NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

## RIKEN Clone ID : ARe30F07

Lot# : 7672_B5I2

Vector : pKA1U5

| Gene | ARAP1 | |
|---|---|---|
| RefSeq_mRNA | NM_001040118.3 | 5156 bp |

### ● Plasmid DNA purification

Date : 2025/09/02 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2025/09/03 Purification : QIAGEN Miniprep kit -> $dH_2O$ 100 ul

### ● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/09/03

DNA concentration (O.D.): 461 ng/ul

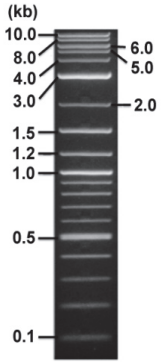
< Size of fragment expected from this clone >

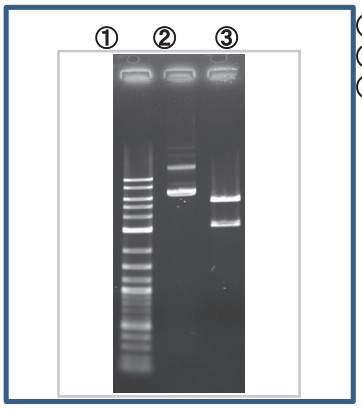
| | | |
|---|---|---|
| DNA | 0.2 | ul |
| Enzyme (BamHI ) | 1 | ul |
| Buffer H | 1 | ul |
| $dH_2O$ | 7.8 | ul |
| Total | 10 | ul |

BamHI 3.1kb (vector), 5.4 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 : 2025/09/09

| full sequence | ARe30F07hts01.seq |
|---|---|
| | |
| | |
| | |

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

Date : 2025/09/09

| | | |
|---|---|---|
| DNA ( 461 ng/ul) | 84 | ul |
| 10x TE | 155 | ul |
| $dH_2O$ | 1,310 | ul |
| Total | 1,549 | ul |

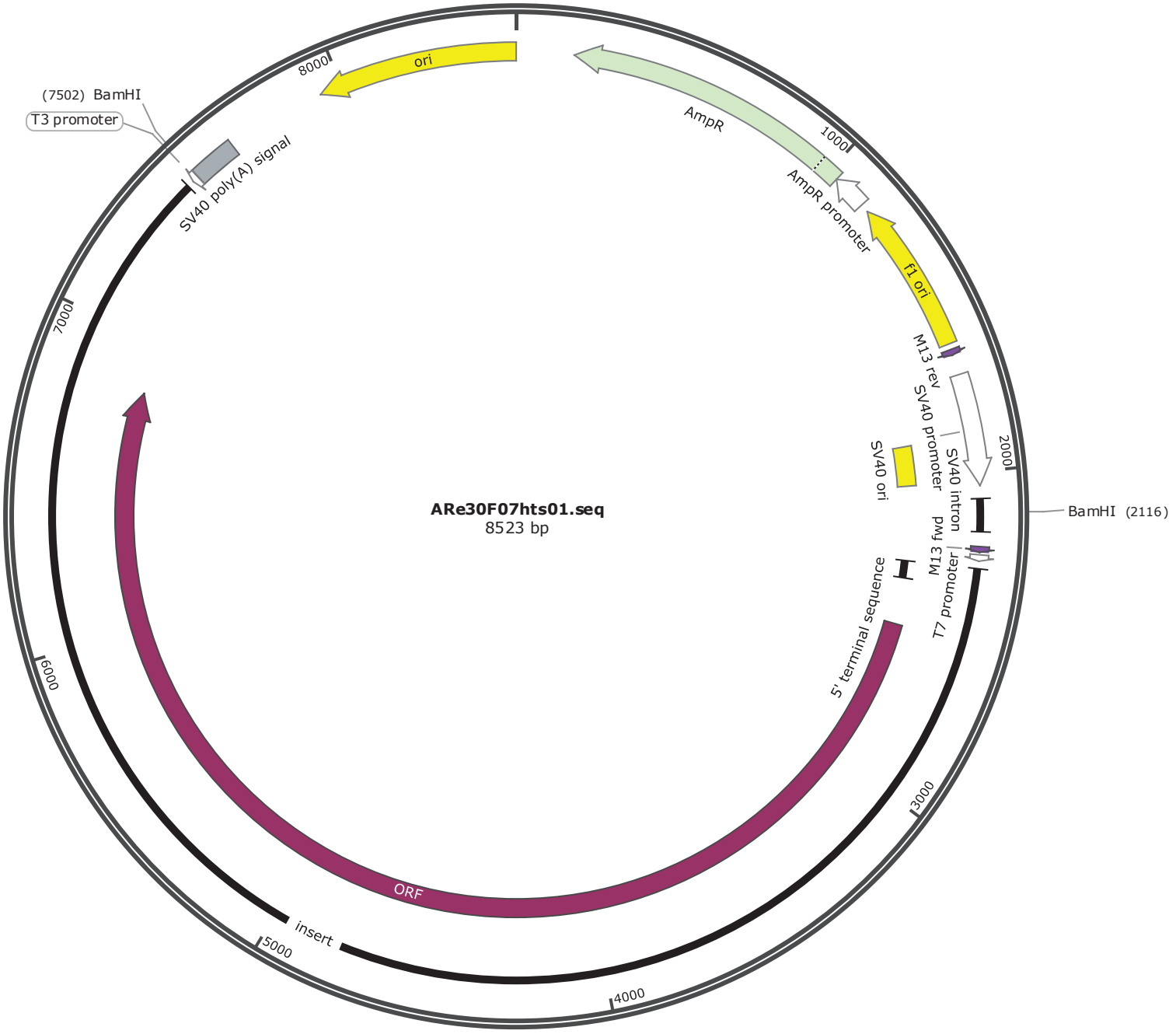
### ● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '25.09.09 笹沼

