NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARe93E11

Lot# : 7672_B5Er

Vector : pKA1U5

Gene	ADAMTSL4	
RefSeq_mRNA	NM_019032.6	4212 bp

● Plasmid DNA purification

Date : 2025/05/27 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2025/05/28 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/05/28

DNA concentration (O.D.): 66 ng/ul

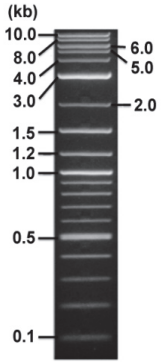
DNA	1.5 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	6.5 ul
Total	10 ul

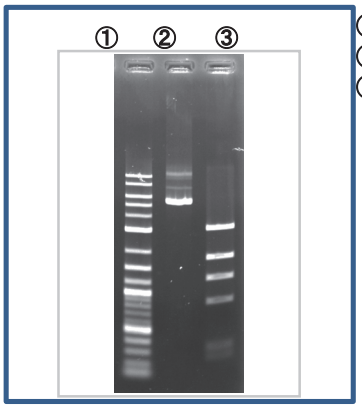
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 1.8, 1.3, 0.8, 0.3, 0.2 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 : 2025/05/30

full sequence	ARe93E11hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/06/10

DNA (66 ng/ul)	84 ul
10x TE	22 ul
dH_2O	116 ul
Total	222 ul

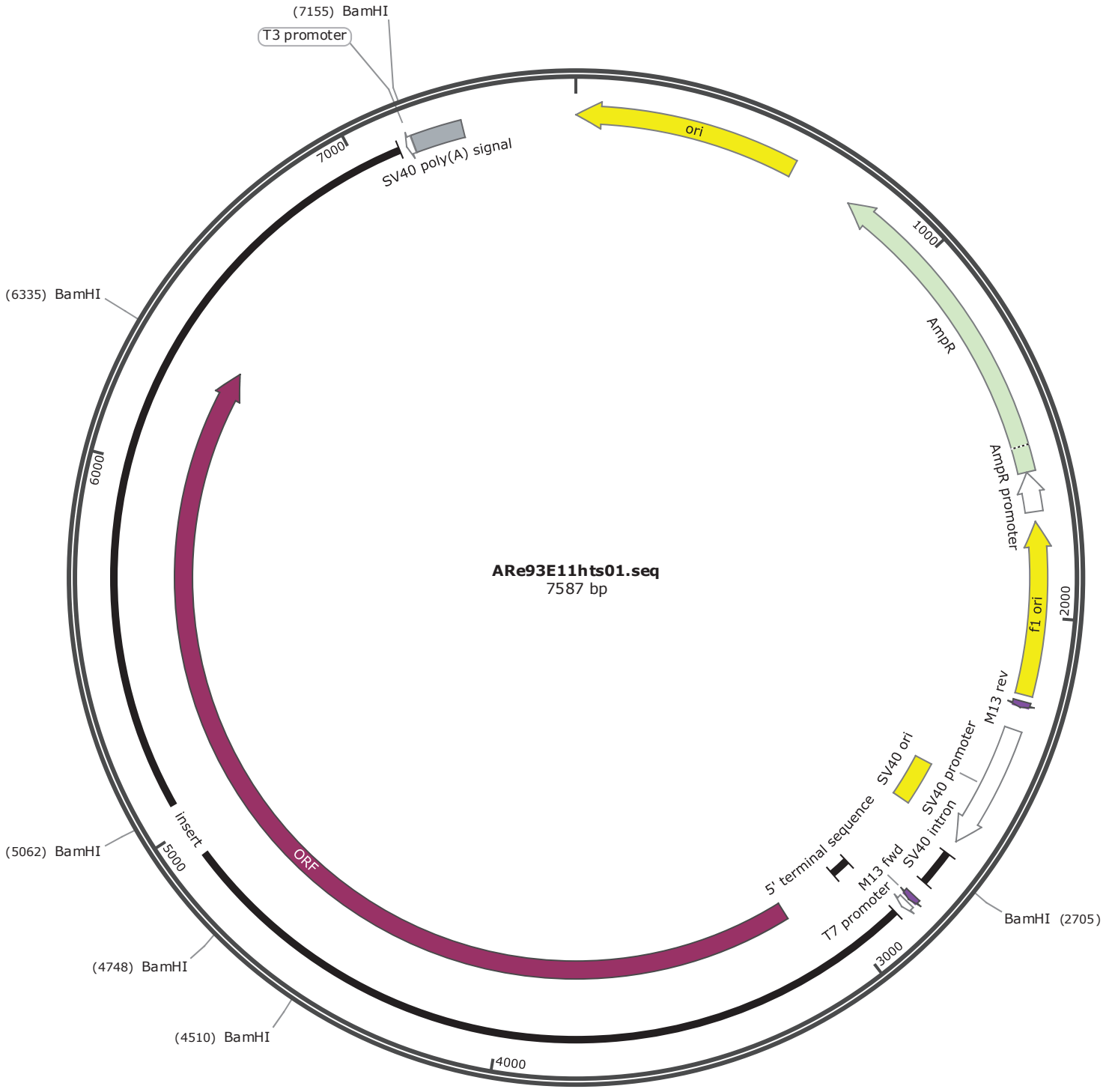
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '25.06.10 笹沼

