NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : RBd19G04

Lot# : 7677_B5KI

Vector : pGCAP10

Gene	FAM108A1	
RefSeq_mRNA	NM_031213.4	1859 bp

● Plasmid DNA purification

Date : 2025/11/25

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

Date : 2025/11/26

Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/11/26

DNA concentration (O.D.): 284 ng/ul

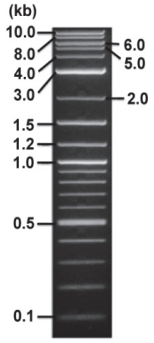
< Size of fragment expected from this clone >

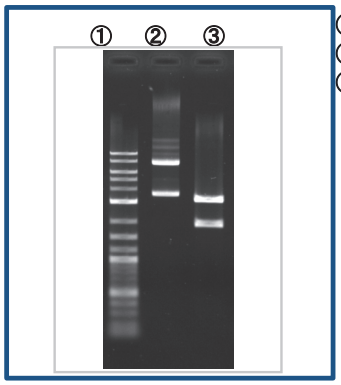
DNA	0.35	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.65	ul
Total	10	ul

BamHI 3.1kb (vector), 1.9 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 : 2025/11/27

full sequence	RBd19G04hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/12/02

DNA (284 ng/ul)	84	ul
10x TE	95	ul
dH_2O	775	ul
Total	954	ul

● Shipping

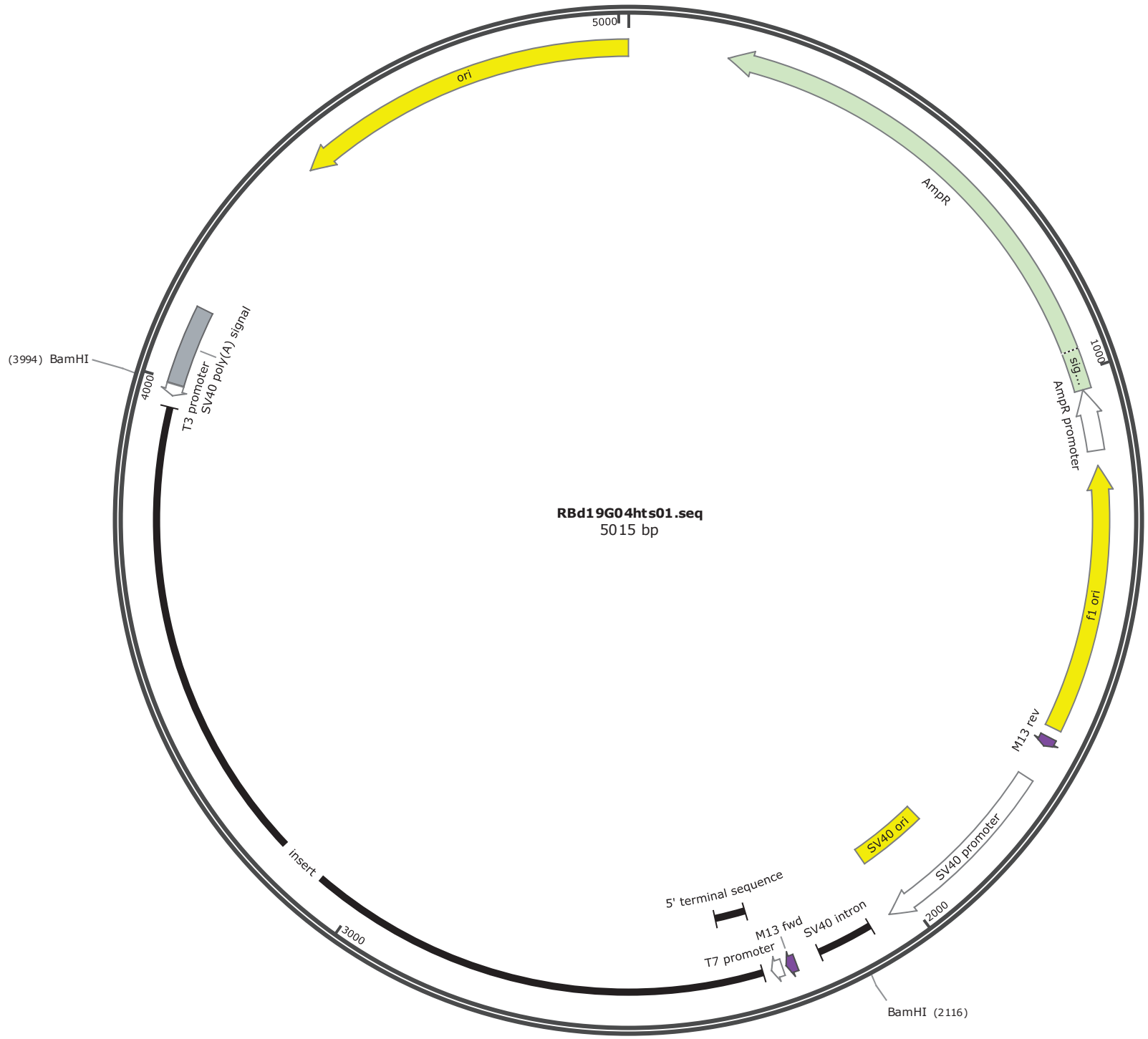
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY :

