NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARe19F12

Lot# : 7672_B4Hm

Vector : pKA1U5

Gene	CCN2	
RefSeq_mRNA	NM_001901.4	2338 bp

● Plasmid DNA purification

Date : 2024/08/22 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2024/08/23 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2024/08/23

DNA concentration (O.D.): 361 ng/ul

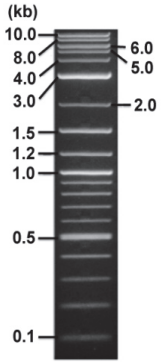
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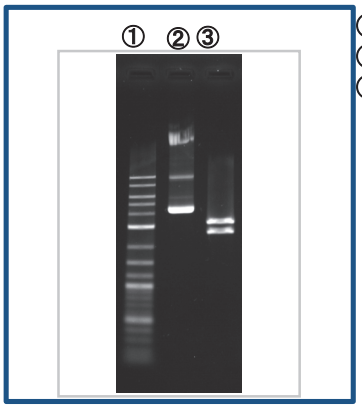
DNA	0.25 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.75 ul
Total	10 ul

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 : 2024/08/30

Primer A	-
Primer B	-
Primer C	ARe19F12hts01.seq
List of Sequencing Primers	-

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2024/09/06

DNA (361 ng/ul)	86 ul
10x TE	124 ul
dH_2O	1,032 ul
Total	1,242 ul

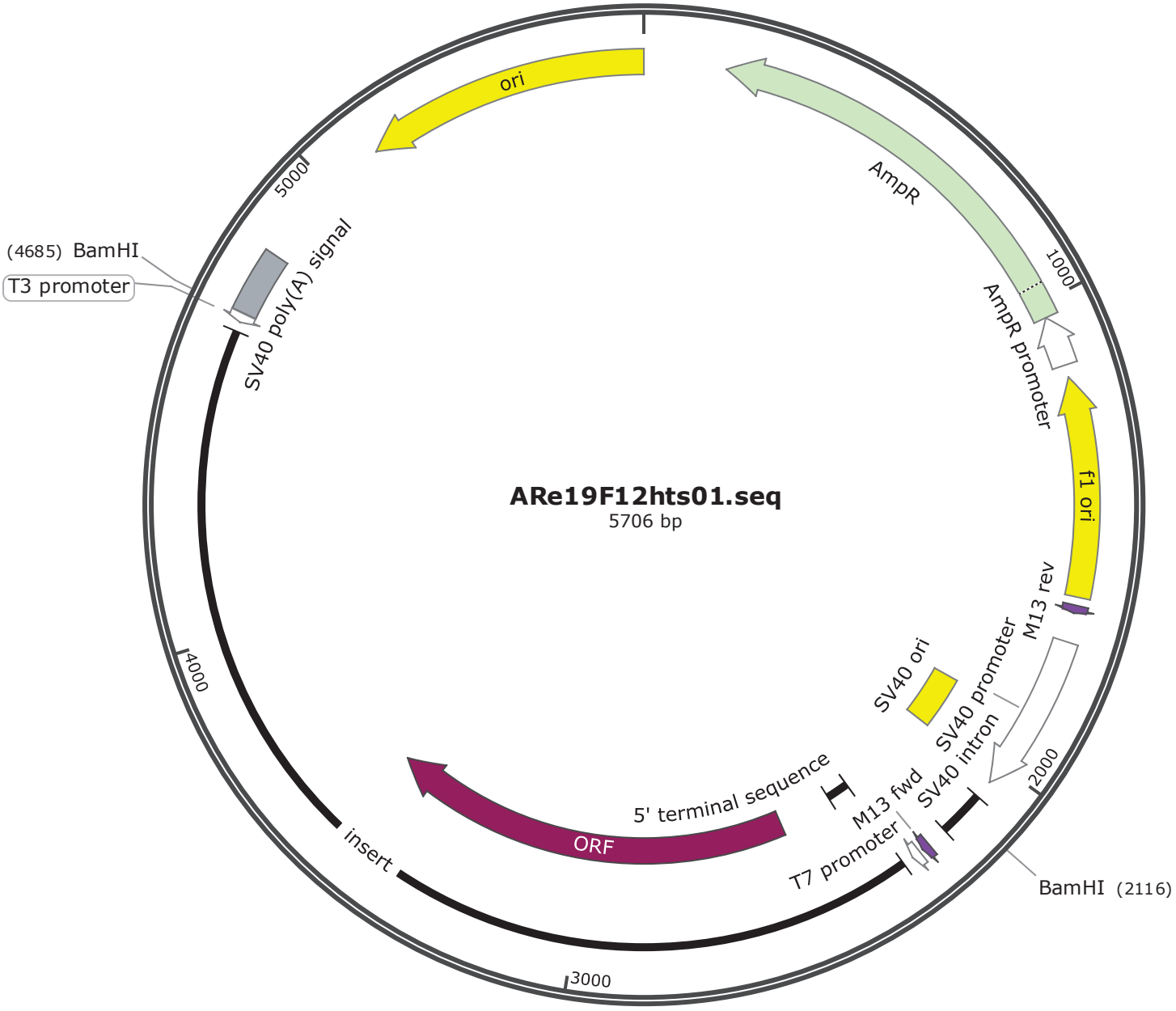
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '24.09.06 笹沼

