NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : ARi06E08

Lot# : 7675_B6Jj

Vector : pGCAP10

Gene	CHKA	
RefSeq_mRNA	NM_212469.2	2660 bp

● Plasmid DNA purification

Date : 2026/10/19 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2026/10/20 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2026/10/20

DNA concentration (O.D.): 306 ng/ul

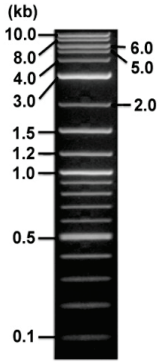
DNA	0.33 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.67 ul
Total	10 ul

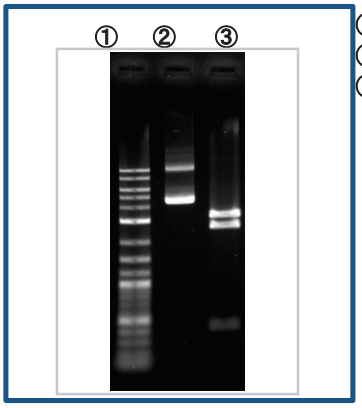
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.5, 0.4 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 : 2026/10/27

full sequence	ARi06E08hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/10/30

DNA (306 ng/ul)	84 ul
10x TE	103 ul
dH_2O	841 ul
Total	1,028 ul

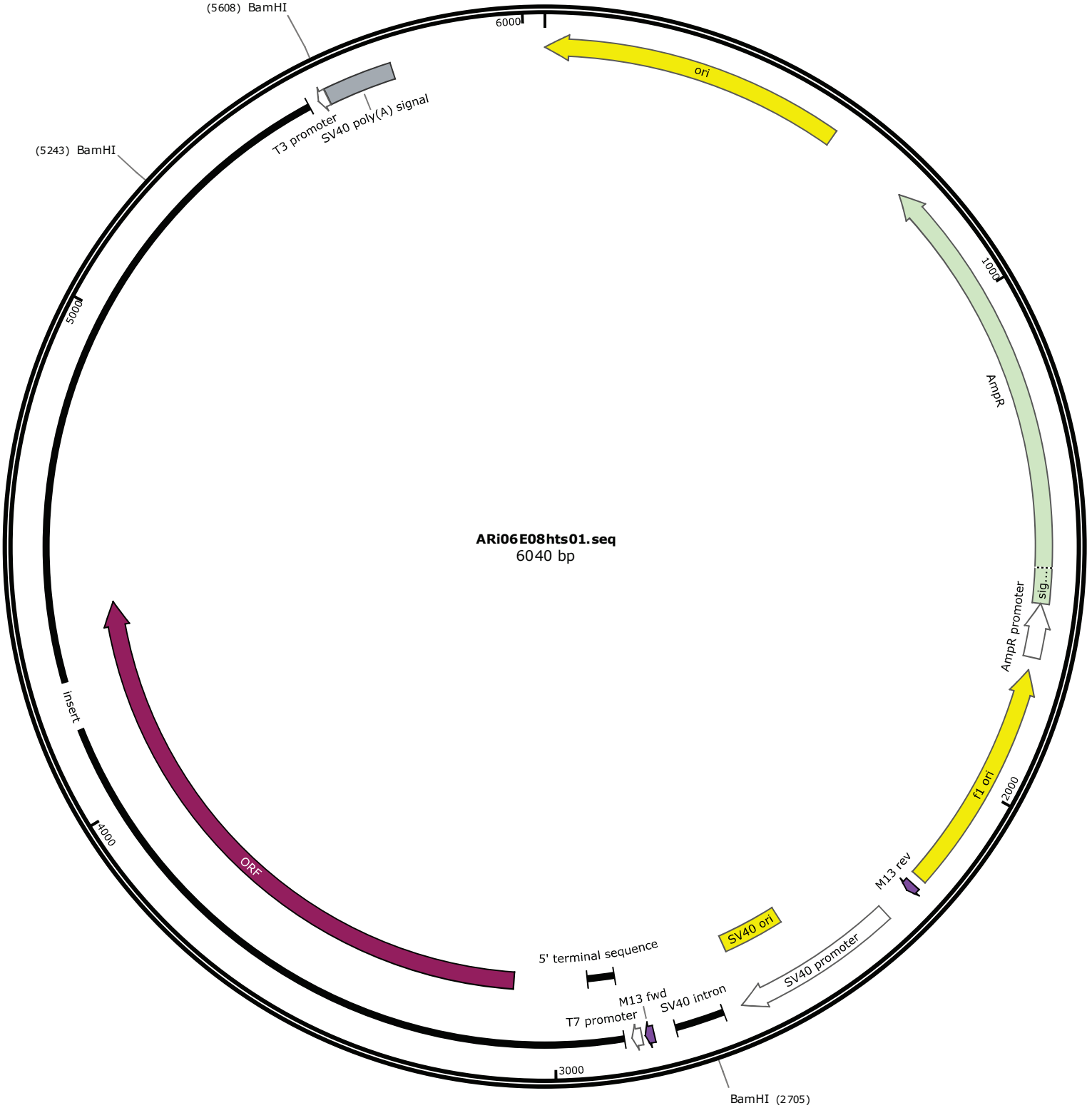
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '26.10.30 笹沼