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


ARe30F07hts01.seq
8523 bp
8000
ori
AmpR
1000
AmpR promoter
f1 ori
M13 rev
SV40 promoter
SV40 intron
2000
BamHI (2116)
SV40 ori
pwy
M13
T7 promoter
5' terminal sequence
3000
4000
insert
5000
ORF
6000
7000
(7502) BamHI
T3 promoter
SV40 poly(A) signal

**BLAST Results**

Questions/comments

**Blast 2 sequences**

**Job title: NM_001040118:Homo sapiens ArfGAP with RhoGAP...**

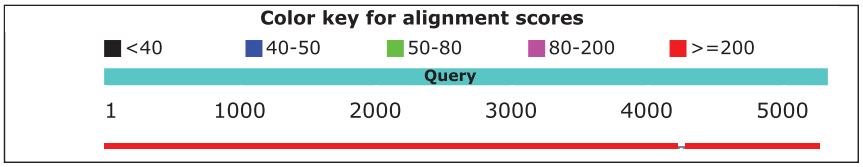
**RID** BZH1N3V0114 (Expires on 09-10 14:07 pm)

| | | | |
|---|---|---|---|
| **Query ID** | NM_001040118.3 | **Subject ID** | lcl\|Query_7073735 |
| **Description** | Homo sapiens ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1 (ARAP1), transcript variant 3, mRNA | **Description** | None<br>See details |
| **Molecule type** | nucleic acid | **Molecule type** | dna |
| **Query Length** | 5156 | **Subject Length** | 8523 |
| | | **Program** | BLASTN 2.17.0+ |

ARe30F07hts01.seq

## Graphic Summary

**Distribution of the top 2 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 | 7685 | 9451 | 99% | 0.0 | 99.98% | Query_7073735 |

## Alignments

Sequence ID: Query_7073735 Length: 8523 Number of Matches: 2
Range 1: 2298 to 6461

| Score | Expect | Identities | Gaps | Strand | Frame |
|---|---|---|---|---|---|
| 7685 bits(4161) | 0.0() | 4163/4164(99%) | 0/4164(0%) | Plus/Plus | |

