NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBdS187P14

Lot# : 6608_B5H6

Vector : pGCAP10

Gene	STMN1	
RefSeq_mRNA	NM_005563.4	1443 bp

● Plasmid DNA purification

Date : 2025/08/06 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2025/08/07 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/08/07

DNA concentration (O.D.): 198 ng/ul

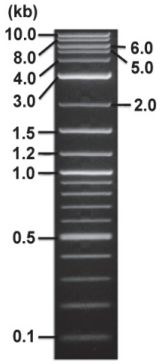
< Size of fragment expected from this clone >

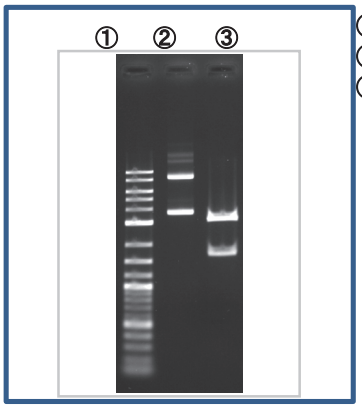
DNA	0.5 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.5 ul
Total	10 ul

BamHI 3.1kb (vector), 1.7 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 : 2025/08/18

full sequence	RBdS187P14hts01.se

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/08/19

DNA (198 ng/ul)	86 ul
10x TE	68 ul
dH_2O	527 ul
Total	681 ul

● Shipping

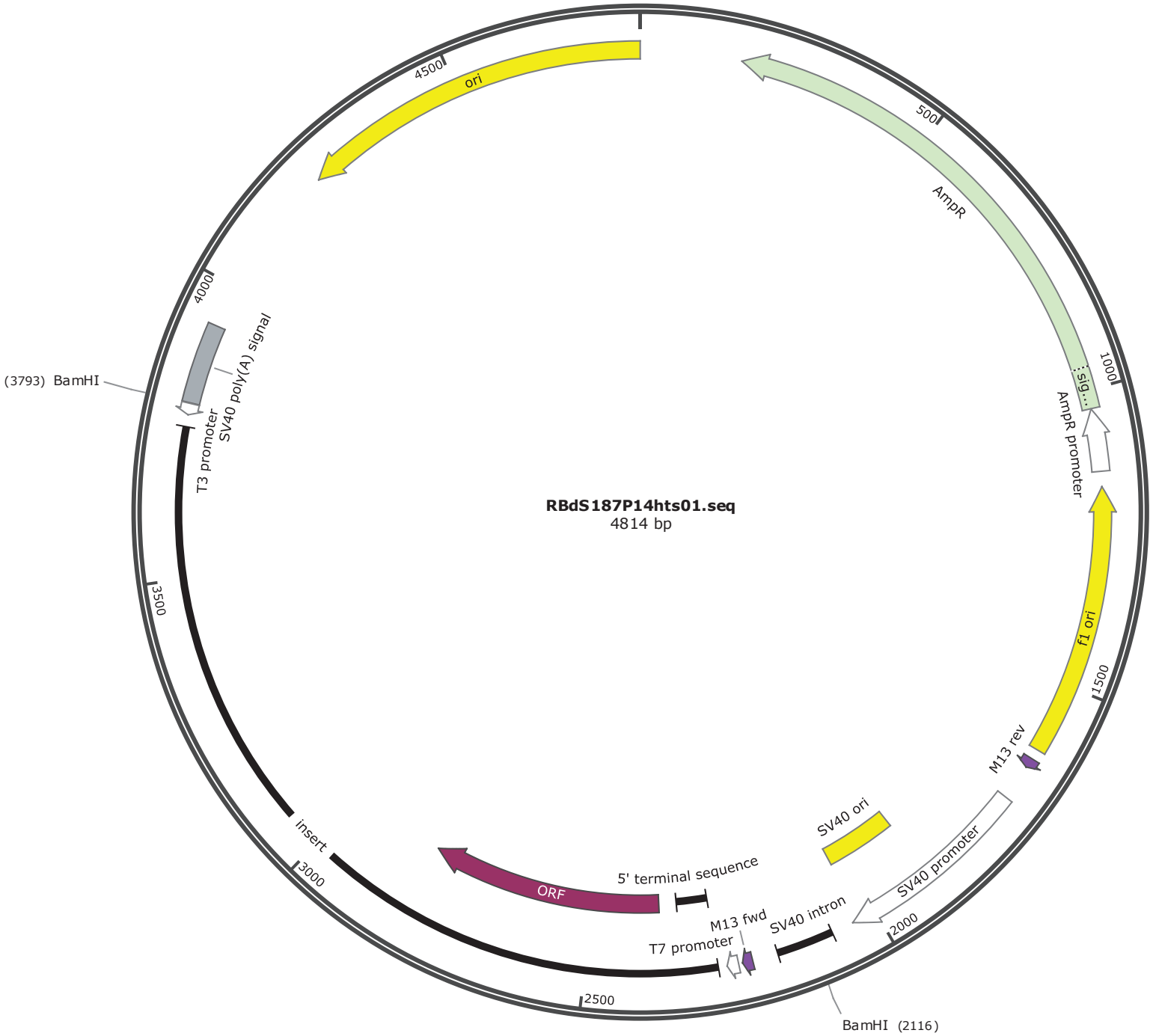
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY :

