NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARi79A03

Lot# : 7675_B5Hm

Vector : pGCAP10

Gene	IRAK1	
RefSeq_mRNA	NM_001025242.2	3491 bp

● Plasmid DNA purification

Date : 2025/08/21 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2025/08/22 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/08/22

DNA concentration (O.D.): 474 ng/ul

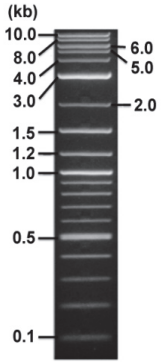
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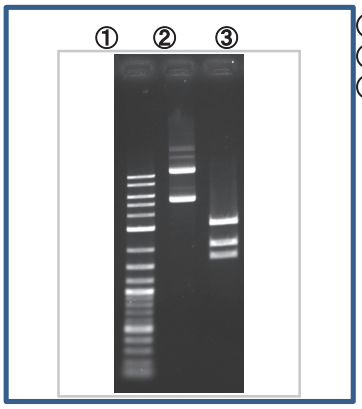
DNA	0.2	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.8	ul
Total	10	ul

BamHI 3.1kb (vector), 2.1, 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 : 2025/08/29

full sequence	ARi79A03hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/09/17

DNA (474 ng/ul)	84	ul
10x TE	159	ul
dH_2O	1,349	ul
Total	1,593	ul

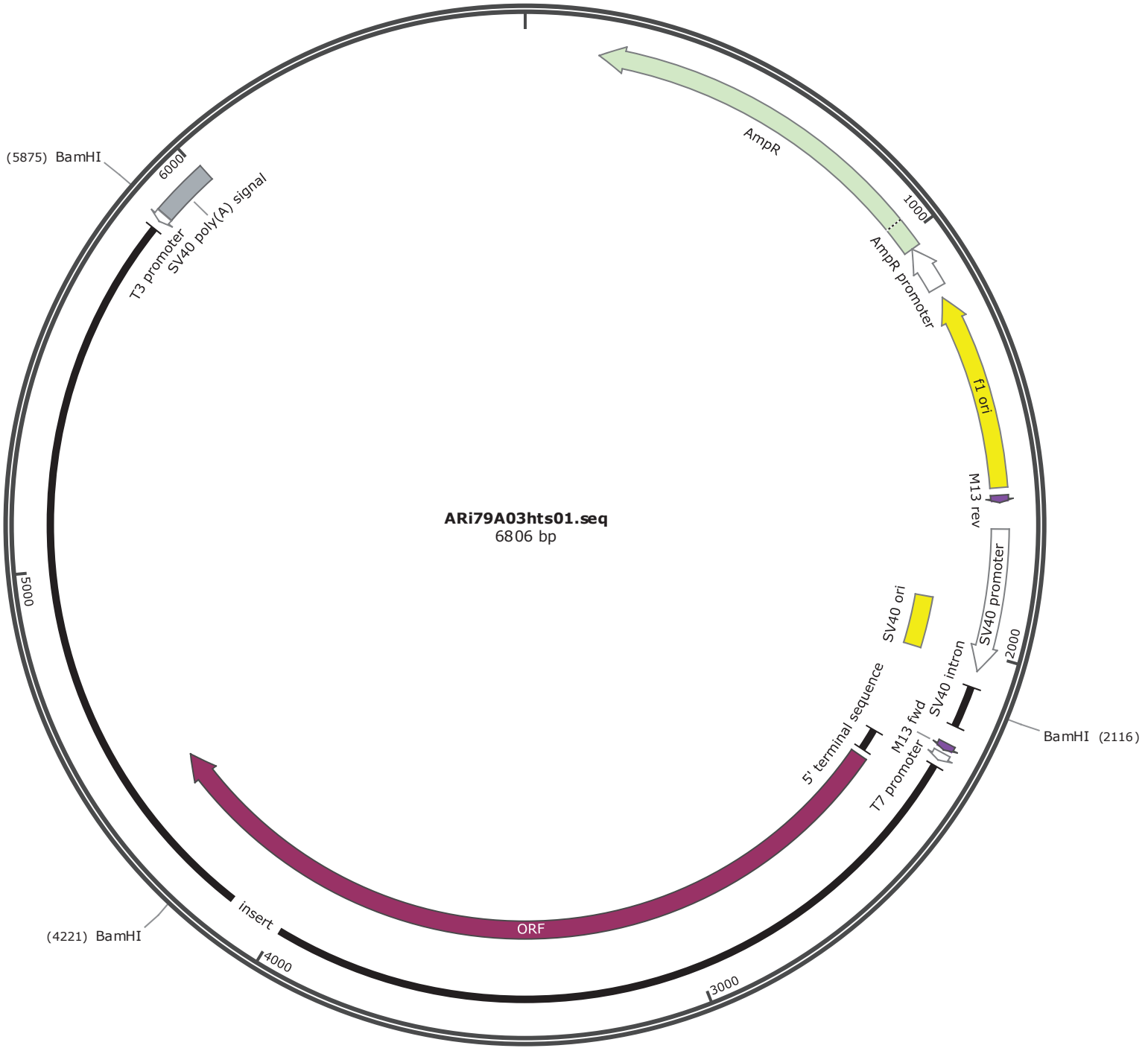
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '25.09.17 笹沼