Features:

```
Query          1     GCTGCAATTTGGCGGTGGCGGTGTAAGTCGGTGGCGGCGCCGGTACGCCTGGTCCCCGCG  60
Sbjct          2298  ............................................................  2357

Query          61    TGGAGTCTTTACTCAAAACAGCTCCCGCCTCAGGCCGAGATGAGGAGCCCTTCAGAATAG  120
Sbjct          2358  ............................................................  2417

Query          121   CTGCTGTCTCTGGGAGGACCCGGGCGTCCTTGGCAGCCCAGCTGCTCTGGACAAAGCCCT  180
Sbjct          2418  ............................................................  2477

CDS:arf-GAP with Rho 1                                 M  A  E  A  G  D  A  A  L  S  V
Query          181   GCCAGTCAGGCCTCCGCTGGCAGGAACCATGGCAGAGGCTGGGGATGCTGCGCTATCGGT  240
Sbjct          2478  ............................................................  2537

CDS:arf-GAP with Rho 12    A  E  W  L  R  A  L  H  L  E  Q  Y  T  G  L  F  E  Q  H  G
Query          241   GGCCGAGTGGCTGCGGGCATTGCACCTGGAGCAGTACACGGGGCTCTTTGAGCAGCATGG  300
Sbjct          2538  ............................................................  2597

CDS:arf-GAP with Rho 32    L  V  W  A  T  E  C  Q  G  L  S  D  T  R  L  M  D  M  G  M
Query          301   CCTGGTGTGGGCCACTGAGTGCCAAGGCCTCAGCGACACCCGCCTGATGGACATGGGCAT  360
Sbjct          2598  ............................................................  2657

CDS:arf-GAP with Rho 52    L  L  P  G  H  R  R  R  I  L  A  G  L  L  R  A  H  T  S  P
Query          361   GCTACTCCCTGGTCACCGCCGCCGCATCCTGGCTGGCCTGCTCCGTGCCCATACCTCACC  420
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Sbjct                2658 ..........................................................  2717

CDS:arf-GAP with Rho   72    A  P  A  P  R  P  T  P  R  P  V  P  M  K  R  H  I  F  R  S
Query                421 GGCCCCTGCACCCCGCCCCACCCCACGGCCTGTGCCCATGAAGCGCCACATCTTCCGCTC  480
Sbjct                2718 ..........................................................  2777

CDS:arf-GAP with Rho   92    P  P  V  P  A  T  P  P  E  P  L  P  T  T  T  E  D  E  G  L
Query                481 ACCACCTGTGCCTGCCACTCCACCCGAGCCGCTGCCCACCACTACAGAGGATGAGGGGCT  540
Sbjct                2778 ..........................................................  2837

CDS:arf-GAP with Rho  112    P  A  A  P  P  I  P  P  R  R  S  C  L  P  P  T  C  F  T  T
Query                541 CCCCGCTGCCCCACCCATCCCGCCCCGGAGGAGCTGCCTTCCGCCCACCTGCTTCACCAC  600
Sbjct                2838 ..........................................................  2897

CDS:arf-GAP with Rho  132    P  S  T  A  A  P  D  P  V  L  P  P  L  P  A  K  R  H  L  A
Query                601 CCCATCCACAGCTGCCCCAGACCCTGTGCTGCCCCCGCTGCCTGCTAAGCGGCATTTGGC  660
Sbjct                2898 ..........................................................  2957

CDS:arf-GAP with Rho  152    E  L  S  V  P  P  V  P  P  R  T  G  P  P  R  L  L  V  S  L
Query                661 AGAGCTGAGCGTTCCACCCGTGCCGCCCCGCACCGGAccccccccGCCTGCTGGTGAGCCT  720
Sbjct                2958 ..........................................................  3017

CDS:arf-GAP with Rho  172    P  T  K  E  E  E  S  L  L  P  S  L  S  S  P  P  Q  P  Q  S
Query                721 GCCCACTAAGGAGGAGGAGGAGTCATTGCTGCCATCATTATCAtcccctccccagccacagtc  780
Sbjct                3018 ..........................................................  3077

CDS:arf-GAP with Rho  192    E  E  P  L  S  T  L  P  Q  G  P  P  Q  P  P  S  P  P  P  C
Query                781 tgaggagcccctgtccacccctccccaggggcctccccagcctccctctccacctccctg  840
Sbjct                3078 ..........................................................  3137

CDS:arf-GAP with Rho  212    P  P  E  I  P  P  K  P  V  R  L  F  P  E  F  D  D  S  D  Y
Query                841 ccccccGGAGATACCTCCAAAGCCGGTACGCCTGTTCCCAGAGTTCGATGACTCTGACTA  900
Sbjct                3138 ..........................................................  3197

