NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARe67B02

Lot# : 7672_B5KI

Vector : pKA1U5

Gene	FAM108C1	
RefSeq_mRNA	NM_021214.2	2361 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.): 353 ng/ul

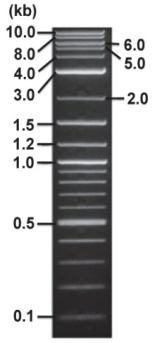
< Size of fragment expected from this clone >

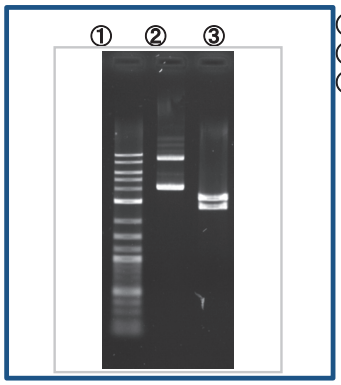
DNA	0.3	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.7	ul
Total	10	ul

BamHI 3.1kb (vector), 2.6 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	ARe67B02hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/12/02

DNA (353 ng/ul)	84	ul
10x TE	119	ul
dH_2O	983	ul
Total	1,186	ul

● Shipping

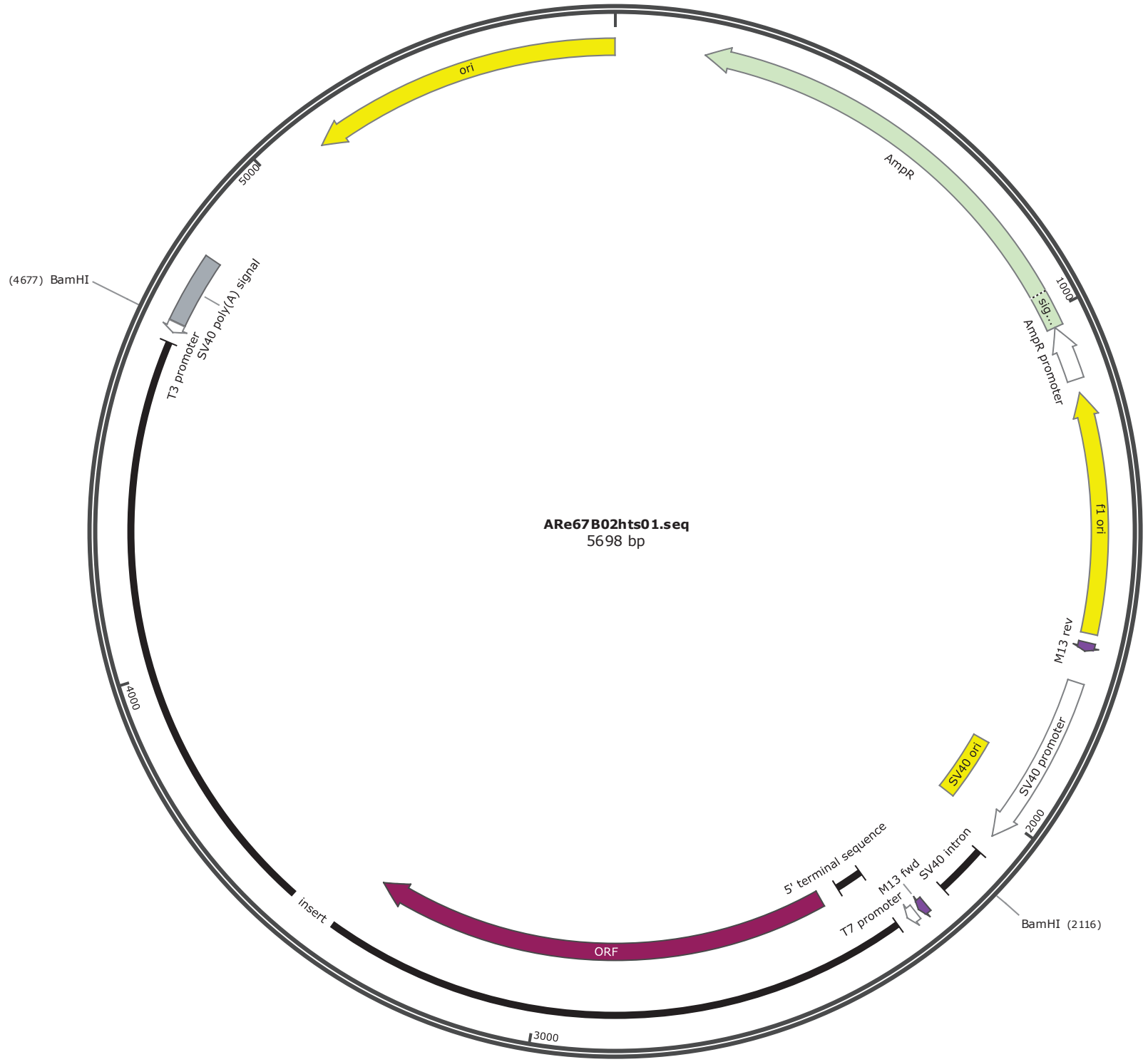
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ 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


