NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARf05E07

Lot# : 7673_B5Gt

Vector : pKA1U5

Gene	TRIM58	
RefSeq_mRNA	NM_015431.4	5170 bp

● Plasmid DNA purification

Date : 2025/07/29 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2025/07/30 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/07/30

DNA concentration (O.D.): 417 ng/ul

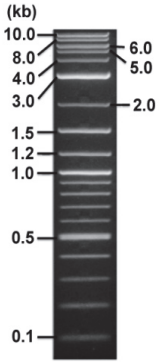
< Size of fragment expected from this clone >

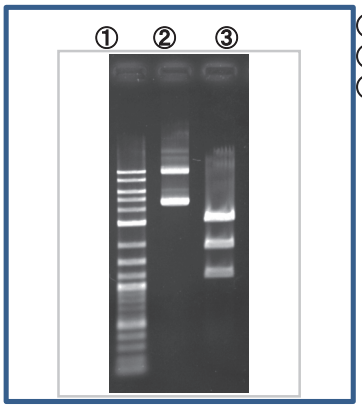
DNA	0.25 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.75 ul
Total	10 ul

BamHI 3.1kb (vector), 1.8, 1.1 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 : 2025/08/01

full sequence	ARf05E07hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/08/05

DNA (417 ng/ul)	80 ul
10x TE	133 ul
dH_2O	1,121 ul
Total	1,334 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '25.08.05 笹沼

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

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_033452:Homo sapiens tripartite motif containing...

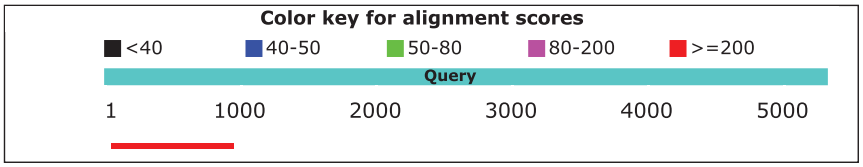
RID 8SHGV46H114 (Expires on 08-02 12:44 pm)

Query ID	NM_015431.4	**Subject ID**	lcl|Query_6513673
Description	Homo sapiens tripartite motif containing 58 (TRIM58), mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	5170	**Subject Length**	6121
		Program	BLASTN 2.17.0+

ARf05E07hts01.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	1605	1605	17%	0.0	99.77%	Query_6513673

Alignments

Sequence ID: Query_6513673 Length: 6121 Number of Matches: 1
Range 1: 2285 to 3159

Score	Expect	Identities	Gaps	Strand	Frame
1605 bits(869)	0.0()	873/875(99%)	0/875(0%)	Plus/Plus	

Features:

```
CDS:E3 ubiquitin-pro  1      M  A  W  A  P  P  G  E  R  L  R  E  D  A  R  C  P  V  C
Query                 57     GGTCATGGCCTGGGCGCCGCCCGGGGAGCGGCTGCGCGAGGATGCGCGGTGCCCGGTGTG  116
Sbjct                 2285   ..........C..............................................  2344

CDS:E3 ubiquitin-pro  20     L  D  F  L  Q  E  P  V  S  V  D  C  G  H  S  F  C  L  R  C
Query                 117    CCTGGATTTCCTGCAGGAGCCGGTCAGCGTGGACTGCGGCCACAGCTTCTGCCTCAGGTG  176
Sbjct                 2345   ..............................................................  2404

CDS:E3 ubiquitin-pro  40     I  S  E  F  C  E  K  S  D  G  A  Q  G  G  V  Y  A  C  P  Q
Query                 177    CATCTCCGAGTTCTGCGAGAAGTCGGACGGCGCGCAGGGCGGCGTCTACGCCTGTCCGCA  236
Sbjct                 2405   ..............................................................  2464

CDS:E3 ubiquitin-pro  60     C  R  G  P  F  R  P  S  G  F  R  P  N  R  Q  L  A  G  L  V
Query                 237    GTGCCGGGGCCCCTTCCGGCCCTCGGGCTTTCGCCCCAACCGGCAGCtggcgggcctggt  296
Sbjct                 2465   ..............................................................  2524

CDS:E3 ubiquitin-pro  80     E  S  V  R  R  L  G  L  G  A  G  P  G  A  R  R  C  A  R  H
Query                 297    ggagagcgtgcggcggctggggttgggcgcggggcccggggcgcggcgatgcgcgcggca  356
Sbjct                 2525   ..............................................................  2584

CDS:E3 ubiquitin-pro  100    G  E  D  L  S  R  F  C  E  E  D  E  A  A  L  C  W  V  C  D
Query                 357    cggcgAGGACCTGAGCCGCTTCTGCGAGGAGGACGAGGCGGCGCTGTGCTGGGTGTGCGA  416
Sbjct                 2585   ..............................................................  2644
```