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


(7155) BamHI
T3 promoter
SV40 poly(A) signal
ori
AmpR
AmpR promoter
f1 ori
M13 rev
SV40 ori
SV40 promoter
SV40 intron
M13 fwd
T7 promoter
5' terminal sequence
ORF
insert
(6335) BamHI
(5062) BamHI
(4748) BamHI
(4510) BamHI
BamHI (2705)
1000
2000
3000
4000
5000
6000
7000
ARe93E11hts01.seq
7587 bp

BLAST Results

Questions/comments

Blast 2 sequences

Job title: ref|NM_019032.6|

RID 3JM88EK2114 (Expires on 05-31 14:32 pm)

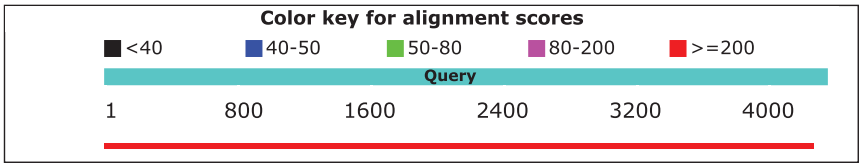
Query ID NM_019032.6
Description Homo sapiens ADAMTS like 4 (ADAMTSL4), transcript variant 1, mRNA
Molecule type nucleic acid
Query Length 4212

Subject ID lcl|Query_1550029
Description None
See details
Molecule type dna
Subject Length 7587
Program BLASTN 2.16.1+

Graphic Summary

ARe93E11hts01.seq

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	7755	7755	100%	0.0	99.91%	Query_1550029

Alignments

Sequence ID: Query_1550029 Length: 7587 Number of Matches: 1
Range 1: 2874 to 7084

Score	Expect	Identities	Gaps	Strand	Frame
7755 bits(4199)	0.0()	4207/4211(99%)	0/4211(0%)	Plus/Plus	

Features:

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Query          2     GGGGCCCCAGTGGCCGCCGCGGAGCGAGGTTGCCTGGAGAGAGCGCCTGGGCGCAGAAGG  61
Sbjct          2874  ............................................................  2933

Query          62    GTTAACGGGCCACCGGGGGCTCGCAGAGCAGGAGGGTGCTCTCGGACGGTGTGTCCCCCA  121
Sbjct          2934  ............................................................  2993

Query          122   CTGCACTCCTGAACTTGGAGGACAGGGTCGCCGCGAGGGACGCAGAGAGCACCCTCCACG  181
Sbjct          2994  ............................................................  3053

Query          182   CCCAGATGCCTGCGTAGTTTTTGTGACCAGTCCGCTCCTGCCTCCCCCTGGGGCAGTAGA  241
Sbjct          3054  ............................................................  3113

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Query          242   GGGGGAGCGATGGAGAACTGGACTGGCAGGCCCTGGCTGTATCTGCTGCTGCTTCTGTCC  301
Sbjct          3114  ............................................................  3173

