NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

Lot# : 7676_B3Bd

RIKEN Clone ID : RBb37D02

Vector : pGCAP1

Gene	ST8SIA1	
RefSeq_mRNA	NM_003034.4	9707 bp

● Plasmid DNA purification

Date : 2023/03/08 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2023/03/09 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2023/03/09

DNA concentration (O.D.): 171 ng/ul

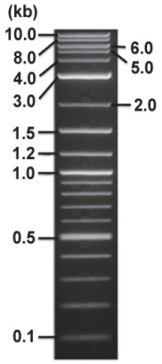
DNA	0.6	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.4	ul
Total	10	ul

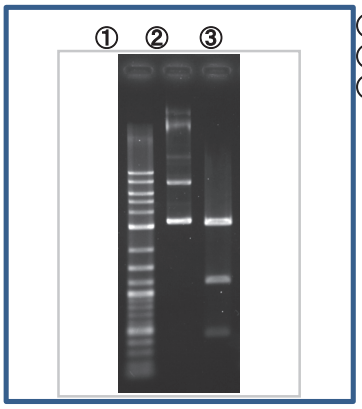
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 1.1, 0.4 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 : 2024/09/20

Primer A	-
Primer B	-
Primer C	RBb37D02hts01.seq
List of Sequencing Primers	-

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2024/09/20

DNA (171 ng/ul)	72	ul
10x TE	49	ul
dH_2O	371	ul
Total	492	ul

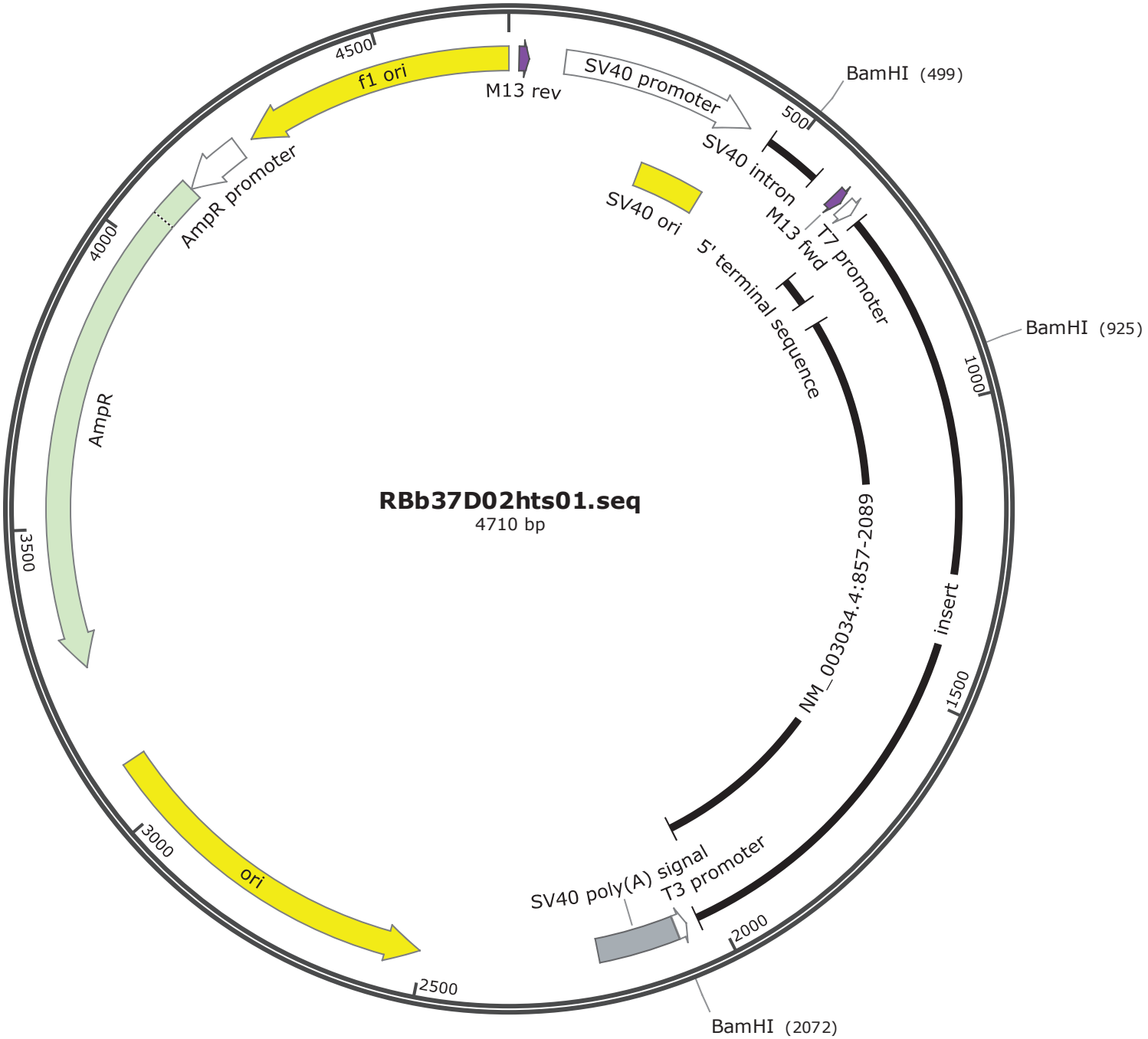
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '24.09.24 笹沼

