2-8

NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

**RIKEN_Clone_ID : ARe60A01**
Vector : pKA1U5

Lot# : 7672_B3Bd

| | | |
|---|---|---|
| Gene | PPP1R3G | |
| RefSeq_mRNA | NM_001145115.3 | 4147 bp |

● **Plasmid DNA purification**

Date : 23.02.20 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.02.21 Purification : QIAGEN Miniprep kit -> $dH_2O$ 100 ul

● **Digestion by restriction enzyme/Concentrarion calibration**

Date : 23.02.21

DNA concentration (O.D.): 209 ng/ul

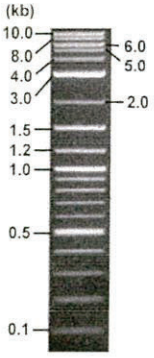
| | |
|---|---|
| DNA | 0.5 ul |
| Enzyme (BamHI ) | 1 ul |
| Buffer H | 1 ul |
| $dH_2O$ | 7.5 ul |
| Total | 10 ul |

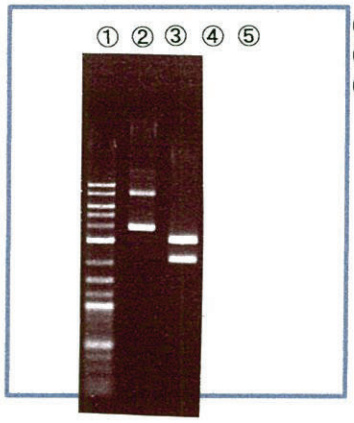
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.2 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 : ARe60A01hts01.seq

● **Adjust plasmid DNA solution to 25 ng/ul**

Date : 2026/07/23

| | |
|---|---|
| DNA (209 ng/ul) | 78 ul |
| 10x TE | 65 ul |
| $dH_2O$ | 509 ul |
| Total | 652 ul |

