NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : ARiS191L06

Lot# : 6607_B6Aj

Vector : pGCAP10

Gene	TMEM37	
RefSeq_mRNA	NM_183240.3	1687 bp

● Plasmid DNA purification

Date :2026/01/19 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date :2026/01/20 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date :2026/01/20

DNA concentration (O.D.): 299 ng/ul

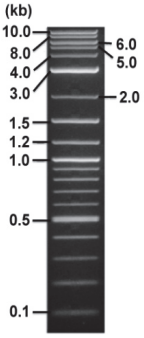
DNA	0.35 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.65 ul
Total	10 ul

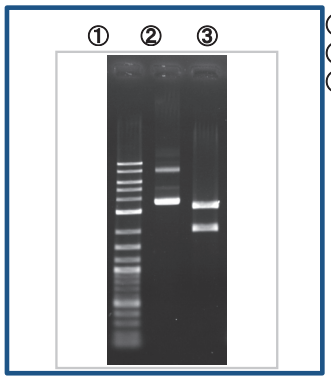
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.0 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 : 2026/02/03

full sequence	ARiS191L06hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/02/05

DNA (299 ng/ul)	86 ul
10x TE	103 ul
dH_2O	840 ul
Total	1,029 ul

● Shipping

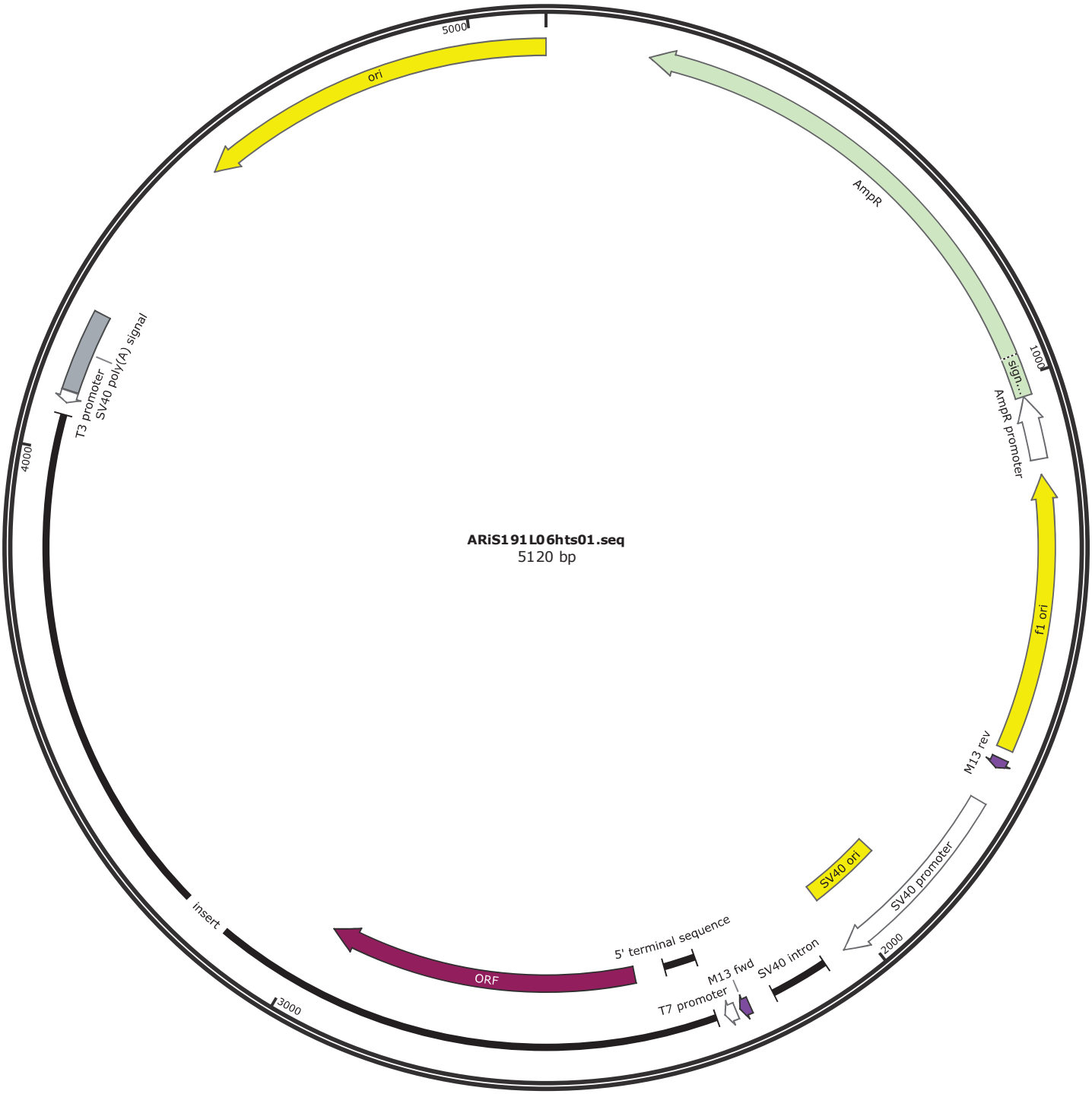
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY :