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


RBb37D02hts01.seq
4710 bp
4500
f1 ori
M13 rev
SV40 promoter
BamHI (499)
500
SV40 intron
M13 fwd
T7 promoter
SV40 ori
5' terminal sequence
BamHI (925)
1000
AmpR promoter
4000
AmpR
NM_003034.4:857-2089
insert
1500
3500
3000
ori
SV40 poly(A) signal
T3 promoter
2000
2500
BamHI (2072)

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_003034:Homo sapiens ST8 alpha-N-acetyl-neuraminide...

RID ETNB8BBD114 (Expires on 09-21 09:52 am)

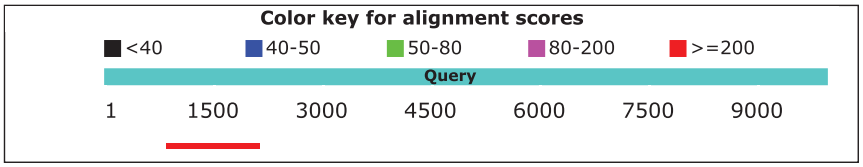
Query ID NM_003034.4
Description Homo sapiens ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1 (ST8SIA1), transcript variant 1, mRNA
Molecule type nucleic acid
Query Length 9707

Subject ID lcl|Query_4593327
Description None
See details
Molecule type dna
Subject Length 4710
Program BLASTN 2.16.0+

RBb37D02hts01.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	2266	2266	12%	0.0	99.84%	Query_4593327

Alignments

Sequence ID: Query_4593327 Length: 4710 Number of Matches: 1
Range 1: 772 to 2004

Score	Expect	Identities	Gaps	Strand	Frame
2266 bits(1227)	0.0()	1231/1233(99%)	0/1233(0%)	Plus/Plus	