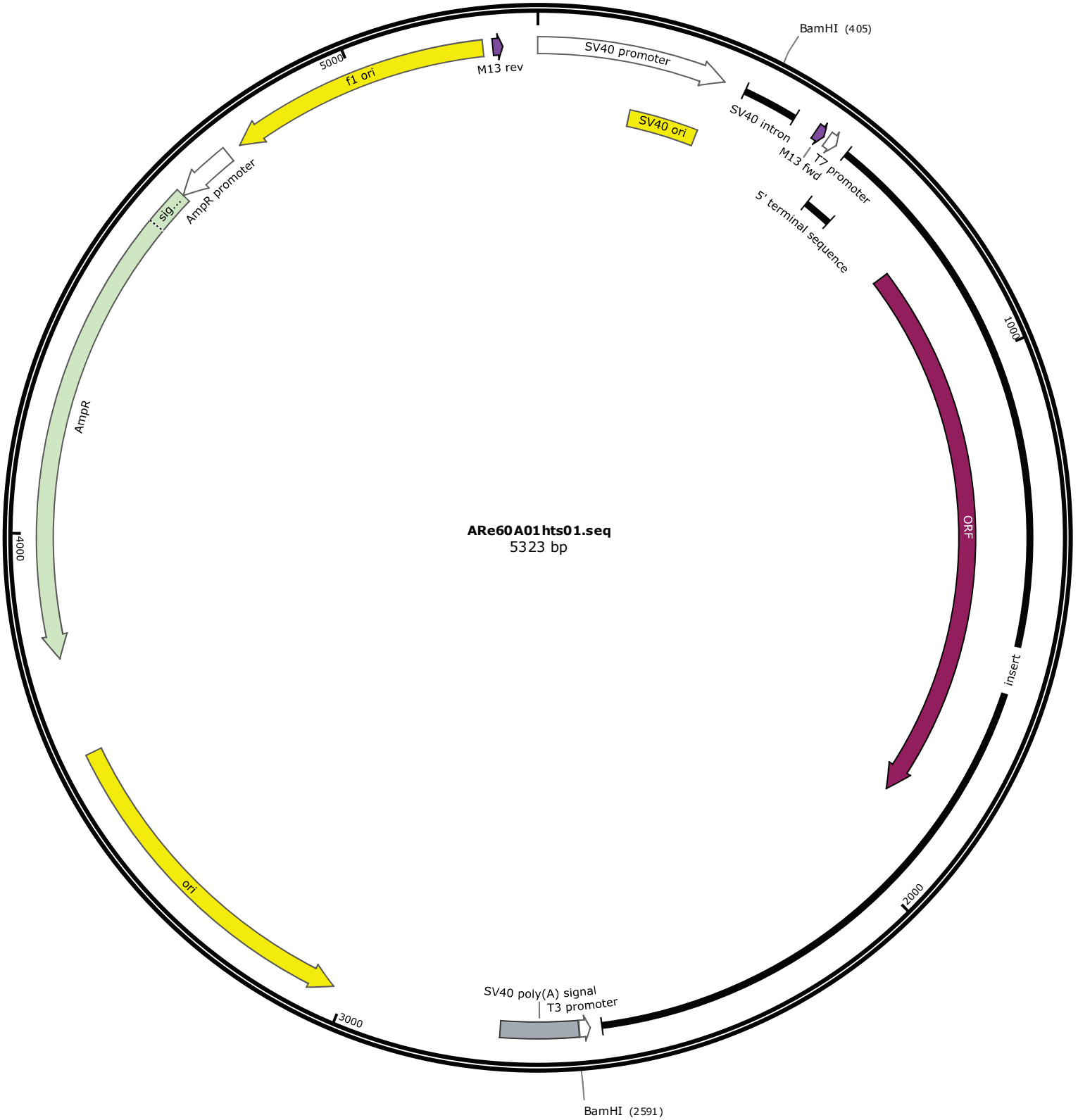
● **Shipping**

☑ 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


BamHI (405)
SV40 promoter
M13 rev
5000
f1 ori
SV40 ori
SV40 intron
M13 fwd
T7 promoter
5' terminal sequence
AmpR promoter
sig...
AmpR
ORF
1000
insert
4000
ARe60A01hts01.seq
5323 bp
ori
2000
SV40 poly(A) signal
T3 promoter
3000
BamHI (2591)

**BLAST Results**

Questions/comments

**Blast 2 sequences**

**Job title: NM_001410779:Homo sapiens shroom family member...**

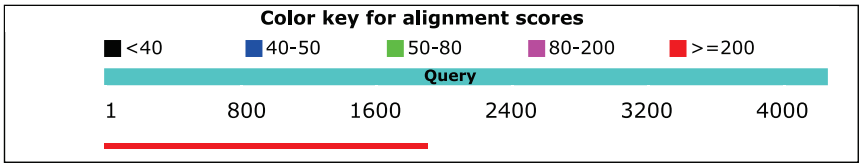
**RID** 34CVN54U114 (Expires on 06-18 13:41 pm)

| | | | |
|---|---|---|---|
| **Query ID** | NM_001145115.3 | **Subject ID** | lcl\|Query_4130615 |
| **Description** | Homo sapiens protein phosphatase 1 regulatory subunit 3G (PPP1R3G), mRNA | **Description** | None<br>See details |
| **Molecule type** | nucleic acid | **Molecule type** | dna |
| **Query Length** | 4147 | **Subject Length** | 5323 |
| | | **Program** | BLASTN 2.17.0+ |

ARe60A01hts01.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 | 3458 | 3458 | 45% | 0.0 | 99.84% | Query_4130615 |

## Alignments

Sequence ID: Query_4130615 Length: 5323 Number of Matches: 1
Range 1: 638 to 2518

| Score | Expect | Identities | Gaps | Strand | Frame |
|---|---|---|---|---|---|
| 3458 bits(1872) | 0.0() | 1878/1881(99%) | 0/1881(0%) | Plus/Plus | |

