NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARe06A04

Lot# : 7672_B4Lb

Vector : pKA1U5

Gene	MATN2	
RefSeq_mRNA	NM_002380.5	4133 bp

● Plasmid DNA purification

Date : 2024/12/11 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2024/12/12 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2024/12/12

DNA concentration (O.D.): 114 ng/ul

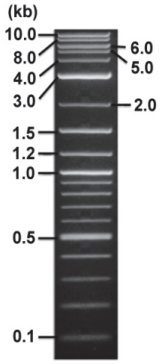
DNA	0.9 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.1 ul
Total	10 ul

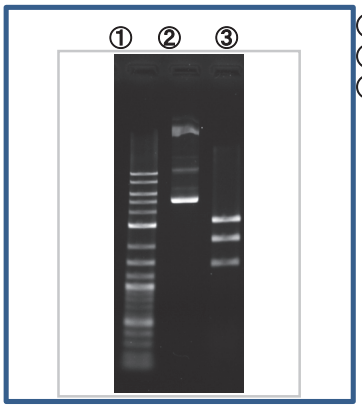
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.2, 1.4 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 : 2024/12/18

full sequence	ARe06A04hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/01/21

DNA (114 ng/ul)	84 ul
10x TE	38 ul
dH_2O	261 ul
Total	383 ul

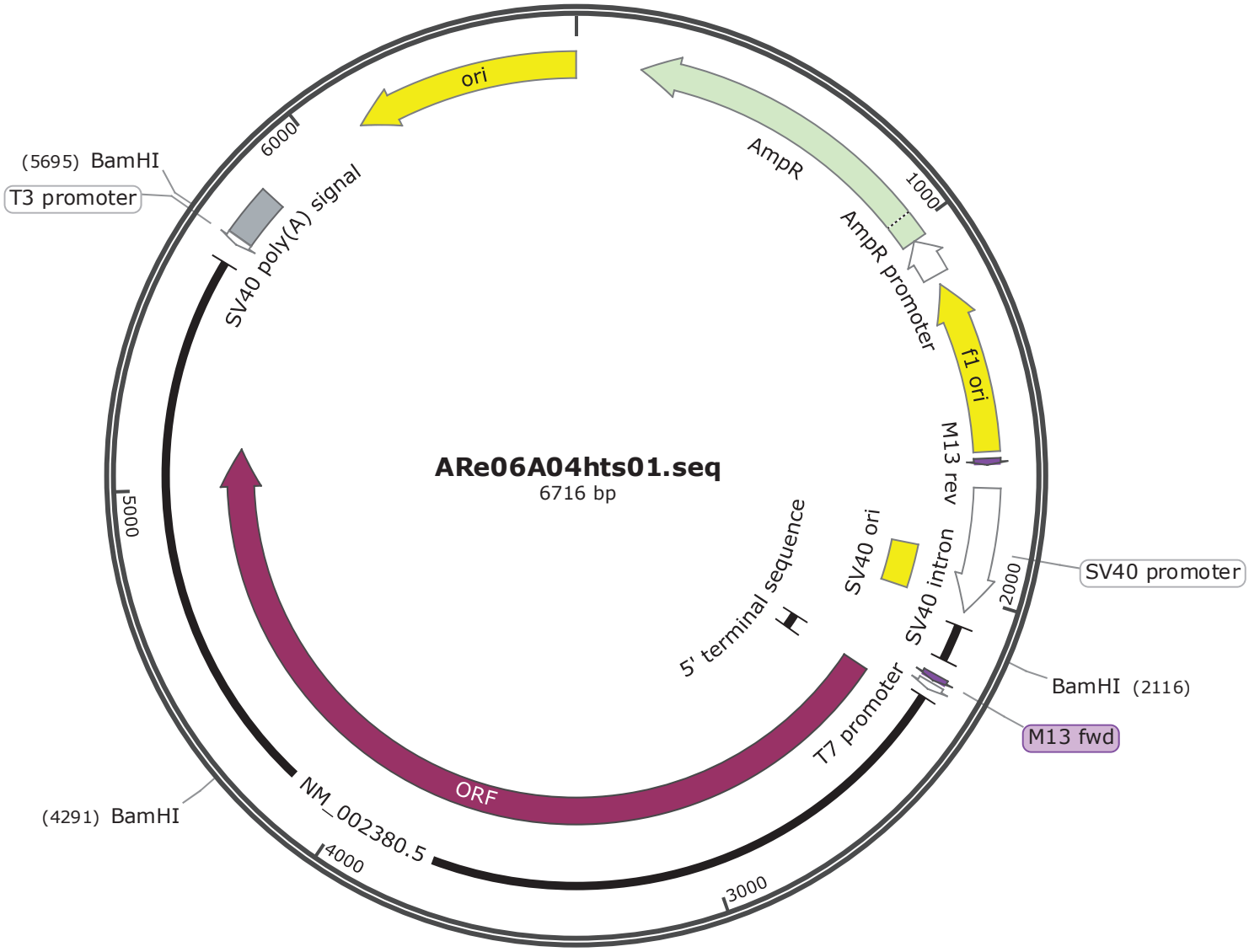
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '25.01.21 笹沼

