NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARe70D06

Vector : pKA1U5

USP30-AS1 Lot# : 7672_B3Bd

Gene	LOC100131733	
Accession No.	AB371497	656 bp

● Plasmid DNA purification

Date : 23.03.14 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.03.15 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 23.03.15

DNA concentration (O.D.): 193 ng/ul

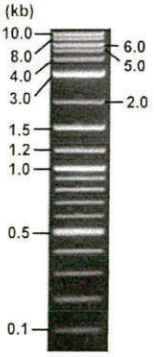
DNA	0.5 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.5 ul
Total	10 ul

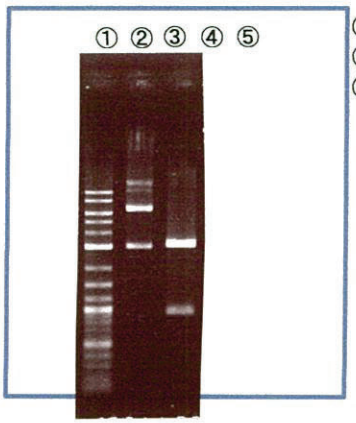
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 0.9 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 : 2026/06/17

full sequence : ARe70D06hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/07/23

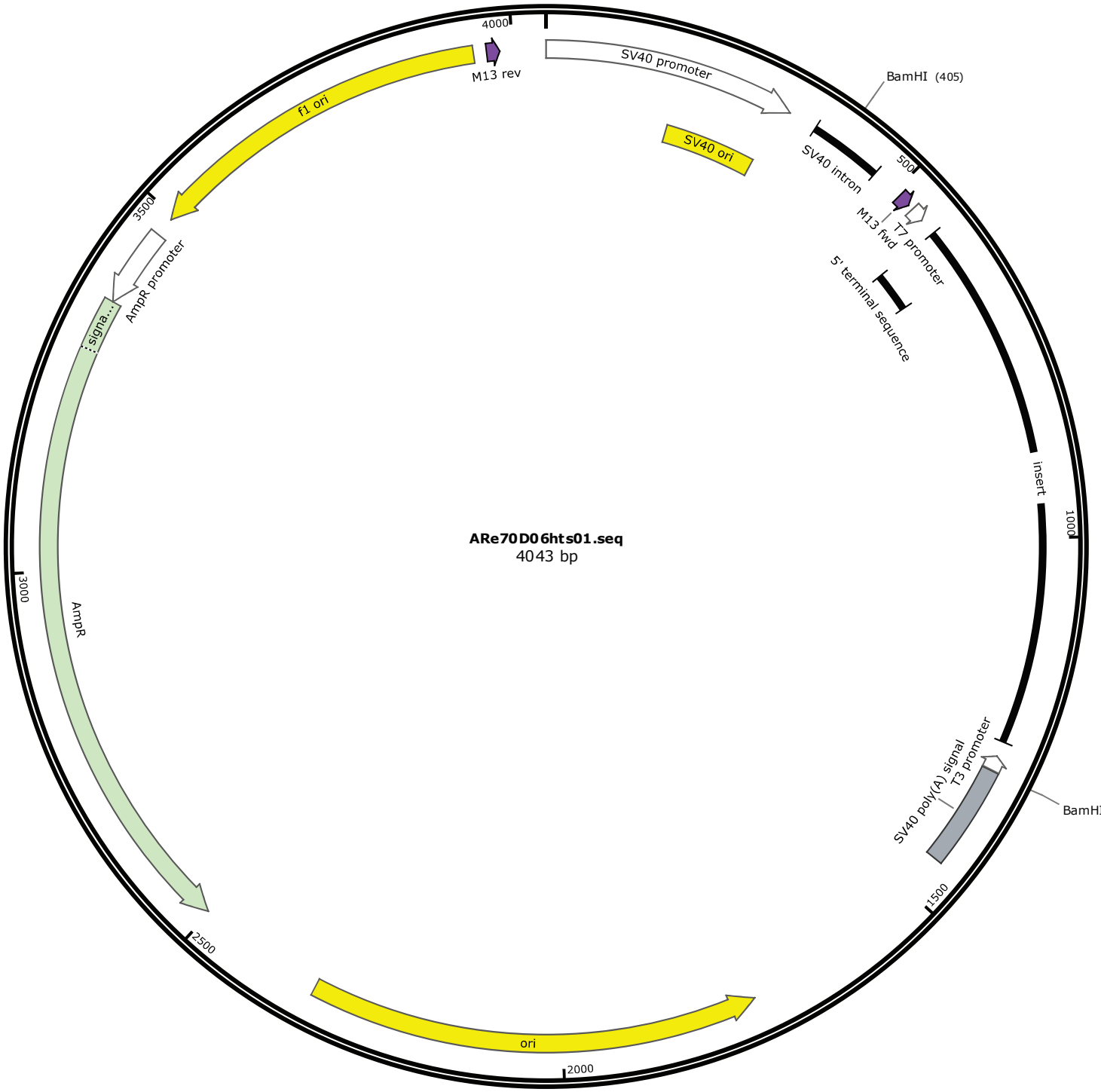
DNA (193 ng/ul)	74 ul
10x TE	57 ul
dH_2O	440 ul
Total	571 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '26.07.23 笹沼