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


ARi79A03hts01.seq
6806 bp
(5875) BamHI
6000
T3 promoter
SV40 poly(A) signal
AmpR
1000
AmpR promoter
f1 ori
M13 rev
SV40 promoter
2000
BamHI (2116)
SV40 ori
SV40 intron
M13 fwd
T7 promoter
5' terminal sequence
ORF
insert
(4221) BamHI
4000
3000
5000

BLAST Results

Questions/comments

Blast 2 sequences

Job title: XM_054327034:PREDICTED: Homo sapiens interleukin...

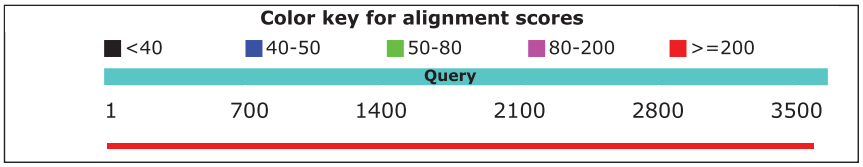
RID B2M6EB8D114 (Expires on 08-30 15:03 pm)

Query ID	XM_054327034.1	**Subject ID**	lcl|Query_5384923
Description	PREDICTED: Homo sapiens interleukin 1 receptor associated kinase 1 (IRAK1), transcript variant X1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	3536	**Subject Length**	6806
		Program	BLASTN 2.17.0+

ARi79A03hts01.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	6477	6477	100%	0.0	99.83%	Query_5384923

Alignments

Sequence ID: Query_5384923 Length: 6806 Number of Matches: 1
Range 1: 2279 to 5806

Score	Expect	Identities	Gaps	Strand	Frame
6477 bits(3507)	0.0()	3522/3528(99%)	6/3528(0%)	Plus/Plus	

Features:

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Query              15   ggacccggccggcccaggcccgcgcccgccgcggccctgagaggccccggcaggtcccgg  74
Sbjct              2279 ............................................................  2338

CDS:interleukin-1 re 1                    M  A  G  G  P  G  P  G  E  P  A  A  P  G  A
Query              75   cccggcggcggcagccatggccgggggccgggcccgggggagcccgcagcccccggcgc  134
Sbjct              2339 ............................................................  2398

CDS:interleukin-1 re 16     Q  H  F  L  Y  E  V  P  P  W  V  M  C  R  F  Y  K  V  M  D
Query              135  ccAGCACTTCTTGTACGAGGTGCCGCCCTGGGTCATGTGCCGCTTCTACAAAGTGATGGA  194
Sbjct              2399 ............................................................  2458

CDS:interleukin-1 re 36     A  L  E  P  A  D  W  C  Q  F  A  A  L  I  V  R  D  Q  T  E
Query              195  CGCCCTGGAGCCCGCCGACTGGTGCCAGTTCGCCGCCCTGATCGTGCGCGACCAGACCGA  254
Sbjct              2459 ............................................................  2518

