NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : RBdS110P05

Lot# : 6608_B5Lm

Vector : pGCAP10

Gene	SUMO2	
RefSeq_mRNA	NM_006937.4	3166 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.): 89 ng/ul

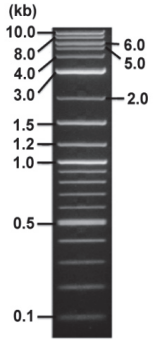
< Size of fragment expected from this clone >

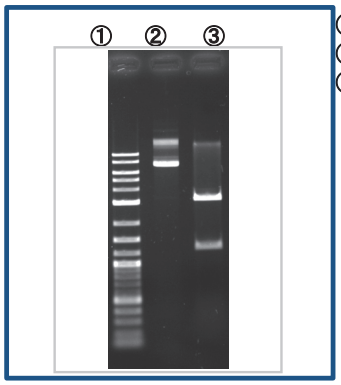
DNA	1.2	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	6.8	ul
Total	10	ul

BamHI 3.1kb (vector), 1.3 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	RBdS110P05hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/01/20

DNA (89 ng/ul)	86	ul
10x TE	31	ul
dH_2O	190	ul
Total	306	ul

● Shipping

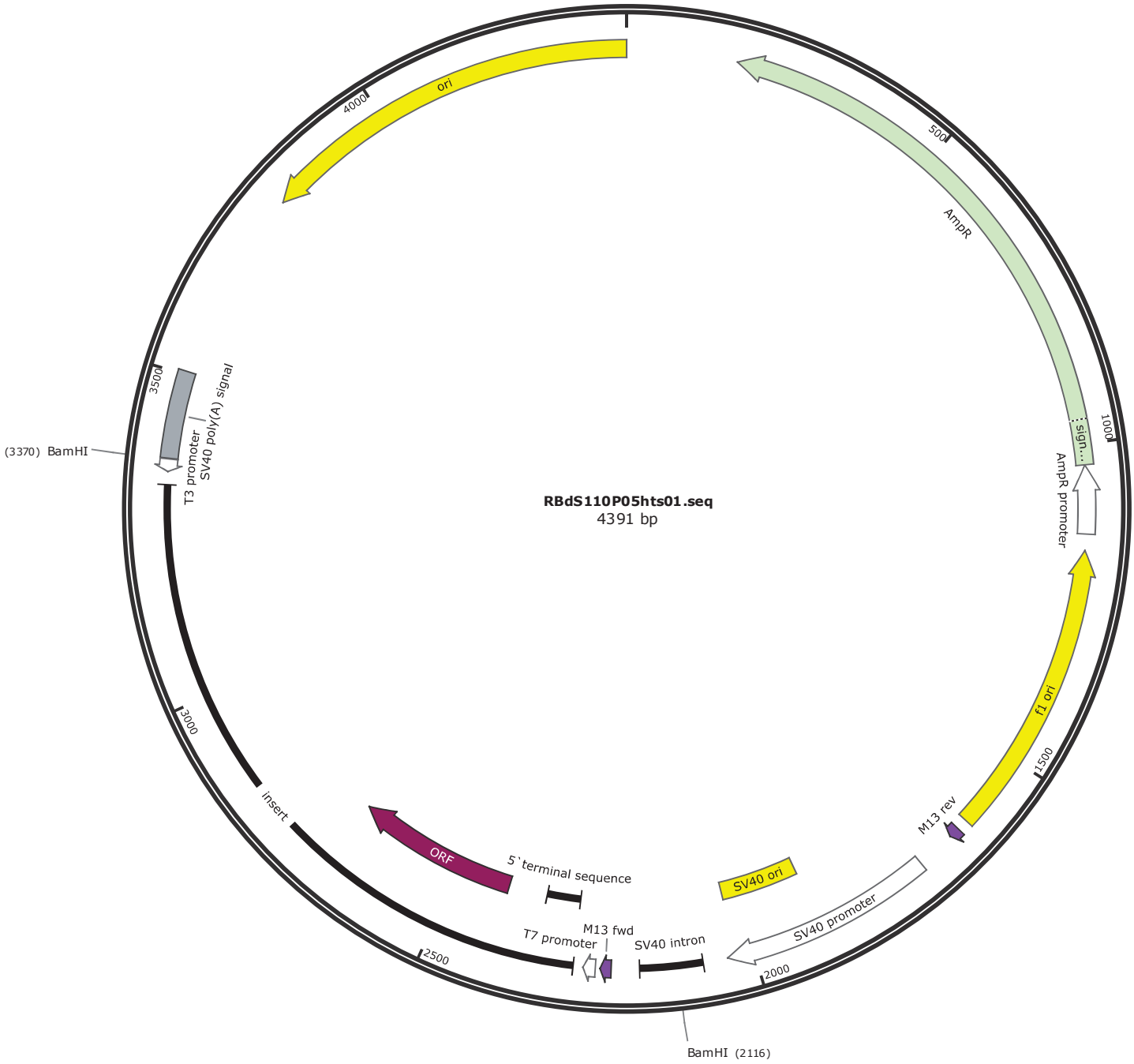
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY :

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


RBdS110P05hts01.seq
4391 bp
ori
4000
AmpR
500
sign...
1000
AmpR promoter
f1 ori
1500
M13 rev
SV40 promoter
2000
SV40 ori
SV40 intron
M13 fwd
T7 promoter
2500
5`terminal sequence
ORF
insert
3000
T3 promoter
SV40 poly(A) signal
3500
(3370) BamHI
BamHI (2116)