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


ARe19F12hts01.seq
5706 bp
ori
AmpR
AmpR promoter
f1 ori
M13 rev
SV40 promoter
SV40 intron
SV40 ori
M13 fwd
T7 promoter
5' terminal sequence
ORF
insert
SV40 poly(A) signal
T3 promoter
(4685) BamHI
BamHI (2116)
1000
2000
3000
4000
5000

BLAST Results

Questions/comments

Blast 2 sequences

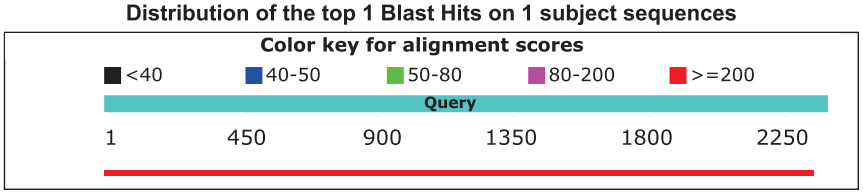
Job title: NM_001901:Homo sapiens cellular communication...

RID CXER58NX114 (Expires on 08-29 13:51 pm)

Query ID	NM_001901.4	**Subject ID**	lcl|Query_4006937
Description	Homo sapiens cellular communication network factor 2 (CCN2), mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	2338	**Subject Length**	5706
		Program	BLASTN 2.16.0+

ARe19F12hts01.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	4283	4283	100%	0.0	99.74%	Query_4006937

Alignments

Sequence ID: Query_4006937 Length: 5706 Number of Matches: 1
Range 1: 2286 to 4621

Score	Expect	Identities	Gaps	Strand	Frame
4283 bits(2319)	0.0()	2332/2338(99%)	2/2338(0%)	Plus/Plus	

Features:

```
Query                1     ACACAACAACTCTTCCCCGCTGAGAGGAGACAGCCAGTGCGACTCCACCCTCCAGCTCGA  60
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2286  ACACAACAACTCTTCCCCGCTGAGAGGAGACAGCCAGTGCGACTCCACCCTCCAGCTCGA  2345

Query                61    CGGCAGCCGCCCCGGCCGACAGCCCCGAGACGACAGCCCGGCGCGTCCCGGtccccacct  120
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2346  CGGCAGCCGCCCCGGCCGACAGCCCCGAGACGACAGCCCGGCGCGTCCCGGTCCCCACCT  2405

Query                121   ccgaccaccgccagcgctccaggccccgccgctccccgctcgccgccaccgcgccctccg  180
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2406  CCGACCACCGCCAGCGCTCCAGGCCCCGCCGCTCCCCGCTCGCCGCCACCGCGCCCTCCG  2465

CDS:CCN family membe 1                          M  T  A  A  S  M  G  P  V  R  V  A  F
Query                181   ctccgcccgcagtgccaaccatgaccgccgccaGTATGGGCCCCGTCCGCGTCGCCTTCG  240
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2466  CTCCGCCCGCAGTGCCAACCATGACCGCCGCCAGTATGGGCCCCGTCCGCGTCGCCTTCG  2525

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                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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419 A>C

440 A>C

447 C>G (H83D)

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