CDS:arf-GAP with Rho  232    D  E  V  P  E  E  G  P  G  A  P  A  R  V  M  T  K  K  E  E
Query                901 CGATGAGGTCCCAGAGGAGGGGCCGGGGGCCCCAGCCAGAGTGATGACCAAGAAGGAGGA  960
Sbjct                3198 ..........................................................  3257

CDS:arf-GAP with Rho  252    P  P  P  S  R  V  P  R  A  V  R  V  A  S  L  L  S  E  G  E
Query                961 GCCCCCACCGAGCCGAGTCCCACGGGCCGTGCGCGTGGCCAGTCTGCTGAGCGAGGGAGA 1020
Sbjct                3258 ..........................................................  3317

CDS:arf-GAP with Rho  272    E  L  S  G  D  D  Q  G  D  E  E  E  D  D  H  A  Y  E  G  V
Query                1021 GGAACTGTCTGGGGACGACCAAGGGGATGAGGAAGAGGATGACCACGCCTATGAGGGCGT 1080
Sbjct                3318 ..........................................................  3377

CDS:arf-GAP with Rho  292    P  N  G  G  W  H  T  S  S  L  S  L  S  L  P  S  T  I  A  A
Query                1081 CCCCAATGGCGGATGGCATACCAGCAGCCTGAGCTTGTCCTTGCCCAGCACAATAGCTGC 1140
Sbjct                3378 ..........................................................  3437

CDS:arf-GAP with Rho  312    P  H  P  M  D  G  P  P  G  G  S  T  P  V  T  P  V  I  K  A
Query                1141 GCCACACCCCATGGACGGGCCGCCTGGGGGCTCCACCCCCGTCACACCAGTCATCAAGGC 1200
Sbjct                3438 ..........................................................  3497

CDS:arf-GAP with Rho  332    G  W  L  D  K  N  P  P  Q  G  S  Y  I  Y  Q  K  R  W  V  R
Query                1201 TGGCTGGCTGGACAAGAACCCACCGCAGGGATCTTACATCTATCAGAAACGATGGGTGAG 1260
Sbjct                3498 ..........................................................  3557

CDS:arf-GAP with Rho  352    L  D  T  D  H  L  R  Y  F  D  S  N  K  D  A  Y  S  K  R  F
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Query                1261 ACTGGATACTGATCACCTGCGATACTTTGACAGTAACAAGGACGCTTACTCTAAGCGCTT 1320
Sbjct                3558 ..........................................................  3617

CDS:arf-GAP with Rho  372    I  S  V  A  C  I  S  H  V  A  A  I  G  D  Q  K  F  E  V  I
Query                1321 TATCTCTGTGGCCTGCATCTCCCACGTGGCTGCCATCGGGGACCAGAAGTTTGAAGTGAT 1380
Sbjct                3618 ..........................................................  3677

CDS:arf-GAP with Rho  392    T  N  N  R  T  F  A  F  R  A  E  S  D  V  E  R  K  E  W  M
Query                1381 CACAAACAACCGAACCTTTGCCTTCCGGGCAGAGAGTGATGTGGAGCGGAAGGAGTGGAT 1440
Sbjct                3678 ..........................................................  3737

CDS:arf-GAP with Rho  412    Q  A  L  Q  Q  A  M  A  E  Q  R  A  R  A  R  L  S  S  A  Y
Query                1441 GCAGGCCCTGCAGCAGGCCATGGCTGAGCAGCGTGCCCGGGCCCGGCTCTCTAGCGCTTA 1500
Sbjct                3738 ..........................................................  3797

CDS:arf-GAP with Rho  432    L  L  G  V  P  G  S  E  Q  P  D  R  A  G  S  L  E  L  R  G
Query                1501 TCTGCTGGGAGTTCCAGGCTCAGAGCAGCCTGACCGCGCTGGCAGCCTGGAGCTTCGTGG 1560
Sbjct                3798 ..........................................................  3857

CDS:arf-GAP with Rho  452    F  K  N  K  L  Y  V  A  V  V  G  D  K  V  Q  L  Y  K  N  L
Query                1561 CTTCAAGAATAAGCTGTACGTGGCCGTGGTCGGGGACAAAGTGCAGCTCTACAAGAATCT 1620
Sbjct                3858 ..........................................................  3917

CDS:arf-GAP with Rho  472    E  E  Y  H  L  G  I  G  I  T  F  I  D  M  S  V  G  N  V  K
Query                1621 AGAGGAGTACCACCTGGGCATTGGCATCACCTTCATCGACATGAGCGTGGGCAACGTGAA 1680
Sbjct                3918 ..........................................................  3977

CDS:arf-GAP with Rho  492    E  V  D  R  R  S  F  D  L  T  T  P  Y  R  I  F  S  F  S  A
Query                1681 GGAAGTGGACCGGCGCAGCTTCGACCTCACCACGCCCTACCGCATCTTCAGCTTCTCTGC 1740
Sbjct                3978 ..........................................................  4037