ARe70D06hts01.seq
4043 bp
4000
M13 rev
SV40 promoter
BamHI (405)
f1 ori
SV40 ori
SV40 intron
500
M13 fwd
T7 promoter
3500
AmpR promoter
5' terminal sequence
signa...
insert
1000
3000
AmpR
SV40 poly(A) signal
T3 promoter
BamHI (1311)
1500
2500
ori
2000

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_175872:Homo sapiens zinc finger protein...

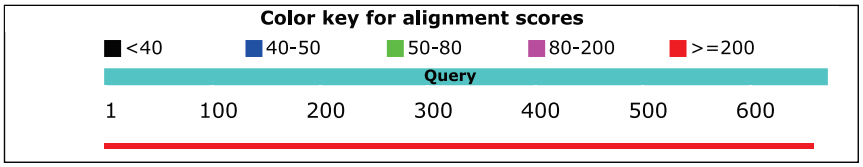
RID 34K92Z5P114 (Expires on 06-18 15:30 pm)

Query ID	AB371497.1	**Subject ID**	lcl|Query_8185115
Description	AB371497 pKA1U5/ARPE-19 vector-capped full-length cDNA Homo sapiens cDNA clone HP10988-ARe70D06 5'.	**Description**	None See details
Molecule type	rna	**Molecule type**	dna
Query Length	656	**Subject Length**	4043
		Program	BLASTN 2.17.0+

ARe70D06hts01.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	1212	1212	100%	0.0	100.00%	Query_8185115

Alignments

Sequence ID: Query_8185115 Length: 4043 Number of Matches: 1
Range 1: 575 to 1230

Score	Expect	Identities	Gaps	Strand	Frame
1212 bits(656)	0.0()	656/656(100%)	0/656(0%)	Plus/Plus	

Features:

```
Query  1    GAGTGAAGGAACATGGCTCTGAATCATGCCTGTCTGTCTCCCCAGGTCTGTGCTTAAAAC  60
Sbjct  575  ............................................................  634

Query  61   CACGAAGTTCAAGATGGAAACTGAAGGGAAGAGTGTCAAGGGGATGGGAGAGAGGACTTG  120
Sbjct  635  ............................................................  694

Query  121  TCCATGACTTTGGCAGCATAAGGAAAAAATACCCAGGGACAAGTGGCGACTTTGGAAACT  180
Sbjct  695  ............................................................  754

Query  181  CCATTCCTCTGCAAAATGACATCACGAGGAGAGTGGTGGGGCCTGCGGATGAAAAGATCT  240
Sbjct  755  ............................................................  814

Query  241  GGCTTCTCCTCCCAACTCTGCTATGAGGAAGCGCTGGATGGCCCTGTCGGCCGCGGTCAT  300
Sbjct  815  ............................................................  874

Query  301  CGCCGCCTCGGCCCGGGAGCTCAGCATTGCAGCCGCACCGGAGGCCTGAAACCGTCTCCT  360
Sbjct  875  ............................................................  934

Query  361  CCGCTAccgccgccgccgccgccgGACCGAGGGATACGACGGTTCCCGAAACAGCGGAAC  420
Sbjct  935  ............................................................  994
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Query  421   CTGCGGCCGCAGTCCCAGCACCTCGGGGGAACGTAGACCGCAGGACAGCTCCCAGGGGGA  480
Sbjct  995   ............................................................  1054

Query  481   CCGGAAGTAGCTGCCCCCGGAGAGCAATAGCTGACGGACCACGTCCTTTCTTTCTTTTCC  540
Sbjct  1055  ............................................................  1114

Query  541   CTTAGCAACAGGCCCCGGCGTCGGTTGCTACGCTGGGCTCAGTTGCCTGGGGCTGCTTGG  600
Sbjct  1115  ............................................................  1174

Query  601   TTTTCAGATTTGCTTAGGCTCCATTCATAAATACAGATGGCACACTTCTAGGATGG  656
Sbjct  1175  ......................................................  1230
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