NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARi75E06

Lot# : 7675_B5Hp

Vector : pGCAP10

Gene	MEGF9	
RefSeq_mRNA	NM_001080497.3	6300 bp

● Plasmid DNA purification

Date : 2025/08/25 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2025/08/26 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/08/26

DNA concentration (O.D.): 444 ng/ul

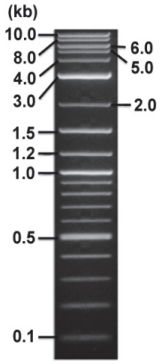
< Size of fragment expected from this clone >

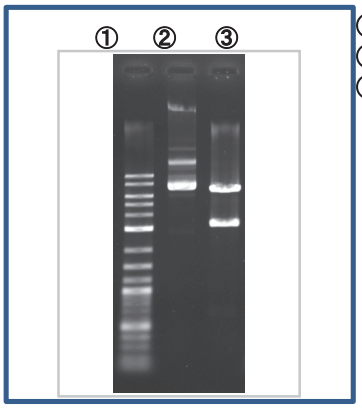
DNA	0.25 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.75 ul
Total	10 ul

BamHI 3.1kb (vector), 6.4 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 : 2025/08/29

full sequence	ARi75E06hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/09/09

DNA (444 ng/ul)	84 ul
10x TE	149 ul
dH_2O	1,259 ul
Total	1,492 ul

● Shipping

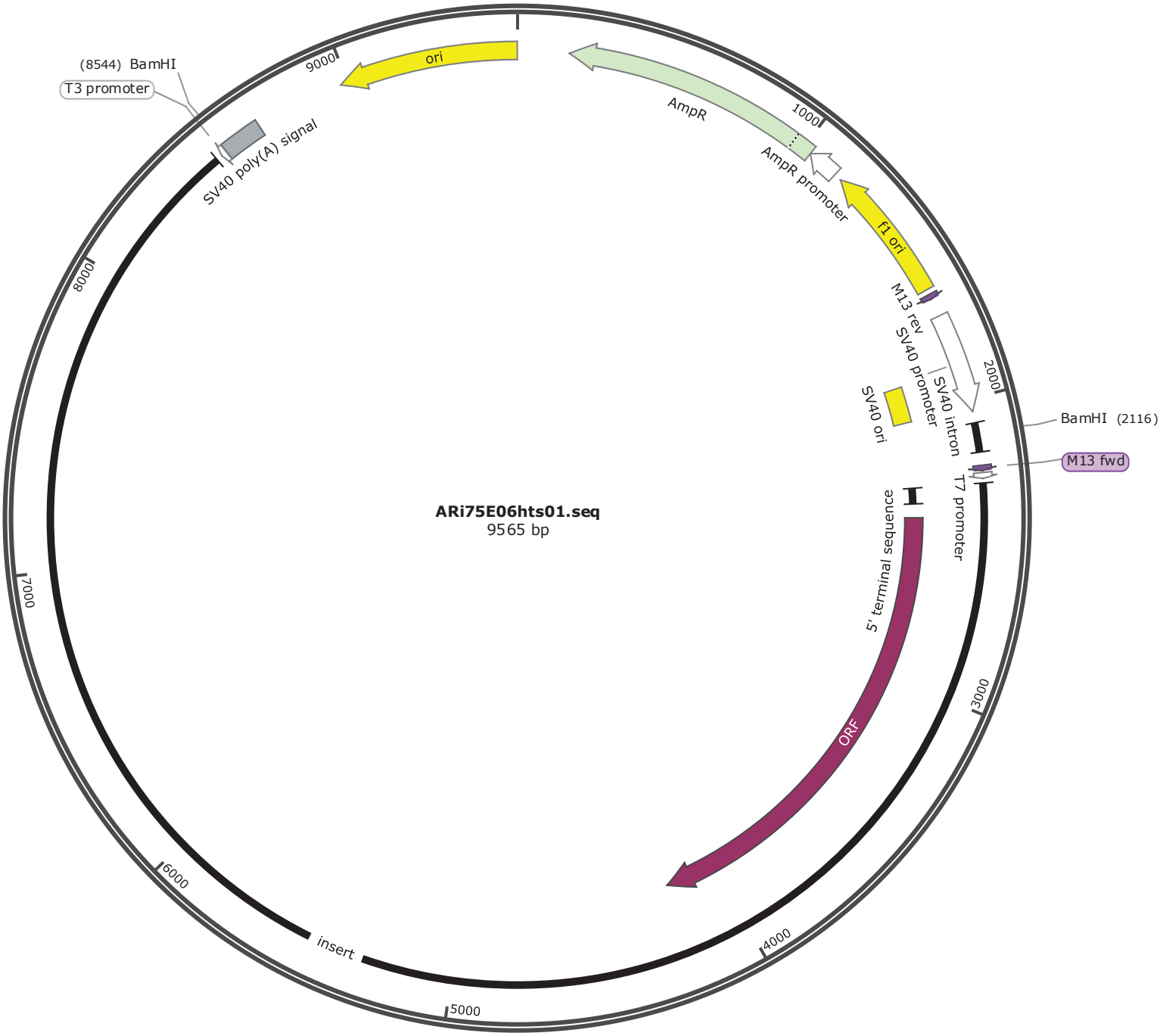
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY :

検 '25.09.09 笹沼

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


ARi75E06hts01.seq
9565 bp
ori
AmpR
AmpR promoter
f1 ori
M13 rev
SV40 promoter
SV40 intron
SV40 ori
BamHI (2116)
M13 fwd
T7 promoter
5' terminal sequence
ORF
insert
(8544) BamHI
T3 promoter
SV40 poly(A) signal
1000
2000
3000
4000
5000
6000
7000
8000
9000

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_001080497:Homo sapiens multiple EGF like...

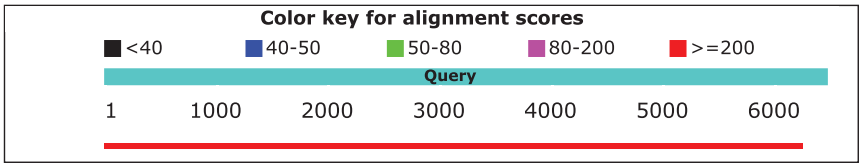
RID B202GU75114 (Expires on 08-30 09:20 am)

Query ID	NM_001080497.3	**Subject ID**	lcl|Query_591655
Description	Homo sapiens multiple EGF like domains 9 (MEGF9), mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	6300	**Subject Length**	9565
		Program	BLASTN 2.17.0+

ARi75E06hts01.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	11393	11393	98%	0.0	99.89%	Query_591655

Alignments

Sequence ID: Query_591655 Length: 9565 Number of Matches: 1
Range 1: 2279 to 8465

Score	Expect	Identities	Gaps	Strand	Frame
11393 bits(6169)	0.0()	6186/6193(99%)	6/6193(0%)	Plus/Plus	

Features:

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Query          1     AGAGGGAGGTGGCGATGGTGCGCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCT  60
Sbjct          2279  ............................................................  2338

CDS:multiple epiderm 1                                                    M  N  G
Query          61    TGGTCGGATTGCAACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGG  120
Sbjct          2339  ............................................................  2398

CDS:multiple epiderm 4       G  A  E  R  A  M  R  S  L  P  S  L  G  G  L  A  L  L  C  C
Query          121   CGGAGCCGAGCGCGCCATGAGGAGCCTGCCGAGCCTGGGCGGCCTCGCCCTGTTGTGCTG  180
Sbjct          2399  ............................................................  2458

CDS:multiple epiderm 24        A  A  A  A  A  A  A  A  V  A  S  A  A  S  A  G  N  V  T  G
Query          181   cacgaccgccgccgccgccgccgccgtcgcctcagccgccTCGGCGGGGAATGTCACCGG  240
Sbjct          2459  ------........................................................  2512

CDS:multiple epiderm 44        G  G  G  A  A  G  Q  V  D  A  S  P  G  P  G  L  R  G  E  P
Query          241   TGGCGGCGGGGCCGCGGGGCAGGTGGACGCGTCGCCGGGCCCCGGGTTGCGGGGCGAGCC  300
Sbjct          2513  ............................................................  2572

CDS:multiple epiderm 64        S  H  P  F  P  R  A  T  A  P  T  A  Q  A  P  R  T  G  P  P
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Sbjct          2573  ............................................................  2632
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181_186 del