ARe67B02hts01.seq
5698 bp
ori
AmpR
::sig...
AmpR promoter
f1 ori
M13 rev
SV40 promoter
SV40 ori
SV40 intron
M13 fwd
T7 promoter
5' terminal sequence
ORF
insert
T3 promoter
SV40 poly(A) signal
(4677) BamHI
BamHI (2116)
1000
2000
3000
4000
5000

BLAST ® » blastn suite-2sequences » RID-JFVDZVAE114

BLAST Results

Questions/comments

Blast 2 sequences

Job title: BC063844:Homo sapiens family with sequence...

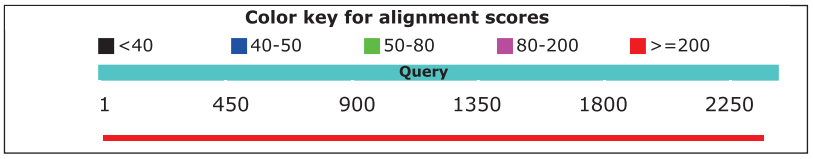
RID JFVDZVAE114 (Expires on 11-28 13:20 pm)

Query ID	NM_021214.2	**Subject ID**	lcl|Query_8114159
Description	Homo sapiens abhydrolase domain containing 17C, depalmitoylase (ABHD17C), mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	2361	**Subject Length**	5698
		Program	BLASTN 2.17.0+

ARe67B02hts01.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	4316	4316	99%	0.0	99.96%	Query_8114159

Alignments

Sequence ID: Query_8114159 Length: 5698 Number of Matches: 1
Range 1: 2286 to 4625

Score	Expect	Identities	Gaps	Strand	Frame
4316 bits(2337)	0.0()	2339/2340(99%)	0/2340(0%)	Plus/Plus	

Features:

```
Query              19   GCGCTCGCCTGCCAGCTCCCTCGCCGCGCGTCCGTCCTCCGTCCTCCCGGgccagccagc  78
Sbjct              2286 ............................................................  2345

CDS:alpha/beta hydro 1                                          M  P  E  P  G  P
Query              79   cagccagccagccGGGCCGGCGGCGGGCACCAGGCCGTCCCGATGCCCGAGCCAGGCCCC  138
Sbjct              2346 ............................................................  2405

CDS:alpha/beta hydro 7    R  M  N  G  F  S  L  G  E  L  C  W  L  F  C  C  P  P  C  P
Query              139  AGGATGAACGGCTTCTCGCTGGGTGAGCTGTGCTGGCTCTTCTGCTGCCCGCCCTGCCCG  198
Sbjct              2406 ......................C.......................................  2465

CDS:alpha/beta hydro 27   S  R  I  A  A  K  L  A  F  L  P  P  E  P  T  Y  T  V  L  A
Query              199  AGCCGCATCGCCGCCAAGCTGGCCTTCCTGCCGCCCGAGCCCACCTACACGGTGCTggcg  258
Sbjct              2466 ............................................................  2525

CDS:alpha/beta hydro 47   P  E  Q  R  G  A  G  A  S  A  P  A  P  A  Q  A  T  A  A  A
Query              259  ccggagcagcgcggcgccggcgcgtccgccccggccccggcccaggctaccgccgccgcc  318
Sbjct              2526 ............................................................  2585

CDS:alpha/beta hydro 67   A  A  A  Q  P  A  P  Q  Q  P  E  E  G  A  G  A  G  P  G  A
Query              319  gccgcggcccagccggcaccgcagcagcccgaggagggcgcgggcgcggggcccgGTGCG  378
Sbjct              2586 ............................................................  2645
```