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


(5608) BamHI
6000
ori
T3 promoter
SV40 poly(A) signal
(5243) BamHI
5000
1000
AmpR
sig...
AmpR promoter
ARi06E08hts01.seq
6040 bp
insert
4000
ORF
f1 ori
2000
M13 rev
SV40 ori
SV40 promoter
5' terminal sequence
M13 fwd
SV40 intron
T7 promoter
3000
BamHI (2705)

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_001277:Homo sapiens choline kinase alpha...

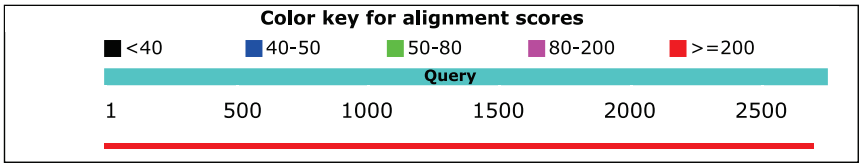
RID E09UTKDZ114 (Expires on 10-28 12:23 pm)

Query ID	NM_212469.2	**Subject ID**	lcl|Query_3604921
Description	Homo sapiens choline kinase alpha (CHKA), transcript variant 2, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	2660	**Subject Length**	6040
		Program	BLASTN 2.17.0+

ARi06E08hts01.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	4865	4865	100%	0.0	99.63%	Query_3604921

Alignments

Sequence ID: Query_3604921 Length: 6040 Number of Matches: 1
Range 1: 2869 to 5537

Score	Expect	Identities	Gaps	Strand	Frame
4865 bits(2634)	0.0()	2659/2669(99%)	9/2669(0%)	Plus/Plus	