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


ARe06A04hts01.seq
6716 bp
ori
AmpR
AmpR promoter
f1 ori
M13 rev
SV40 promoter
SV40 intron
SV40 ori
5' terminal sequence
T7 promoter
BamHI (2116)
M13 fwd
ORF
NM_002380.5
(4291) BamHI
SV40 poly(A) signal
T3 promoter
(5695) BamHI
1000
2000
3000
4000
5000
6000

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_030583:Homo sapiens matrilin 2 (MATN2),...

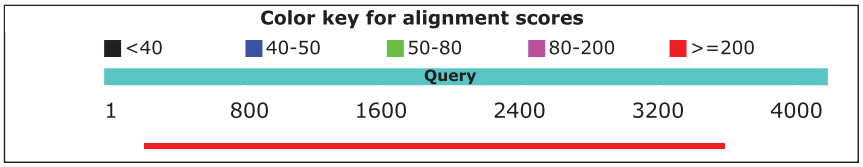
RID P4PYMD5D114 (Expires on 12-19 12:21 pm)

Query ID	NM_030583.4	**Subject ID**	lcl|Query_4367823
Description	Homo sapiens matrilin 2 (MATN2), transcript variant 2, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	4076	**Subject Length**	6716
		Program	BLASTN 2.16.1+

ARe06A04hts01.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	6148	6148	81%	0.0	99.94%	Query_4367823

Alignments

Sequence ID: Query_4367823 Length: 6716 Number of Matches: 1
Range 1: 2286 to 5620

Score	Expect	Identities	Gaps	Strand	Frame
6148 bits(3329)	0.0()	3333/3335(99%)	0/3335(0%)	Plus/Plus	

Features:

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CDS:matrilin-2 isofo  1                        M  E  K  M  L  A  G  C  F  L  L  I  L
Query                 229  GCCCCTCTTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCTGCTTTCTGCTGATCCT  288
Sbjct                 2286 ............................................................  2345

CDS:matrilin-2 isofo  14     G  Q  I  V  L  L  P  A  E  A  R  E  R  S  R  G  R  S  I  S
Query                 289  CGGACAGATCGTCCTCCTCCCTGCCGAGGCCAGGGAGCGGTCACGTGGGAGGTCCATCTC  348
Sbjct                 2346 ............................................................  2405

CDS:matrilin-2 isofo  34     R  G  R  H  A  R  T  H  P  Q  T  A  L  L  E  S  S  C  E  N
Query                 349  TAGGGGCAGACACGCTCGGACCCACCCGCAGACGGCCCTTCTGGAGAGTTCCTGTGAGAA  408
Sbjct                 2406 ............................................................  2465

CDS:matrilin-2 isofo  54     K  R  A  D  L  V  F  I  I  D  S  S  R  S  V  N  T  H  D  Y
Query                 409  CAAGCGGGCAGACCTGGTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTA  468
Sbjct                 2466 ............................................................  2525

CDS:matrilin-2 isofo  74     A  K  V  K  E  F  I  V  D  I  L  Q  F  L  D  I  G  P  D  V
Query                 469  TGCAAAGGTCAAGGAGTTCATCGTGGACATCTTGCAATTCTTGGACATTGGTCCTGATGT  528
Sbjct                 2526 ............................................................  2585

CDS:matrilin-2 isofo  94     T  R  V  G  L  L  Q  Y  G  S  T  V  K  N  E  F  S  L  K  T
Query                 529  CACCCGAGTGGGCCTGCTCCAATATGGCAGCACTGTCAAGAATGAGTTCTCCCTCAAGAC  588
Sbjct                 2586 ............................................................  2645
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CDS:matrilin-2 isofo  114    F  K  R  K  S  E  V  E  R  A  V  K  R  M  R  H  L  S  T  G
Query                 589    CTTCAAGAGGAAGTCCGAGGTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACGGG  648
Sbjct                 2646   ............................................................  2705