CDS:interleukin-1 re 56     L  R  L  C  E  R  S  G  Q  R  T  A  S  V  L  W  P  W  I  N
Query              255  GCTGCGGCTGTGCGAGCGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAA  314
Sbjct              2519 ............................................................  2578

CDS:interleukin-1 re 76     R  N  A  R  V  A  D  L  V  H  I  L  T  H  L  Q  L  L  R  A
Query              315  CCGCAACGCCCGTGTGGCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGC  374
Sbjct              2579 ............................................................  2638
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Query                 375   GCGGGACATCATCACAGCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGC  434
Sbjct                 2639  ............................................................  2698

CDS:interleukin-1 re  116   P R P S S I P A P A E A E A W S P R K L
Query                 435   CCCGAGGCCCAGCAGCATCCCTGCACCCGCCGAGGCCGAGGCCTGGAGCCCCCGGAAGTT  494
Sbjct                 2699  ............................................................  2758

CDS:interleukin-1 re  136   P S S A S T F L S P A F P G S Q T H S G
Query                 495   GCCATCCTCAGCCTCCACCTTCCTCTCCCCAGCTTTTCCAGGCTCCCAGACCCATTCAGG  554
Sbjct                 2759  ............................................................  2818

CDS:interleukin-1 re  156   P E L G L V P S P A S L W P P P P S P A
Query                 555   GCCTGAGCTCGGCCTGGTTCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCAGC  614
Sbjct                 2819  ............................................................  2878

CDS:interleukin-1 re  176   P S S T K P G P E S S V S L L Q G A R P
Query                 615   CCCTTCTTCTACCAAGCCAGGCCCAGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGCCC  674
Sbjct                 2879  ............................................................  2938

CDS:interleukin-1 re  196   S P F C W P L C E I S R G T H N F S E E
Query                 675   CTCTCCGTTTTGCTGGCCCCTCTGTGAGATTTCCCGGGGCACCCACAACTTCTCGGAGGA  734
Sbjct                 2939  ............................................................  2998

CDS:interleukin-1 re  216   L K I G E G G F G C V Y R A V M R N T V
Query                 735   GCTCAAGATCGGGGAGGGTGGCTTTGGGTGCGTGTACCGGGCGGTGATGAGGAACACGGT  794
Sbjct                 2999  ............................................................  3058

CDS:interleukin-1 re  236   Y A V K R L K E N A D L E W T A V K Q S
Query                 795   GTATGCTGTGAAGAGGCTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAGAG  854
Sbjct                 3059  ............................................................  3118

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Query                 855   CTTCCTGACCGAGGTGGAGCAGCTGTCCAGGTTTCGTCACCCAAACATTGTGGACTTTGC  914
Sbjct                 3119  ............................................................  3178

CDS:interleukin-1 re  276   G Y C A Q N G F Y C L V Y G F L P N G S
Query                 915   TGGCTACTGTGCTCAGAACGGCTTCTACTGCCTGGTGTACGGCTTCCTGCCCAACGGCTC  974
Sbjct                 3179  ............................................................  3238

CDS:interleukin-1 re  296   L E D R L H C Q T Q A C P P L S W P Q R
Query                 975   CCTGGAGGACCGTCTCCACTGCCAGACCCAGGCCTGCCCACCTCTCTCCTGGCCTCAGCG  1034
Sbjct                 3239  ............................................................  3298

CDS:interleukin-1 re  316   L D I L L G T A R A I Q F L H Q D S P S
Query                 1035  ACTGGACATCCTTCTGGGTACAGCCCGGGCAATTCAGTTTCTACATCAGGACAGCCCCAG  1094
Sbjct                 3299  ............................................................  3358

CDS:interleukin-1 re  336   L I H G D I K S S N V L L D E R L T P K
Query                 1095  CCTCATCCATGGAGACATCAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCCAA  1154
Sbjct                 3359  ............................................................  3418

CDS:interleukin-1 re  356   L G D F G L A R F S R F A G S S P S Q S
Query                 1155  GCTGGGAGACTTTGGCCTGGCCCGGTTCAGCCGCTTTGCCGGGTCCAGCCCCAGCCAGAG  1214
Sbjct                 3419  ............................................................  3478