Features:

```
Query          1     AGAGGAGCGAGTGCAGCGGCCAGCAGCACATCCCCGCTCCA---------CAGTcgccgc  51
Sbjct          2869  ..........................................CAGTCGCCG.........  2928

Query          52    agtcgccgcagccgccgccgccccgcgcgcccaaccgccgcggccccctgccccgcc  111
Sbjct          2929  ..........................................................  2988

Query          112   ggcctgccAGTGAGAGAGCGGCGAGGGGGCGCCCGGCCGGACTCTGAGCCTAGTCCTCTC  171
Sbjct          2989  ..........................................................  3048

CDS:choline k  1                                                  M  K  T  K  F  C  T
Query          172   GCGCTGCGGCCGCCCGCGCCTCCTCGGCCGCCTGTCGGGCATGAAAACCAAATTCTGCAC  231
Sbjct          3049  ..........................................................  3108

CDS:choline k  8        G  G  E  A  E  P  S  P  L  G  L  L  L  S  C  G  S  G  S  A
Query          232   CGGGGGCGAGGCGGAGCCCTCGCCGCTCGGGCTGCTGCTGAGCTGCGGTAGCGGCAGCGC  291
Sbjct          3109  ..........................................................  3168

CDS:choline k  28       A  P  A  P  G  V  G  Q  Q  R  D  A  A  S  D  L  E  S  K  Q
Query          292   GGCCCCGGCGCCCGGCGTGGGGCAGCAGCGCGACGCCGCCAGCGACCTCGAGTCCAAGCA  351
Sbjct          3169  ..........................................................  3228
```

```
CDS:choline kinase a  48    L  G  G  Q  Q  P  P  L  A  L  P  P  P  P  P  L  P  L  P  L
Query                 352   GCTGGGCGGCCAACAgccgccgctcgcgctgccccctccgccgccgctgccgctgccgct  411
Sbjct                 3229  ............................................................  3288

CDS:choline kinase a  68    P  L  P  Q  P  P  P  P  Q  P  P  A  D  E  Q  P  E  P  R  T
Query                 412   gccgctgccccagccccgccgccgcagccgcccgcagacgagcagccggagccccggac  471
Sbjct                 3289  ............................................................  3348

CDS:choline kinase a  88    R  R  R  A  Y  L  W  C  K  E  F  L  P  G  A  W  R  G  L  R
Query                 472   gcggcgcagGGCCTATCTGTGGTGCAAGGAGTTCCTGCCCGGCGCCTGGCGGGGCCTCCG  531
Sbjct                 3349  ............................................................  3408

CDS:choline kinase a  108   E  D  E  F  H  I  S  V  I  R  G  G  L  S  N  M  L  F  Q  C
Query                 532   CGAGGACGAGTTCCACATCAGTGTCATCAGAGGCGGCCTTAGCAACATGCTGTTCCAGTG  591
Sbjct                 3409  ............................................................  3468

CDS:choline kinase a  128   S  L  P  D  T  T  A  T  L  G  D  E  P  R  K  V  L  L  R  L
Query                 592   CTCCCTACCTGACACCACAGCCACCCTTGGTGATGAGCCTCGGAAAGTGCTCCTGCGGCT  651
Sbjct                 3469  ............................................................  3528

CDS:choline kinase a  148   Y  G  A  I  L  Q  M  G  A  E  A  M  V  L  E  S  V  M  F  A
Query                 652   GTATGGAGCGATTTTGCAGATGGGGGCTGAGGCCATGGTTCTGGAGAGCGTTATGTTTGC  711
Sbjct                 3529  ............................................................  3588

CDS:choline kinase a  168   I  L  A  E  R  S  L  G  P  K  L  Y  G  I  F  P  Q  G  R  L
Query                 712   CATTCTCGCAGAGAGGTCACTTGGGCCAAAACTCTATGGCATCTTTCCCCAAGGCCGACT  771
Sbjct                 3589  ............................................................  3648

CDS:choline kinase a  188   E  Q  F  I  P  S  R  R  L  D  T  E  E  L  S  L  P  D  I  S
Query                 772   GGAGCAGTTCATCCCGAGCCGGCGATTAGATACTGAAGAATTAAGTTTGCCAGATATTTC  831
Sbjct                 3649  ............................................................  3708

CDS:choline kinase a  208   A  E  I  A  E  K  M  A  T  F  H  G  M  K  M  P  F  N  K  E
