5 - 3

NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : ARi12G04
Vector : pGCAP10

Lot# : 7675_B3Bd

Gene	TRIM7	
RefSeq_mRNA	NM_203293.3	2864 bp

● Plasmid DNA purification

Date : 23.03.14 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.03.15 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 23.03.15

DNA concentration (O.D.): 88 ng/ul

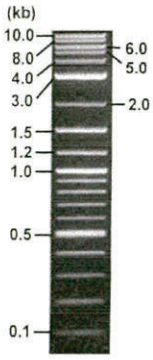
DNA	1.1 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	6.9 ul
Total	10 ul

< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 1.3, 1.0, 0.9 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 : 2026/06/19

full sequence : ARi12G04hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/07/23

DNA (8888 ng/ul)	72 ul
10x TE	25 ul
dH_2O	156 ul
Total	253 ul

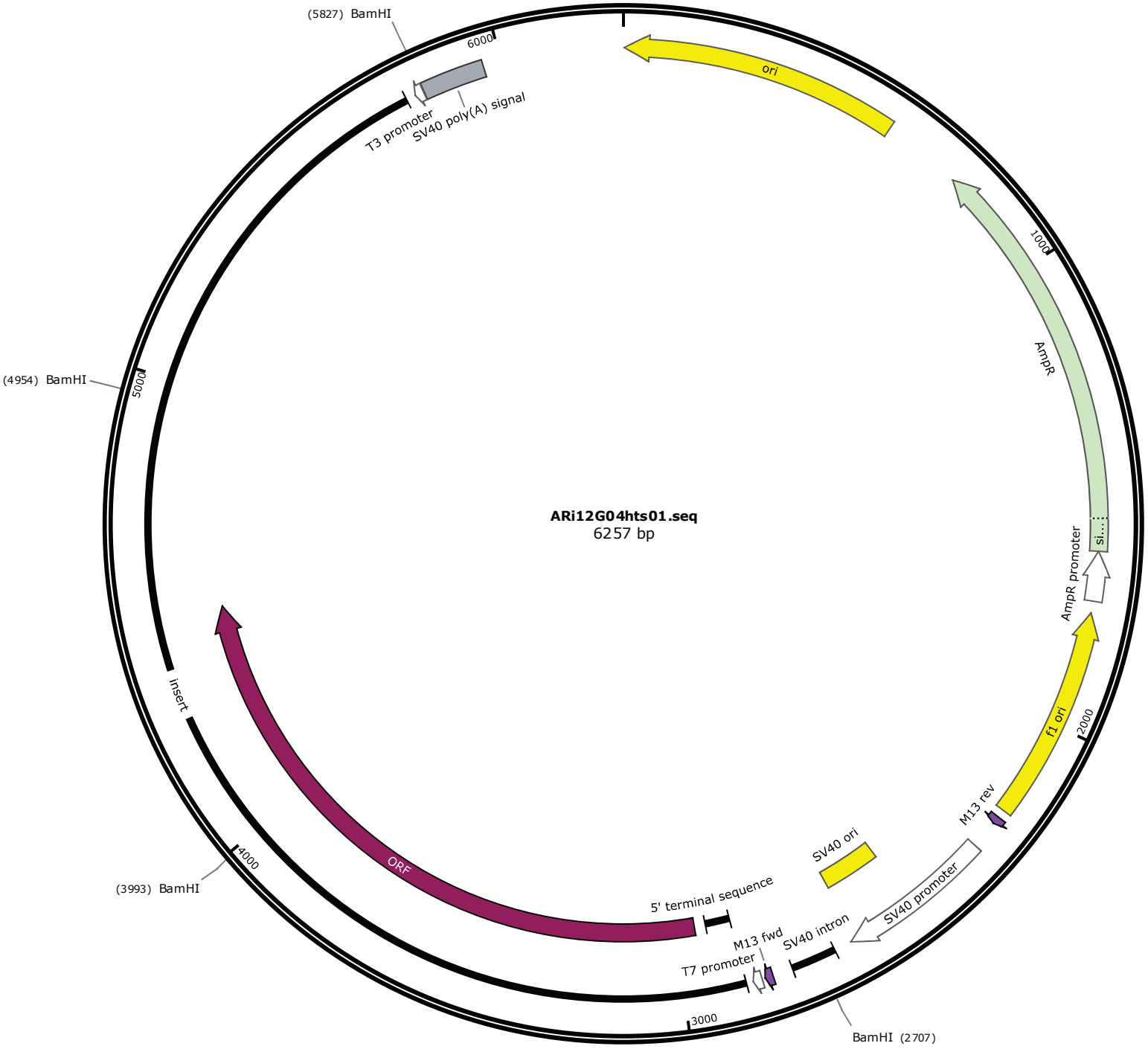
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '26.07.23 笹沼

