N  G  L  S  D  P  Y  V  K  L  K  L  I
Query                784   ATCTAATCCCTATGGATCCAAACGGGCTTTCAGATCCTTATGTGAAGCTGAAACTTATTC  843
Sbjct                1425  ..........................................................  1484

CDS:protein kinase C   202  P  D  P  K  N  E  S  K  Q  K  T  K  T  I  R  S  T  L  N  P
Query                844   CTGATCCCAAGAATGAAAGCAAGCAAAAAACCAAAACCATCCGCTCCACACTAAATCCGC  903
Sbjct                1485  ..........................................................  1544

CDS:protein kinase C   222  Q  W  N  E  S  F  T  F  K  L  K  P  S  D  K  D  R  R  L  S
Query                904   AGTGGAATGAGTCCTTTACATTCAAATTGAAACCTTCAGACAAAGACCGACGACTGTCTG  963
Sbjct                1545  ..........................................................  1604

CDS:protein kinase C   242  V  E  I  W  D  W  D  R  T  T  R  N  D  F  M  G  S  L  S  F
Query                964   TAGAAATCTGGGACTGGGATCGAACAACAAGGAATGACTTCATGGGATCCCTTTCCTTTG  1023
Sbjct                1605  ..........................................................  1664

CDS:protein kinase C   262  G  V  S  E  L  M  K  M  P  A  S  G  W  Y  K  L  L  N  Q  E
Query                1024  GAGTTTCGGAGCTGATGAAGATGCCGGCCAGTGGATGGTACAAGTTGCTTAACCAAGAAG  1083
Sbjct                1665  ..........................................................  1724

CDS:protein kinase C   282  E  G  E  Y  Y  N  V  P  I  P  E  G  D  E  E  G  N  M  E  L
Query                1084  AAGGTGAGTACTACAACGTACCCATTCCGGAAGGGGACGAGGAAGGAAACATGGAACTCA  1143
Sbjct                1725  ..........................................................  1784

CDS:protein kinase C   302  R  Q  K  F  E
Query                1144  GGCAGAAATTCGAG  1157
Sbjct                1785  ..............  1798
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