Query                 832   TGCAGAAATCGCCGAGAAAATGGCTACATTTCATGGTATGAAAATGCCATTCAATAAGGA  891
Sbjct                 3709  ............................................................  3768

CDS:choline kinase a  228   P  K  W  L  F  G  T  M  E  K  Y  L  K  E  V  L  R  I  K  F
Query                 892   ACCAAAATGGCTTTTTGGCACAATGGAAAAGTATCTAAAGGAAGTGCTGAGAATTAAATT  951
Sbjct                 3769  ............................................................  3828

CDS:choline kinase a  248   T  E  E  S  R  I  K  K  L  H  K  L  L  S  Y  N  L  P  L  E
Query                 952   TACTGAGGAATCCAGAATTAAAAAGCTCCACAAATTGCTCAGTTACAATCTGCCCTTGGA  1011
Sbjct                 3829  ............................................................  3888

CDS:choline kinase a  268   L  E  N  L  R  S  L  L  E  S  T  P  S  P  V  V  F  C  H  N
Query                 1012  ACTGGAAAACCTGAGATCATTGCTTGAATCTACTCCATCTCCAGTTGTATTTTGTCATAA  1071
Sbjct                 3889  ............................................................  3948

CDS:choline kinase a  288   D  C  Q  E  G  N  I  L  L  L  E  G  R  E  N  S  E  K  Q  K
Query                 1072  TGACTGTCAAGAAGGTAATATCTTGTTGCTGGAAGGCCGAGAGAATTCTGAAAAACAGAA  1131
Sbjct                 3949  ............................................................  4008

CDS:choline kinase a  308   L  M  L  I  D  F  E  Y  S  S  Y  N  Y  R  G  F  D  I  G  N
Query                 1132  ACTGATGCTCATTGATTTCGAATACAGCAGTTACAATTACAGGGGATTCGACATTGGAAA  1191
Sbjct                 4009  ............................................................  4068

CDS:choline kinase a  328   H  F  C  E  W  M  Y  D  Y  S  Y  E  K  Y  P  F  F  R  A  N
Query                 1192  TCACTTCTGTGAGTGGATGTATGATTATAGCTATGAAAAATACCCTTTTTTCAGAGCAAA  1251
Sbjct                 4069  ............................................................  4128
```

```
CDS:choline kinase a  348   I  R  K  Y  P  T  K  K  Q  Q  L  H  F  I  S  S  Y  L  P  A
Query                 1252  CATCCGGAAGTATCCCACCAAGAAACAACAGCTCCATTTTATTTCCAGTTACTTGCCTGC  1311
Sbjct                 4129  ............................................................  4188

CDS:choline kinase a  368   F  Q  N  D  F  E  N  L  S  T  E  E  K  S  I  I  K  E  E  M
Query                 1312  ATTCCAAAATGACTTTGAAAACCTCAGTACTGAAGAAAAATCCATTATAAAAGAAGAAAT  1371
Sbjct                 4189  ............................................................  4248

CDS:choline kinase a  388   L  L  E  V  N  R  F  A  L  A  S  H  F  L  W  G  L  W  S  I
Query                 1372  GTTGCTTGAAGTTAATAGGTTTGCCCTTGCATCTCATTTCCTCTGGGGACTGTGGTCCAT  1431
Sbjct                 4249  ............................................................  4308

CDS:choline kinase a  408   V  Q  A  K  I  S  S  I  E  F  G  Y  M  D  Y  A  Q  A  R  F
Query                 1432  TGTACAAGCCAAGATTTCATCTATTGAATTTGGGTACATGGACTACGCCCAAGCAAGGTT  1491
Sbjct                 4309  ............................................................  4368

CDS:choline kinase a  428   D  A  Y  F  H  Q  K  R  K  L  G  V
Query                 1492  TGATGCCTATTTCCACCAGAAGAGGAAGCTTGGGGTGTGACTGTGGGGAGGACTCCATCC  1551
Sbjct                 4369  ............................................................  4428

Query                 1552  ACCTCATCACTGGACTGCATGGGGAGGCAGCAGAGCGGGGTCCCCTCTGTGCTTCGACTA  1611
Sbjct                 4429  ............................................................  4488

Query                 1612  CTGCTCCTGTGGCAGGAGGCTTTGGGTGGCTCACTACTGAACACATGTGTATGATACTAA  1671
Sbjct                 4489  ............................................................  4548

