NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARe80F12

Lot# : 7672_B3Bd

Vector : pKA1U5

Gene	SHB	
RefSeq_mRNA	NM_003028.3	6035 bp

● Plasmid DNA purification

Date : 2023/02/21 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2023/02/22 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2023/02/22

DNA concentration (O.D.): 126 ng/ul

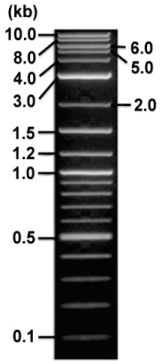
DNA	0.8	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.2	ul
Total	10	ul

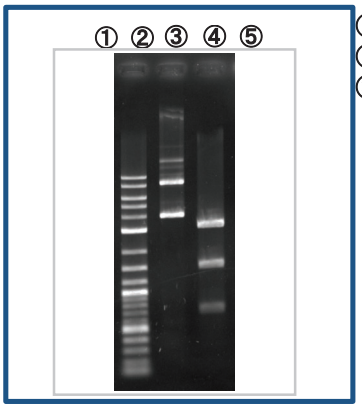
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 1.5, 0.7, <0.1 kb

Erectrophoresis : 1% agarose gel, 1x TAE Buffer

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





①:Marker
②:uncut
③:BamHI

● Confirmation of sequence

Date : 2026/06/18

full sequence	ARe80F12hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/07/23

DNA (126 ng/ul)	70	ul
10x TE	35	ul
dH_2O	248	ul
Total	353	ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '26.07.23 笹沼

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


ARe80F12hts01.seq
5401 bp
BamHI (405)
SV40 promoter
M13 rev
f1 ori
5000
SV40 ori
SV40 intron
M13 fwd
T7 promoter
5' terminal sequence
1000
ORF
insert
BamHI (1904)
BamHI (1923)
2000
SV40 poly(A) signal
T3 promoter
3000
BamHI (2669)
ori
4000
AmpR
sig...
AmpR promoter

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_147128:Homo sapiens zinc and ring finger...

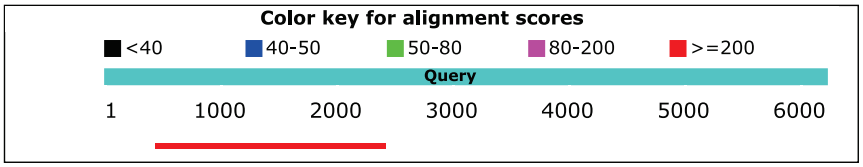
RID 36NF584V114 (Expires on 06-19 10:20 am)

Query ID	NM_003028.3	**Subject ID**	lcl|Query_2046141
Description	Homo sapiens SH2 domain containing adaptor protein B (SHB), mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	6035	**Subject Length**	5401
		Program	BLASTN 2.17.0+

ARe80F12hts01.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	3602	3602	32%	0.0	99.95%	Query_2046141

Alignments

Sequence ID: Query_2046141 Length: 5401 Number of Matches: 1
Range 1: 575 to 2527

Score	Expect	Identities	Gaps	Strand	Frame
3602 bits(1950)	0.0()	1952/1953(99%)	0/1953(0%)	Plus/Plus	

