NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBdS007K04

Lot# : 6608_B4F4

Vector : pGCAP10

Gene	EMD	
RefSeq_mRNA	NM_000117.3	1281 bp

● Plasmid DNA purification

Date : 2024/06/04 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2024/06/05 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2024/06/05

DNA concentration (O.D.): 284 ng/ul

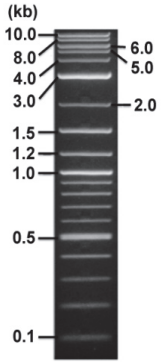
DNA	0.35 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.65 ul
Total	10 ul

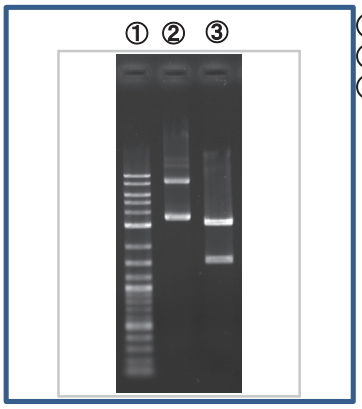
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 1.5 kb

Erectrophoresis : 1% agarose gel, 1x TAE Buffer

Marker : 2-Log DNA Ladder (NEB#N3200L)





①:Marker
②:uncut
③:BamHI

● Confirmation of the insert/vector junction sequence

Date : 2024/06/10

Primer A	pGCAP-F
Primer B	pGCAP-R
Primer C	
List of Sequencing Primers	http://dna.brc.riken.jp/en/NRCDhum2en.html

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2024/06/12

DNA (284 ng/ul)	86 ul
10x TE	98 ul
dH_2O	793 ul
Total	977 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '24.06.12 笹沼

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

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_032806:Homo sapiens protein O-linked mannose...

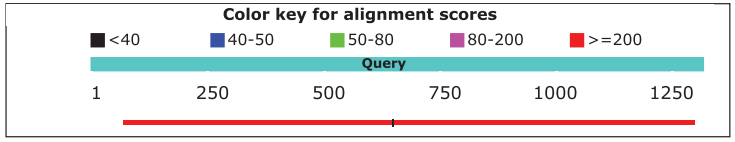
RID 64V527ZE114 (Expires on 06-08 10:12 am)

Query ID	NM_000117.3	**Subject ID**	lcl|Query_2147269
Description	Homo sapiens emerin (EMD), mRNA	**Description**	None
Molecule type	nucleic acid		See details
Query Length	1281	**Molecule type**	dna
		Subject Length	1317
		Program	BLASTN 2.15.0+

RBdS007K04hts.seq

Graphic Summary

Distribution of the top 2 Blast Hits on 1 subject sequences



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'24.06.07
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Dot Matrix View

Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
None provided	1190	2220	94%	0.0	100.00%	Query_2147269

Alignments

Sequence ID: Query_2147269 Length: 1317 Number of Matches: 2
Range 1: 645 to 1288

Score	Expect	Identities	Gaps	Strand	Frame
1190 bits(644)	0.0()	644/644(100%)	0/644(0%)	Plus/Plus	