Features:

```
CDS:alpha-N-acetylne  128   A  T  P  F  Q  L  P  L  K  K  C  A  V  V  G  N  G  G  I  L
Query                 857   GCAACCCCATTCCAGCTGCCATTGAAGAAATGCGCGGTGGTGGGAAATGGTGGGATTCTG  916
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 772   GCAACCCCATTCCAGCTGCCATTGAAGAAATGCGCGGTGGTGGGAAATGGTGGGATTCTG  831

CDS:alpha-N-acetylne  148   K  K  S  G  C  G  R  Q  I  D  E  A  N  F  V  M  R  C  N  L
Query                 917   AAGAAGAGTGGCTGTGGCCGTCAAATAGATGAAGCAAATTTTGTCATGCGATGCAATCTC  976
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 832   AAGAAGAGTGGCTGTGGCCGTCAAATAGATGAAGCAAATTTTGTCATGCGATGCAATCTC  891

CDS:alpha-N-acetylne  168   P  P  L  S  S  E  Y  T  K  D  V  G  S  K  S  Q  L  V  T  A
Query                 977   CCTCCTTTGTCAAGTGAATACACTAAGGATGTTGGATCCAAAAGTCAGTTAGTGACAGCT  1036
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 892   CCTCCTTTGTCAAGTGAATACACTAAGGATGTTGGATCCAAAAGTCAGTTAGTGACAGCT  951

CDS:alpha-N-acetylne  188   N  P  S  I  I  R  Q  R  F  Q  N  L  L  W  S  R  K  T  F  V
Query                 1037  AATCCCAGCATAATTCGGCAAAGGTTTCAGAACCTTCTGTGGTCCAGAAAGACATTTGTG  1096
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 952   AATCCCAGCATAATTCGGCAAAGGTTTCAGAACCTTCTGTGGTCCAGAAAGACATTTGTG  1011

CDS:alpha-N-acetylne  208   D  N  M  K  I  Y  N  H  S  Y  I  Y  M  P  A  F  S  M  K  T
Query                 1097  GACAACATGAAAATTTATAACCACAGTTACATCTACATGCCTGCCTTTTCTATGAAGACA  1156
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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1111 T>C

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Sbjct                1012  GACAACATGAAAATCTATAACCACAGTTACATCTACATGCCTGCCTTTTCTATGAAGACA  1071

CDS:alpha-N-acetylne  228   G  T  E  P  S  L  R  V  Y  Y  T  L  S  D  V  G  A  N  Q  T
Query                1157  GGAACAGAGCCATCTTTGAGGGTTTATTATACACTGTCAGATGTTGGTGCCAATCAAACA  1216

Sbjct                1072  GGAACAGAGCCATCTTTGAGGGTTTATTATACACTGTCAGATGTTGGTGCCAATCAAACA  1131

CDS:alpha-N-acetylne  248   V  L  F  A  N  P  N  F  L  R  S  I  G  K  F  W  K  S  R  G
Query                1217  GTGCTGTTTGCCAACCCCAACTTTCTGCGTAGCATTGGAAAGTTCTGGAAAAGTAGAGGA  1276

Sbjct                1132  GTGCTGTTTGCCAACCCCAACTTTCTGCGTAGCATTGGAAAGTTCTGGAAAAGTAGAGGA  1191

CDS:alpha-N-acetylne  268   I  H  A  K  R  L  S  T  G  L  F  L  V  S  A  A  L  G  L  C
Query                1277  ATCCATGCCAAGCGCCTGTCCACAGGACTTTTTCTGGTGAGCGCAGCTCTGGGTCTCTGT  1336

Sbjct                1192  ATCCATGCCAAGCGCCTGTCCACAGGACTTTTTCTGGTGAGCGCAGCTCTGGGTCTCTGT  1251

CDS:alpha-N-acetylne  288   E  E  V  A  I  Y  G  F  W  P  F  S  V  N  M  H  E  Q  P  I
Query                1337  GAAGAGGTGGCCATCTATGGCTTCTGGCCCTTCTCTGTGAATATGCATGAGCAGCCCATC  1396