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


RBdS187P14hts01.seq
4814 bp
4500
ori
500
AmpR
1000
:sig...
AmpR promoter
1500
f1 ori
M13 rev
SV40 promoter
2000
SV40 intron
M13 fwd
T7 promoter
2500
BamHI (2116)
5' terminal sequence
ORF
SV40 ori
insert
3000
3500
T3 promoter
SV40 poly(A) signal
4000
(3793) BamHI

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_004753:Homo sapiens dehydrogenase/reductase...

RID A5BWBVFJ114 (Expires on 08-19 12:43 pm)

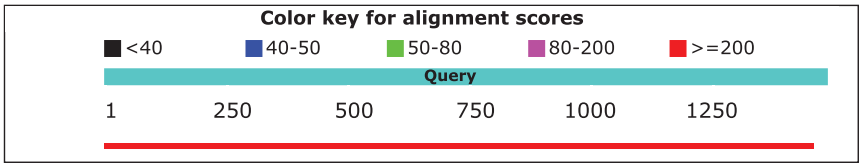
Query ID NM_005563.4
Description Homo sapiens stathmin 1 (STMN1), transcript variant 3, mRNA
Molecule type nucleic acid
Query Length 1443

Subject ID lcl|Query_6787511
Description None
See details
Molecule type dna
Subject Length 4814
Program BLASTN 2.17.0+

RBdS187P14hts01.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	2665	2665	100%	0.0	100.00%	Query_6787511

Alignments

Sequence ID: Query_6787511 Length: 4814 Number of Matches: 1
Range 1: 2279 to 3721

Score	Expect	Identities	Gaps	Strand	Frame
2665 bits(1443)	0.0()	1443/1443(100%)	0/1443(0%)	Plus/Plus	