CDS:matrilin-2 isofo  134    T  M  T  G  L  A  I  Q  Y  A  L  N  I  A  F  S  E  A  E  G
Query                 649    CACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGG  708
Sbjct                 2706   ............................................................  2765

CDS:matrilin-2 isofo  154    A  R  P  L  R  E  N  V  P  R  V  I  M  I  V  T  D  G  R  P
Query                 709    GGCCCGGCCCCTGAGGGAGAATGTGCCACGGGTCATAATGATCGTGACAGATGGGAGACC  768   757 A>G
Sbjct                 2766   ............................................G...............  2825

CDS:matrilin-2 isofo  174    Q  D  S  V  A  E  V  A  A  K  A  R  D  T  G  I  L  I  F  A
Query                 769    TCAGGACTCCGTGGCCGAGGTGGCTGCTAAGGCACGGGACACGGGCATCCTAATCTTTGC  828
Sbjct                 2826   ............................................................  2885

CDS:matrilin-2 isofo  194    I  G  V  G  Q  V  D  F  N  T  L  K  S  I  G  S  E  P  H  E
Query                 829    CATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTGGGAGTGAGCCCCATGA  888
Sbjct                 2886   ............................................................  2945

CDS:matrilin-2 isofo  214    D  H  V  F  L  V  A  N  F  S  Q  I  E  T  L  T  S  V  F  Q
Query                 889    GGACCATGTCTTCCTTGTGGCCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCCA  948
Sbjct                 2946   ............................................................  3005

CDS:matrilin-2 isofo  234    K  K  L  C  T  A  H  M  C  S  T  L  E  H  N  C  A  H  F  C
Query                 949    GAAGAAGTTGTGCACGGCCCATATGTGCAGCACCCTGGAGCATAACTGTGCCCACTTCTG  1008  970 T>C
Sbjct                 3006   ..................C.........................................  3065

CDS:matrilin-2 isofo  254    I  N  I  P  G  S  Y  V  C  R  C  K  Q  G  Y  I  L  N  S  D
Query                 1009   CATCAACATCCCTGGCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGA  1068
Sbjct                 3066   ............................................................  3125

CDS:matrilin-2 isofo  274    Q  T  T  C  R  I  Q  D  L  C  A  M  E  D  H  N  C  E  Q  L
Query                 1069   TCAGACGACTTGCAGAATCCAGGATCTGTGTGCCATGGAGGACCACAACTGTGAGCAGCT  1128
Sbjct                 3126   ............................................................  3185

CDS:matrilin-2 isofo  294    C  V  N  V  P  G  S  F  V  C  Q  C  Y  S  G  Y  A  L  A  E
Query                 1129   CTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGTGCTACAGTGGCTACGCCCTGGCTGA  1188
Sbjct                 3186   ............................................................  3245

CDS:matrilin-2 isofo  314    D  G  K  R  C  V  A  V  D  Y  C  A  S  E  N  H  G  C  E  H
Query                 1189   GGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAACCACGGATGTGAACA  1248
Sbjct                 3246   ............................................................  3305

CDS:matrilin-2 isofo  334    E  C  V  N  A  D  G  S  Y  L  C  Q  C  H  E  G  F  A  L  N
Query                 1249   TGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAA  1308
Sbjct                 3306   ............................................................  3365

CDS:matrilin-2 isofo  354    P  D  K  K  T  C  T  K  I  D  Y  C  A  S  S  N  H  G  C  Q
Query                 1309   CCCAGATaaaaaaaCGTGCACAAAGATAGACTACTGTGCCTCATCTAATCACGGATGTCA  1368
Sbjct                 3366   ............................................................  3425

CDS:matrilin-2 isofo  374    H  E  C  V  N  T  D  D  S  Y  S  C  H  C  L  K  G  F  T  L
Query                 1369   GCACGAGTGTGTTAACACAGATGATTCCTATTCCTGCCACTGCCTGAAAGGCTTTACCCT  1428
Sbjct                 3426   ............................................................  3485

CDS:matrilin-2 isofo  394    N  P  D  K  K  T  C  R  R  I  N  Y  C  A  L  N  K  P  G  C
Query                 1429   GAATCCAGATAAGAAAACCTGCAGAAGGATCAACTACTGTGCACTGAACAAACCGGGCTG  1488
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Sbjct                 3486   ............................................................  3545

CDS:matrilin-2 isofo  414    E  H  E  C  V  N  M  E  E  S  Y  Y  C  R  C  H  R  G  Y  T
Query                 1489   TGAGCATGAGTGCGTCAACATGGAGGAGAGCTACTACTGCCGCTGCCACCGTGGCTACAC  1548
Sbjct                 3546   ............................................................  3605