CDS:arf-GAP with Rho  512    D  S  E  L  E  K  E  Q  W  L  E  A  M  Q  G  A  I  A  E  A
Query                1741 TGACTCAGAGCTAGAGAAGGAGCAGTGGTTGGAGGCCATGCAGGGAGCCATCGCTGAGGC 1800
Sbjct                4038 ..........................................................  4097

CDS:arf-GAP with Rho  532    L  S  T  S  E  V  A  E  R  I  W  A  A  A  P  N  R  F  C  A
Query                1801 CCTGTCTACCTCGGAGGTGGCCGAGCGCATCTGGGCTGCAGCCCCCAACAGGTTCTGTGC 1860
Sbjct                4098 ..........................................................  4157

CDS:arf-GAP with Rho  552    D  C  G  A  P  Q  P  D  W  A  S  I  N  L  C  V  V  I  C  K
Query                1861 TGACTGCGGGGCTCCTCAGCCTGACTGGGCCTCCATCAACCTCTGTGTTGTTATCTGCAA 1920
Sbjct                4158 ..........................................................  4217

CDS:arf-GAP with Rho  572    R  C  A  G  E  H  R  G  L  G  A  G  V  S  K  V  R  S  L  K
Query                1921 GCGCTGTGCAGGGGAGCACCGTGGCCTGGGCGCTGGCGTCTCCAAGGTGCGGAGCCTGAA 1980
Sbjct                4218 ..........................................................  4277

CDS:arf-GAP with Rho  592    M  D  R  K  V  W  T  E  T  L  I  E  L  F  L  Q  L  G  N  G
Query                1981 GATGGACAGGAAGGTGTGGACAGAAACACTTATCGAGCTCTTCTTACAGCTGGGGAATGG 2040
Sbjct                4278 ..........................................................  4337

CDS:arf-GAP with Rho  612    A  G  N  R  F  W  A  A  N  V  P  P  S  E  A  L  Q  P  S  S
Query                2041 CGCTGGGAACCGCTTCTGGGCAGCCAACGTGCCCCCCAGTGAGGCCCTGCAGCCCAGCAG 2100
Sbjct                4338 ..........................................................  4397

CDS:arf-GAP with Rho  632    S  P  S  T  R  R  C  H  L  E  A  K  Y  R  E  G  K  Y  R  R
Query                2101 CAGCCCCAGCACCCGGCGGTGCCACCTGGAGGCCAAGTACCGTGAGGGCAAGTACCGCCG 2160
Sbjct                4398 ..........................................................  4457
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CDS:arf-GAP with Rho  652    Y  H  P  L  F  G  N  Q  E  E  L  D  K  A  L  C  A  A  V  T
Query                2161   CTACCACCCGCTCTTTGGCAACCAGGAGGAGCTGGACAAGGCCCTGTGTGCTGCAGTCAC  2220
Sbjct                4458   ............................................................  4517

CDS:arf-GAP with Rho  672    T  T  D  L  A  E  T  Q  A  L  L  G  C  G  A  G  I  N  C  F
Query                2221   CACCACAGACCTGGCTGAGACCCAGGCGCTCCTGGGCTGTGGGGCTGGGATCAACTGCTT  2280
Sbjct                4518   ............................................................  4577

CDS:arf-GAP with Rho  692    S  G  D  P  E  A  P  T  P  L  A  L  A  E  Q  A  G  Q  T  L
Query                2281   CTCGGGGGACCCTGAGGCCCCCACGCCCCTGGCTCTTGCAGAGCAGGCGGGGCAGACGCT  2340
Sbjct                4578   ............................................................  4637

CDS:arf-GAP with Rho  712    Q  M  E  F  L  R  N  N  R  T  T  E  V  P  R  L  D  S  M  K
Query                2341   GCAGATGGAATTCCTTCGGAACAACCGGACCACAGAGGTGCCTCGGCTGGACTCGATGAA  2400
Sbjct                4638   ............................................................  4697

CDS:arf-GAP with Rho  732    P  L  E  K  H  Y  S  V  V  L  P  T  V  S  H  S  G  F  L  Y
Query                2401   GCCCCTGGAAAAGCACTACTCAGTTGTCCTGCCGACCGTGAGCCACAGTGGCTTCCTCTA  2460
Sbjct                4698   ............................................................  4757

CDS:arf-GAP with Rho  752    K  T  A  S  A  G  K  L  L  Q  D  R  R  A  R  E  E  F  S  R
Query                2461   CAAGACTGCCTCTGCCGGCAAGCTGCTACAGGACCGCCGGGCCCGGGAAGAGTTCAGCCG  2520
Sbjct                4758   ............................................................  4817

CDS:arf-GAP with Rho  772    R  W  C  V  L  G  D  G  V  L  S  Y  F  E  N  E  R  A  V  T
Query                2521   GCGCTGGTGTGTCCTTGGTGACGGGGTCCTGAGCTACTTTGAGAATGAGCGGGCAGTGAC  2580
