NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : RBdS007D08

Lot# : 6608_B5Lm

Vector : pGCAP10

Gene	SUMO1	
RefSeq_mRNA	NM_003352.8	1523 bp

● Plasmid DNA purification

Date : 2026/01/08 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2026/01/13 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2026/01/13

DNA concentration (O.D.): 358 ng/ul

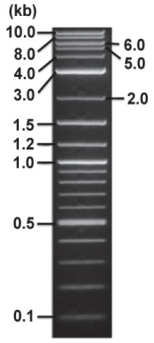
DNA	0.3	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.7	ul
Total	10	ul

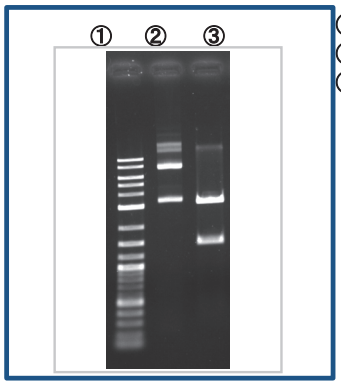
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 1.4 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 : 2026/01/15

full sequence	RBdS007D08hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/01/20

DNA (358 ng/ul)	86	ul
10x TE	123	ul
dH_2O	1,022	ul
Total	1,232	ul

● Shipping

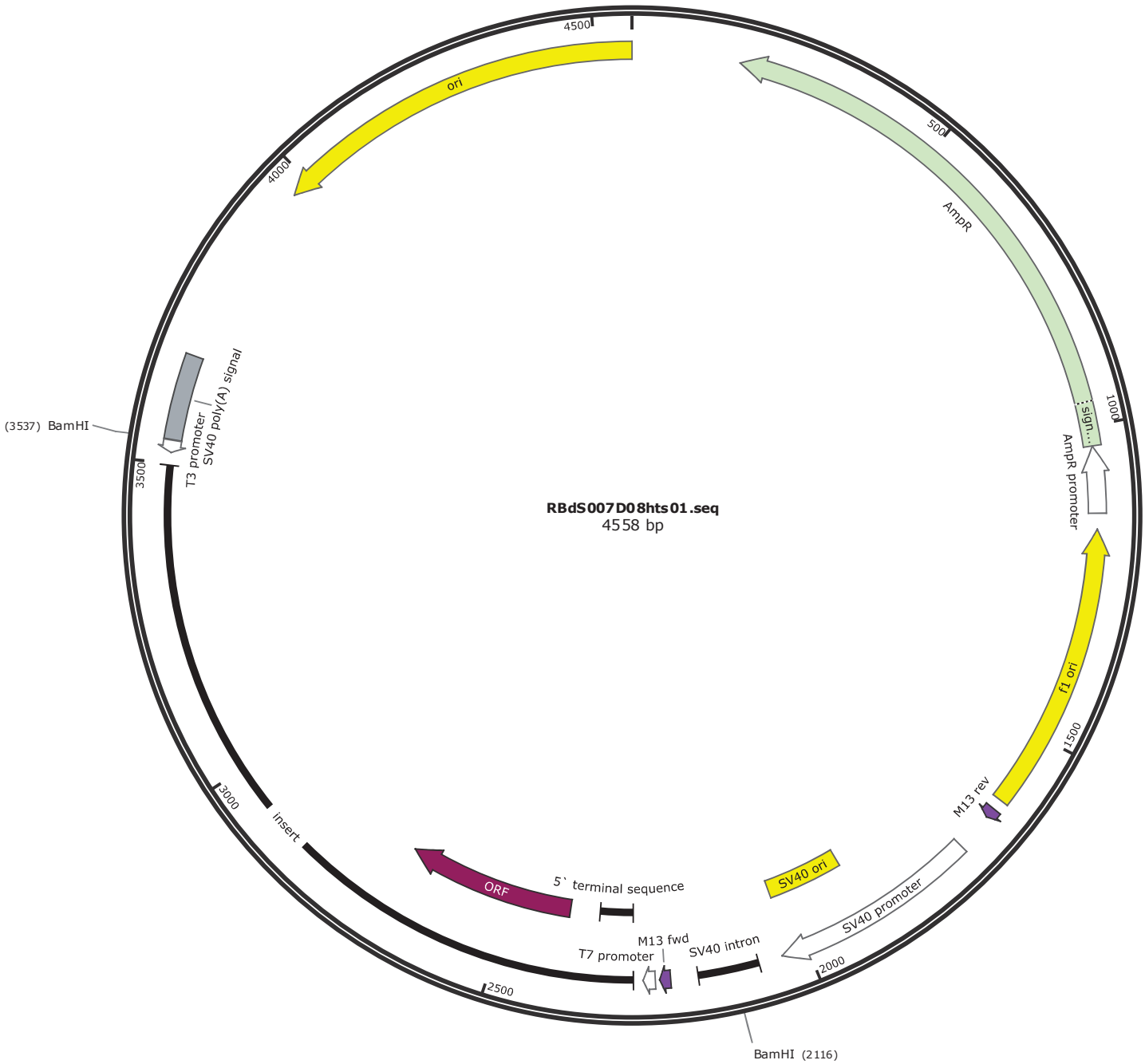
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY :

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'26.01.20
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http://dna.brc.riken.jp/index.html


RBdS007D08hts01.seq
4558 bp
4500
ori
4000
500
AmpR
1000
AmpR promoter
1500
f1 ori
M13 rev
SV40 promoter
SV40 ori
SV40 intron
M13 fwd
T7 promoter
5` terminal sequence
ORF
2000
2500
BamHI (2116)
3000
insert
3500
T3 promoter
SV40 poly(A) signal
(3537) BamHI

BLAST ® » blastn suite-2sequences » RID-PH7PUY6D114

BLAST Results

Questions/comments

Blast 2 sequences

Job title: ref|NM_003352.8|

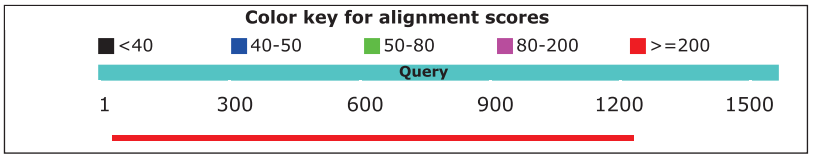
RID PH7PUY6D114 (Expires on 01-16 15:01 pm)

Query ID	NM_003352.8	**Subject ID**	lcl|Query_4741965
Description	Homo sapiens small ubiquitin like modifier 1 (SUMO1), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	1523	**Subject Length**	4558
		Program	BLASTN 2.17.0+

RBdS007D08hts01.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	2196	2196	78%	0.0	100.00%	Query_4741965

Alignments

Sequence ID: Query_4741965 Length: 4558 Number of Matches: 1
Range 1: 2279 to 3467

Score	Expect	Identities	Gaps	Strand	Frame
2196 bits(1189)	0.0()	1189/1189(100%)	0/1189(0%)	Plus/Plus	

