NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARi07H12

Lot# : 7675_B4G4

Vector : pGCAP10

Gene	FSTL3	
RefSeq_mRNA	NM_005860.3	2501 bp

● Plasmid DNA purification

Date : 2024/07/04 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2024/07/05 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2024/07/05

DNA concentration (O.D.): 253 ng/ul

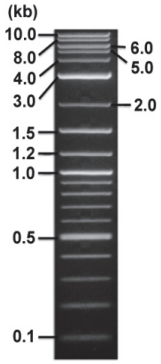
DNA	0.4	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.6	ul
Total	10	ul

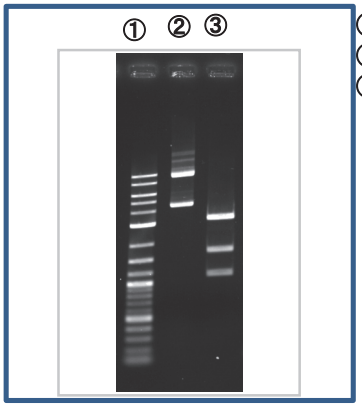
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 1.6, 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 : 2024/07/09

Primer A	-
Primer B	-
Primer C	ARi07H12hts01.seq
List of Sequencing Primers	-

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2024/07/09

DNA (253 ng/ul)	86	ul
10x TE	87	ul
dH_2O	697	ul
Total	870	ul

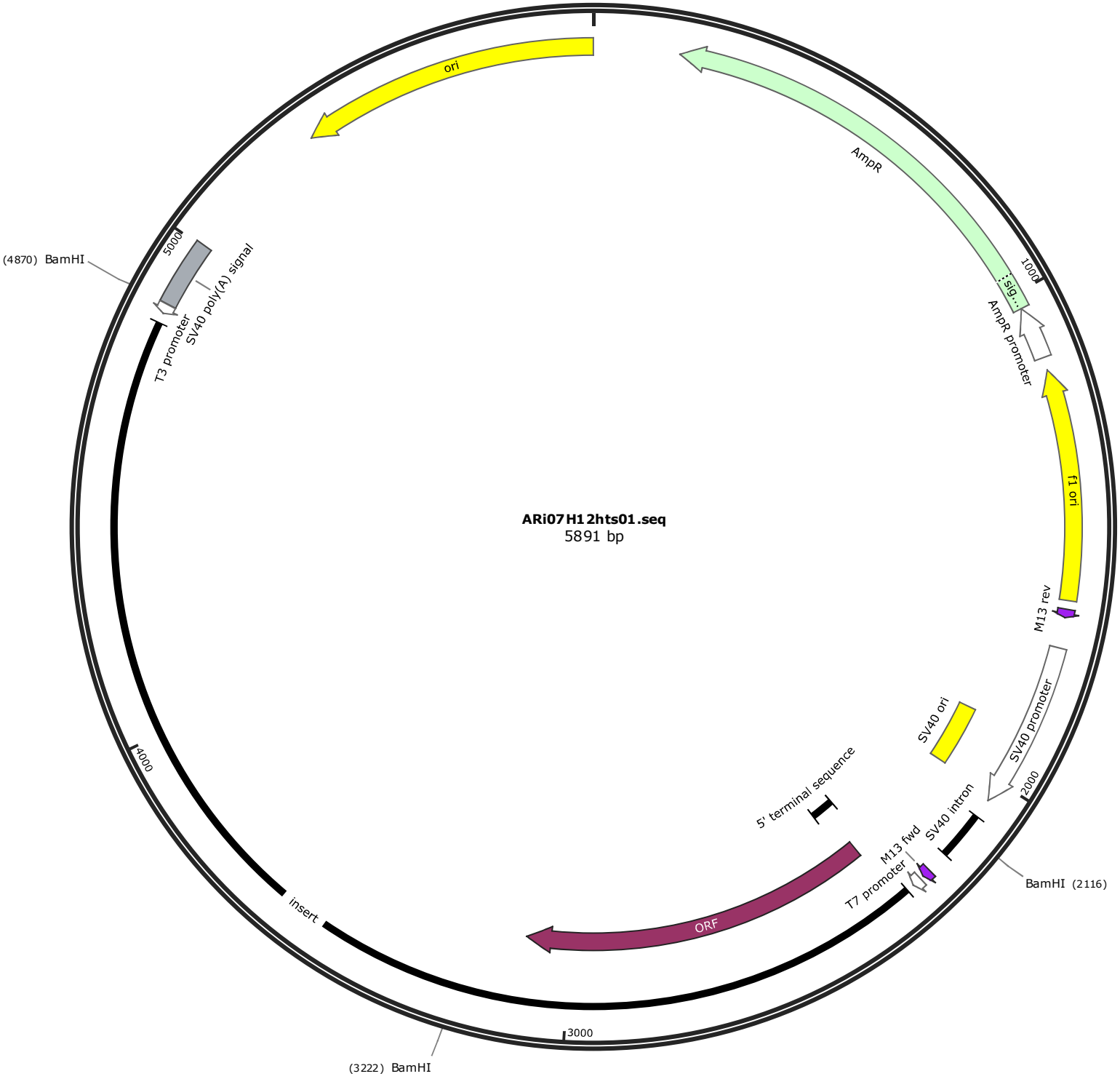
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '24.07.09 笹沼