Sbjct                4818   ............................................................  4877

CDS:arf-GAP with Rho  792    P  N  G  E  I  R  A  S  E  I  V  C  L  A  V  P  P  P  D  T
Query                2581   CCCCAATGGAGAGATTCGGGCCAGCGAGATTGTGTGCCTGGCAGTGCCCCCTCCTGACAC  2640
Sbjct                4878   ............................................................  4937

CDS:arf-GAP with Rho  812    H  G  F  E  H  T  F  E  V  Y  T  E  G  E  R  L  Y  L  F  G
Query                2641   CCATGGCTTTGAGCACACCTTTGAGGTGTACACGGAGGGAGAACGGCTGTACCTGTTTGG  2700
Sbjct                4938   ............................................................  4997

CDS:arf-GAP with Rho  832    L  E  S  A  E  Q  A  H  E  W  V  K  C  I  A  K  A  F  V  P
Query                2701   GCTGGAGAGTGCGGAGCAGGCTCATGAGTGGGTCAAGTGTATTGCTAAGGCATTCGTGCC  2760
Sbjct                4998   ............................................................  5057

CDS:arf-GAP with Rho  852    P  L  A  E  D  L  L  A  R  D  F  E  R  L  G  R  L  P  Y  K
Query                2761   TCCCCTAGCCGAGGATCTGCTGGCCCGGGATTTTGAGCGGCTGGGACGCCTACCCTACAA  2820
Sbjct                5058   ............................................................  5117

CDS:arf-GAP with Rho  872    A  G  L  S  L  Q  R  A  Q  E  G  W  F  S  L  S  G  S  E  L
Query                2821   AGCTGGCCTGAGCCTACAGCGGGCCCAGGAGGGCTGGTTCTCTCTCAGTGGCTCGGAGCT  2880
Sbjct                5118   ............................................................  5177

CDS:arf-GAP with Rho  892    R  A  V  F  P  E  G  P  C  E  E  P  L  Q  L  R  K  L  Q  E
Query                2881   CCGTGCTGTCTTCCCGGAGGGGCCCTGCGAAGAGCCGCTGCAACTACGGAAACTGCAGGA  2940
Sbjct                5178   ............................................................  5237

CDS:arf-GAP with Rho  912    L  S  I  Q  G  D  S  E  N  Q  V  L  V  L  V  E  R  R  R  T
Query                2941   GCTTTCCATCCAGGGGGACAGTGAGAACCAGGTGCTGGTGCTGGTGGAGCGAAGGAGGAC  3000
Sbjct                5238   ...........................A................................  5297

CDS:arf-GAP with Rho  932    L  Y  I  Q  G  E  R  R  L  D  F  M  G  W  L  G  A  I  Q  K
Query                3001   ACTGTACATACAGGGCGAGCGGCGGCTGGACTTCATGGGTTGGCTGGGGGCCATCCAGAA  3060
Sbjct                5298   ............................................................  5357
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2983 G>A

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CDS:arf-GAP with Rho  952    A  A  A  S  M  G  D  T  L  S  E  Q  Q  L  G  D  S  D  I  P
Query                3061   AGCAGCCGCCAGCATGGGGGACACGCTGTCGGAGCAGCAGCTTGGGGACTCGGATATCCC  3120
Sbjct                5358   ............................................................  5417

CDS:arf-GAP with Rho  972    V  I  V  Y  R  C  V  D  Y  I  T  Q  C  G  L  T  S  E  G  I
Query                3121   GGTGATCGTGTACCGCTGTGTGGACTACATCACGCAGTGCGGCCTGACCTCCGAGGGCAT  3180
Sbjct                5418   ............................................................  5477

CDS:arf-GAP with Rho  992    Y  R  K  C  G  Q  T  S  K  T  Q  R  L  L  E  S  L  R  Q  D
Query                3181   CTACCGCAAGTGTGGGCAGACATCGAAGACACAGCGGCTGCTGGAGAGCCTGCGGCAGGA  3240
Sbjct                5478   ............................................................  5537

CDS:arf-GAP with Rho  1012   A  R  S  V  H  L  K  E  G  E  Q  H  V  D  D  V  S  S  A  L
Query                3241   TGCGCGCTCTGTGCACCTCAAGGAGGGCGAGCAGCACGTGGATGATGTTTCCTCGGCGCT  3300
Sbjct                5538   ............................................................  5597

CDS:arf-GAP with Rho  1032   K  R  F  L  R  D  L  P  D  G  L  F  T  R  A  Q  R  L  T  W
Query                3301   CAAGCGCTTCCTGCGCGACCTGCCTGATGGGCTCTTCACTCGCGCCCAGCGCCTAACCTG  3360
Sbjct                5598   ............................................................  5657