Features:

```
CDS:emerin [Homo sap 150   R  E  R  P  M  Y  G  R  D  S  A  Y  Q  S  I  T  H  Y  R  P
Query               638   AGGGAACGCCCCATGTACGGCCGGGACAGTGCCTACCAGAGCATCACGCACTACCGCCCT  697
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct               645   AGGGAACGCCCCATGTACGGCCGGGACAGTGCCTACCAGAGCATCACGCACTACCGCCCT  704

CDS:emerin [Homo sap 170   V  S  A  S  R  S  S  L  D  L  S  Y  Y  P  T  S  S  S  T  S
Query               698   GTTTCAGCCTCCAGGAGCTCCCTGGACCTGTCCTATTATCCTACTTCCTCCTCCACCTCT  757
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct               705   GTTTCAGCCTCCAGGAGCTCCCTGGACCTGTCCTATTATCCTACTTCCTCCTCCACCTCT  764

CDS:emerin [Homo sap 190   F  M  S  S  S  S  S  S  S  S  W  L  T  R  R  A  I  R  P  E
Query               758   TTTATGTCCTCCTCATCATCTTCCTCTTCATGGCTCACCCGCCGTGCCATCCGGCCTGAA  817
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct               765   TTTATGTCCTCCTCATCATCTTCCTCTTCATGGCTCACCCGCCGTGCCATCCGGCCTGAA  824

CDS:emerin [Homo sap 210   N  R  A  P  G  A  G  L  G  Q  D  R  Q  V  P  L  W  G  Q  L
Query               818   AACCGTGCTCCTGGGGCTGGGCTGGGCCAGGATCGCCAGGTCCCGCTCTGGGGCCAGCTG  877
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct               825   AACCGTGCTCCTGGGGCTGGGCTGGGCCAGGATCGCCAGGTCCCGCTCTGGGGCCAGCTG  884

CDS:emerin [Homo sap 230   L  L  F  L  V  F  V  I  V  L  F  F  I  Y  H  F  M  Q  A  E
Query               878   CTGCTTTTCCTGGTCTTTGTGATCGTCCTCTTCTTCATTTACCACTTCATGCAGGCTGAA  937
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct               885   CTGCTTTTCCTGGTCTTTGTGATCGTCCTCTTCTTCATTTACCACTTCATGCAGGCTGAA  944

CDS:emerin [Homo sap 250   E  G  N  P  F
Query               938   GAAGGCAACCCCTTCTAGAGGGAGCCATGAGGGTCTGGGCTTCAGAGCTAGGTCTTTGGG  997
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct               945   GAAGGCAACCCCTTCTAGAGGGAGCCATGAGGGTCTGGGCTTCAGAGCTAGGTCTTTGGG  1004

Query               998   GAAGTCCTGGCTGACTGCCTTAGCAGTggggggtgggggtgggggcagggggcagggggcttt  1057
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct               1005  GAAGTCCTGGCTGACTGCCTTAGCAGTGGGGGTGGGGGTGGGGGCAGGGGCAGGGGCTTT  1064

Query               1058  atgtgtttttgcttgggggggcgctgggcCTAGCCCAGAGTAGTGCTTGCTCCCCCTGCCT  1117
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct               1065  ATGTGTTTTTGCTTGGGGGGCGCTGGGCCTAGCCCAGAGTAGTGCTTGCTCCCCCTGCCT  1124

Query               1118  TGTCCCACCAGGGAGGCAGCAGACTCAGGCCCTCCATGGTCCTCTTTGTCATTTTGTTGA  1177
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct               1125  TGTCCCACCAGGGAGGCAGCAGACTCAGGCCCTCCATGGTCCTCTTTGTCATTTTGTTGA  1184

Query               1178  CATGCATTCCTCCTTTTGTCATCTTGTTGGGGGGAGGGGATTAACCAAAGGCCACCCTGA  1237
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct               1185  CATGCATTCCTCCTTTTGTCATCTTGTTGGGGGGAGGGGATTAACCAAAGGCCACCCTGA  1244

Query               1238  CTTTGTTTTTGTGGACACACAATAAAAGCCCCGTTTATTTGTAA  1281
                          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct               1245  CTTTGTTTTTGTGGACACACAATAAAAGCCCCGTTTATTTGTAA  1288
```

Range 2: 2 to 568

Score	Expect	Identities	Gaps	Strand	Frame
1029 bits(557)	0.0()	567/571(99%)	4/571(0%)	Plus/Plus	