68 G>C (W3S)

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CDS:E3 ubiquitin-pro  120    A  G  P  E  H  R  T  H  R  T  A  P  L  Q  E  A  A  G  S  Y
Query                 417    CGCCGGCCCCGAGCACAGGACGCACCGCACGGCGCCGCTGCAGGAGGCCGCCGGCAGCTA  476
Sbjct                 2645   ............................................................  2704

CDS:E3 ubiquitin-pro  140    Q  V  K  L  Q  M  A  L  E  L  M  R  K  E  L  E  D  A  L  T
Query                 477    CCAGGTAAAGCTCCAGATGGCTCTGGAACTTATGAGGAAAGAGTTGGAGGACGCCTTGAC  536
Sbjct                 2705   ............................................................  2764

CDS:E3 ubiquitin-pro  160    Q  E  A  N  V  G  K  K  T  V  I  W  K  E  K  V  E  M  Q  R
Query                 537    TCAGGAGGCCAACGTGGGGAAAAAGACTGTCATTTGGAAGGAGAAAGTGGAAATGCAGAG  596
Sbjct                 2765   ............................................................  2824

CDS:E3 ubiquitin-pro  180    Q  R  F  R  L  E  F  E  K  H  R  G  F  L  A  Q  E  E  Q  R
Query                 597    GCAGCGCTTCAGATTGGAGTTTGAGAAGCATCGTGGCTTTCTGGCCCAGGAGGAGCAACG  656
Sbjct                 2825   ............................................................  2884

CDS:E3 ubiquitin-pro  200    Q  L  R  R  L  E  A  E  E  R  A  T  L  Q  R  L  R  E  S  K
Query                 657    GCAGCTGAGGCGGCTGGAGGCGGAGGAGCGAGCGACGCTGCAGAGACTGCGGGAGAGCAA  716
Sbjct                 2885   ............................................................  2944

CDS:E3 ubiquitin-pro  220    S  R  L  V  Q  Q  S  K  A  L  K  E  L  A  D  E  L  Q  E  R
Query                 717    GAGCCGGCTGGTCCAGCAGAGCAAGGCCCTGAAGGAGCTGGCGGATGAGCTGCAGGAGAG  776
Sbjct                 2945   ............................................................  3004

CDS:E3 ubiquitin-pro  240    C  Q  R  P  A  L  G  L  L  E  G  V  R  G  V  L  S  R  S  K
Query                 777    GTGCCAGCGCCCGGCCCTGGGTCTGCTGGAGGGTGTGAGAGGAGTCCTGAGCAGAAGTAA  836
Sbjct                 3005   ............A...............................................  3064

CDS:E3 ubiquitin-pro  260    A  V  T  R  L  E  A  E  N  I  P  M  E  L  K  T  A  C  C  I
Query                 837    GGCTGTCACAAGGCTGGAAGCAGAGAACATCCCCATGGAACTGAAGACAGCATGCTGCAT  896
Sbjct                 3065   ............................................................  3124

CDS:E3 ubiquitin-pro  280    P  G  R  R  E  L  L  R  K  F  Q
Query                 897    CCCTGGGAGGAGGGAGCTCTTAAGGAAGTTCCAAG  931
Sbjct                 3125   ...................................  3159
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789 G>A

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