

Product datasheet for **MC212845**

Arfgap1 (NM_001177710) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Arfgap1 (NM_001177710) Mouse Untagged Clone
Tag: Tag Free
Symbol: Arfgap1
Synonyms: A115377; Arf1gap
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC212845 representing NM_001177710
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**GCGATCGCC**

ATGAGAATAATCTTTGTGCGCTCTGTTACAATGGACAAATGGAAGGACATTGAGCTGGAGAAGATGAAGG
CTGGTGGGAATGCTAAGTTCGAGAGTTCCTGGAGACACAGGACGACTATGAGCCTAGCTGGTCACTGCA
GGACAAGTACAGCAGCAGAGCCGCGGCTCTTCAGGGATAAGGTGGCTACTTTGGCAGAAGGTAAGAG
TGGTCTCTGGAGTCATCGCTGCACAGAACTGGACCCACCTCAGCCCAAGACACTGCAGTTCACCTGCC
ACCGAGCCTCTGGCCAGCCACAGAGTGCAGCCGCTCTGGGGACAAGGCTTTTGAAGATTGGCTGAATGA
TGACCTGGGTTCTACCAGGGTCTCAGGAGAATCGCTATGTAGGGTTTGGGAACACAGTGCCACCTCAG
AAGAGAGAAGATGACTTCCTCAACAATGCCATGTCATCGCTGACTCGGGCTGGAGCAGTTTTACCACTG
GGGCGAGCAAGTTTGCATCTGCAGCAAAGGAGGGTGTACAAAATTTGGATCTCAAGCAAGTCAGAAGGC
TTCGGAGTTGGGCCACAGCCTGAATGAGAATGTTCTCAAGCCTGCACAGGAGAAGGTGAAGGAGGGAAGG
ATTTTTGATGATGTGCCAGTGGGTCTCTCAGTTGCCATCCAAGTCCAGGGAGTTGCCAGTAAGGGAT
GGCGTGATGCTACTACTTTCTCTGGGAAAGCCGAAGACTCTCAGACAGACCCTTAGAGGGCCACAG
CTACCAGAACAGCAGTGGAGACAACTCTCAGAACAGCAACATAGACCAGAGCTTCTGGGAGACCTTTGGG
AGTGCTGAGCCCCCAAGGCCAAGTCCCCAAGCAGTGACAGCTGGACCTGTGCAGATGCTTCAACAGGGA
GGAGGAGCTCGGACAGCTGGGACGTTTGGGGCTCAGGTTCCGCATCCAACAACAAGAACAGCAATAGCGA
TGGCTGGGAGAGTTGGGAGGGAGCCAGTGGGGAGGGCAGGGCAAAGGCCACCAAGAAGGCAGCCCCATCC
ACGGCTGATGAGGGCTGGGACAACCAGAAGCTGGTAG

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI
ACCN: NM_001177710



Insert Size:	1086 bp
OTI Disclaimer:	Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).
Components:	The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).
Reconstitution Method:	<ol style="list-style-type: none">1. Centrifuge at 5,000xg for 5min.2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.3. Close the tube and incubate for 10 minutes at room temperature.4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.
RefSeq:	<u>NM_001177710.1, NP_001171181.1</u>
RefSeq Size:	2398 bp
RefSeq ORF:	1086 bp
Locus ID:	228998
Cytogenetics:	2 103.53 cM
Gene Summary:	<p>GTPase-activating protein (GAP) for the ADP ribosylation factor 1 (ARF1). Involved in membrane trafficking and /or vesicle transport. Promotes hydrolysis of the ARF1-bound GTP and thus, is required for the dissociation of coat proteins from Golgi-derived membranes and vesicles, a prerequisite for vesicle's fusion with target compartment. Probably regulates ARF1-mediated transport via its interaction with the KDELR proteins and TMED2. Overexpression induces the redistribution of the entire Golgi complex to the endoplasmic reticulum, as when ARF1 is deactivated. Its activity is stimulated by phosphoinositides and inhibited by phosphatidylcholine (By similarity).[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (6) differs in the 5' UTR and lacks an alternate in-frame exon in the 5' coding region, compared to variant 1. The resulting isoform (d) lacks an internal segment near the N-terminus, compared to isoform a. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.</p>