Features:

```
Query               70    GCGAGCGCGGCCGCTCCCGATGCGCTCGTGCCGCCCCCGCCGTGCTCCTCGGCAGCCGTT  129
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct               2     GCGAGCGCGGCCGCTCCCGATGCGCTCGTGCCGCCCCCGCCGTGCTCCTCGGCAGCCGTT  61
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Query                130  GCTCGGCCGGTTTTGGTAGGCCCGGGCCGCCGCCAGGCCTCCGCCTGAGCCCGCACCCGC  189
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                62   GCTCGGCCGGTTTTGGTAGGCCCGGGCCGCCGCCAGGCCTCCGCCTGAGCCCGCACCCGC  121

CDS:emerin [Homo sap 1      M  D  N  Y  A  D  L  S  D  T  E  L  T  T  L  L  R  R  Y  N
Query                190  CATGGACAACTACGCAGATCTTTCGGATACCGAGCTGACCACCTTGCTGCGCCGGTACAA  249
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                122  CATGGACAACTACGCAGATCTTTCGGATACCGAGCTGACCACCTTGCTGCGCCGGTACAA  181

CDS:emerin [Homo sap 21     I  P  H  G  P  V  V  G  S  T  R  R  L  Y  E  K  K  I  F  E
Query                250  CATCCCGCACGGGCCTGTAGTAGGATCAACTCGTAGGCTTTACGAGAAGAAGATCTTCGA  309
                          ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Sbjct                182  CATCCCGCACGGGCCTGTA----GATCAACTCGTAGGCTTTACGAGAAGAAGATCTTCGA  237

CDS:emerin [Homo sap 41     Y  E  T  Q  R  R  R  L  S  P  P  S  S  S  A  A  S  S  Y  S
Query                310  GTACGAGACCCAGAGGCGGCGGCTCTCGCCCCCCAGCTCGTCCGCCGCCTCCTCTTATAG  369
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                238  GTACGAGACCCAGAGGCGGCGGCTCTCGCCCCCCAGCTCGTCCGCCGCCTCCTCTTATAG  297

CDS:emerin [Homo sap 61     F  S  D  L  N  S  T  R  G  D  A  D  M  Y  D  L  P  K  K  E
Query                370  CTTCTCTGACTTGAATTCGACTAGAGGGGATGCAGATATGTATGATCTTCCCAAGAAAGA  429
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                298  CTTCTCTGACTTGAATTCGACTAGAGGGGATGCAGATATGTATGATCTTCCCAAGAAAGA  357

CDS:emerin [Homo sap 81     D  A  L  L  Y  Q  S  K  G  Y  N  D  D  Y  Y  E  E  S  Y  F
Query                430  GGACGCTTTACTCTACCAGAGCAAGGGCTACAATGACGACTACTATGAAGAGAGCTACTT  489