162 T>C

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CDS:alpha/beta hydro  87    C  S  L  H  L  S  E  R  A  D  W  Q  Y  S  Q  R  E  L  D  A
Query                 379   TGCAGCCTGCACCTCAGCGAGCGCGCCGACTGGCAGTACTCGCAGCGCGAGCTGGACGCC  438
Sbjct                 2646  ............................................................  2705

CDS:alpha/beta hydro  107   V  E  V  F  F  S  R  T  A  R  D  N  R  L  G  C  M  F  V  R
Query                 439   GTCGAGGTCTTCTTCTCGCGCACGGCCCGGGACAACCGGCTCGGCTGCATGTTCGTGCGC  498
Sbjct                 2706  ............................................................  2765

CDS:alpha/beta hydro  127   C  A  P  S  S  R  Y  T  L  L  F  S  H  G  N  A  V  D  L  G
Query                 499   TGCGCGCCCTCCAGCCGCTACACGCTGCTCTTCTCGCACGGCAACGCCGTGGACCTGGGC  558
Sbjct                 2766  ............................................................  2825

CDS:alpha/beta hydro  147   Q  M  C  S  F  Y  I  G  L  G  S  R  I  N  C  N  I  F  S  Y
Query                 559   CAGATGTGCAGCTTCTACATTGGCCTCGGCTCCCGCATCAACTGCAACATCTTCTCCTAC  618
Sbjct                 2826  ............................................................  2885

CDS:alpha/beta hydro  167   D  Y  S  G  Y  G  V  S  S  G  K  P  S  E  K  N  L  Y  A  D
Query                 619   GACTACTCGGGATACGGCGTCAGCTCGGGCAAGCCCTCCGAGAAGAACCTCTACGCCGAC  678
Sbjct                 2886  ............................................................  2945

CDS:alpha/beta hydro  187   I  D  A  A  W  Q  A  L  R  T  R  Y  G  V  S  P  E  N  I  I
Query                 679   ATCGACGCCGCGTGGCAGGCGCTGCGCACCCGGTATGGCGTGAGTCCCGAGAACATTATC  738
Sbjct                 2946  ............................................................  3005

CDS:alpha/beta hydro  207   L  Y  G  Q  S  I  G  T  V  P  T  V  D  L  A  S  R  Y  E  C
Query                 739   CTCTATGGTCAGAGCATTGGGACTGTCCCCACGGTAGACTTGGCCTCGAGGTATGAATGC  798
Sbjct                 3006  ............................................................  3065

CDS:alpha/beta hydro  227   A  A  V  I  L  H  S  P  L  M  S  G  L  R  V  A  F  P  D  T
Query                 799   GCAGCGGTAATTCTCCATTCCCCTCTGATGTCTGGTTTGCGTGTGGCTTTTCCGGATACC  858
Sbjct                 3066  ............................................................  3125

CDS:alpha/beta hydro  247   R  K  T  Y  C  F  D  A  F  P  S  I  D  K  I  S  K  V  T  S
Query                 859   AGGAAAACATACTGCTTTGATGCTTTCCCCAGCATTGACAAGATATCTAAAGTCACCTCT  918
Sbjct                 3126  ............................................................  3185

CDS:alpha/beta hydro  267   P  V  L  V  I  H  G  T  E  D  E  V  I  D  F  S  H  G  L  A
Query                 919   CCTGTGTTGGTCATTCATGGTACAGAGGATGAGGTCATCGATTTCTCCCATGGCCTAGCG  978
Sbjct                 3186  ............................................................  3245

CDS:alpha/beta hydro  287   M  Y  E  R  C  P  R  A  V  E  P  L  W  V  E  G  A  G  H  N
Query                 979   ATGTACGAGCGCTGTCCCCGAGCCGTGGAGCCCCTTTGGGTTGAAGGGGCTGGGCATAAT  1038
Sbjct                 3246  ............................................................  3305

CDS:alpha/beta hydro  307   D  I  E  L  Y  A  Q  Y  L  E  R  L  K  Q  F  I  S  H  E  L
Query                 1039  GACATAGAGCTTTATGCACAATACCTAGAAAGACTAAAACAGTTCATATCTCACGAACTT  1098
Sbjct                 3306  ............................................................  3365