CDS:matrilin-2 isofo  434    L  D  P  N  G  K  T  C  S  R  V  D  H  C  A  Q  Q  D  H  G
Query                 1549   TCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCACTGTGCACAGCAGGACCATGG  1608
Sbjct                 3606   ............................................................  3665

CDS:matrilin-2 isofo  454    C  E  Q  L  C  L  N  T  E  D  S  F  V  C  Q  C  S  E  G  F
Query                 1609   CTGTGAGCAGCTGTGTCTGAACACGGAGGATTCCTTCGTCTGCCAGTGCTCAGAAGGCTT  1668
Sbjct                 3666   ............................................................  3725

CDS:matrilin-2 isofo  474    L  I  N  E  D  L  K  T  C  S  R  V  D  Y  C  L  L  S  D  H
Query                 1669   CCTCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTGAGTGACCA  1728
Sbjct                 3726   ............................................................  3785

CDS:matrilin-2 isofo  494    G  C  E  Y  S  C  V  N  M  D  R  S  F  A  C  Q  C  P  E  G
Query                 1729   TGGTTGTGAATACTCCTGTGTCAACATGGACAGATCCTTTGCCTGTCAGTGTCCTGAGGG  1788
Sbjct                 3786   ............................................................  3845

CDS:matrilin-2 isofo  514    H  V  L  R  S  D  G  K  T  C  A  K  L  D  S  C  A  L  G  D
Query                 1789   ACACGTGCTCCGCAGCGATGGGAAGACGTGTGCAAAATTGGACTCTTGTGCTCTGGGGGA  1848
Sbjct                 3846   ............................................................  3905

CDS:matrilin-2 isofo  534    H  G  C  E  H  S  C  V  S  S  E  D  S  F  V  C  Q  C  F  E
Query                 1849   CCACGGTTGTGAACATTCGTGTGTAAGCAGTGAAGATTCGTTTGTGTGCCAGTGCTTTGA  1908
Sbjct                 3906   ............................................................  3965

CDS:matrilin-2 isofo  554    G  Y  I  L  R  E  D  G  K  T  C  R  R  K  D  V  C  Q  A  I
Query                 1909   AGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTAT  1968
Sbjct                 3966   ............................................................  4025

CDS:matrilin-2 isofo  574    D  H  G  C  E  H  I  C  V  N  S  D  D  S  Y  T  C  E  C  L
Query                 1969   AGACCATGGCTGTGAACACATTTGTGTGAACAGTGATGACTCATACACGTGCGAGTGCTT  2028
Sbjct                 4026   ............................................................  4085

CDS:matrilin-2 isofo  594    E  G  F  R  L  A  E  D  G  K  R  C  R  R  K  D  V  C  K  S
Query                 2029   GGAGGGATTCCGGCTCGCTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAAATC  2088
Sbjct                 4086   ............................................................  4145

CDS:matrilin-2 isofo  614    T  H  H  G  C  E  H  I  C  V  N  N  G  N  S  Y  I  C  K  C
Query                 2089   AACCCACCATGGCTGCGAACACATTTGTGTTAATAATGGGAATTCCTACATCTGCAAATG  2148
Sbjct                 4146   ............................................................  4205

CDS:matrilin-2 isofo  634    S  E  G  F  V  L  A  E  D  G  R  R  C  K  K  C  T  E  G  P
Query                 2149   CTCAGAGGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAATGCACTGAAGGCCC  2208
Sbjct                 4206   ............................................................  4265

CDS:matrilin-2 isofo  654    I  D  L  V  F  V  I  D  G  S  K  S  L  G  E  E  N  F  E  V
Query                 2209   AATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGT  2268
Sbjct                 4266   ............................................................  4325

CDS:matrilin-2 isofo  674    V  K  Q  F  V  T  G  I  I  D  S  L  T  I  S  P  K  A  A  R
Query                 2269   CGTGAAGCAGTTTGTCACTGGAATTATAGATTCCTTGACAATTTCCCCCAAAGCCGCTCG  2328
Sbjct                 4326   ............................................................  4385

CDS:matrilin-2 isofo  694    V  G  L  L  Q  Y  S  T  Q  V  H  T  E  F  T  L  R  N  F  N
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Query                2329  AGTGGGGCTGCTCCAGTATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAA  2388
Sbjct                4386  ............................................................  4445

CDS:matrilin-2 isofo  714    S  A  K  D  M  K  K  A  V  A  H  M  K  Y  M  G  K  G  S  M
Query                2389  CTCAGCCAAAGACATGAAAAAAGCCGTGGCCCACATGAAATACATGGGAAAGGGCTCTAT  2448
Sbjct                4446  ............................................................  4505