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


ARi07H12hts01.seq
5891 bp
ori
AmpR
(4870) BamHI
5000
SV40 poly(A) signal
T3 promoter
1000
AmpR promoter
f1 ori
M13 rev
SV40 promoter
2000
SV40 ori
5' terminal sequence
SV40 intron
M13 fwd
T7 promoter
BamHI (2116)
4000
insert
ORF
3000
(3222) BamHI

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_016441:Homo sapiens cysteine rich transmembrane...

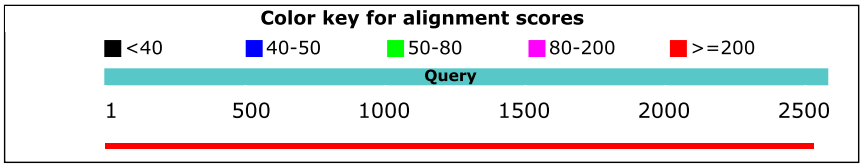
RID TZA3DTWN114 (Expires on 02-27 08:57 am)

Query ID	NM_005860.3	**Subject ID**	lcl|Query_2743431
Description	Homo sapiens follistatin like 3 (FSTL3), mRNA	**Description**	None
Molecule type	nucleic acid		See details
Query Length	2501	**Molecule type**	dna
		Subject Length	5891
		Program	BLASTN 2.17.0+

ARi07H12hts01.seq

Graphic Summary

Distribution of the top 11 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	4599	7696	100%	0.0	99.92%	Query_2743431

Alignments

Sequence ID: Query_2743431 Length: 5891 Number of Matches: 11
Range 1: 2279 to 4774

Score	Expect	Identities	Gaps	Strand	Frame
4599 bits(2490)	0.0()	2494/2496(99%)	0/2496(0%)	Plus/Plus	

Features:

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CDS:follistatin-rela  1                                   M  R  P  G  A  P  G  P  L  W  P
Query                 6     GGTGCCGCTGCCGTCTCTGCGTTCGCCATGCGTCCCGGGGCGCCAGGGCCACTCTGGCCT  65
Sbjct                 2279  ............................................................  2338

CDS:follistatin-rela  12     L  P  W  G  A  L  A  W  A  V  G  F  V  S  S  M  G  S  G  N
Query                 66    CTGCCCTGGGGGGCCCTGGCTTGGGCCGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAAC  125
Sbjct                 2339  ............................................................  2398

CDS:follistatin-rela  32     P  A  P  G  G  V  C  W  L  Q  Q  G  Q  E  A  T  C  S  L  V
Query                 126   CCCGCGCCCGGTGGTGTTTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTG  185
Sbjct                 2399  ............................................................  2458

CDS:follistatin-rela  52     L  Q  T  D  V  T  R  A  E  C  C  A  S  G  N  I  D  T  A  W
Query                 186   CTCCAGACTGATGTCACCCGGGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGG  245
Sbjct                 2459  ............................................................  2518

CDS:follistatin-rela  72     S  N  L  T  H  P  G  N  K  I  N  L  L  G  F  L  G  L  V  H
Query                 246   TCCAACCTCACCCACCCGGGGAACAAGATCAACCTCCTCGGCTTCTTGGGCCTTGTCCAC  305
Sbjct                 2519  ............................................................  2578