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


(5827) BamHI
6000
ori
T3 promoter
SV40 poly(A) signal
1000
AmpR
(4954) BamHI
5000
ARi12G04hts01.seq
6257 bp
AmpR promoter
f1 ori
2000
insert
ORF
4000
(3993) BamHI
M13 rev
SV40 ori
SV40 promoter
5' terminal sequence
M13 fwd
SV40 intron
T7 promoter
3000
BamHI (2707)

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_015323:Homo sapiens UFM1 specific ligase...

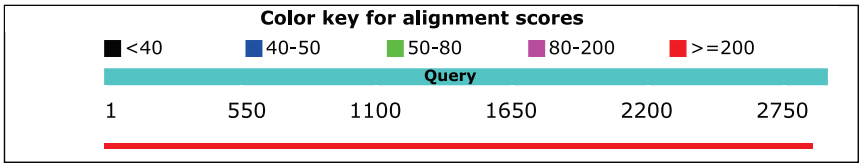
RID 399FD132114 (Expires on 06-20 10:14 am)

Query ID	NM_203293.3	**Subject ID**	lcl|Query_4124943
Description	Homo sapiens tripartite motif containing 7 (TRIM7), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	2864	**Subject Length**	6257
		Program	BLASTN 2.17.0+

ARi12G04hts01.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	5210	5210	100%	0.0	99.58%	Query_4124943

Alignments

Sequence ID: Query_4124943 Length: 6257 Number of Matches: 1
Range 1: 2870 to 5726

Score	Expect	Identities	Gaps	Strand	Frame
5210 bits(2821)	0.0()	2847/2859(99%)	3/2859(0%)	Plus/Plus	