CDS:alpha/beta hydro  327   P  N  S
Query                 1099  CCTAATTCCTGAAGACAACAACTTGATCTTACCTCATTTACTGTGAACAGAAGAGTCCTC  1158
Sbjct                 3366  ............................................................  3425

Query                 1159  TGTTTTGCACATGCTTTAACTGGGTAGCTGTAAAGGCTTGATAACCATGAAGAAGTGCCC  1218
Sbjct                 3426  ............................................................  3485

Query                 1219  AACCTTTAGGGTGTTCTAATCAAAGAGCTGATGAAATCTCAGTCTTTTGTATCTAGAGGT  1278
Sbjct                 3486  ............................................................  3545

Query                 1279  GGTTCTGCTAATTCACACAACACGTTAAACTGAACAGTCGTGATTCCCAGCTTCATTACC  1338
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Sbjct                 3546  ............................................................  3605

Query                 1339  TTGCAGGAATGGGAATGAGAGCTGAATGTAGGGACAATTTTCTAGTGCTGTATAAAGTAG  1398
Sbjct                 3606  ............................................................  3665

Query                 1399  CCTCGCATCTGTTTCTCAACCTTATCCATCATTTCTGACATTCATGCAGGACTTGCCCTG  1458
Sbjct                 3666  ............................................................  3725

Query                 1459  TTGCCACCAATGTTCTCGGTATTTCACATGCAGCTCTCTTTCTGCCACTGGATACATGGG  1518
Sbjct                 3726  ............................................................  3785

Query                 1519  TTCAATCCATTTGTGAAGCTGTGATAGTGTAACTGGAAAGCTAGTGTGGTGAAAATTCCT  1578
Sbjct                 3786  ............................................................  3845

Query                 1579  TTATTATTTTTTGTTAACATGCTGATCTTTCCCGGACAAATGAACTGAAGGGTAATTTAC  1638
Sbjct                 3846  ............................................................  3905

Query                 1639  TGGAACTCTCGTGTACAGCTTCATCAACTGTAACCATATAAATATAACTGGAATATTCTT  1698
Sbjct                 3906  ............................................................  3965

Query                 1699  AAACAAAAAGAAACTAGGGGttttttttAAGTGTAAATTTATTACTAGCCAACAGAGTTTT  1758
Sbjct                 3966  ............................................................  4025

Query                 1759  ACTATTTTGATTGTCTGGTTGGTTTAACAAAGAGCCTAGCTGACTTTCCTTCTGTAAAGT  1818
Sbjct                 4026  ............................................................  4085

Query                 1819  CCTCCTTGTAGGCTTTTTTAAAGTACTGTACATATTTGCAATCACATTGTGCATAGATTC  1878
Sbjct                 4086  ............................................................  4145

Query                 1879  TTAATGGTAGATATGATTTCTTTTGTCAGGCTACAACAATGAACTGCAGATTCCTTGTTT  1938
Sbjct                 4146  ............................................................  4205

Query                 1939  GTAATGTAAATGATTGAATACATTTTGTTAATATGTTTTTATTCCTATGTTTTGCTATTA  1998
Sbjct                 4206  ............................................................  4265

Query                 1999  AAAATTTTATAACATTTCCAAGACAAAAATTCCAAGTTTATGCTTTGAAGAATTTATGTA  2058
Sbjct                 4266  ............................................................  4325

Query                 2059  ATTAAAATTTCACTAAACTAATCTTTTTAGTTTAGGAATTATTTGGGTTTTGACACTGGA  2118
Sbjct                 4326  ............................................................  4385

Query                 2119  AGTTGCGCCAAATAAGCATCAGAAATAGGAGATGCTTAACATTGCTATACTACTTGTGTT  2178
Sbjct                 4386  ............................................................  4445

Query                 2179  GGTTAGGGGTTTGGATTTGGGGGTTCTTTGGTTTTAAttttttttttCCACATTTAAAAGC  2238
Sbjct                 4446  ............................................................  4505

Query                 2239  CTTAAATGTACTGTAAGCCTCAGATCGTTGTACAACTGGACTGCGGTTGATTGCCAGTTT  2298
Sbjct                 4506  ............................................................  4565

Query                 2299  GTGTACTGTTGCTTGGATGCGGCACAGTGGTTGGTAATGGAATAAAGGATGCATGGATCA  2358
Sbjct                 4566  ............................................................  4625
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