NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

**RIKEN_Clone_ID : ARi20G08**
Vector : pGCAP10

Lot# : 7675_B3Bd

| | | |
|---|---|---|
| Gene | PPP4R1L | |
| RefSeq_mRNA | NR_003505.3 | 2398 bp |

## ● Plasmid DNA purification

Date : 23.02.21 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.02.22 Purification : QIAGEN Miniprep kit -> $dH_2O$ 100 ul

## ● Digestion by restriction enzyme/Concentrarion calibration

Date : 23.02.22

DNA concentration (O.D.): 260 ng/ul

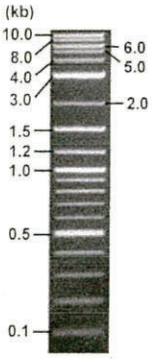
| | |
|---|---|
| DNA | 0.4 ul |
| Enzyme (BamHI ) | 1 ul |
| Buffer H | 1 ul |
| $dH_2O$ | 7.6 ul |
| Total | 10 ul |

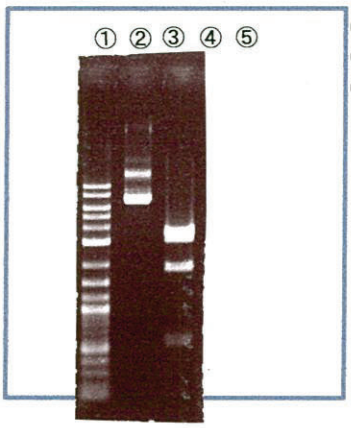
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 3.5, 1.9, 0.5 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 : 2026/06/19

full sequence : ARi20G08hts01.seq

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

Date : 2026/07/23

| | |
|---|---|
| DNA (260 ng/ul) | 74 ul |
| 10x TE | 77 ul |
| $dH_2O$ | 619 ul |
| Total | 770 ul |