CDS:follistatin-rela  92     C  L  P  C  K  D  S  C  D  G  V  E  C  G  P  G  K  A  C  R
Query                 306   TGCCTTCCCTGCAAAGATTCGTGCGACGGCGTGGAGTGCGGCCCGGGCAAGGCGTGCCGC  365
Sbjct                 2579  ............................................................  2638
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CDS:follistatin-rela  112   M  L  G  G  R  P  R  C  E  C  A  P  D  C  S  G  L  P  A  R
Query                 366   ATGCTGGGGGGCCGCCCGCGCTGCGAGTGCGCGCCCGACTGCTCGGGGCTCCCGGCGCGG  425
Sbjct                 2639  ............................................................  2698

CDS:follistatin-rela  132   L  Q  V  C  G  S  D  G  A  T  Y  R  D  E  C  E  L  R  A  A
Query                 426   CTGCAGGTCTGCGGCTCAGACGGCGCCACCTACCGCGACGAGTGCGAGCTGCGCGCCGCG  485
Sbjct                 2699  ............................................................  2758

CDS:follistatin-rela  152   R  C  R  G  H  P  D  L  S  V  M  Y  R  G  R  C  R  K  S  C
Query                 486   CGCTGCCGCGGCCACCCGGACCTGAGCGTCATGTACCGGGGCCGCTGCCGCAAGTCCTGT  545
Sbjct                 2759  ............................................................  2818

CDS:follistatin-rela  172   E  H  V  V  C  P  R  P  Q  S  C  V  V  D  Q  T  G  S  A  H
Query                 546   GAGCACGTGGTGTGCCCGCGGCCACAGTCGTGCGTCGTGGACCAGACGGGCAGCGCCCAC  605
Sbjct                 2819  ............................................................  2878

CDS:follistatin-rela  192   C  V  V  C  R  A  A  P  C  P  V  P  S  S  P  G  Q  E  L  C
Query                 606   TGCGTGGTGTGTCGAGCGGCGCCCTGCCCTGTGCCCTCCAGCCCCGGCCAGGAGCTTTGC  665
Sbjct                 2879  ............................................................  2938

CDS:follistatin-rela  212   G  N  N  N  V  T  Y  I  S  S  C  H  M  R  Q  A  T  C  F  L
Query                 666   GGCAACAACAACGTCACCTACATCTCCTCGTGCCACATGCGCCAGGCCACCTGCTTCCTG  725
Sbjct                 2939  ............................................................  2998

CDS:follistatin-rela  232   G  R  S  I  G  V  R  H  A  G  S  C  A  G  T  P  E  E  P  P
Query                 726   GGCCGCTCCATCGGCGTGCGCCACGCGGGCAGCTGCGCAGGCACCCCTGAGGAGCCGCCA  785
Sbjct                 2999  ............................................................  3058

CDS:follistatin-rela  252   G  G  E  S  A  E  E  E  E  N  F  V
Query                 786   GGTGGTGAGTCTGCAGAAGAGGAAGAGAACTTCGTGTGAGCCTGCAGGACAGGCCTGGGC  845
Sbjct                 3059  ............................................................  3118

Query                 846   CTGGTGCCCGAGGCCCCCCATCATCCCCTGTTATTTATTGCCACAGCAGAGTCTAATTTA  905
Sbjct                 3119  ............................................................  3178

Query                 906   TATGCCACGGACACTCCTTAGAGCCCGGATTCGGACCACTTGGGGATCCCAGAACCTCCC  965
Sbjct                 3179  ............................................................  3238

Query                 966   TGACGATATCCTGGAAGGACTGAGGAAGGGAGGCCTGGGGGCCGGCTGGTGGGTGGGATA  1025
Sbjct                 3239  ............................................................  3298

Query                 1026  GACCTGCGTTCCGGACACTGAGCGCCTGATTTAGGGCCCTTCTCTAGGATGCCCCAGCCC  1085
Sbjct                 3299  ............................................................  3358

Query                 1086  CTACCCTAAGACCTATTGCCGGGGAGGATTCCACACTTCCGCTCCTTTGGGGATAAACCT  1145
Sbjct                 3359  ............................................................  3418

