NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : RBd60C12

Lot# : 7677_B6F1

Vector : pGCAP10

Gene	ARGLU1	
RefSeq_mRNA	NM_018011.4	3363 bp

● Plasmid DNA purification

Date : 2026/06/01

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

Date : 2026/06/02

Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2026/06/02

DNA concentration (O.D.): 251 ng/ul

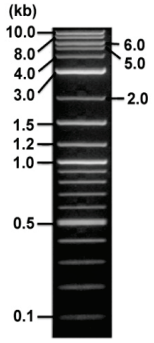
< Size of fragment expected from this clone >

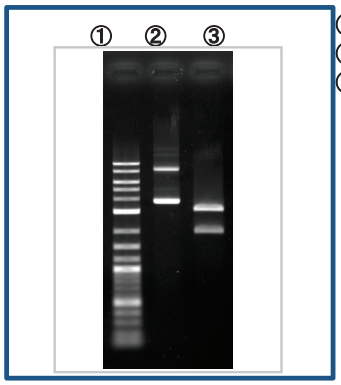
DNA	0.4	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.6	ul
Total	10	ul

BamHI 3.1kb (vector), 2.0 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 : 2026/06/04

full sequence	RBd60C12hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/06/05

DNA (251 ng/ul)	82	ul
10x TE	82	ul
dH_2O	659	ul
Total	823	ul

● Shipping

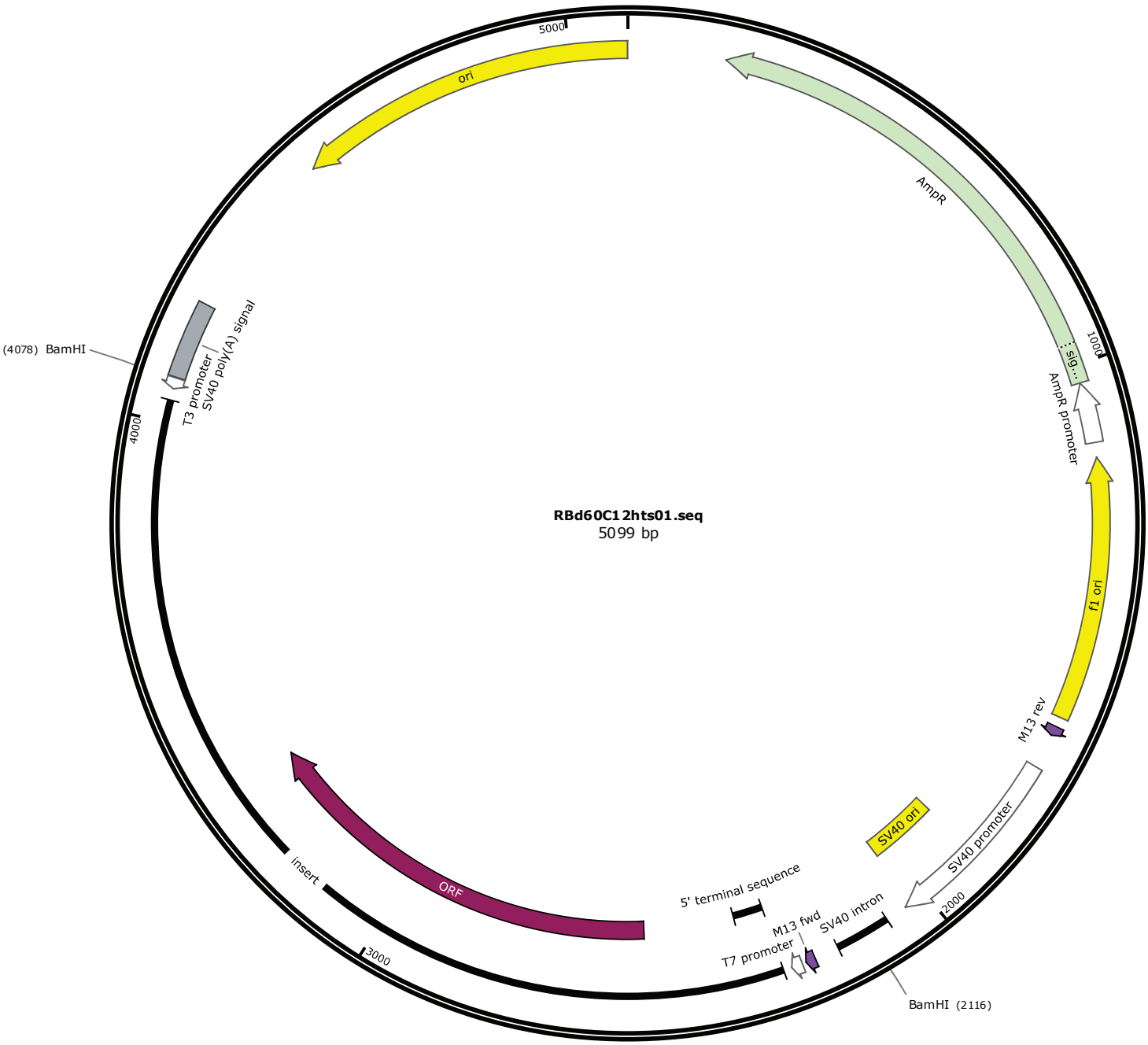
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY :

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'26.06.05
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http://dna.brc.riken.jp/index.html


RBd60C12hts01.seq
5099 bp
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
ORF
insert
3000
4000
T3 promoter
SV40 poly(A) signal
(4078) BamHI

BLAST Results

Questions/comments

Blast 2 sequences

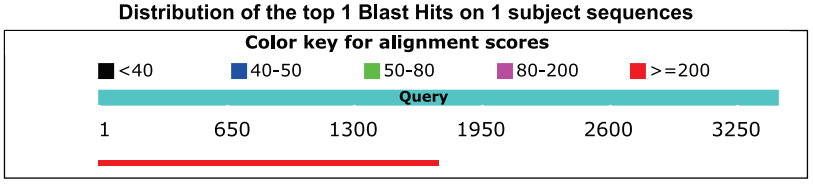
Job title: BC063242:Homo sapiens fatty acid synthase,...

RID 22671R2D114 (Expires on 06-05 14:19 pm)

Query ID	NM_018011.4	**Subject ID**	lcl|Query_3532065
Description	Homo sapiens arginine and glutamate rich 1 (ARGLU1), mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	3363	**Subject Length**	5099
		Program	BLASTN 2.17.0+

RBd60C12hts01.seq

Graphic Summary



Dot Matrix View

Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
None provided	3157	3157	51%	0.0	100.00%	Query_3532065

Alignments

Sequence ID: Query_3532065 Length: 5099 Number of Matches: 1
Range 1: 2300 to 4008

Score	Expect	Identities	Gaps	Strand	Frame
3157 bits(1709)	0.0()	1709/1709(100%)	0/1709(0%)	Plus/Plus	

