NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARe17H01
Vector : pKA1U5

Lot# : 7672_B3Bd

Gene	ZSWIM7	
RefSeq_mRNA	NM_001042697.2	2020 bp

● Plasmid DNA purification

Date : 23.03.22 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.03.24 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 23.03.24

DNA concentration (O.D.): 212 ng/ul

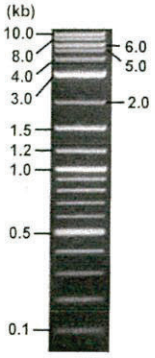
DNA	0.5 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.5 ul
Total	10 ul

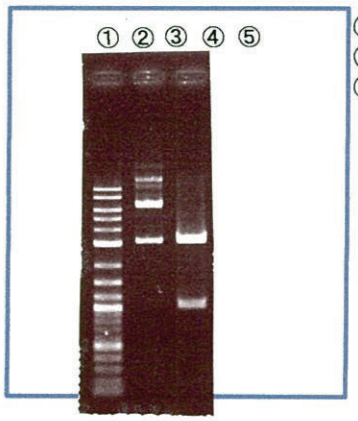
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 1.1 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 : 2026/07/23

full sequence : ARe17H01hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/07/23

DNA (212 ng/ul)	76 ul
10x TE	64 ul
dH_2O	504 ul
Total	644 ul

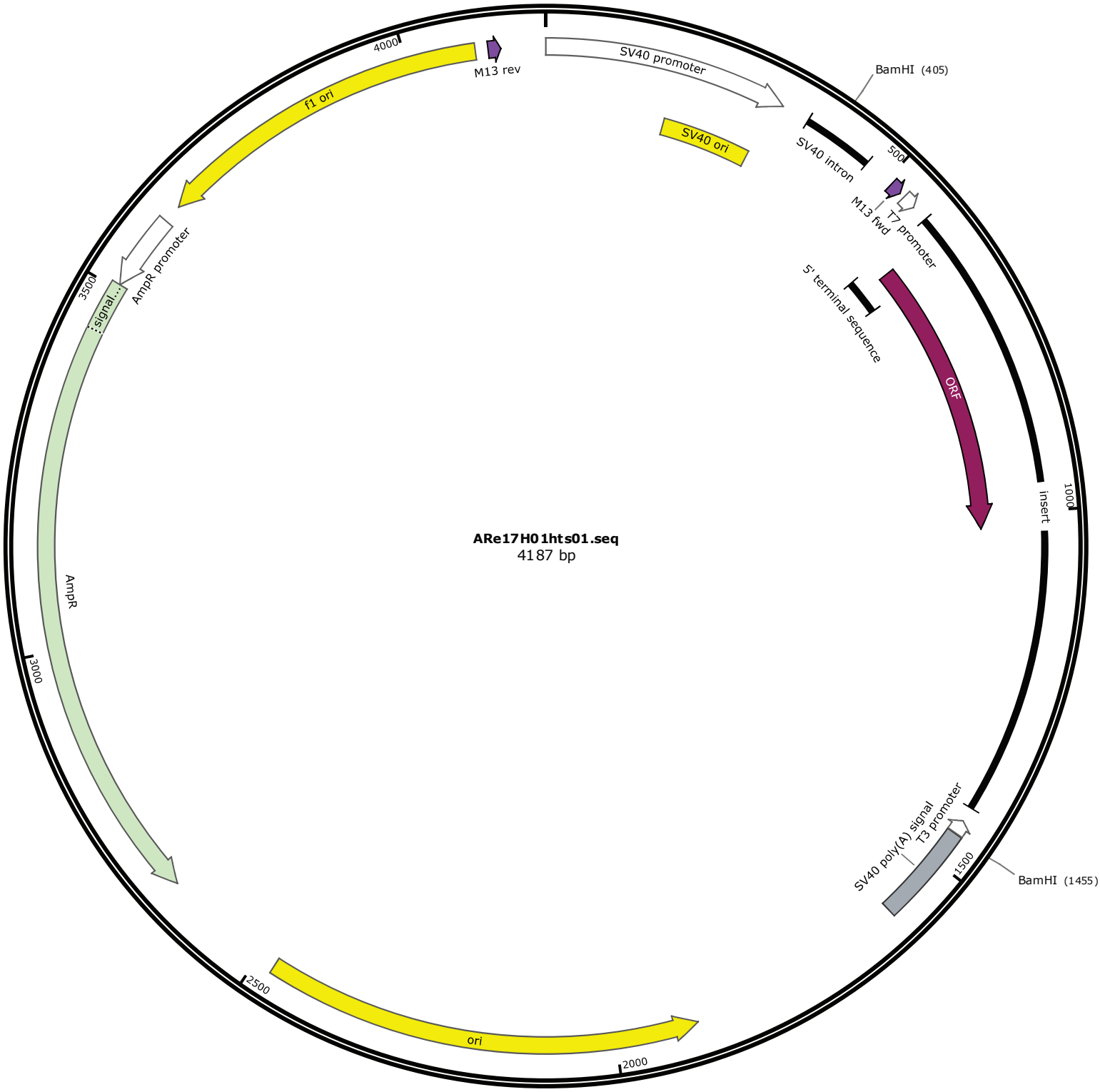
● Shipping

☑ 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


ARe17H01hts01.seq
4187 bp
4000
M13 rev
f1 ori
SV40 promoter
BamHI (405)
SV40 ori
SV40 intron
500
M13 fwd
T7 promoter
5' terminal sequence
ORF
insert
1000
3500
signal...
AmpR promoter
AmpR
3000
2500
ori
2000
SV40 poly(A) signal
T3 promoter
1500
BamHI (1455)