Features:

```
Query              1     AGTGGGCCCTCGGCGCCCAGCTCCGCGTCCTGTGAGGTCCAGTGGCCGCCCAGGCGCGAC  60
Sbjct              2870  ............................................................  2929

CDS:E3 ubiquitin-pro 1                                  M  A  A  V  G  P  R  T  G  P  G
Query              61    CAGATCTGGGTGCGCGGAGAGCGCGCATGGCGGCTGTGGGACCGCGGACCGGCCCCGGAA  120
Sbjct              2930  ............................................................  2989

CDS:E3 ubiquitin-pro 12    T  G  A  E  A  L  A  L  A  A  E  L  Q  G  E  A  T  C  S  I
Query              121   CCGGCGCCGAGGCTCTAGCGCTGGCGGCAGAGCTGCAGGGCGAGGCGACGTGCTCCATCT  180
Sbjct              2990  ............................................................  3049

CDS:E3 ubiquitin-pro 32    C  L  E  L  F  R  E  P  V  S  V  E  C  G  H  S  F  C  R  A
Query              181   GCCTAGAGCTCTTTCGTGAGCCGGTGTCCGTCGAGTGCGGCCACAGCTTCTGCCGCGCCT  240
Sbjct              3050  ............................................................  3109

CDS:E3 ubiquitin-pro 52    C  I  G  R  C  W  E  R  P  G  A  G  S  V  G  A  A  T  R  A
Query              241   GCATAGGGCGCTGCTGGGAGCGCCCGGGCGCGGGGTCTGTTGGGgccgccacccgcgcgc  300
Sbjct              3110  ............................................................  3169

CDS:E3 ubiquitin-pro 72    P  P  F  P  L  P  C  P  Q  C  R  E  P  A  R  P  S  Q  L  R
Query              301   cccccttcccactgccctgtccgcagtgccgcgagcccgcgcgccccAGTCAGCTGCGGC  360
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303 C>T (P73S)

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Sbjct                3170  ..T.....................................................  3229

CDS:E3 ubiquitin-pro   92  P N R Q L A A V A T L L R R F S L P A A
Query                 361  CCAACCGGCAGCTGGCGGCAGTGGCCACGCTCCTGCGGCGCTTCAGCCTGCCCGCGGCTG  420
Sbjct                3230  .....................G.....................C.  3289

CDS:E3 ubiquitin-pro  112  A P G E H G S Q A A A A A R A A A A A R C G
Query                 421  CCCCGGGAGAGCACGGGTCTCAGGCGGCCGCGGCCCGGGCAGCGGCTGCCCGCTGCGGGC  480
Sbjct                3290  .....................................................  3349

CDS:E3 ubiquitin-pro  132  Q H G E P F K L Y C Q D D G R A I C V V
Query                 481  AGCATGGCGAACCCTTCAAGCTCTACTGCCAGGACGACGGACGCGCCATCTGCGTGGTGT  540
Sbjct                3350  .....................................................  3409

CDS:E3 ubiquitin-pro  152  C D R A R E H R E H A V L P L D E A V Q
Query                 541  GCGACCGCGCCCGCGAGCACCGCGAGCACGCCGTGCTGCCGCTGGACGAGGCGGTGCAGG  600
Sbjct                3410  .....................................................  3469

CDS:E3 ubiquitin-pro  172  E A K E L L E S R L R V L K K E L E D C
Query                 601  AGGCCAAGGAGCTCTTGGAGTCCAGGCTGAGGGTCTTGAAGAAGGAACTGGAGGACTGTG  660
Sbjct                3470  .....................................................  3529

CDS:E3 ubiquitin-pro  192  E V F R S T E K K E S K E L L K Q M A A
Query                 661  AGGTGTTCCGGTCCACGGAAAAGAAGGAGAGCAAGGAGCTGCTGAAACAGATGGCAGCGG  720
Sbjct                3530  .....................................................  3589

CDS:E3 ubiquitin-pro  212  E Q E K V G A E F Q A L R A F L V E Q E
Query                 721  AGCAGGAGAAGGTGGGGGCAGAGTTCCAGGCACTGAGGGCTTTCCTGGTGGAGCAGGAGG  780
Sbjct                3590  .....................................................  3649

CDS:E3 ubiquitin-pro  232  G R L L G R L E E L S R E V A Q K Q N E
Query                 781  GTCGGCTGCTAGGCCGCCTGGAGGAACTGTCCCGGGAGGTGGCACAGAAGCAGAATGAGA  840