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Sbjct                 2633  ............................................................  2692

CDS:multiple epiderm  104   P L W A T A G P S S T T F Q A P L G P S
Query                 421   CCCTCTTTGGGCGACTGCTGGACCCTCTTCCACCACCTTTCAGGCGCCGCTCGGCCCCTC  480
Sbjct                 2693  ............................................................  2752

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Sbjct                 2753  ............................................................  2812

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Query                 541   CGCGCCGACCACCCTTTCGACGACCACTGGCCCGGCGCCGACCACCCCTGTAGCGACCAC  600
Sbjct                 2813  ............................................................  2872

CDS:multiple epiderm  164   V P A P T T P R T P T P D L P S S S N S
Query                 601   CGTACCGGCGCCCACGACtccccggaccccgacccccgatctccccagcagcagcaacag  660
Sbjct                 2873  ............................................................  2932

CDS:multiple epiderm  184   S V L P T P P A T E A P S S P P P E Y V
Query                 661   cagcgtcctccccaccccACCTGCCACCGAGGCCCCCTCTTCGCCTCCTCCAGAGTATGT  720
Sbjct                 2933  ............................................................  2992

CDS:multiple epiderm  204   C N C S V V G S L N V N R C N Q T T G Q
Query                 721   ATGTAACTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCTGCAACCAGACCACAGGGCA  780
Sbjct                 2993  ............................................................  3052

CDS:multiple epiderm  224   C E C R P G Y Q G L H C E T C K E G F Y
Query                 781   GTGTGAGTGTCGGCCAGGTTATCAGGGGCTTCACTGTGAAACCTGCAAAGAGGGCTTTTA  840
Sbjct                 3053  ............................................................  3112

CDS:multiple epiderm  244   L N Y T S G L C Q P C D C S P H G A L S
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Sbjct                 3113  ............................................................  3172

CDS:multiple epiderm  264   I P C N S S G K C Q C K V G V I G S I C
Query                 901   CATACCGTGCAACAGTTCTGGGAAATGCCAGTGCAAAGTGGGTGTCATTGGCTCTATATG  960
Sbjct                 3173  ............................................................  3232

CDS:multiple epiderm  284   D R C Q D G Y Y G F S K N G C L P C Q C
Query                 961   TGACCGATGCCAAGATGGATATTATGGCTTTAGTAAGAATGGCTGCTTGCCCTGCCAATG  1020
Sbjct                 3233  ............................................................  3292

CDS:multiple epiderm  304   N N R S A S C D A L T G A C L N C Q E N
Query                 1021  CAATAATCGGTCTGCCAGTTGCGATGCCCTCACAGGTGCTTGTTTAAACTGCCAGGAAAA  1080
Sbjct                 3293  ............................................................  3352

CDS:multiple epiderm  324   S K G N H C E E C K E G F Y Q S P D A T
Query                 1081  TAGCAAAGGAAATCACTGTGAAGAATGTAAAGAAGGATTTTATCAGAGTCCTGATGCCAC  1140
Sbjct                 3353  ............................................................  3412

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Sbjct                 3413  ............................................................  3472

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Sbjct                 3473  ............................................................  3532
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Sbjct                 3533  ............................................................  3592

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Query                 1321  CGGCCATGTGGACCCAGTTAAAACTCCAAAGATTTGTAAGCCCGAGAGTGGTGAGTGCAT  1380
Sbjct                 3593  ............................................................  3652

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Sbjct                 3653  ............................................................  3712

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Sbjct                 3713  ............................................................  3772

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Sbjct                 3773  ............................................................  3832

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Sbjct                 4013  ............................................................  4072

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Query                 1801  CAGCTACCATGACAGCATTCCCAATGCAGATGTTTCGGGATTGTTGGAAGATGATGGCAA  1860
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Sbjct                 4373  ............................................................  4432

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Sbjct                 4433  ............................................................  4492
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Sbjct  8033  ............................................................  8092

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Sbjct  8273  ............................................................  8332

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Sbjct  8393  ............................................................  8452

Query  6181  TGTACCTATTGTA  6193
Sbjct  8453  .............  8465
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