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'25.12.02
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http://dna.brc.riken.jp/index.html


5000
ori
AmpR
1000
sig...
AmpR promoter
f1 ori
M13 rev
SV40 promoter
2000
BamHI (2116)
SV40 ori
SV40 intron
M13 fwd
T7 promoter
5' terminal sequence
3000
insert
4000
T3 promoter
SV40 poly(A) signal
(3994) BamHI
RBd19G04hts01.seq
5015 bp

BLAST ® » blastn suite-2sequences » RID-JG19061E114

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_031213:Homo sapiens abhydrolase domain...

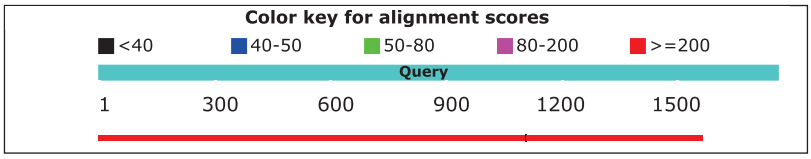
RID JG19061E114 (Expires on 11-28 15:00 pm)

Query ID	NM_001130111.2	**Subject ID**	lcl|Query_841311
Description	Homo sapiens abhydrolase domain containing 17A, depalmitoylase (ABHD17A), transcript variant 2, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	1706	**Subject Length**	5015
		Program	BLASTN 2.17.0+

RBd19G04hts01.seq

Graphic Summary

Distribution of the top 2 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	2013	2846	90%	0.0	100.00%	Query_841311

Alignments

Sequence ID: Query_841311 Length: 5015 Number of Matches: 2
Range 1: 2302 to 3391

Score	Expect	Identities	Gaps	Strand	Frame
2013 bits(1090)	0.0()	1090/1090(100%)	0/1090(0%)	Plus/Plus	

Features:

```
Query          1     GAGGCTCACTTCCGTCCGTGGGGGGAGCTGCGGCGGTGGCGGTGCAGGAGGCCGGGCAGG  60
Sbjct          2302  ............................................................  2361

Query          61    GGTGCGGAGGGACCGACGGACGCACgggcgggcggccgggagccatggagcgcggccctg  120
Sbjct          2362  ............................................................  2421

Query          121   gggcccgggggcgcgggccggggtgggcTTCCCACGGCACGACATGGAGACCTGTGGTTG  180
Sbjct          2422  ............................................................  2481

Query          181   CGAGGCTCCCTGGGGCTCGGCTTGGACCGCGATGGGGCTGGGCCCTGGCCTCCTAACGGG  240
Sbjct          2482  ............................................................  2541

Query          241   GCTGCTGTCTGGGGCGGTAGCTgggggggCGCTCTCCCCCCTGCCCGCGACTCGGAGCAC  300
Sbjct          2542  ............................................................  2601

Query          301   CCCCACCCCTCCCCTgccgggccaggccgggcggcgttgttggcgggggccccggtggag  360
Sbjct          2602  ............................................................  2661

CDS:alpha/beta hydro 1                         M  N  G  L  S  L  S  E  L  C  C  L
Query          361   gcccggcctgggcggcgcccgCCATGAATGGGCTGTCGCTGAGTGAGCTCTGCTGCCTCT  420
Sbjct          2662  ............................................................  2721

CDS:alpha/beta hydro 13    F  C  C  P  P  C  P  G  R  I  A  A  K  L  A  F  L  P  P  E
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Query              421  TCTGCTGCCCGCCCTGCCCCGGCCGCATCGCTGCCAAGCTCGCCTTCCTGCCGCCGGAGG  480
Sbjct             2722  ............................................................  2781

CDS:alpha/beta hydro  33   A  T  Y  S  L  V  P  E  P  E  P  G  P  G  G  A  G  A  A  P
Query              481  CCACCTACTCCCTGGTGCCTGAGCCCGAGCCGGGGCCTGGTGGGGCCGGGGCCGCCCCCT  540
Sbjct             2782  ............................................................  2841

CDS:alpha/beta hydro  53   L  G  T  L  R  A  S  S  G  A  P  G  R  W  K  L  H  L  T  E
Query              541  TGGGGACCCTGAGAGCCTCCTCGGGCGCACCCGGGCGCTGGAAGCTGCACCTGACGGAGC  600
Sbjct             2842  ............................................................  2901

CDS:alpha/beta hydro  73   R  A  D  F  Q  Y  S  Q  R  E  L  D  T  I  E  V  F  P  T  K
Query              601  GTGCCGACTTCCAGTACAGCCAGCGCGAGCTGGACACCATCGAGGTCTTCCCCACCAAGA  660
Sbjct             2902  ............................................................  2961

CDS:alpha/beta hydro  93   S  A  R  G  N  R  V  S  C  M  Y  V  R  C  V  P  G  A  R  Y
Query              661  GCGCCCGCGGCAACCGCGTCTCCTGCATGTATGTTCGCTGCGTGCCTGGTGCCAGGTACA  720
Sbjct             2962  ............................................................  3021

CDS:alpha/beta hydro  113  T  V  L  F  S  H  G  N  A  V  D  L  G  Q  M  S  S  F  Y  I
Query              721  CGGTCCTCTTCTCGCACGGCAATGCCGTGGACCTGGGCCAGATGAGCAGCTTCTACATTG  780
Sbjct             3022  ............................................................  3081

CDS:alpha/beta hydro  133  G  L  G  S  R  L  H  C  N  I  F  S  Y  D  Y  S  G  Y  G  A
Query              781  GCCTGGGCTCCCGCCTCCACTGCAACATCTTCTCCTACGACTACTCCGGCTACGGTGCCA  840
Sbjct             3082  ............................................................  3141

CDS:alpha/beta hydro  153  S  S  G  R  P  S  E  R  N  L  Y  A  D  I  D  A  A  W  Q  A
Query              841  GCTCGGGCAGGCCTTCCGAGAGGAACCTCTATGCCGACATCGACGCCGCCTGGCAGGCCC  900
Sbjct             3142  ............................................................  3201

CDS:alpha/beta hydro  173  L  R  T  R  Y  G  I  S  P  D  S  I  I  L  Y  G  Q  S  I  G
Query              901  TGCGCACCAGGTACGGCATCAGCCCGGACAGCATCATCCTGTACGGGCAGAGCATCGGCA  960
Sbjct             3202  ............................................................  3261

CDS:alpha/beta hydro  193  T  V  P  T  V  D  L  A  S  R  Y  F  C  A  A  V  V  L  H  S
Query              961  CGGTGCCCACCGTGGACCTGGCCTCGCGCTACGAGTGTGCCGCGGTGGTGCTGCACTCGC  1020
Sbjct             3262  ............................................................  3321

CDS:alpha/beta hydro  213  P  L  T  S  G  M  R  V  A  F  P  D  T  K  K  T  Y  C  F  D
Query             1021  CGCTCACCTCGGGCATGCGCGTCGCCTTCCCCGACACCAAGAAGACCTACTGCTTCGACG  1080
Sbjct             3322  ............................................................  3381

CDS:alpha/beta hydro  233  A  F  P  N
Query             1081  CCTTCCCTAA  1090
Sbjct             3382  ..........  3391
```