Features:

```
Query   431  GGCAAGAACTTGAACTTGGCGTCGGGAGCGGgcgccccggacgccccccgccggggccgg  490
Sbjct   575  ............................................................  634

Query   491  ggcgccgagggacctgcgccgcagcgctgccccccgAATGGCCGCGGCGGCGGACCGGGC  550
Sbjct   635  ............................................................  694

CDS:SH2 domain-conta  1                                  M  A  K  W  L  N  K  Y  F
Query   551  TCCCGCGCCGCGGCCCTAGGCGGCCTCTCGCCATGGCCAAGTGGCTAAACAAGTACTTCA  610
Sbjct   695  ............................................................  754

CDS:SH2 domain-conta  10   S  L  G  N  S  K  T  K  S  P  P  Q  P  P  R  P  D  Y  R  E
Query   611  GCTTGGGCAACAGCAAGACCAAGAGCCCCCCGCAGCCGCCGCGGCCAGACTACCGCGAGC  670
Sbjct   755  ............................................................  814

CDS:SH2 domain-conta  30   Q  R  R  R  G  E  R  P  S  Q  P  P  Q  A  V  P  Q  A  S  S
Query   671  AGCGGCGCCGAGGCGAGCGGCCTTCGCAGccccccccAGGCCGTGCCGCAGGCCTCCTCCG  730
Sbjct   815  ......................C.....................................  874

CDS:SH2 domain-conta  50   A  A  S  A  S  C  G  P  A  T  A  S  C  F  S  A  S  S  G  S
Query   731  CCGCCTCGGCGTCCTGCGGTCCGGCCACCGCCTCCTGCTTCTCAGCCTCTTCGGGCTCGC  790
Sbjct   875  ............................................................  934
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693 T>C

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CDS:SH2 domain-conta  70    L  P  D  D  S  G  S  T  S  D  L  I  R  A  Y  R  A  Q  K  E
Query                 791   TGCCCGACGACAGCGGCAGCACCAGCGACCTCATCCGCGCCTACCGCGCGCAGAAGGAGC  850
Sbjct                 935   ............................................................  994

CDS:SH2 domain-conta  90    R  D  F  E  D  P  Y  N  G  P  G  S  S  L  R  K  L  R  A  M
Query                 851   GAGACTTCGAGGACCCCTACAACGGGCCTGGCTCGTCGCTGCGCAAACTGCGCGCCATGT  910
Sbjct                 995   ............................................................  1054

CDS:SH2 domain-conta  110   C  R  L  D  Y  C  G  G  S  G  E  P  G  G  V  Q  R  A  F  S
Query                 911   GCCGCCTGGACTACTGCGGCGGCAGCGGGGAGCCAGGCGGGGTCCAGCGCGCCTTCTCGG  970
Sbjct                 1055  ............................................................  1114

CDS:SH2 domain-conta  130   A  S  S  A  S  G  A  A  G  C  C  C  A  S  S  G  A  G  A  A
Query                 971   CCTCGTCCGCGTCGGGCGCCGCGGGCTGTTGCTGCGCCTCCTCGGGCGCGGGGGCCGCCG  1030
Sbjct                 1115  ............................................................  1174

CDS:SH2 domain-conta  150   A  S  S  S  S  S  S  G  S  P  H  L  Y  R  S  S  S  E  R  R
Query                 1031  CGTCCTCGTCCTCGTCCTCCGGCTCTCCGCATCTCTACCGCAGCAGCAGCGAGCGGCGGC  1090
Sbjct                 1175  ............................................................  1234

CDS:SH2 domain-conta  170   P  A  T  P  A  E  V  R  Y  I  S  P  K  H  R  L  I  K  V  E
Query                 1091  CCGCCACGCCGGCCGAGGTGCGCTACATCTCCCCCAAGCACCGCCTCATCAAAGTGGAGA  1150
Sbjct                 1235  ............................................................  1294

CDS:SH2 domain-conta  190   S  A  A  G  G  G  A  G  D  P  L  G  G  A  C  A  G  G  R  T
Query                 1151  gcgccgcgggcggtggggccggggaccccctgggggcgcctgcgcgggcggccgcACCT  1210
Sbjct                 1295  ............................................................  1354

CDS:SH2 domain-conta  210   W  S  P  T  A  C  G  G  K  K  L  L  N  K  C  A  A  S  A  A
Query                 1211  GGAGCCCGACGGCCTGCGGAGGCAAGAAACTGCTCAACAAGTGCGCCGCCTCAGCCGCGG  1270
Sbjct                 1355  ............................................................  1414

CDS:SH2 domain-conta  230   E  E  S  G  A  G  K  K  D  K  V  T  I  A  D  D  Y  S  D  P
Query                 1271  AGGAGAGCGGGGCCGGCAAGAAGGACAAGGTGACCATAGCCGATGACTACTCAGATCCCT  1330
Sbjct                 1415  ............................................................  1474

CDS:SH2 domain-conta  250   F  D  A  K  N  D  L  K  S  K  A  G  K  G  E  S  A  G  Y  M
Query                 1331  TTGATGCCAAGAATGATCTCAAGAGCAAAGCAGGAAAGGGGGAGAGTGCTGGCTACATGG  1390
Sbjct                 1475  ............................................................  1534

CDS:SH2 domain-conta  270   E  P  Y  E  A  Q  R  I  M  T  E  F  Q  R  Q  E  S  V  R  S