CDS:arf-GAP with Rho  1052   L  E  A  S  E  I  E  D  E  E  E  K  V  S  R  Y  R  E  L  L
Query                3361   GCTGGAGGCCTCAGAGATTGAGGACGAGGAGGAGAAGGTCTCCAGGTACCGAGAGCTGCT  3420
Sbjct                5658   ............................................................  5717

CDS:arf-GAP with Rho  1072   V  R  L  P  P  V  N  R  A  T  V  K  A  L  I  S  H  L  Y  C
Query                3421   GGTGCGGCTGCCCCCTGTCAACCGGGCCACAGTGAAGGCCCTTATCAGCCACCTGTACTG  3480
Sbjct                5718   ............................................................  5777

CDS:arf-GAP with Rho  1092   V  Q  C  F  S  D  T  N  Q  M  N  V  H  N  L  A  I  V  F  G
Query                3481   TGTTCAGTGCTTCTCAGACACGAACCAGATGAACGTGCACAACCTGGCAATTGTGTTTGG  3540
Sbjct                5778   ............................................................  5837

CDS:arf-GAP with Rho  1112   P  T  L  F  Q  T  D  G  Q  D  Y  K  A  G  R  V  V  E  D  L
Query                3541   GCCCACGCTCTTCCAGACAGATGGGCAGGACTACAAGGCTGGCCGTGTGGTGGAAGACCT  3600
Sbjct                5838   ............................................................  5897

CDS:arf-GAP with Rho  1132   I  N  H  Y  V  V  V  F  S  V  D  E  E  E  L  R  K  Q  R  E
Query                3601   CATTAACCACTATGTGGTGGTGTTTAGTGTGGATGAGGAAGAGCTCAGGAAGCAGCGGGA  3660
Sbjct                5898   ............................................................  5957

CDS:arf-GAP with Rho  1152   E  I  T  A  I  V  K  M  R  V  A  G  T  A  S  G  T  Q  H  A
Query                3661   GGAGATCACTGCCATTGTGAAGATGCGCGTGGCTGGCACTGCCAGTGGGACCCAGCATGC  3720
Sbjct                5958   ............................................................  6017

CDS:arf-GAP with Rho  1172   G  D  F  I  C  T  V  Y  L  E  E  K  K  A  E  T  E  Q  H  I
Query                3721   CGGTGACTTCATCTGCACAGTGTATCTGGAAGAGAAGAAGGCAGAGACTGAGCAGCATAT  3780
Sbjct                6018   ............................................................  6077

CDS:arf-GAP with Rho  1192   K  V  P  A  S  M  T  A  E  E  L  T  L  E  I  L  D  R  R  N
Query                3781   CAAGGTCCCAGCATCCATGACTGCTGAGGAGCTCACCCTGGAGATCCTGGATCGCCGGAA  3840
Sbjct                6078   ............................................................  6137

CDS:arf-GAP with Rho  1212   V  G  I  R  E  K  D  Y  W  T  C  F  E  V  N  E  R  E  E  A
Query                3841   CGTGGGCATCAGGGAGAAGGACTATTGGACCTGCTTTGAGGTCAACGAGAGGGAGGAGGC  3900
Sbjct                6138   ............................................................  6197

CDS:arf-GAP with Rho  1232   E  R  P  L  H  F  A  E  K  V  L  P  I  L  H  G  L  G  T  D
Query                3901   AGAGCGCCCCCTGCACTTTGCGGAGAAGGTGCTGCCCATCCTGCACGGGCTGGGCACGGA  3960
```

```
Sbjct                6198 ..........................................................  6257

CDS:arf-GAP with Rho 1252   S  H  L  V  V  K  K  H  Q  A  M  E  A  M  L  L  Y  L  A  S
Query                3961 CAGCCACCTGGTGGTGAAGAAGCACCAGGCCATGGAGGCCATGCTGCTGTACCTGGCCAG  4020
Sbjct                6258 ..........................................................  6317

CDS:arf-GAP with Rho 1272   R  V  G  D  T  K  H  G  M  M  K  F  R  E  D  R  S  L  L  G
Query                4021 CCGTGTCGGTGACACCAAGCATGGCATGATGAAGTTCCGTGAGGACCGCAGCCTCCTGGG  4080
Sbjct                6318 ..........................................................  6377

CDS:arf-GAP with Rho 1292   L  G  L  P  S  G  G  F  H  D  R  Y  F  I  L  N  S  S  C  L
Query                4081 CCTGGGCCTGCCCTCAGGTGGCTTCCACGATCGCTACTTCATCCTCAACAGCAGCTGCTT  4140
Sbjct                6378 ..........................................................  6437

CDS:arf-GAP with Rho 1312   R  L  Y  K  E  V  R  S
Query                4141 GCGGCTCTACAAGGAGGTCCGGAG  4164
Sbjct                6438 .........................  6461
```