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Query          302   CTCCCTCAGCTCTGCTTGGATCAGGAGGTGTTGTCCGGACACTCTCTTCAGACACCTACA  361
Sbjct          3174  ............................................................  3233

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Sbjct          3234  ............................................................  3293
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Sbjct                3294  ............................................................  3353

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Sbjct                3354  ............................................................  3413

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Sbjct                3414  ............................................................  3473

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Sbjct                3474  ............................................................  3533

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Sbjct                3534  ............................................................  3593

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Query                722   GGTTATGGGAGAGTGCCCTTTGCATTGCCACTGCACCGGAACCGCAGGCACCCTCGGAGC  781
Sbjct                3594  ............................................................  3653

CDS:ADAMTS-like prot  178   P  P  R  S  E  L  S  L  I  S  S  R  G  E  E  A  I  P  S  P
Query                782   CCACCCAGATCTGAGCTGTCCCTGATCTCTTCTAGAGGGGAAGAGGCTATTCCGTCCCCT  841   827 G>C (A193P)
Sbjct                3654  ..........................C.................................  3713

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Sbjct                3714  ............................................................  3773

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Sbjct                3774  ............................................................  3833

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Sbjct                3834  ............................................................  3893

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Sbjct                3894  ............................................................  3953

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Sbjct                3954  ............................................................  4013

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Query                1142  CGCCCTGATCCTTTTCCTTCGGTCCCTCGGGGCCGAGGCCAGCAGGGCCAAGGGCCTTGG  1201  1189 C>T
Sbjct                4014  ..........................T.................................  4073

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Query                1202  GGAACgggggggACTCCTCACGGGCCCCGCCTGGAGCCTGACCCTCAGCACCCGGGCGCC  1261
Sbjct                4074  ............................................................  4133

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Query                1382  CCCTGCCCCCCTGAGCAGCCAGACCCCCGGGCCCTGCAGTGCGCAGCCTTTAACTCCCAG  1441
Sbjct                4254  ............................................................  4313

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Sbjct                4434  ............................................................  4493

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Sbjct                4614  ............................................................  4673

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Query                1802  CTCCGGCCTAGCTCCAACTACCTGGCACTTCGTGGCCCTGGGGGCCGGTCCATCATCAAT  1861
Sbjct                4674  ............................................................  4733

CDS:ADAMTS-like prot  538   G  N  W  A  V  D  P  P  G  S  Y  R  A  G  G  T  V  F  R  Y
Query                1862  GGGAACTGGGCTGTGGATCCCCCTGGGTCCTACAGGGCCGGCGGGACCGTCTTTCGATAT  1921
Sbjct                4734  ............................................................  4793

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Sbjct                4794  ............................................................  4853

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Sbjct                4854  ............................................................  4913

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Sbjct                4914  ............................................................  4973

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Query                2102  CTTCAGCCGGAGATTCTGAGGGTGGAGCCCCCACTTGCTCCGGCACCCCGCCCAGCCCGG  2161
Sbjct                4974  ............................................................  5033

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Query                2222  AGGACACCCCTGGGGTCTCCAGCTGCGTACTGGAAACGAGTGGGACACTCTGCATGCTCA  2281
Sbjct                5094  ............................................................  5153

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Query                2282  GCGTCCTGCGGGAAAGGTGTCTGGCGCCCCATTTTCCTCTGCATCTCCCGTGAGTCGGGA  2341
Sbjct                5154  ............................................................  5213

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Query                2342  GAGGAACTGGATGAACGCAGCTGTGCCGCGGGTGCCAGGCCCCCAGCCTCCCCTGAACCC  2401
Sbjct                5214  ............................................................  5273

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Sbjct                5274  ............................................................  5333

CDS:ADAMTS-like prot  738   S  C  G  P  G  T  Q  H  R  Q  L  Q  C  R  Q  E  F  G  G  G
Query                2462  TCCTGTGGCCCCGGCACCCAGCACCGCCAGCTGCAGTGCCGGCAGGAATTTgggggggT  2521
Sbjct                5334  ............................................................  5393

CDS:ADAMTS-like prot  758   G  S  S  V  P  P  E  R  C  G  H  L  P  R  P  N  I  T  Q  S
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Sbjct                5394  ............................................................  5453