Query                 1391  AGCCCTATGAGGCACAGAGGATCATGACAGAATTTCAGAGGCAGGAAAGTGTCCGGTCCC  1450
Sbjct                 1535  ............................................................  1594

CDS:SH2 domain-conta  290   Q  H  K  G  I  Q  L  Y  D  T  P  Y  E  P  E  G  Q  S  V  D
Query                 1451  AGCATAAAGGTATCCAGTTATATGACACCCCTTACGAACCTGAAGGCCAAAGTGTTGACT  1510
Sbjct                 1595  ............................................................  1654

CDS:SH2 domain-conta  310   S  D  S  E  S  T  V  S  P  R  L  R  E  S  K  L  P  Q  D  D
Query                 1511  CAGACTCGGAGAGCACAGTCAGCCCCCGACTGCGGGAGAGCAAGCTGCCCCAGGATGACG  1570
Sbjct                 1655  ............................................................  1714

CDS:SH2 domain-conta  330   D  R  P  A  D  E  Y  D  Q  P  W  E  W  N  R  V  T  I  P  A
Query                 1571  ACAGGCCCGCCGATGAGTACGACCAGCCTTGGGAGTGGAACCGGGTCACCATCCCAGCCC  1630
Sbjct                 1715  ............................................................  1774

CDS:SH2 domain-conta  350   L  A  A  Q  F  N  G  N  E  K  R  Q  S  S  P  S  P  S  R  D
Query                 1631  TGGCAGCACAGTTTAATGGCAACGAGAAGCGGCAGTCATCCCCCTCACCTTCGCGGGACC  1690
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Sbjct                 1775  ............................................................  1834

CDS:SH2 domain-conta  370   R  R  R  Q  L  R  A  P  G  G  G  F  K  P  I  K  H  G  S  P
Query                 1691  GGCGGCGCCAGCTTCGTGCCCCTGGAGGGGGCTTTAAGCCTATCAAACATGGGAGCCCTG  1750
Sbjct                 1835  ............................................................  1894

CDS:SH2 domain-conta  390   F  F  C  G  I  L  G  E  R  V  D  P  A  V  P  L  E  K  Q  I
Query                 1751  AGTTCTGCGGGATCCTAGGAGAAAGGGTGGATCCTGCCGTCCCCCTGGAGAAGCAAATAT  1810
Sbjct                 1895  ............................................................  1954

CDS:SH2 domain-conta  410   W  Y  H  G  A  I  S  R  G  D  A  E  N  L  L  R  L  C  K  E
Query                 1811  GGTATCACGGAGCCATCAGCAGAGGAGACGCCGAGAACCTGCTGCGACTCTGCAAGGAGT  1870
Sbjct                 1955  ............................................................  2014

CDS:SH2 domain-conta  430   C  S  Y  L  V  R  N  S  Q  T  S  K  H  D  Y  S  L  S  L  R
Query                 1871  GTAGCTACCTTGTCCGGAACAGCCAGACCAGCAAGCATGACTACTCCCTCTCCCTGAGGA  1930
Sbjct                 2015  ............................................................  2074

CDS:SH2 domain-conta  450   S  N  Q  G  F  M  H  M  K  L  A  K  T  K  E  K  Y  V  L  G
Query                 1931  GCAACCAGGGTTTTATGCACATGAAACTGGCCAAAACCAAAGAGAAATACGTTCTGGGTC  1990
Sbjct                 2075  ............................................................  2134

CDS:SH2 domain-conta  470   Q  N  S  P  P  F  D  S  V  P  E  V  I  H  Y  Y  T  T  R  K
Query                 1991  AGAACAGCCCTCCGTTCGACAGTGTCCCGGAAGTCATCCACTACTACACCACCAGAAAGC  2050
Sbjct                 2135  ............................................................  2194

CDS:SH2 domain-conta  490   L  P  I  K  G  A  E  H  L  S  L  L  Y  P  V  A  V  R  T  L
Query                 2051  TACCCATCAAAGGGGCTGAGCACTTGTCCCTCCTCTATCCCGTGGCTGTGAGGACCCTGT  2110
Sbjct                 2195  ............................................................  2254

Query                 2111  GAGCGGACCAGACCTGCCCTGCTCTGTGACAGAGCCTGAGACTTGGAGGTGCCAGAGGCC  2170
Sbjct                 2255  ............................................................  2314

Query                 2171  CCCCACCAACCAGCCCAGCCACTGTTGCTGGCTGTGTCGTTTGTGTTGTGTGTATGGTAC  2230
Sbjct                 2315  ............................................................  2374

Query                 2231  TAGCACACCACTGCATGTCTCTAGAATGCTGTTGCCACTTACGGGGGCTGGAGAAGGCCT  2290
Sbjct                 2375  ............................................................  2434

Query                 2291  GGATAAAGACAGAAGGGCGGCAACAcaccaccccagcccccaccccacccTCTCCTTGA  2350
Sbjct                 2435  ............................................................  2494

Query                 2351  GTTTCTGTGAATTAAAATATTTGCAAATCCAAA  2383
Sbjct                 2495  .................................  2527
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