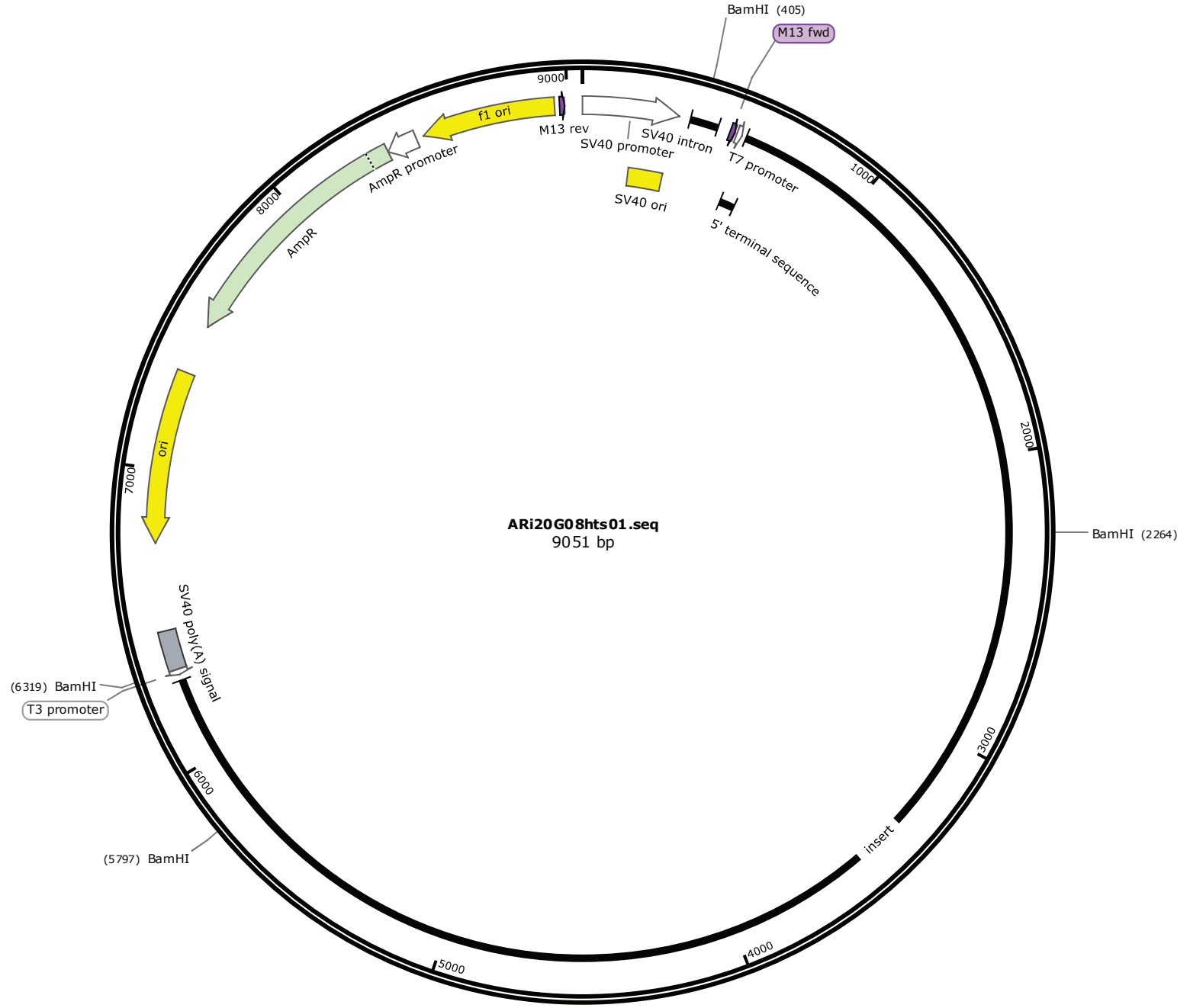
## ● Shipping

☑ 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)
M13 fwd
9000
f1 ori
M13 rev
SV40 promoter
SV40 intron
T7 promoter
1000
AmpR promoter
SV40 ori
5' terminal sequence
8000
AmpR
ori
7000
2000
BamHI (2264)
ARi20G08hts01.seq
9051 bp
SV40 polyA signal
(6319) BamHI
T3 promoter
6000
3000
insert
(5797) BamHI
5000
4000

**BLAST Results**

Questions/comments

**Blast 2 sequences**

**Job title: NM_001144068:Homo sapiens zinc finger protein...**

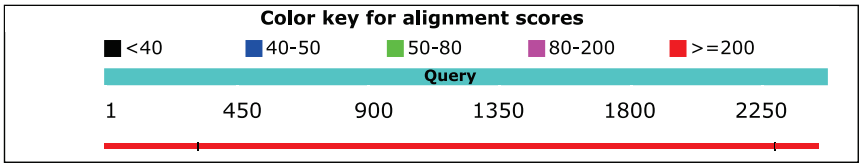
**RID** 39HUY9XS114 (Expires on 06-20 12:36 pm)

| | | | |
|---|---|---|---|
| **Query ID** | NR_003505.3 | **Subject ID** | lcl\|Query_7938375 |
| **Description** | Homo sapiens protein phosphatase 4 regulatory subunit 1 like (pseudogene) (PPP4R1L), non-coding RNA | **Description** | None<br>See details |
| **Molecule type** | nucleic acid | **Molecule type** | dna |
| **Query Length** | 2398 | **Subject Length** | 9051 |
| | | **Program** | BLASTN 2.17.0+ |

ARi20G08hts01.seq

## Graphic Summary

**Distribution of the top 3 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 | 3583 | 4416 | 100% | 0.0 | 99.85% | Query_7938375 |

## Alignments

Sequence ID: Query_7938375 Length: 9051 Number of Matches: 3
Range 1: 1023 to 2971

| Score | Expect | Identities | Gaps | Strand | Frame |
|---|---|---|---|---|---|
| 3583 bits(1940) | 0.0() | 1946/1949(99%) | 0/1949(0%) | Plus/Plus | |