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Sbjct                5454  ............................................................  5513

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Query                2642  CGGTGCGGCCGGGGCCAGAGAAGCCGGCAGGTTCGCTGTGTTGGGAACAATGGTGATGAA  2701  2692 T>C
Sbjct                5514  ..........................C.................  5573

CDS:ADAMTS-like prot  818   V  S  E  Q  E  C  A  S  G  P  P  Q  P  P  S  R  E  A  C  D
Query                2702  GTGAGCGAGCAGGAGTGTGCGTCAGGcccccccagcgcccccAGCAGAGAGGCCTGTGAC  2761  2734 G>A
Sbjct                5574  ..............A.............................  5633

CDS:ADAMTS-like prot  838   M  G  P  C  T  T  A  W  F  H  S  D  W  S  S  K  C  S  A  E
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Sbjct                5634  ............................................................  5693

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Sbjct                5694  ............................................................  5753

CDS:ADAMTS-like prot  878   P  G  Q  G  E  A  G  A  G  T  G  Q  S  C  P  T  G  S  R  P
Query                2882  CCAGGCCAGGGGGAAGCAGGAGCAGGAACTGGGCAGAGCTGTCCAACAGGAAGCCGGCCC  2941
Sbjct                5754  ............................................................  5813

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Query                2942  CCTGACATGCGCGCCTGCAGCCTGGGGCCCTGTGAGAGAACTTGGCGCTGGTACACAGGG  3001
Sbjct                5814  ............................................................  5873

CDS:ADAMTS-like prot  918   P  W  G  E  C  S  S  E  C  G  S  G  T  Q  R  R  D  I  I  C
Query                3002  CCCTGGGGTGAGTGCTCCTCCGAATGTGGCTCTGGCACACAGCGTAGAGACATCATCTGT  3061
Sbjct                5874  ............................................................  5933
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Query                3062  GTATCCAAACTGGGGACGGAGTTCAACGTGACTTCTCCGAGCAACTGTTCTCACCTCCCC  3121
Sbjct                5934  ............................................................  5993

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Query                3122  AGGCCCCCTGCCCTGCAGCCCTGTCAAGGGCAGGCCTGCCAGGACCGATGGTTTTCCACG  3181
Sbjct                5994  ............................................................  6053

CDS:ADAMTS-like prot  978   P  W  S  P  C  S  R  S  C  Q  G  G  T  Q  T  R  E  V  Q  C
Query                3182  CCCTGGAGCCCATGTTCTCGCTCCTGCCAAGGGGGAACGCAGACACGGGAGGTCCAGTGC  3241
Sbjct                6054  ............................................................  6113

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Sbjct                6114  ............................................................  6173

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Sbjct                6174  ............................................................  6233

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Sbjct                6234  ............................................................  6293

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Sbjct                6294  ............................................................  6353

Query                3482  TCCGGGGCACCTTCACGGTTTTCTGTGCCACCATCGGTCACCCATTGATCGGCCCACTCT  3541
Sbjct                6354  ............................................................  6413

Query                3542  GAACCCCCTGGCTCTCCAGCCTGTCCCAGTCTCAGCAGGGATGTCCTCCAGGTGACAGAG  3601
Sbjct                6414  ............................................................  6473

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Query                3662  GTGATGGGTGTGTGCACATATGCCTCAGGTGTGCTTTTGGGACTGCATGGATATGTGTGT  3721
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Sbjct                6714  ............................................................  6773

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Query                4022  TACTCAGGAAGGCAGGAGGAAAGAGACTGCCTCTCCAGAGCAAGGCCCAGCTGGGCAGAG  4081
Sbjct                6894  ............................................................  6953

Query                4082  GGTGAAAAAGAGAAATGTGAGCATCCGCTcccccaccaccccgcccagcccctagcccca  4141
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Sbjct  6954  ..........................................................  7013

Query  4142  ctcccTGCCTCCTGAAATGGTTCCCACCCAGAACTAATTTATTTTTTATTAAAGATGGTC  4201
Sbjct  7014  ..........................................................  7073

Query  4202  ATGACAAATGA  4212
Sbjct  7074  ...........  7084
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