Sbjct                3650  .....................................................  3709

CDS:E3 ubiquitin-pro  252  N L A Q L G V E I T Q L S K L S S Q I Q
Query                 841  ACCTGGCCCAGCTCGGGGTTGAGATCACCCAGCTGTCCAAGCTCAGCAGCCAGATCCAGG  900
Sbjct                3710  .....................C.....................................  3769

CDS:E3 ubiquitin-pro  272  E T A Q K P D L D F L Q E F K S T L S R
Query                 901  AGACAGCTCAAAAGCCTGACCTTGACTTTCTCCAGGAATTCAAAAGCACGCTGAGCAGGT  960
Sbjct                3770  .....................................................  3829

CDS:E3 ubiquitin-pro  292  C S N V P G P K P T T V S S E M K N K V
Query                 961  GTAGCAATGTGCCTGGCCCCAAGCCAACCACAGTCTCTTCTGAGATGAAGAATAAAGTCT  1020
Sbjct                3830  .....................................................  3889

CDS:E3 ubiquitin-pro  312  W N V S L K T F V L K G M L K K F K E D
Query                1021  GGAATGTTTCTCTCAAGACCTTTGTCTTAAAAGGGATGCTGAAGAAGTTCAAAGAGGACC  1080
Sbjct                3890  .....................................................  3949

CDS:E3 ubiquitin-pro  332  L R G E L E K E E K V E L T L D P D T A
Query                1081  TTCGGGGAGAGCTGGAGAAAGAGGAGAAAGTGGAGCTCACCTTGGATCCCGACACGGCCA  1140
Sbjct                3950  .....................................................  4009

CDS:E3 ubiquitin-pro  352  N P R L I L S L D L K G V R L G E R A Q
Query                1141  ACCCGCGCCTCATCCTCTCTCTGGATCTTAAGGGCGTGCGCCTCGGCGAGCGGGCCCAGG  1200
Sbjct                4010  .....................................................  4069

CDS:E3 ubiquitin-pro  372  D L P N H P C R F D T N T R V L A S C G


Query                1201  ACCTGCCCAACCACCCCTGCCGCTTCGACACCAACACCCGCGTCCTGGCGTCCTGCGGCT  1260
Sbjct                4070  .....................................................  4129

CDS:E3 ubiquitin-pro  392  F S S G R H H W E V E V G S K D G W A F
Query                1261  TCTCCTCGGGCCGGCATCACTGGGAGGTGGAGGTGGGCTCTAAGGACGGCTGGGCCTTTG  1320
Sbjct                4130  .....................................................  4189

CDS:E3 ubiquitin-pro  412  G V A R E S V R R K G L T P F T P E E G
Query                1321  GCGTGGCCCGCGAGAGCGTGCGCCGAAAGGGCCTGACGCCCTTCACTCCCGAGGAGGGCG  1380
Sbjct                4190  .....................................................  4249

CDS:E3 ubiquitin-pro  432  V W A L Q L N G G Q Y W A V T S P E R S
Query                1381  TCTGGGCCCTGCAGCTCAACGGCGGCCAGTACTGGGCCGTGACCAGCCCCGAGCGGTCGC  1440
Sbjct                4250  .....................................................  4309

CDS:E3 ubiquitin-pro  452  P L S C G H L S R V R V A L D L E V G A
Query                1441  CCCTCAGCTGCGGGCACCTGTCGCGCGTGCGGGTGGCCCTGGACCTGGAGGTGGGAGCCG  1500
Sbjct                4310  .....................................................  4369

CDS:E3 ubiquitin-pro  472  V S F Y A V E D M R H L Y T F R V N F Q
Query                1501  TGTCCTTCTACGCTGTGGAGGACATGCGCCACCTCTACACCTTCCGCGTCAACTTCCAGG  1560
Sbjct                4370  .....................................................  4429

CDS:E3 ubiquitin-pro  492  E R V F P L F S V C S T G T Y L R I W P
Query                1561  AGCGCGTGTTCCCGCTTTTCTCTGTTTGCTCCACGGGCACCTACTTGCGAATCTGGCCTT  1620
Sbjct                4430  .....................................................  4489

Query                1621  GAGGGGCACTGCTGGGGAGCTCCTGTCTCTGGGCTGCCGGTGGGAGGGGATGTCGCCTCC  1680
Sbjct                4490  .....................................................  4549