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'26.02.05
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http://dna.brc.riken.jp/index.html


ARiS191L06hts01.seq
5120 bp
5000
ori
AmpR
1000
AmpR promoter
f1 ori
M13 rev
SV40 promoter
2000
SV40 intron
M13 fwd
T7 promoter
5' terminal sequence
ORF
3000
insert
4000
T3 promoter
SV40 poly(A) signal
SV40 ori

BLAST ® » blastn suite-2sequences » RID-S2K4VTWR114

BLAST Results

Questions/comments

Blast 2 sequences

Job title: BC031592:Homo sapiens serpin peptidase inhibitor,...

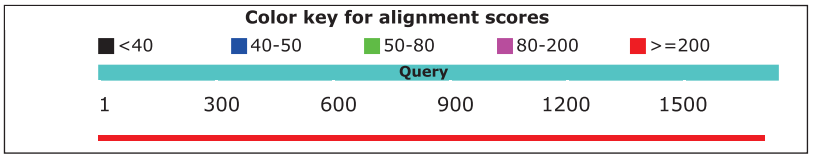
RID S2K4VTWR114 (Expires on 02-04 08:17 am)

Query ID	NM_183240.3	**Subject ID**	lcl|Query_2723579
Description	Homo sapiens transmembrane protein 37 (TMEM37), mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	1687	**Subject Length**	5120
		Program	BLASTN 2.17.0+

ARiS191L06hts01.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	3035	3035	100%	0.0	99.17%	Query_2723579

Alignments

Sequence ID: Query_2723579 Length: 5120 Number of Matches: 1
Range 1: 2345 to 4030

Score	Expect	Identities	Gaps	Strand	Frame
3035 bits(1643)	0.0()	1677/1691(99%)	12/1691(0%)	Plus/Plus	