Features:

```
Query              1     AGAGTGTGGTCAGGCGGCTCGGACTGAGCAGGACTTTCCTTATCCCAGTTGATTGTGCAG  60
Sbjct              2279  ............................................................  2338

CDS:stathmin isoform  1                                      M  A  S  S  D  I  Q  V  K
Query              61    AATACACTGCCTGTCGCTTGTCTTCTATTCACCATGGCTTCTTCTGATATCCAGGTGAAA  120
Sbjct              2339  ............................................................  2398

CDS:stathmin isoform  10    E  L  E  K  R  A  S  G  Q  A  F  E  L  I  L  S  P  R  S  K
Query              121   GAACTGGAGAAGCGTGCCTCAGGCCAGGCTTTTGAGCTGATTCTCAGCCCTCGGTCAAAA  180
Sbjct              2399  ............................................................  2458

CDS:stathmin isoform  30    E  S  V  P  E  F  P  L  S  P  P  K  K  K  D  L  S  L  E  E
Query              181   GAATCTGTTCCAGAATTCCCCCTTTCCCCTCCAAAGAAGAAGGATCTTTCCCTGGAGGAA  240
Sbjct              2459  ............................................................  2518

CDS:stathmin isoform  50    I  Q  K  K  L  E  A  A  E  E  R  R  K  S  H  E  A  E  V  L
Query              241   ATTCAGAAGAAATTAGAAGCTGCAGAAGAAAGACGCAAGTCCCATGAAGCTGAGGTCTTG  300
Sbjct              2519  ............................................................  2578

CDS:stathmin isoform  70    K  Q  L  A  E  K  R  E  H  E  K  E  V  L  Q  K  A  I  E  E
Query              301   AAGCAGCTGGCTGAGAAACGAGAGCACGAGAAAGAAGTGCTTCAGAAGGCAATAGAAGAG  360
Sbjct              2579  ............................................................  2638
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CDS:stathmin isoform  90    N  N  N  F  S  K  M  A  E  E  K  L  T  H  K  M  E  A  N  K
Query                 361   AACAACAACTTCAGTAAAATGGCAGAAGAGAAACTGACCCACAAAATGGAAGCTAATAAA  420
Sbjct                 2639  ............................................................  2698

CDS:stathmin isoform  110   E  N  R  E  A  Q  M  A  A  K  L  E  R  L  R  E  K  D  K  H
Query                 421   GAGAACCGAGAGGCACAAATGGCTGCCAAACTGGAACGTTTGCGAGAGAAGGATAAGCAC  480
Sbjct                 2699  ............................................................  2758

CDS:stathmin isoform  130   I  E  E  V  R  K  N  K  E  S  K  D  P  A  D  E  T  E  A  D
Query                 481   ATTGAAGAAGTGCGGAAGAACAAAGAATCCAAAGACCCTGCTGACGAGACTGAAGCTGAC  540
Sbjct                 2759  ............................................................  2818

Query                 541   TAATTTGTTCTGAGAACTGACTTTCTCCCCATCCCCTTCCTAAATATCCAAAGACTGTAC  600
Sbjct                 2819  ............................................................  2878

Query                 601   TGGCCAGTGTCATTTTATTTTTTCCCTCCTGACAAATATTTTAGAAGCTAATGTAGGACT  660
Sbjct                 2879  ............................................................  2938

Query                 661   GTATAGGTAGATCCAGATCCAGACTGTAAGATGTTGTTTTAGGGGCTAAAGGGGAGAAAC  720
Sbjct                 2939  ............................................................  2998

Query                 721   TGAAAGTGTTTTACTCTTTTTCTAAAGTGTTGGTCTTTCTAATGTAGCTATTTTTCTTGT  780
Sbjct                 2999  ............................................................  3058

Query                 781   TGCATCTTTTCTACTTCAGTACACTTGGTGTACTGGGTTAATGGCTAGTACTGTATTGGC  840
Sbjct                 3059  ............................................................  3118

Query                 841   TCTGTGAAAACATATTTGTGAAAAGAGTATGTAGTGGCTTCTTTTGAACTGTTAGATGCT  900
Sbjct                 3119  ............................................................  3178

Query                 901   GAATATCTGTTCACTTTTCAATCCCAATTCTGTCCCAATCTTACCAGATGCTACTGGACT  960
Sbjct                 3179  ............................................................  3238

Query                 961   TGAATGGTTAATAAAACTGCACAGTGCTGTTGGTGGCAGTGACTTCTTTTGAGTTAGGTT  1020
Sbjct                 3239  ............................................................  3298

Query                 1021  AATAAATCAAGCCATAGAGCCCCTCCTGGTTGATACTTGTTCCAGATGGGGCCTTTGGGG  1080
Sbjct                 3299  ............................................................  3358

Query                 1081  CTGGTAGAAATACCCAACGCACAAATGACCGCACGTTCTCTGCCCCGTTTCTTGCCCCAG  1140
Sbjct                 3359  ............................................................  3418

Query                 1141  TGTGGTTTGCATTGTCTCCTTCCACAATGACTGCTTTGTTTGGATGCCTCAGCCCAGGTC  1200
Sbjct                 3419  ............................................................  3478

Query                 1201  AGCTGTTACTTTCTTTCAGATGTTTATTTGCAAACAACCATTTTTTGTTCTGTGTCCCTT  1260
Sbjct                 3479  ............................................................  3538

Query                 1261  TTAAAAGGCAGATTAAAAGCACAAGCGTGTTTCTAGAGAACAGTTGAGAGAGAATCTCAA  1320
Sbjct                 3539  ............................................................  3598

Query                 1321  GATTCTACTTGGTGGTTTGCTTGCTCTACGTTACAGGTGGGGCATGTCCTCATCCTTTCC  1380
Sbjct                 3599  ............................................................  3658

Query                 1381  TGCCATAAAAGCTATGACACGAGAATCAGAATATTAATAAAACTTTATGTACTGCTGTAG  1440
Sbjct                 3659  ............................................................  3718

Query                 1441  CAA  1443
Sbjct                 3719  ...  3721
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