Features:

```
Query  304   CAGATAATCTGCAAAATGGCTTCAATGCTGAGTAAGAGTACCGTTGAACGCCTGCTACTC  363
Sbjct  1023  ............................................................  1082

Query  364   CCCCGATTCTGTGAACTGTGTGGTGACAGGAAGCTCTTTCAAGTTCGGAAGGTTTGTGCT  423
Sbjct  1083  ............................................................  1142

Query  424   GCAAATTTTGGTGATATTTGTCATGCTGTTGGACAAGAAGCCACTGAGAAATTTTTGATC  483
Sbjct  1143  ............................................................  1202

Query  484   CCAAAGTTCTTTGAGCTCTGCTCTGATGCTGTTTGGGGCATGCGGAAAGCCTGTGCAGAA  543
Sbjct  1203  ............................................................  1262

Query  544   TGCTTCACGGCTGTGTCGCACAGCTCCTCCCCTGGGGTCCGCAGAACCCAGCTCTTCCCG  603
Sbjct  1263  ............................................................  1322

Query  604   CTCTTCATCAGACTTGTCAGCGACCCCTGCCGATGGGTGCACCAGGCTGCCTTCCAGTCC  663
Sbjct  1323  ............................................................  1382

Query  664   CTCGGCCCCTTCACTTCCACCTTTGCAAACCCCTCCAGGGCTGGCCTTTATCTTCGAGAG  723
Sbjct  1383  ..T.........................................................  1442
```

```
Query  724   GATGGCGCCCTGAGCATCTGGCCACTCACCCAGGATTTGGACTCTGGTTTTGCCTCTGGC  783
Sbjct  1443  ............................................................  1502

Query  784   TCCCCTGCTCCCAGCAGTGGTGGTAACACTTCCCCTGCCAGTTTAACTCGTTCAGCAAAG  843
Sbjct  1503  ............................................................  1562

Query  844   CCTGTGCGGAGCGAGCCAGAGCTACCTGTGGAAGGGACCTCAGCGAAAACCAGTGATTGC  903
Sbjct  1563  ............................................................  1622

Query  904   CCACACAGCAGTAGCTCCTCTGACGGCCCAGCGGAAAGCCCTGTGGAAAGCTGTGTGTCG  963
Sbjct  1623  ............................................................  1682

Query  964   GCTGGAGCTGAGTGGACCAGGGTTTCCCCAGAGACCAGCGCCTGCTCAAAGCTTTCTGAC  1023
Sbjct  1683  ...........................................C................  1742

Query  1024  ATGAATGACCTCCCCATCAGCAGCTACCCTGGATCAGATTCCTGGGCCTGCCCAGGGAAC  1083
Sbjct  1743  ............................................................  1802

Query  1084  ACTGAGGATGTGTTCAGTCATTTTCTTTATTGGTGAACTCCTCTCCCTGACATAAGCAAG  1143
Sbjct  1803  ............................................................  1862

Query  1144  GACTTAGAGCTGCTTCTGAGTGAGGCTGGGCCTCAGGAGGACGACTGCAGCAGACCTGGG  1203
Sbjct  1863  ............................................................  1922

Query  1204  GTTGTGCACAACAGCTGTGTGGCCCGGAGTGAGATTCAGAAAGTCCTTGGTAGCTTGCAG  1263
Sbjct  1923  ..............................................A.............  1982

Query  1264  GAGCATCTGATGAATGATCCAGATGTTCAAGCTCAAGTTCAGGTATTATCCGCTGCACTG  1323
Sbjct  1983  ............................................................  2042

Query  1324  AGAGCTGCACAGCTCGACTGCGTGAATGAAGCTGAGAGCAAGCCAACAGCAGGCCTAAAG  1383
Sbjct  2043  ............................................................  2102

Query  1384  GAAGTGTCCATTTCACATCCCAGCTCTGCCTCTGACAATCAGATCGCTCTGGCGGCCTCA  1443
Sbjct  2103  ............................................................  2162

Query  1444  TCATCTCAGGATGAGCTCTTTGTGGCCAGGATATTACAAAGCCCAGATCCAGGTGGACCC  1503
Sbjct  2163  ............................................................  2222

Query  1504  AGAAATGGAACCAGTGACCATCTGGAGACTGACCAGAGGCAGGATCCCACCCCACTTGAA  1563
Sbjct  2223  ............................................................  2282

Query  1564  GAGAATAAATCTAAATTACAGGATGTAATACCTCAGCCGCTGCTAGATCAGTATGTGTCC  1623
Sbjct  2283  ............................................................  2342

Query  1624  ATGACTGACCCAGCTCGAGCCCAGACTGTCGATACTGACATAGCCAAACACTGTGCCTAC  1683
Sbjct  2343  ............................................................  2402

Query  1684  AGCCTCCCAGGGGTGGCACTGACCCTGGGCAGGCAAAATTGGCACTGCCTGAAAGATACA  1743
Sbjct  2403  ............................................................  2462

Query  1744  TATGAAACACTGGCTTCTGATGTACAGTGGAAGGTACGGCGAGCCCTAGCCTTCTCCATT  1803
Sbjct  2463  ............................................................  2522

Query  1804  CACGAGCTGGCTGTGATTCTTGGGGATCAGTTAACAGCAGCTGACCTGGTGCCTATCTTC  1863
Sbjct  2523  ............................................................  2582

Query  1864  AATGGATTTTTAAAGGATCTGGATGAAGTGCGAATAGGAGTTCTTAGACACCTGTATGAT  1923
Sbjct  2583  ............................................................  2642

Query  1924  TTTCTAAAGTTGCTTCATGAAGACAAGAGGAGAGACTATCTTTATCAGCTTCAAGAATTT  1983
Sbjct  2643  ............................................................  2702

Query  1984  GTAGTGACTGATAACAGCAGGAATTGGAGGTTTCGATATGAACTAGCAGAACAGCTGATA  2043
Sbjct  2703  ............................................................  2762

Query  2044  CTGATTCTGGAACTCTATAGTCCCAATGATGTTTATGATTACCTAATGCACATTGCCTTA  2103
Sbjct  2763  ............................................................  2822

Query  2104  AAGTTGTGTGCAGATCAAGTTTCTGAAGTTCGGTGGATCTCCTTCAAACTAGTCGTGGCA  2163
Sbjct  2823  ............................................................  2882

Query  2164  ATTCTGCAGAAGTTCTATTCCAACAGTGAAAGTGCATTGGGGTTAAATTTCATCAATGAG  2223
Sbjct  2883  ............................................................  2942

Query  2224  CTCATCATAAGGTTCCGGCACTGTTCTAA  2252
Sbjct  2943  ............................  2971
```