BLAST ® » blastn suite-2sequences » RID-PH6H4K2W114

BLAST Results

Questions/comments

Blast 2 sequences

Job title: ref|NM_006937.4|

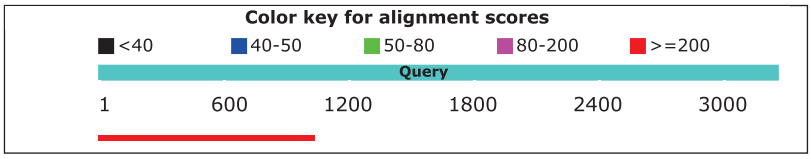
RID PH6H4K2W114 (Expires on 01-16 14:41 pm)

Query ID	NM_006937.4	**Subject ID**	lcl|Query_4369327
Description	Homo sapiens small ubiquitin like modifier 2 (SUMO2), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	3166	**Subject Length**	4391
		Program	BLASTN 2.17.0+

RBdS110P05hts01.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	1888	1888	32%	0.0	100.00%	Query_4369327

Alignments

Sequence ID: Query_4369327 Length: 4391 Number of Matches: 1
Range 1: 2282 to 3303

Score	Expect	Identities	Gaps	Strand	Frame
1888 bits(1022)	0.0()	1022/1022(100%)	0/1022(0%)	Plus/Plus	

Features:

```
Query              1    CTCTCCCCTCGTCCACCGCTGCCGCCTCCTTCTTCTGCCGCTCCTGGTGCTGCTTGTGTG  60
Sbjct           2282    ............................................................  2341

Query             61    CTCGTTTGGTGCGGACCTGGTACCTCTTTTGTGAAGCGGCAGCTGAGGAGACTCCGGCGC  120
Sbjct           2342    ............................................................  2401

CDS:small ubiquitin-   1          M  A  D  E  K  P  K  E  G  V  K  T  E  N  N  D  H  I
Query            121    TCGCCATGGCCGACGAAAAGCCCAAGGAAGGAGTCAAGACTGAGAACAACGATCATATTA  180
Sbjct           2402    ............................................................  2461

CDS:small ubiquitin-  19    N  L  K  V  A  G  Q  D  G  S  V  V  Q  F  K  I  K  R  H  T
Query            181    ATTTGAAGGTGGCGGGGCAGGATGGTTCTGTGGTGCAGTTTAAGATTAAGAGGCATACAC  240
Sbjct           2462    ............................................................  2521

CDS:small ubiquitin-  39    P  L  S  K  L  M  K  A  Y  C  E  R  Q  G  L  S  M  R  Q  I
Query            241    CACTTAGTAAACTAATGAAAGCCTATTGTGAACGACAGGGATTGTCAATGAGGCAGATCA  300
Sbjct           2522    ............................................................  2581

CDS:small ubiquitin-  59    R  F  R  F  D  G  Q  P  I  N  E  T  D  T  P  A  Q  L  E  M
Query            301    GATTCCGATTTGACGGGCAACCAATCAATGAAACAGACACACCTGCACAGTTGGAAATGG  360
Sbjct           2582    ............................................................  2641

CDS:small ubiquitin-  79    E  D  E  D  T  I  D  V  F  Q  Q  Q  T  G  G  V  Y
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Query  361   AGGATGAAGATACAATTGATGTGTTCCAACAGCAGACGGGAGGTGTCTACTGAAAAGGGA  420
Sbjct  2642  ............................................................  2701

Query  421   ACCTGCTTCTTTACTCCAGAACTCTGTTCTTTAAAGACCAAGATTACATTCTCAATTAGA  480
Sbjct  2702  ............................................................  2761

Query  481   AAACTGCAATTTGGTTCCACCACATCCTGACTACTACCGTATAGTTTTCTCTATTCTTTC  540
Sbjct  2762  ............................................................  2821

Query  541   ATTTCCCCCTTCCCCATTCCTTTATTGTACATAAAGTAACTGGTATATGTGCACAAGCAT  600
Sbjct  2822  ............................................................  2881

Query  601   ATTGCAttttttttttttttAACTAAACAGCCAATGGTATGTTTTGATTGACATCAAGTG  660
Sbjct  2882  ............................................................  2941

Query  661   GAGACGGGATGGGGAAAAATACTGATTCTGTGAAAATACCCCCTTTCTCCATTAGTGGCA  720
Sbjct  2942  ............................................................  3001

Query  721   TGCTCATTCAGCTCTTATCTTTATATTCCAGTAAGTTATTTTGCTCTCACTGTTTTAACa  780
Sbjct  3002  ............................................................  3061

Query  781   aaaaaaaaaaCAACAACATAAAAATCCTTGCATACCTTGTTCAATTGGAGAATTTTAAT  840
Sbjct  3062  ............................................................  3121

Query  841   GTTTTTCATTTATCATTGTAAAACCAAGGACAATTTTATAACTTTTTTGTACGTAGCTGT  900
Sbjct  3122  ............................................................  3181

Query  901   TACATGTAGGGCAATCTGTCTTTAAGTAGGGATAAATTACTCTAAAACAAAAAAGAATCC  960
Sbjct  3182  ............................................................  3241

Query  961   TAGATAGTTTTCCCTTCAAGTCAAGCGTCTTGTTGTTTAAATAAACTTCTTGTTTAAAAT  1020
Sbjct  3242  ............................................................  3301

Query  1021  GA  1022
Sbjct  3302  ..  3303
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