CDS:matrilin-2 isofo  734    T  G  L  A  L  K  H  M  F  E  R  S  F  T  Q  G  E  G  A  R
Query                2449  GACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTTACCCAAGGAGAAGGGGCCAG  2508
Sbjct                4506  ............................................................  4565

CDS:matrilin-2 isofo  754    P  L  S  T  R  V  P  R  A  A  I  V  F  T  D  G  R  A  Q  D
Query                2509  GCCCCTTTCCACAAGGGTGCCCAGAGCAGCCATTGTGTTCACCGACGGACGGGCTCAGGA  2568
Sbjct                4566  ............................................................  4625

CDS:matrilin-2 isofo  774    D  V  S  E  W  A  S  K  A  K  A  N  G  I  T  M  Y  A  V  G
Query                2569  TGACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGG  2628
Sbjct                4626  ............................................................  4685

CDS:matrilin-2 isofo  794    V  G  K  A  I  E  E  E  L  Q  E  I  A  S  E  P  T  N  K  H
Query                2629  GGTAGGAAAAGCCATTGAGGAGGAACTACAAGAGATTGCCTCTGAGCCCACAAACAAGCA  2688
Sbjct                4686  ............................................................  4745

CDS:matrilin-2 isofo  814    L  F  Y  A  E  D  F  S  T  M  D  E  I  S  E  K  L  K  K  G
Query                2689  TCTCTTCTATGCCGAAGACTTCAGCACAATGGATGAGATAAGTGAAAAACTCAAGAAAGG  2748
Sbjct                4746  ............................................................  4805

CDS:matrilin-2 isofo  834    I  C  E  A  L  E  D  S  D  G  R  Q  D  S  P  A  G  E  L  P
Query                2749  CATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAGCAGGGGAACTGCC  2808
Sbjct                4806  ............................................................  4865

CDS:matrilin-2 isofo  854    K  T  V  Q  Q  P  T  V  Q  H  R  Y  L  F  E  E  D  N  L  L
Query                2809  AAAAACGGTCCAACAGCCAACAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTT  2868
Sbjct                4866  ............................................................  4925

CDS:matrilin-2 isofo  874    R  S  T  Q  K  L  S  H  S  T  K  P  S  G  S  P  L  E  E  K
Query                2869  ACGGTCTACACAAAAGCTTTCCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAA  2928
Sbjct                4926  ............................................................  4985

CDS:matrilin-2 isofo  894    H  D  Q  C  K  C  E  N  L  I  M  F  Q  N  L  A  N  E  E  V
Query                2929  ACACGATCAATGCAAATGTGAAAACCTTATAATGTTCCAGAACCTTGCAAACGAAGAAGT  2988
Sbjct                4986  ............................................................  5045

CDS:matrilin-2 isofo  914    R  K  L  T  Q  R  L  E  E  M  T  Q  R  M  E  A  L  E  N  R
Query                2989  AAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCCTGGAAAATCG  3048
Sbjct                5046  ............................................................  5105

CDS:matrilin-2 isofo  934    L  R  Y  R
Query                3049  CCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTATCACGGATT  3108
Sbjct                5106  ............................................................  5165

Query                3109  ACAATGAACGCAGTGCAGAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGA  3168
Sbjct                5166  ............................................................  5225

Query                3169  AGTAAAACAATCAGTACTGAGAAACCTGGTTTGCCACAGAACAAAGACAAGAAGTATACA  3228
Sbjct                5226  ............................................................  5285

Query                3229  CTAACTTGTATAAATTTATCTAGGaaaaaaaTCCTTCAGAATTCTAAGATGAATTTACCA  3288
Sbjct                5286  ............................................................  5345

Query                3289  GGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAATATACTGTGGACACAACTTGCTTC  3348
Sbjct                5346  ............................................................  5405

Query                3349  TGCCTCATCCTGCCTTAGTGTGCAATCTCATTTGACTATACGATAAAGTTTGCACAGTCT  3408
Sbjct                5406  ............................................................  5465

Query                3409  TACTTCTGTAGAACACTGGCCATAGGAAATGCTGttttttttGTACTGGACTTTACCTTGA  3468
Sbjct                5466  ............................................................  5525

Query                3469  TATATGTATATGGATGTATGCATAAAATCATAGGACATATGTACTTGTGGAACAAGTTGG  3528
Sbjct                5526  ............................................................  5585

Query                3529  ATTTTTTATACAATATTAAAATTCACCACTTCAGA  3563
Sbjct                5586  .................................    5620
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