Range 2: 577 to 883

| Score | Expect | Identities | Gaps | Strand | Frame |
|---|---|---|---|---|---|
| 568 bits(307) | 2e-164() | 307/307(100%) | 0/307(0%) | Plus/Plus | |

Features:

```
Query  1    ATGCCCATCCCAAGATGGCGGAGATCCCCCTGTACTTTGTGGACTTGCAGGATGACTTAG  60
Sbjct  577  ............................................................  636

Query  61   ACGACTATGGATTTGAAGACTATGGTACAGATTGCGACAACATGAGAGTAACGGCCTTCT  120
Sbjct  637  ............................................................  696

Query  121  TGGACATTCCAGGCCAGGATAACCTGCCTCCACTCACTCGCCTGGAGAAGTATGCTTTCA  180
Sbjct  697  ............................................................  756

Query  181  GCGAGAACACCTTCAACCGGCAGATTATTGCCAGAGGGCTGCTTGATATCTTCCGGGACT  240
Sbjct  757  ............................................................  816

Query  241  TCGGTAACAATGAAGAAGACTTCCTCACGGTAATGGAGATTGTAGTCAGATTGTCAGAAG  300
Sbjct  817  ............................................................  876

Query  301  ATGCAGA  307
Sbjct  877  .......  883
```

Range 3: 3009 to 3154

| Score | Expect | Identities | Gaps | Strand | Frame |
|---|---|---|---|---|---|
| 265 bits(143) | 3e-73() | 145/146(99%) | 0/146(0%) | Plus/Plus | |

Features:

```
Query  2253  ATTCTGAAATGACTTCTTTGGGATTAAAGAAGTGTATGTTTCTAGAAGACTGCGGAAAAC  2312
Sbjct  3009  .........C.............................................  3068

Query  2313  ATCATTTCTTTGGCTGTGACTTTCTTGGAGCAGGCAGTGGTGAGCAAGGAGTGTGTCCCC  2372
Sbjct  3069  ............................................................  3128

Query  2373  GTGGACCAGTTCATGGAGCACCTGCT  2398
Sbjct  3129  .........................  3154
```




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RDB : No. 7675

**RIKEN_Clone_ID : ARi20G08**
開始Stock

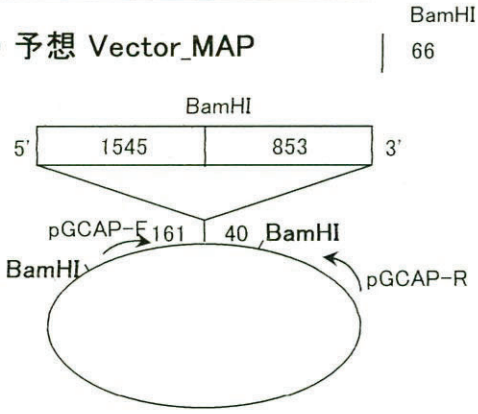
作業開始日 B3Bd QA – 保管場所 60B0329
作業者 古谷・112, Page 128

| | |
|---|---|
| Accession No. | – |
| RefSeq_mRNA | NR_003505.3 |
| Gene | PPP4R1L |
| Gene_ID | 55370 |
| lot. No. | 7675_B3Bd |

検 '26.07.23 笹沼
提供担当者確認印

K.Nakashima '26.11.12 confirmed
承認印

## ● 予想 Vector_MAP




pGCAP10 : Amp

## ● 構造確認

BamHI cut での予想バンドサイズ

Vector : 3138 bp
Insert : 1706, 893 bp (unsure)

## ● 配列確認

DNA 量 : 83.80994

追加プライマー : GNP mix primer

古谷

業務進捗（提供担当チェックリスト）

- [x] 構造チェック（泳動写真確認）
- [x] 配列決定
- [x] 濃度調製 （25 ng/ul）

（承認担当チェックリスト）

- [x] 構造チェック（泳動写真確認）判定
- [x] 配列確認判定

クローンの質

- [ ] y : 構造確認・予想サイズと異なる
- [ ] z : Insert 情報が異なる
- [x] p : 問題なく検定終了

<MEMO>

HTS解析済み