Features:

```
Query              1     GCAGCTGCCATCTTAGGGGCGCCTGGCGCTACGGGTTTCTCGTTGGAGGCGGCCTTCGTG  60
Sbjct              2300  ............................................................  2359

Query              61    GCAGCTGTAGACGCCGGGAAAAGGCATAAAGTCCGTTGGCCGACACCTTTCTTTCCTCCG  120
Sbjct              2360  ............................................................  2419

Query              121   GCCTCGGTAGAACCGCCAGCCCGCGTCCGAAGGCGGAGGCGAGGGGAACTGGCCGCGTGA  180
Sbjct              2420  ............................................................  2479

CDS:arginine and glu 1                                        M  G  R  S  R  S  R
Query              181   GGGGCCTGAGGCGAGCGGTTAGAGCGTCTCCCGGAAGGATGGGCCGGTCTCGGAGCCGGA  240
Sbjct              2480  ............................................................  2539

CDS:arginine and glu 8     S  S  S  R  S  K  H  T  K  S  S  K  H  N  K  K  R  S  R  S
Query              241   GCTCGTCCCGCTCCAAGCACACCAAGAGCAGCAAGCACAACAAGAAGCGCAGCCGGTCCC  300
Sbjct              2540  ............................................................  2599

CDS:arginine and glu 28    R  S  R  S  R  D  K  E  R  V  R  K  R  S  K  S  R  E  S  K
Query              301   GGTCGCGATCCCGGGACAAGGAGCGCGTGCGGAAGCGTTCCAAATCTCGGGAAAGTAAAC  360
Sbjct              2600  ............................................................  2659
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CDS:arginine and glu  48    R  N  R  R  R  E  S  R  S  R  S  R  S  T  N  T  A  V  S  R
Query                 361   GGAACCGGCGGCGGGAGTCGCGGTCCCGTTCGCGCTCCACCAACACGGCCGTGTCCCGGC  420
Sbjct                 2660  ............................................................  2719

CDS:arginine and glu  68    R  E  R  D  R  E  R  A  S  S  P  P  D  R  I  D  I  F  G  R
Query                 421   GCGAGCGGGACCGGGAGCGCGCCTCGTCCCCGCCCGACCGCATCGACATCTTCGGGCGCA  480
Sbjct                 2720  ............................................................  2779

CDS:arginine and glu  88    T  V  S  K  R  S  S  L  D  E  K  Q  K  R  E  E  E  E  K  K
Query                 481   CGGTGAGCAAGCGCAGCAGCCTGGACGAGAAGCAGAAGCGAGAGGAGGAGGAGAAGAAAG  540
Sbjct                 2780  ............................................................  2839

CDS:arginine and glu  108   A  E  F  E  R  Q  R  K  I  R  Q  Q  E  I  E  E  K  L  I  E
Query                 541   CGGAGTTCGAGCGGCAGCGAAAAATTCGACAGCAAGAAATAGAAGAAAAACTCATCGAGG  600
Sbjct                 2840  ............................................................  2899

CDS:arginine and glu  128   E  E  T  A  R  R  V  E  E  L  V  A  K  R  V  E  E  E  L  E
Query                 601   AAGAAACAGCACGAAGAGTAGAAGAATTGGTAGCAAAAAGGGTGGAGGAAGAACTGGAGA  660
Sbjct                 2900  ............................................................  2959

CDS:arginine and glu  148   K  R  K  D  E  I  E  R  E  V  L  R  R  V  E  E  A  K  R  I
Query                 661   AAAGGAAGGATGAAATTGAACGAGAAGTTCTCCGAAGGGTGGAGGAAGCCAAACGCATCA  720
Sbjct                 2960  ............................................................  3019

CDS:arginine and glu  168   M  E  K  Q  L  L  E  E  L  E  R  Q  R  Q  A  E  L  A  A  Q
Query                 721   TGGAAAAGCAGTTGCTCGAAGAACTCGAGCGACAGAGACAAGCTGAGCTTGCCGCACAAA  780
Sbjct                 3020  ............................................................  3079

CDS:arginine and glu  188   K  A  R  E  E  E  E  R  A  K  R  E  E  L  E  R  I  L  E  E
Query                 781   AAGCTAGAGAGGAGGAAGAACGTGCAAAACGTGAGGAGCTAGAGCGAATACTGGAAGAGA  840
Sbjct                 3080  ............................................................  3139

CDS:arginine and glu  208   N  N  R  K  I  A  E  A  Q  A  K  L  A  E  E  Q  L  R  I  V
Query                 841   ATAACCGAAAAATTGCAGAAGCACAAGCCAAACTGGCCGAAGAACAGTTGAGAATTGTTG  900
Sbjct                 3140  ............................................................  3199

CDS:arginine and glu  228   E  E  Q  R  K  I  H  E  E  R  M  K  L  E  Q  E  R  Q  R  Q
Query                 901   AAGAACAAAGAAAGATTCATGAGGAAAGGATGAAACTAGAACAAGAACGACAACGTCAAC  960
Sbjct                 3200  ............................................................  3259

CDS:arginine and glu  248   Q  K  E  E  Q  K  I  I  L  G  K  G  K  S  R  P  K  L  S  F
Query                 961   AAAAAGAAGAACAAAAAATTATCCTGGGCAAGGGGAAGTCCAGGCCAAAACTGTCCTTCT  1020
Sbjct                 3260  ............................................................  3319

CDS:arginine and glu  268   S  L  K  T  Q  D
Query                 1021  CATTAAAAACCCAGGATTAAATTGCAAACTCTGAACTTTTTACAAAGAAAAATGGAAAAA  1080
Sbjct                 3320  ............................................................  3379

Query                 1081  CTTTGTATGGTAGCTTCATGTTGAAGTGGttttttgttttttgttttttgttttttttAATTT  1140
Sbjct                 3380  ............................................................  3439

Query                 1141  GTAAAATCTGGAAAGTTAGCTTGTTCTAATAGGGGCTATGCTCTGCAATTCCCttttttt  1200
Sbjct                 3440  ............................................................  3499

Query                 1201  ttttttttttCCTTCCACTAAGTCAAATCCTTATCAGATCATTGTTGTATTCTAAGGAGT  1260
Sbjct                 3500  ............................................................  3559

Query                 1261  GACGTATTTTTCACCTGTTTGGATTCTATATTAGTGGTCTGAGGAAGAGCAGATCACATT  1320
Sbjct                 3560  ............................................................  3619

Query                 1321  GTAAAACTATGGATGGTCTGATAAGGCTTTTACTGACCCCACTGACTTCAGAGTTATACT  1380
Sbjct                 3620  ............................................................  3679

Query                 1381  CTGTTTGCTACATCATAATGCTGGTTTTGCTGACttttgttttttttATATATTTATaaa  1440
Sbjct                 3680  ............................................................  3739

Query                 1441  aaaagaaaaaGTTGGTGATTGCATTGGGAAATTCCCAGGGTATTACTGGACCTATGTGGT  1500
Sbjct                 3740  ............................................................  3799

Query                 1501  GTATTGTTAAACCAGTGTCCTTGTGATACTGTTGCTCTTGATGTTCCTGATACAGGTAAG  1560
Sbjct                 3800  ............................................................  3859

Query                 1561  GAAACAGTTGGTCAACTCTGATACAAAGTATATATACAGTTCAGTATTGTCTCTGTTCAT  1620
Sbjct                 3860  ............................................................  3919

Query                 1621  TTTGTTTTTATTTCATTGACAAAATCAAACCAGCATTCCCCATTGTGTAAATAAATGATT  1680
Sbjct                 3920  ............................................................  3979

Query                 1681  TTGCTGAATAAAGTAAAGTCTTAAATTCA  1709
Sbjct                 3980  ...........................    4008
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