CDS:interleukin-1 re  376   S M V A R T Q T V R G T L A Y L P E E Y
Query                 1215  CAGCATGGTGGCCCGGACACAGACAGTGCGGGGCACCCTGGCCTACCTGCCCGAGGAGTA  1274
Sbjct                 3479  ............................................................  3538
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CDS:interleukin-1 re  396   I K T G R L A V D T D T F S F G V V V L
Query                 1275  CATCAAGACGGGAAGGCTGGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTGCT  1334
Sbjct                 3539  ............................................................  3598

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Query                 1335  AGAGACCTTGGCTGGTCAGAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTGAA  1394
Sbjct                 3599  ............................................................  3658

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Query                 1395  AGACCTGGTGGAAGAGGAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAGCAC  1454
Sbjct                 3659  ............................................................  3718

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Query                 1455  ACTGCAAGCAGGTCTGGCTGCAGATGCCTGGGCTGCTCCCATCGCCATGCAGATCTACAA  1514
Sbjct                 3719  ............................................................  3778

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Sbjct                 3779  ......CCTGGG............................................  3838
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1520_1521 ins 6bp

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Query                 1569  GCCTCCTATGACCCAGGTGTACGAGAGGCTAGAGAAGCTGCAGGCAGTGGTGGCGGGGGT  1628
Sbjct                 3839  ............................................................  3898

CDS:interleukin-1 re  514   P G H L E A A S C I P P S P Q E N S Y V
Query                 1629  GCCCGGGCATTTGGAGGCCGCCAGCTGCATCCCCCCTTCCCCGCAGGAGAACTCCTACGT  1688
Sbjct                 3899  ............................................................  3958

CDS:interleukin-1 re  534   S S T G R A H S G A A P W Q P L A A P S
Query                 1689  GTCCAGCACTGGCAGAGCCCACAGTGGGGCTGCTCCATGGCAGCCCCTGGCAGCGCCATC  1748
Sbjct                 3959  ............................................................  4018

CDS:interleukin-1 re  554   G A S A Q A A E Q L Q R G P N Q P V E S
Query                 1749  AGGAGCCAGTGCCCAGGCAGCAGAGCAGCTGCAGAGAGGCCCCAACCAGCCCGTGGAGAG  1808
Sbjct                 4019  ............................................................  4078

CDS:interleukin-1 re  574   D E S L G G L S A A L R S W H L T P S C
Query                 1809  TGACGAGAGCCTAGGCGGCCTCTCTGCTGCCCTGCGCTCCTGGCACTTGACTCCAAGCTG  1868
Sbjct                 4079  ............................................................  4138

CDS:interleukin-1 re  594   P L D P A P L R E A G C P Q G D T A G E
Query                 1869  CCCTCTGGACCCAGCACCCCTCAGGGAGGCCGGCTGTCCTCAGGGGGACACGGCAGGAGA  1928
Sbjct                 4139  ............................................................  4198

CDS:interleukin-1 re  614   S S W G S G P G S R P T A V E G L A L G
Query                 1929  ATCGAGCTGGGGGAGTGGCCCAGGATCCCGGCCCACAGCCGTGGAAGGACTGGCCCTTGG  1988
Sbjct                 4199  ............................................................  4258

CDS:interleukin-1 re  634   S S A S S S S E P P Q I I I N P A R Q K
Query                 1989  CAGCTCTGCATCATCGTCGTCAGAGCCACCGCAGATTATCATCAACCCTGCCCGACAGAA  2048
Sbjct                 4259  ............................................................  4318

CDS:interleukin-1 re  654   M V Q K L A L Y E D G A L D S L Q L L S
Query                 2049  GATGGTCCAGAAGCTGGCCCTGTACGAGGATGGGGCCCTGGACAGCCTGCAGCTGCTGTC  2108
Sbjct                 4319  ............................................................  4378

CDS:interleukin-1 re  674   S S S L P G L G L E Q D R Q G P E E S D
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Query                2229 TCATGGTCAGAAGTTCTCATGGTGCACGAGTCCTCAGCACTCTGCCGGCAGTGGGGGTGG  2288
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