Range 2: 6460 to 7415

| Score | Expect | Identities | Gaps | Strand | Frame |
|---|---|---|---|---|---|
| 1766 bits(956) | 0.0() | 956/956(100%) | 0/956(0%) | Plus/Plus | |

Features:

```
CDS:arf-GAP with Rho 1330   S  H  R  P  E  K  E  W  P  I  K  S  L  K  V  Y  L  G  V  K
Query                4196 AGTCACCGGCCTGAGAAGGAGTGGCCTATTAAGAGTCTCAAAGTCTACCTGGGAGTGAAG  4255
Sbjct                6460 ..........................................................  6519

CDS:arf-GAP with Rho 1350   K  K  L  R  P  P  T  C  W  G  F  T  V  V  H  E  T  E  K  H
Query                4256 AAGAAACTCAGGCCACCCACCTGCTGGGGCTTCACAGTGGTGCATGAGACAGAGAAACAT  4315
Sbjct                6520 ..........................................................  6579

CDS:arf-GAP with Rho 1370   E  K  Q  Q  W  Y  L  C  C  D  T  Q  M  F  L  R  F  W  F  A
Query                4316 GAGAAGCAGCAGTGGTACCTCTGCTGTGACACACAGATGGAGCTCCGGGAGTGGTTCGCT  4375
Sbjct                6580 ..........................................................  6639

CDS:arf-GAP with Rho 1390   T  F  L  F  V  Q  H  D  G  L  V  W  P  S  E  P  S  R  V  S
Query                4376 ACCTTTCTGTTTGTGCAGCATGACGGCCTGGTGTGGCCCTCAGAGCCCTCACGCGTGTCC  4435
Sbjct                6640 ..........................................................  6699

CDS:arf-GAP with Rho 1410   R  A  V  P  E  V  R  L  G  S  V  S  L  I  P  L  R  G  S  E
Query                4436 CGGGCAGTGCCTGAGGTCCGGCTGGGTAGTGTGTCACTGATCCCCCTTCGAGGTAGTGAA  4495
Sbjct                6700 ..........................................................  6759

CDS:arf-GAP with Rho 1430   N  E  M  R  R  S  V  A  A  F  T  A  D  P  L  S  L  L  R  N
Query                4496 AATGAAATGCGCCGGAGTGTGGCTGCCTTCACCGCGGACCCTCTGTCTCTTCTGCGCAAC  4555
Sbjct                6760 ..........................................................  6819

CDS:arf-GAP with Rho 1450   V
Query                4556 GTCTGAGCACAGGAGCCCATCCTTGGCTCTAGGATTCCGCCGCTGGAAGCCTTCTGTTCA  4615
Sbjct                6820 ..........................................................  6879

Query                4616 GACACCCCTTATGCTCCAAGGCCTGATGTGAGCCAGCGGGGGGTGCATGGGAAACTGCAC  4675
Sbjct                6880 ..........................................................  6939

Query                4676 CCCACAACCCACATCCTCCATCCTGACTGCAGCATGGGGTTCCCCGGCAGGGGTGGGAGG  4735
```

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Sbjct                6940 ..........................................................  6999

Query                4736 CAGCAGGGGTCAGCCTGGGCAGGAACCTCTCCCAACTCTGTCCAGGTGTTCAGACCTCTT  4795
Sbjct                7000 ..........................................................  7059

Query                4796 GGCCCAACCTGCTCACCCCACCGGGTTCACTGTCCTTGTGGGGCTGGAGAGATGGGCATA  4855
Sbjct                7060 ..........................................................  7119

Query                4856 AGTCAGGAACTTGGGAGGACCACCACCCTTTCAGAGGCGTGAGGCCCTGGGGCCCTGCCG  4915
Sbjct                7120 ..........................................................  7179

Query                4916 GAAGGGAGCCCCCTGCTCCTCCCAACAAACTCCAGAACAGCAGAAAGCGGGTGCTGTAGA  4975
Sbjct                7180 ..........................................................  7239

Query                4976 GGAGCACTCAGCTCACGGGGAGGGAGCTCTTGGCTGAGCTTCTACAGGGCTGAGAGCTGC  5035
Sbjct                7240 ..........................................................  7299

Query                5036 GCTTTGGGGACTTCAGCCTTCCTTCCAGTCTGGGCTGAGTGGGGGGTCCAGACTACCTGA  5095
Sbjct                7300 ..........................................................  7359

Query                5096 TGCCCCTTCCCCAATTTGGGGACTTTTTGATAATATAAATATATCTGTATATTTTA  5151
Sbjct                7360 ..........................................................  7415
```

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