Query                1681  CCAGAGATGCCTGGTCCGTCTTGGGTCTGCCCTCCGTGCTCCTGACCCCTGCTGCCCAAG  1740
Sbjct                4550  .....................................................  4609

Query                1741  AGAGCCTGCTACAGACACAACCCCGAGGCAGGAGAGTGACTGTGGCCAACCGAGCAGGGG  1800
Sbjct                4610  .....................................................  4669

Query                1801  AACAGGGGCTTTGGACTCCTGAGGGTGTTCCCTTCCTGAGGTCACATGTGGATTTGGCCA  1860
Sbjct                4670  .....................................................  4729

Query                1861  GAGCCTTCAGGAGGTGGAGGCCGGTGAGGTCAGGAGCCCAGCTCTCCAGGGGGCTTCTGC  1920
Sbjct                4730  .....................................................  4789

Query                1921  CCTGACTGGGAAGGGTGCCTGGCTCCCTAAAACAATGTCAAAGCCAGTCCTGCTGTTCTC  1980
Sbjct                4790  .....................................................  4849

Query                1981  TGTTGCCAGGGGGCAGGTCTGGGCCTGGGCCAACCACGTTTGTTATCATGGCTGCTGCCT  2040
Sbjct                4850  .....................................................  4909

Query                2041  TCTGGACAGCTGCCAGCTCTGCCTTGAGAGGTTGTGGGACCTCTGGATCCAGCTGACCTG  2100
Sbjct                4910  .....................................................  4969

Query                2101  ACAGGTCATCTACTCAGGGAGGAGCCCTGTGCTCCCAGCTCAGAGGACAGTCTGGGCCAG  2160
Sbjct                4970  .....................................................A.....  5029

Query                2161  AACTGGAAGGAGACATCTGTCCCGTCTTTGAGTGACAAGCCCGGGACAACAGCCAGTGGG  2220
Sbjct                5030  .....................G.....................................  5089

Query                2221  CATCACGGCTCTCCAGCACTCCTTAGCCGGAGGATACAGAGTGATGGGTGCATCCTGACC  2280
Sbjct                5090  .....................................................  5149
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380 A>G

419 T>C

859 T>C (V258A)

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Query  2281  AATGCGACAACCAACACGTGCTCTCACAAACCCCTGACTCCCGCACTTTCCAGTGCCAAA  2340
Sbjct  5150  ..............................--..........................  5207

Query  2341  GTACAAACGCTGCTTGGATAAGGAGAGCAAAGCTTCTGGAActttatttactctttcttt  2400
Sbjct  5208  ..................................A.......................  5267

Query  2401  ttaattttctttttaAGAGACTGGGTCTTGCTATGTTGCCCAGGCTGGTCTTGAACTCCTG  2460
Sbjct  5268  ............................................................  5327

Query  2461  GCCTCAAGTGATCCTCCAGTTTCCATCTCCCTAAGAGCTGGGATTACAGGTGTGAGCCGC  2520
Sbjct  5328  ............................................................  5387

Query  2521  TGTACCCGAACtttttttgtttttGCTTCTGGAACTTTGAAACACAAAACACAAGTTGGC  2580
Sbjct  5388  ............................................................  5447

Query  2581  ACTTACAATTTTAAAGATGCAGCCAGCTCTAAACAACACACAGAGCACAAATATGCTCCT  2640
Sbjct  5448  ............................................................  5507

Query  2641  GACGGACTCAGGAAAATGCCAACAGCAGAGCACCCTGGTGCCAAGGCCTTCTCAGCCCAT  2700
Sbjct  5508  ..............................C.............................  5567

Query  2701  GCCCTGGAGGGCATTCCCCTGGCCAGCCTCAGCCCCTTGTCTACTTGTTCTCCAGCTTCT  2760
Sbjct  5568  ............................................................  5627

Query  2761  GGGTAGCTGGGCTTCTGGAAGGGTGGCAGTGGGCTACTCCCTGCTCAGCGCTCCCCTGGG  2820
Sbjct  5628  ..................................................A.........  5687

Query  2821  AAGGGGGTGAGGAGATGAAAATGAA-ACTATGAGCTGTC  2858
Sbjct  5688  ........................G.............  5726
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