Query                 1672  AGACGGTATTAAAATGGAGCGACGTTTATTTCATCTCTTGTTTACGATTTCACTAGGACT  1731
Sbjct                 4549  ............................................................  4608

Query                 1732  CAGAAACGAGATCGGGAAGCAGAAATATAGTGCAATAGTGCAACATCTCTGAATCCTTTT  1791
Sbjct                 4609  ............................................................  4668

Query                 1792  AATCTAGAGAAGGCATTTCATATTTGGGGGCTAAGGTTTCCAGTCAGATGAGGCAAACAG  1851
Sbjct                 4669  ............................................................  4728

Query                 1852  CAAGAGTAAGCAGTGTTACTTGCAGGTACTTTGGTTAATGTTGATTTAAATTTTCATGAA  1911
Sbjct                 4729  ............................................................  4788

Query                 1912  TGTGCTGGTGAACACTGTGACCAGGCTTTTGTAGATGGCGATGTGTTATAGACGGTGCTC  1971
Sbjct                 4789  ............................................................  4848

Query                 1972  ACTCCCAAGGGACAGCAAGTGAGCAGAGATGTACTGCAAAGTCGCCAGTCACTGCTGCAA  2031
Sbjct                 4849  ............................................................  4908

Query                 2032  GGTGGCCTCTGCCTGGGGCCTCCAGAAGCTGCTCCTTTACCCTCTTGGTCCCATGGCTGA  2091
Sbjct                 4909  ............................................................  4968

Query                 2092  AGCTGGAGCAGCGGATTGCTCTGGAGCAGCCAAGGCCGCCAGCGTGTGGAGCAGAGCTCT  2151
Sbjct                 4969  ............................................................  5028

Query                 2152  CCCCTCCTGCTGGGCGTGTGTGACACTGATGAGTTTCACTGTACTGCATGTGACTTCTCC  2211
Sbjct                 5029  ............................................................  5088

Query                 2212  CCTGCCCTTCCTCCTGATGGAGTGTGCAGACAGCCATGCGTGGCCACGGGGGCAGTGTGA  2271
Sbjct                 5089  ............................................................  5148

Query                 2272  GGACCTCCCTGTCTCCCGGCTCCCCTCCCAGGGGAGCCAGCTGCTTGACCTAGCTCTTTG  2331
Sbjct                 5149  ............................................................  5208
```

```
Query  2332  GGCCTCTCCTGCCCTCTGCTCTGCCTGGAGTGTCGGATCCTGTGAGTAGGCTGGGCCTCC  2391
Sbjct  5209  ............................................................  5268

Query  2392  CCTGGGCAGGGTTCTCCAAGGGCCCGGTTTCCCGGCCCTTACCTTTCCTGATGCCCCTGA  2451
Sbjct  5269  ............................................................  5328

Query  2452  CATCATCATTCTTGTGGGAGACAGCAGCCTGTATGTGGTGTGGGGCGTGGATCGAGTGTA  2511
Sbjct  5329  ............................................................  5388

Query  2512  GCTGTGAAATCCATATATATGAAATGTCCTGCGGGATACAGTCTTAGCTGACtttttttt  2571
Sbjct  5389  ............................................................  5448

Query  2572  ACTCTGAACTCTTATTTGAATTGTTTTTTGTGCATATATTTCTGCTACCACAGAGATTGT  2631
Sbjct  5449  ............................................................  5508

Query  2632  ACTATACAAATaaaaaaaataaaaaCCCAA  2660
Sbjct  5509  ..................T.........  5537
```



BLAST is a registered trademark of the National Library of Medicine

NCBI

National Center for Biotechnology Information, U.S. National Library of Medicine 8600 Rockville Pike, Bethesda MD, 20894 USA

Policies and Guidelines | Contact

NIH Websites Are Changing

- Get the Latest Updates and FAQs on the transition
- Per Executive Order 14434, federal agencies are now using "Super Intelligence" (SI) in place of "Artificial Intelligence" (AI). You may see both terms across NIH content during this transition.

HHS Vulnerability Disclosure