Query                 1146  ATTAATTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATTCCTGAAGAGGC  1205
Sbjct                 3419  ............................................................  3478

Query                 1206  ATGACTGCTTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGTCTAGCCTGG  1265
Sbjct                 3479  ............................................................  3538

Query                 1266  GTGTGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAGTACGGAG  1325
Sbjct                 3539  ............................................................  3598

Query                 1326  GGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAGCCTGG  1385
Sbjct                 3599  ......................A.....................................  3658
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1350 G>A

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Query                 1386  GTGAGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAG  1445
Sbjct                 3659  ............................................................  3718

Query                 1446  GGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGG  1505
Sbjct                 3719  ............................................................  3778

Query                 1506  GTGAGTATGGAGGGTCTAGCCTGGGTGTGTACGGAGGGTCTAGTCTGAGTGCGTGTGGGG  1565
Sbjct                 3779  ............................................................  3838

Query                 1566  ACCTCAGAACACTGTGACCTTAGCCCAGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGC  1625
Sbjct                 3839  ............................................................  3898

Query                 1626  TGCCACCATTCCCTGCCAGCCCAAGAACTCCAGCTTCCCCACTGCCTCTGTGTGCCCCTT  1685
Sbjct                 3899  ............................................................  3958

Query                 1686  TGCGTCCTGTGAAGGCCATTGAGAAATGCCCAGTGTGCCCCCTGGGAAAGGGCACGGCCT  1745
Sbjct                 3959  ............................................................  4018

Query                 1746  GTGCTCCTGACACGGGCTGTGCTTGGCCACAGAACCACCCAGCGTCTCCCCTGCTGCTGT  1805
Sbjct                 4019  ............................................................  4078

Query                 1806  CCACGTCAGTTCATGAGGCAACGTCGCGTGGTCTCAGACGTGGAGCAGCCAGCGGCAGCT  1865
Sbjct                 4079  ............................................................  4138

Query                 1866  CAGAGCAGGGCACTGTGTCCGGCGGAGCCAAGTCCACTCTGGGGGAGCTCTGGCGGGGAC  1925
Sbjct                 4139  ............................................................  4198

Query                 1926  CACGGGCCACTGCTCACCCACTGGCCCCGAGGGGGGTGTAGACGCCAAGACTCACGCATG  1985
Sbjct                 4199  ............................................................  4258

Query                 1986  TGTGACATCCGGAGTCCTGGAGCCGGGTGTCCCAGTGGCACCACTAGGTGCCTGCTGCCT  2045
Sbjct                 4259  ............................................................  4318

Query                 2046  CCACAGTGGGGTTCACACCCAGGGCTCCTTGGTCCCCCACAACCTGCCCCGGCCAGGCCT  2105
Sbjct                 4319  ............................................................  4378

Query                 2106  GCAGACCCAGACTCCAGCCAGACCTGCCTCACCCACCAATGCAGCCGGGGCTGGCGACAC  2165
Sbjct                 4379  ............................................................  4438

Query                 2166  CAGCCAGGTGCTGGTCTTGGGCCAGTTCTCCCACGACGGCTCACCCTCCCCTCCATCTGC  2225
Sbjct                 4439  ............................................................  4498

Query                 2226  GTTGATGCTCAGAATCGCCTACCTGTGCCTGCGTGTAAACCACAGCCTCAGACCAGCTAT  2285
Sbjct                 4499  ............................................................  4558

Query                 2286  GGGGAGAGGACAACACGGAGGATATCCAGCTTCCCCGGTCTGGGGTGAGGAATGTGGGGA  2345
Sbjct                 4559  ..........................................G.................  4618
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2337 A>G

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Query                 2346  GCTTGGGCATCCTCCTCCAGCCTCCTCCAGCCCCCAGGCAGTGCCTTACCTGTGGTGCCC  2405
Sbjct                 4619  ............................................................  4678

Query                 2406  AGAAAAGTGCCCCTAGGTTGGTGGGTCTACAGGAGCCTCAGCCAGGCAGCCCACCCCACC  2465
Sbjct                 4679  ............................................................  4738

Query                 2466  CTGGGGCCCTGCCTCACCAAGGAAATAAAGACTCAA  2501
Sbjct                 4739  ....................................  4774
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'26.02.26
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