Sbjct                1252  GAAGAGGTGGCCATCTATGGCTTCTGGCCCTTCTCTGTGAATATGCATGAGCAGCCCATC  1311

CDS:alpha-N-acetylne  308   S  H  H  Y  Y  D  N  V  L  P  F  S  G  F  H  A  M  P  E  E
Query                1397  AGCCACCACTACTATGACAACGTCTTACCCTTTTCTGGCTTCCATGCCATGCCCGAGGAA  1456

Sbjct                1312  AGCCACCACTACTATGACAACGTCTTACCCTTTTCTGGCTTCCATGCCATGCCCGAGGAA  1371

CDS:alpha-N-acetylne  328   F  L  Q  L  W  Y  L  H  K  I  G  A  L  R  M  Q  L  D  P  C
Query                1457  TTTCTCCAACTCTGGTATCTTCATAAAATCGGTGCACTGAGAATGCAGCTGGACCCATGT  1516

Sbjct                1372  TTTCTCCAACTCTGGTATCTTCATAAAATCGGTGCACTGAGAATGCAGCTGGACCCATGT  1431

CDS:alpha-N-acetylne  348   E  D  T  S  L  Q  P  T  S
Query                1517  GAAGATACCTCACTCCAGCCCACTTCCTAGGAACAATGGAAGAAGAAAGGACTGAACCAG  1576

Sbjct                1432  GAAGATACCTCACTCCAGCCCACTTCCTAGGAACAATGGAAGAAGAAAGGACTGAACCAG  1491

Query                1577  GGTATTTTTGTTAGGTTTTCTATGTGACTCCAAGAGGGAATGGTCAAGTTGTTTCATGAG  1636

Sbjct                1492  GGTATTTTTGTTAGGTTTTCTATGTGACTCCAAGAGGGAATGGTCAAGTTGTTTCATGAG  1551

Query                1637  TTTGCATGGGCCCTTGGAAAAACAGGAAAGGAGCAATGAAGATCCAAGCAAAACTTTACT  1696

Sbjct                1552  TTTGCATGGGCCCTTGGAAAAACAGGAAAGGAGCAATGAAGATCCAAGCAAAACTTTACT  1611

Query                1697  TTCAGCGTTGGCTTGGAGGACAAATAAGAAATGAAACATCCTATGAAATACTTTATAGCA  1756

Sbjct                1612  TTCAGCGTTGGCTTGGAGGACAAATAAGAAATGAAACATCCTATGAAATACTTTATAGCA  1671

Query                1757  CATGGCAGATTTGCAACTAGTAAAATGCTGGTGAAATGCTGTTGGTAAAGCACATGGTTC  1816

Sbjct                1672  CATGGCAGATTTGCAACTAGTAAAATGCTGGTGAAATGCTGTTGGTAAAGCACATGGTTC  1731

Query                1817  AAATCTAGAAGATGCAGTTCAAAAACAAGACAGACTCGAGTTGTTAGGGCTGAGGAACCA  1876

Sbjct                1732  AAATCTAGAAGATGCAGTTCAAAAACAAGACAGACTCGAGTTGTTAGGGCTGAGGAACCA  1791

Query                1877  ATCAAGGTAGAACAAAGAAAATGTTGGGGTAAAAGTGTTGCTGATTGTCAACACAAACTG  1936
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Sbjct                1792  ATCAAGGTAGAACAAAGAAAATGTTGGGGTAAAAGTGTTGCTGATTGTCAACACAAACTG  1851

Query                1937  GCTTAATAATATTAATAAGAACCTGTCTTATTAAGACTGGCTTTAGAACCGTAGGtttttt  1996

Sbjct                1852  GCTTAATAATATTAATAAGAACCTGTCTTATTAAGACTGGCTTTAGAACCGTAGGTTTTT  1911

Query                1997  ttaaaaaattattatttatttttGCCCTCTTTGGGGAAGTGGGTGGGTAGATTTAAAAAA  2056

Sbjct                1912  TAAAAAAATTATTATTTATTTTTGCCCTCTTTGGGGAAGTGGGTGGGTAGATTTAAAAAA  1971

Query                2057  TCCCTTCCTGAGTAATAAAGATACAAAATGTTA  2089

Sbjct                1972  TCCCTTCCTGAGTAATAAAGATACAAAATGTTA  2004
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