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                358  GGACGCTTTACTCTACCAGAGCAAGGGCTACAATGACGACTACTATGAAGAGAGCTACTT  417

CDS:emerin [Homo sap 101    T  T  R  T  Y  G  E  P  E  S  A  G  P  S  R  A  V  R  Q  S
Query                490  CACCACCAGGACTTATGGGGAGCCCGAGTCTGCCGGCCCGTCCAGGGCTGTCCGCCAGTC  549
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                418  CACCACCAGGACTTATGGGGAGCCCGAGTCTGCCGGCCCGTCCAGGGCTGTCCGCCAGTC  477

CDS:emerin [Homo sap 121    V  T  S  F  P  D  A  D  A  F  H  H  Q  V  H  D  D  D  L  L
Query                550  AGTGACTTCATTCCCAGATGCTGACGCTTTCCATCACCAGGTGCATGATGACGATCTTTT  609
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                478  AGTGACTTCATTCCCAGATGCTGACGCTTTCCATCACCAGGTGCATGATGACGATCTTTT  537

CDS:emerin [Homo sap 141    S  S  S  E  E  E  C  K  D  R
Query                610  GTCTTCTTCTGAAGAGGAGTGCAAGGATAGG  640
                          ||||||||||||||||||||||||||||||
Sbjct                538  GTCTTCTTCTGAAGAGGAGTGCAAGGATAGG  568
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NM_000117.3 : 640_641ins 81bp

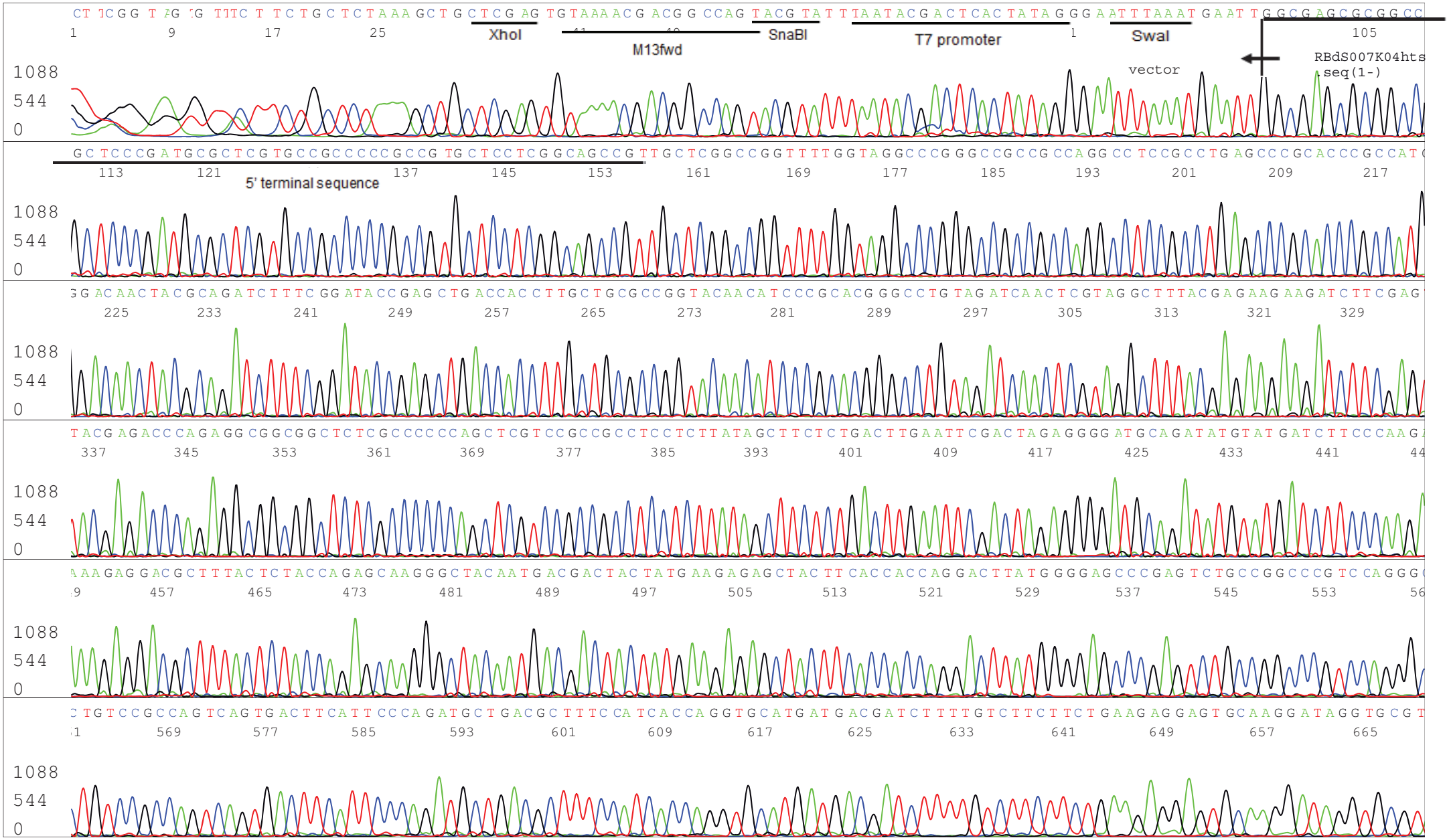
Applied Biosystems

S/N G:303 A:392 T:313 C:511
KB.bcp
KB 1.4.1.8 Cap:2

Primer A : pGCAP-F
5' CTCAGTGGATGTTGCCTTTAC 3'

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KB_3500_POP7_BDTv3.mob
Pts 1577 to 12965 Pk1 Loc:1554
Version 6.0 HiSQV Bases: 876

Inst Model/Name 3500/3500 Instrument
Jun 05,2024 03:16PM, JST
Jun 05,2024 03:43PM, JST
Spacing:11.29 Pts/Panel1350
Plate Name: 20240605_GNP



Applied Biosystems

S/N G:46 A:66 T:76 C:73
KB.bcp
KB 1.4.1.8 Cap:5

Primer B : pGCAP-R
5' GCATTCTAGTTGTGGTTTGTCC 3'

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Pts 1671 to 12598 Pk1 Loc:1648
Version 6.0 HiSQV Bases: 89

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Jun 05,2024 03:16PM, JST
Jun 05,2024 03:43PM, JST
Spacing:13.25 Pts/Panel1350
Plate Name: 20240605_GNP