Features:

```
Query              1    CGTTGTCTTGTCGAGCCTGGGGCGACTCGCCTCGGGGAGGGCGAGCCTGAACTGCAGCCC  60
Sbjct            638    ............................................................  697

Query             61    TGCGCTCCTTCCACGGCCCGAGGAGTTAGTTAAGTCTCCAGAGGGGCCCGGTTCGGCCCG  120
Sbjct            698    ............................................................  757

CDS:protein phosphat  1                                 M  E  P  I  G  A  R  L  S  L  E  A
Query            121    AGCAAGTCCAGGGGCGAACGGCGTCATGGAGCCCATAGGGGCGCGGCTAAGTTTGGAGGC  180
Sbjct            758    ............................................................  817

CDS:protein phosphat  13     P  G  P  A  P  F  R  E  A  P  P  A  E  E  L  P  A  P  V  V
Query            181    GCCGGGACCAGCGCCCTTCCGAGAGGCCCCGCCGGCCGAGGAGCTGCCCGCCCCGGTGGT  240
Sbjct            818    ............................................................  877

CDS:protein phosphat  33     P  C  V  Q  G  G  G  D  G  G  G  A  S  E  T  P  S  P  D  A
Query            241    CCCCTGTGTGCAGGGTGGCGGCGACGGCGGTGGCGCTTCGGAGACCCCGAGTCCTGACGC  300
Sbjct            878    ............................................................  937

CDS:protein phosphat  53     Q  L  G  D  R  P  L  S  P  K  E  E  A  A  P  Q  E  Q  E  E
Query            301    TCAGCTAGGGGATAGGCCCCTGTCCCCGAAGGAAGAGGCCGCCCCCCAGGAGCAGGAGGA  360
Sbjct            938    ............................................................  997
```

```
CDS:protein phosphat  73    L  L  E  C  R  R  R  C  R  A  R  S  F  S  L  P  A  D  P  I
Query                 361   GCTGCTGGAATGCCGCCGCCGCTGCCGCGCGCGCTCCTTTTCCTTGCCCGCCGACCCCAT  420
Sbjct                 998   ............................................................  1057

CDS:protein phosphat  93    L  Q  A  A  K  F  L  Q  Q  Q  Q  Q  Q  A  V  A  L  G  G  E
Query                 421   CTTGCAGGCGGCCAAGTTCCTGCAGCAGCAGCAGCAACAGGCGGTGGCACTGGGCGGCGA  480
Sbjct                 1058  ............................................................  1117

CDS:protein phosphat  113   G  A  E  D  A  Q  L  G  P  G  G  C  C  A  K  C  K  K  R  V
Query                 481   GGGGGCGGAGGACGCACAGCTCGGCCCGGGCGGCTGCTGCGCCAAGTGCAAGAAGCGGGT  540   496 A>G
Sbjct                 1118  .............G..............................................  1177

CDS:protein phosphat  133   Q  F  A  D  T  L  G  L  S  L  A  S  V  K  H  F  S  E  A  E
Query                 541   GCAGTTCGCGGACACGCTGGGGCTAAGCCTGGCCAGCGTGAAGCACTTCAGCGAGGCGGA  600
Sbjct                 1178  ............................................................  1237

CDS:protein phosphat  153   E  P  Q  V  P  P  A  V  L  S  R  L  R  S  F  P  M  R  A  E
Query                 601   GGAGCCGCAGGTGCCGCCCGCCGTGCTCTCGCGCCTCCGAAGCTTCCCTATGCGTGCCGA  660
Sbjct                 1238  ............................................................  1297

CDS:protein phosphat  173   D  L  E  Q  L  G  G  L  L  A  A  A  A  V  A  A  P  L  S  A
Query                 661   GGACCTGGAGCAGCTCGGGGGGCTGCTGGCCGCGGCGGCAGTGGCCGCGCCCCTTTCAGC  720
Sbjct                 1298  ............................................................  1357

CDS:protein phosphat  193   P  P  S  R  L  R  P  L  F  Q  L  P  G  P  S  A  A  A  E  R
Query                 721   GCCGCCTTCCCGGCTCCGGCCGCTCTTCCAGCTCCCGGGGCCGAGCGCCGCGGCCGAGCG  780
Sbjct                 1358  ............................................................  1417

CDS:protein phosphat  213   L  Q  R  Q  R  V  C  L  E  R  V  Q  C  S  T  A  S  G  A  E
Query                 781   TCTGCAGCGGCAGCGCGTGTGCCTGGAGCGCGTGCAGTGCTCGACGGCCTCGGGCGCTGA  840
Sbjct                 1418  ............................................................  1477

CDS:protein phosphat  233   V  K  G  S  G  R  V  L  S  C  P  G  P  R  A  V  T  V  R  Y
Query                 841   GGTGAAGGGCTCCGGCCGGGTGCTCAGCTGCCCTGGGCCCAGGGCCGTGACCGTGCGCTA  900