Features:

```
CDS:voltage-dependen  1                                                   M  T  A
Query                 1     AGCGGAGCAGCTGGAGCGATCGAGGCTGCAGCGCGGCCGCCGGGCGCAGCATGACTGCCG  60
Sbjct                 2345  ...C.........................................................  2404

CDS:voltage-dependen  4     V  G  V  Q  A  Q  R  P  L  G  Q  R  Q  P  R  R  S  F  F  E
Query                 61    TCGGCGTGCAGGCCCAGAGGCCTTTGGGCCAAAGGCAGCCCCGCCGGTCCTTCTTTGAAT  120
Sbjct                 2405  ...........................................................  2464

CDS:voltage-dependen  24    S  F  I  R  T  L  I  I  T  C  V  A  L  A  V  V  L  S  S  V
Query                 121   CCTTCATCCGGACCCTCATCATCACGTGTGTGGCCCTGGCTGTGGTCCTGTCCTCGGTCT  180
Sbjct                 2465  ...........................................................  2524

CDS:voltage-dependen  44    S  I  C  D  G  H  W  L  L  A  E  D  R  L  F  G  L  W  H  F
Query                 181   CCATTTGTGATGGGCACTGGCTCCTGGCTGAGGACCGCCTCTTCGGGCTCTGGCACTTCT  240
Sbjct                 2525  ...........................................................  2584

CDS:voltage-dependen  64    C  T  T  T  N  Q        T  I  C  F  R  D  L  G  Q  A  H  V
Query                 241   GCACCACCACCAACCAGA------CGATCTGCTTCAGAGACCTGGGCCAGGCCCATGTGC  294
Sbjct                 2585  ..................GTGTGC..................................  2644

CDS:voltage-dependen  82    P  G  L  A  V  G  M  G  L  V  R  S  V  G  A  L  A  V  V  A
Query                 295   CCGGGCTGGCCGTGGGCATGGGCCTGGTACGCAGCGTGGGCGCCTTGGCCGTGGTGGCCG  354
Sbjct                 2645  ...........................................................  2704
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258_259 ins 6nt

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CDS:voltage-dependen  102   A  I  F  G  L  E  F  L  M  V  S  Q  L  C  E  D  K  H  S  Q
Query                 355   CCATTTTTGGCCTGGAGTTCCTCATGGTGTCCCAGTTGTGCGAGGACAAACACTCACAGT  414
Sbjct                 2705  ............................................................  2764

CDS:voltage-dependen  122   C  K  W  V  M  G  S  I  L  L  L  V  S  F  V  L  S  S  G  G
Query                 415   GCAAGTGGGTCATGGGTTCCATCCTCCTCCTGGTGTCTTTCGTCCTCTCCTCCGGCGGGC  474
Sbjct                 2765  ............................................................  2824

CDS:voltage-dependen  142   L  L  G  F  V  I  L  L  R  N  Q  V  T  L  I  G  F  T  L  M
Query                 475   TCCTGGGTTTTGTGATCCTCCTCAGGAACCAAGTCACACTCATCGGCTTCACCCTAATGT  534
Sbjct                 2825  ............................................................  2884

CDS:voltage-dependen  162   F  W  C  E  F  T  A  S  F  L  L  F  L  N  A  I  S  G  L  H
Query                 535   TTTGGTGCGAATTCACTGCCTCCTTCCTCCTCTTCCTGAACGCCATCAGCGGCCTTCACA  594
Sbjct                 2885  ............................................................  2944

CDS:voltage-dependen  182   I  N  S  I  T  H  P  W  E
Query                 595   TCAACAGCATCACCCATCCCTGGGAATGACCGTGGAAATTTTAGGCCCCCTCCAGGGACA  654
Sbjct                 2945  ............................................................  3004

Query                 655   TCAGATTCCACAAGAAAATATGGTCAAAATGGGACTTTTCCAGCATGTGGCCTCTGGTGG  714
Sbjct                 3005  ............................................................  3064

Query                 715   GGCTGGGTTGGACAAGGGCCTTGAAACGGCTGCCTGTTTGCCGATAACTTGTGGGTGGTC  774
Sbjct                 3065  ............................................................  3124

Query                 775   AGCCAGAAATGGCCCGGGGGCCTCTGCACCTGGTCTGCAGGGCCAGAGGCCAGGAGGGTG  834
Sbjct                 3125  ............................................................  3184

Query                 835   CCTCAGTGCCACCAACTGCACAGGCTTAGCCAGATGTTGATTTTAGAGGAAGaaaaaaaC  894
Sbjct                 3185  ............................................................  3244

Query                 895   ATTTTAAAACTCCTTCTTGAATTTTCTTCCCTGGACTGGAATACAGTTGGAAGCACAGGG  954
Sbjct                 3245  ............................................................  3304

Query                 955   GTAACTGGTACCTGAGCTAGCTGCACAGCCAAGGATAGTTCATGCCTGTTTCATTGACAC  1014
Sbjct                 3305  ............................................................  3364

Query                 1015  GTGCTGGGATAGGGGCTGCAGAATCCCTGGGGCTCCCAGGGTTGTTAAGAATGGATCATT  1074
Sbjct                 3365  ............................................................  3424

Query                 1075  CTTCCAGCTAAGGGTCCAATCAGTGCCTAGGACTTTCTTCCACCAGCTCAAAGGGCCTTC  1134
Sbjct                 3425  ..........-----..........................................  3479

Query                 1135  GTATGTATGTCCCTGGCTTCAGCTTTGGTCATGCCAAAGAGGCAGAGTTCAGGATTCCCT  1194
Sbjct                 3480  ............................................................  3539

Query                 1195  CAGAATGCCCTGCACACAGTAGGTTTCCAAACCATTTGACTCGGTTTGCCTCCCTGCCCG  1254
Sbjct                 3540  ............................................................  3599

Query                 1255  TTGTTTAAACCTTACAAACCCTGGATAACCCCATCTTCTAGCAGCTGGCTGTG-CCTCTG  1313
Sbjct                 3600  ..........................................................CC..  3659

Query                 1314  GGAGCTCTGCCTATCAGAACCCTACCTTAAGGTGGGTTTCCTTCCGAGAAGAGTTCTTGA  1373
Sbjct                 3660  ............................................................  3719

Query                 1374  GCAAGCTCTCCCAGGAGGGCCCACCTGACTGCTAATACACAGCCCTCCCCAAGGCCCGTG  1433
Sbjct                 3720  ............................................................  3779
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Query                 1434  TGTGCATGTGTCTGTCTTTTGTGAGGGTTAGACAGCCTCAGGGCACCATTTTTAATCCCA  1493
Sbjct                 3780  ............................................................  3839

Query                 1494  GAACACATTTCAAAGAGCACGTATCTAGACCTGCTGGACTCTGCAGGGGGTGAGGGGGAA  1553
Sbjct                 3840  ............................................................  3899

Query                 1554  CAGCGAGAGCTTGGGTAATGATTAACACCCATGCTGGGGATGCATGGAGGTGAAGGGGGC  1613
Sbjct                 3900  ............................................................  3959

Query                 1614  CAGGAACCAGTGGAGATTTCCATCCTTGCCAGCACGTCTGTACTTCTGTTCATTAAAGTG  1673
Sbjct                 3960  ............................................................  4019

Query                 1674  CTCCCTTTCTA  1684
Sbjct                 4020  ...........  4030
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