Features:

```
Query              34   AGCCGCGGTGTTGTGCTGTGGGGAAGGGAGAAGGATTTGTAAACCCCGGAGCGAGGTTCT  93
Sbjct              2279 ............................................................  2338

CDS:small ubiquitin-  1                                                    M  S
Query              94   GCTTACCCGAGGCCGCTGCTGTGCGGAGACCCCCGGGTGAAGCCACCGTCATCATGTCTG  153
Sbjct              2339 ............................................................  2398

CDS:small ubiquitin-  3    D  Q  E  A  K  P  S  T  E  D  L  G  D  K  K  E  G  E  Y  I
Query              154  ACCAGGAGGCAAAACCTTCAACTGAGGACTTGGGGGATAAGAAGGAAGGTGAATATATTA  213
Sbjct              2399 ............................................................  2458

CDS:small ubiquitin-  23   K  L  K  V  I  G  Q  D  S  S  E  I  H  F  K  V  K  M  T  T
Query              214  AACTCAAAGTCATTGGACAGGATAGCAGTGAGATTCACTTCAAAGTGAAAATGACAACAC  273
Sbjct              2459 ............................................................  2518

CDS:small ubiquitin-  43   H  L  K  K  L  K  E  S  Y  C  Q  R  Q  G  V  P  M  N  S  L
Query              274  ATCTCAAGAAACTCAAAGAATCATACTGTCAAAGACAGGGTGTTCCAATGAATTCACTCA  333
Sbjct              2519 ............................................................  2578

CDS:small ubiquitin-  63   R  F  L  F  E  G  Q  R  I  A  D  N  H  T  P  K  E  L  G  M
Query              334  GGTTTCTCTTTGAGGGTCAGAGAATTGCTGATAATCATACTCCAAAAGAACTGGGAATGG  393
Sbjct              2579 ............................................................  2638
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CDS:small ubiquitin-  83    E  E  E  D  V  I  E  V  Y  Q  E  Q  T  G  G  H  S  T  V
Query                 394   AGGAAGAAGATGTGATTGAAGTTTATCAGGAACAAACGGGGGGTCATTCAACAGTTTAGA  453
Sbjct                 2639  ............................................................  2698

Query                 454   TATTCttttttatttttttttctttccctcaatccttttttattttttAAAAATAGTTCTTT  513
Sbjct                 2699  ............................................................  2758

Query                 514   TGTAATGTGGTGTTCAAAACGGAATTGAAAACTGGCACCCCATCTCTTTGAAACATCTGG  573
Sbjct                 2759  ............................................................  2818

Query                 574   TAATTTGAATTCTAGTGCTCATTATTCATTATTGTTTGTTTTCATTGTGCTGATTTTTGG  633
Sbjct                 2819  ............................................................  2878

Query                 634   TGATCAAGCCTCAGTCCCCTTCATATTACCCTCTCCTTTTTAAAAATTACGTGTGCACAG  693
Sbjct                 2879  ............................................................  2938

Query                 694   AGAGGTCACCTTTTTCAGGACATTGCATTTTCAGGCTTGTGGTGATAAATAAGATCGACC  753
Sbjct                 2939  ............................................................  2998

Query                 754   AATGCAAGTGTTCATAATGACTTTCCAATTGGCCCTGATGTTCTAGCATGTGATTACTTC  813
Sbjct                 2999  ............................................................  3058

Query                 814   ACTCCTGGACTGTGACTTTCAGTGGGAGATGGAAGTTTTTCAGAGAACTGAACTGTGGAA  873
Sbjct                 3059  ............................................................  3118

Query                 874   AAATGACCTTTCCTTAACTTGAAGCTACTTTTAAAATTTGAGGGTCTGGACCAAAAGAAG  933
Sbjct                 3119  ............................................................  3178

Query                 934   AGGAATATCAGGTTGAAGTCAAGATGACAGATAAGGTGAGAGTAATGACTAACTCCAAAG  993
Sbjct                 3179  ............................................................  3238

Query                 994   ATGGCTTCACTGAAGAAAAGGCATTTTAAGATTTTTTAAAAATCTTGTCAGAAGATCCCA  1053
Sbjct                 3239  ............................................................  3298

Query                 1054  GAAAAGTTCTAATTTTCATTAGCAATTAATAAAGCTATACATGCAGAAATGAATACAACA  1113
Sbjct                 3299  ............................................................  3358

Query                 1114  GAACACTGCTCTTTTTGATTTTATTTGTACTTTTTGGCCTGGGATATGGGTTTTAAATGG  1173
Sbjct                 3359  ............................................................  3418

Query                 1174  ACATTGTCTGTACCAGCTTCATTAAAATAAACAATATTTGTAAAAATCA  1222
Sbjct                 3419  ..................................................  3467
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