Sbjct                 1478  ............................................................  1537

CDS:protein phosphat  253   T  F  T  E  W  R  S  F  L  D  V  P  A  E  L  Q  P  E  P  L
Query                 901   CACCTTTACCGAGTGGCGCTCCTTCCTGGACGTGCCGGCTGAGCTGCAGCCCGAGCCGCT  960
Sbjct                 1538  ............................................................  1597

CDS:protein phosphat  273   E  P  Q  Q  P  E  A  P  S  G  A  S  E  P  G  S  G  D  A  K
Query                 961   GGAGCCACAGCAGCCAGAGGCACCGTCTGGGGCCTCCGAGCCAGGGTCCGGGGATGCCAA  1020  984 C>A (P280Q)
Sbjct                 1598  ..........A.................................................  1657

CDS:protein phosphat  293   K  E  P  G  A  E  C  F  H  F  S  L  C  L  P  P  G  L  Q  P
Query                 1021  GAAAGAGCCAGGCGCCGAGTGCTTCCACTTCTCGCTGTGCCTGCCCCCGGGCCTGCAGCC  1080
Sbjct                 1658  ............................................................  1717

CDS:protein phosphat  313   E  D  E  E  D  A  D  E  R  G  V  A  V  H  F  A  V  C  Y  R
Query                 1081  TGAGGACGAAGAGGACGCCGACGAGCGCGGCGTCGCGGTCCACTTCGCTGTCTGCTACCG  1140
Sbjct                 1718  ............................................................  1777

CDS:protein phosphat  333   C  A  Q  G  E  Y  W  D  N  N  A  G  A  N  Y  T  L  R  Y  A
Query                 1141  CTGCGCGCAGGGCGAGTACTGGGACAACAACGCGGGCGCCAACTACACGCTGCGCTACGC  1200
Sbjct                 1778  ............................................................  1837

CDS:protein phosphat  353   R  P  A  D  A  L
Query                 1201  GCGCCCTGCGGACGCGCTCTGAGCCTGGAGAGTTTCGAAGAGCCGTGGGGCGGGGTTGAT  1260

Sbjct                 1838  ............................................................  1897

Query                 1261  TAGCACGTGGAGCTCGGGCTGCCGCCTCAAGGAACTTGCTGGGACGCTTTGCTGAGCGTG  1320
Sbjct                 1898  ............................................................  1957

Query                 1321  GCGAGTCTGGCGTGAGGGGCGCGTGGAGGGAAAGGAGGGAGACTTTGAACCGTCGACTCG  1380
Sbjct                 1958  ............................................................  2017

Query                 1381  CACCCCCGCAGACAAGTGAGCGAGCTTAGAGAGCCCGGGCAATGCTCCGAAAGCCTCTGA  1440
Sbjct                 2018  ............................................................  2077

Query                 1441  CCTCAGTCTTCTCGTCCGTTTGACCTTCCTACAAGGCCTCTAGAATTCCCAGCCTGCGTC  1500
Sbjct                 2078  ............................................................  2137

Query                 1501  AGAATAGGAAGAAACTTCCAAGGCCCGGAGCAGCTGCCTCCAAGAAAAAGGCTCCCAACT  1560
Sbjct                 2138  ...G........................................................  2197

Query                 1561  CCCGGGCATGGTTCTAAGGCCTTGGGATTGGTTTTTAACTCTAAATATCATATTGTAGCC  1620
Sbjct                 2198  ............................................................  2257

Query                 1621  CTTGCAGTTTGCTGGAGACCCCTAGGGAAAGAACAAAGCGTCCTGCCACGGTGCACCAGA  1680
Sbjct                 2258  ............................................................  2317

Query                 1681  GGAAGGTGCCACGGACTGTGGGTGCACGCGTGGGACCTTTACACCCCAACCTATTTCTCA  1740
Sbjct                 2318  ............................................................  2377

Query                 1741  GAGAAAACCCTTCGGGGCTGGGCCAGGCCACCCTTTTCTTTTGACTGAGATGTGGGTAAT  1800
Sbjct                 2378  ............................................................  2437

Query                 1801  GTGTGCCCAGACTTGACGTTGTTTATTGTGCGACATTGTGTACAAATGTCCTTTATAAAA  1860
Sbjct                 2438  ............................................................  2497

Query                 1861  GTAAAGGCCACTCGCACCCCC  1881
Sbjct                 2498  .....................  2518
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