BLAST Results

Questions/comments

Blast 2 sequences

Job title: ref|NM_001042697|

RID 33WFPATE114 (Expires on 06-18 09:01 am)

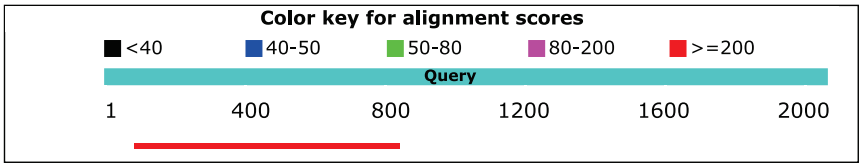
Query ID NM_001042697.2
Description Homo sapiens zinc finger SWIM-type containing 7 (ZSWIM7), transcript variant 1, mRNA
Molecule type nucleic acid
Query Length 2020

Subject ID lcl|Query_4521427
Description None
See details
Molecule type dna
Subject Length 4187
Program BLASTN 2.17.0+

ARe17H01hts01.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	1382	1382	37%	0.0	99.87%	Query_4521427

Alignments

Sequence ID: Query_4521427 Length: 4187 Number of Matches: 1
Range 1: 575 to 1325

Score	Expect	Identities	Gaps	Strand	Frame
1382 bits(748)	0.0()	750/751(99%)	0/751(0%)	Plus/Plus	

Features:

```
CDS:zinc finger SWIM  1                                 M  A  V  V  L  P  A  V  V  F  F  L
Query                 87    GTGGAGGGCGTGTCCTGCGGCGCGATGGCCGTAGTGTTGCCGGCGGTTGTGGAGGAGCTC  146
Sbjct                 575   ............................................................  634

CDS:zinc finger SWIM  13    L  S  E  M  A  A  A  V  Q  E  S  A  R  I  P  D  E  Y  L  L
Query                 147   CTGAGCGAGATGGCGGCGGCGGTGCAGGAGAGCGCGCGAATTCCTGATGAATATCTGTTA  206
Sbjct                 635   ............................................................  694

CDS:zinc finger SWIM  33    S  L  K  F  L  F  G  S  S  A  T  Q  A  L  D  L  V  D  R  Q
Query                 207   TCGCTGAAGTTTCTCTTTGGCTCATCAGCCACCCAGGCCTTGGACCTAGTTGATCGACAG  266
Sbjct                 695   ............................................................  754

CDS:zinc finger SWIM  53    S  I  T  L  I  S  S  P  S  G  R  R  V  Y  Q  V  L  G  S  S
Query                 267   TCCATCACCTTAATCTCATCACCCAGTGGAAGGCGTGTTTACCAGGTCCTTGGAAGTTCC  326
Sbjct                 755   ............................................................  814

CDS:zinc finger SWIM  73    S  K  T  Y  T  C  L  A  S  C  H  Y  C  S  C  P  A  F  A  F
Query                 327   AGTAAAACATACACATGTTTGGCTTCTTGTCATTACTGTTCATGTCCTGCATTTGCATTC  386
Sbjct                 815   ............................................................  874

CDS:zinc finger SWIM  93    S  V  L  R  K  S  D  S  I  L  C  K  H  L  L  A  V  Y  L  S
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Query                387   TCAGTGCTACGGAAGAGTGACAGCATCCTGTGCAAGCATCTCTTGGCAGTTTACCTGAGT  446
Sbjct                875   ............................................................  934

CDS:zinc finger SWIM 113    Q  V  M  R  T  C  Q  Q  L  S  V  S  D  K  Q  L  T  D  I  L
Query                447   CAGGTTATGAGGACCTGTCAGCAGCTAAGTGTCTCTGACAAGCAGTTGACTGACATATTA  506
Sbjct                935   ............................................................  994

CDS:zinc finger SWIM 133    L  M  E  K  K  Q  E  A
Query                507   TTGATGGAGAAGAAACAAGAAGCATAAAAGGTACAGATTGAGCATCATTCTTTCAAAATA  566
Sbjct                995   ............................................................  1054

Query                567   GAATCCTGTCAAGAAATGCATTGAAAGCGTCATGATTCACATGGAAAAGAGGTGAAATGG  626
Sbjct                1055  ............................................................  1114

Query                627   ATCTTCAGACACTTCATGTTACTGTCCCTTTTCCCTCCAGGACTGCAGGAGGTGCTGTGG  686
Sbjct                1115  ............................................................  1174

Query                687   GTTGGAGCCGTGGGCTGTGGAGGGTTTGTGTATGATGAGAAGCCCTGTACAGTCTTGTCA  746
Sbjct                1175  ............................................C...............  1234

Query                747   AGAAATACCCTGAGCCAGTCTCTGAGACGCTTCGGTAAAAAATGTCCCTGGATGGAATCA  806
Sbjct                1235  ............................................................  1294

Query                807   AGATTTTAAATTCAAATAAAGCCTAATATCA  837
Sbjct                1295  ................................  1325
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'26.06.17
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