Range 2: 3474 to 3923

Score	Expect	Identities	Gaps	Strand	Frame
832 bits(450)	0.0()	450/450(100%)	0/450(0%)	Plus/Plus	

Features:

```
CDS:alpha/beta hydro  237    I  E  K  V  S  K  I  T  S  P  V  L  I  I  H  G  T  E  D  E
Query             1091  CATCGAGAAGGTGTCCAAGATCACGTCTCCCGTGCTCATCATCCACGGCACGGAGGACGA  1150
```



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Sbjct             3474  ............................................................  3533

CDS:alpha/beta hydro  257    V  I  D  F  S  H  G  L  A  L  Y  E  R  C  P  K  A  V  E  P
Query             1151  GGTGATCGACTTCTCGCACGGGCTGGCGCTCTACGAGCGCTGCCCCAAGGCGGTGGAGCC  1210
Sbjct             3534  ............................................................  3593

CDS:alpha/beta hydro  277    L  W  V  E  G  A  G  H  N  D  I  E  L  Y  S  Q  Y  L  E  R
Query             1211  GCTGTGGGTGGAGGGCGCCGGGCACAACGACATCGAGCTCTACAGCCAGTACCTGGAGCG  1270
Sbjct             3594  ............................................................  3653

CDS:alpha/beta hydro  297    L  R  R  F  I  S  Q  E  L  P  S  Q  R  A
Query             1271  CCTGCGTCGCTTCATCTCCCAGGAGCTGCCCAGCCAGCGCGCCTAGCGGCGGCCCCAACC  1330
Sbjct             3654  ............................................................  3713

Query             1331  GGCCGGACCTCAGCAATAAGGCGGccccggacctcaccccgcgccggccccccacccagg  1390
Sbjct             3714  ............................................................  3773

Query             1391  ggctgcatgtggacccccgggcggcccaggggacccgccccgacccaggggCTGTGGA  1450
Sbjct             3774  ............................................................  3833

Query             1451  CGATGTACAGGCAACAGAGCTACGCACTCCTTTCCTTTTGGAAGCAAGAAGAAAATACGT  1510
Sbjct             3834  ............................................................  3893

Query             1511  GAAAACGGAAATTAAAGATTTAAAATTTTA  1540
Sbjct             3894  ..............................  3923
```

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