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Product datasheet for SC322936

AP1AR (NM_001128426) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	AP1AR (NM_001128426) Human Untagged Clone
Tag:	Tag Free
Symbol:	AP1AR
Synonyms:	2C18; C4orf16; gamma-BAR; GBAR; PRO0971
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)

Fully Sequenced ORF:

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>SC322936 representing NM_001128426.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGGGGAACTGCTGCTGGACGCAGTGCTTCGGACTGCTTCGCAAGGAAGCGGGGCGGCTGCAGCGAGTA
GGCGGCGGCGGAGGATCCAAGTATTTTAGAACATGCTCAAGAGGTGAGCACTTAACAATAGAGTTTGAG
AATCTAGTAGAAAGTGATGAAGGGGAGAGCCCAGGAAGCAGTCATAGGCCTCTTACTGAGGAAGAAATT
GTTGACCTAAGAGAAAGGCATTATGATTCCATTGCCGAAAAACAAAAAGATCTTGATAAGAAAATTCAA
AAAGAGCAAGAAAGGCAGAGAATTGTGCAGCAATATCATCCTTCCAACAATGGAGAATATCAAAGTTCA
GGACCAGAAGATGACTTCGAATCTTGTTTGAGAAATATGAAGTCACAGTATGAAGTTTTTCGAAGTAGT
AGACTCTCATCAGATGCTACAGTTTTGACACCAAATACAGAAAGCAGTTGTGATTTAATGACCAAAACT
AAATCAACTAGTGGAAATGACGACAGCACATCCTTAGATCTAGAGTGGGAAGATGAAGAAGGAATGAAT
AGAATGCTTCCAATGAGAGAACGTTCCAAAACAGAGGAAGACATTCTACGGGCAGCACTTAAGTATAGC
AACAAGAAGACTGGAAGTAATCCTACATCAGCCTCTGATGATTCCAATGGGCTGGAGTGGGAAAATGAT
TTTGTTAGTGCCGAAATGGATGATAATGGAAATTCCGAGTATTCTGGATTTGTAAATCCTGTATTAGAA
CTGTCTGATTCTGGCATAAGGCATTCTGACACAGATCAACAGACTCGATAG
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
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Restriction Sites:	SgfI-MluI
ACCN:	NM_001128426
Insert Size:	810 bp

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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).
OTI Annotation:	This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.
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:	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:	NM_001128426.2
RefSeq Size:	5878 bp
RefSeq ORF:	810 bp
Locus ID:	55435
UniProt ID:	Q63HQ0
Cytogenetics:	4q25
MW:	30.5 kDa
Gene Summary:	Necessary for adaptor protein complex 1 (AP-1)-dependent transport between the trans-Golgi network and endosomes. Regulates the membrane association of AP1G1/gamma1-adaptin, one of the subunits of the AP-1 adaptor complex. The direct interaction with AP1G1/gamma1-adaptin attenuates the release of the AP-1 complex from membranes. Regulates endosomal membrane traffic via association with AP-1 and KIF5B thus linking kinesin-based plus-end-directed microtubular transport to AP-1-dependent membrane traffic. May act as effector of AP-1 in calcium-induced endo-lysosome secretion. Inhibits Arp2/3 complex function; negatively regulates cell spreading, size and motility via intracellular sequestration of the Arp2/3 complex.[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (2) lacks an in-frame exon in the mid-coding region compared to variant 1. The resulting shorter isoform (2) has the same N- and C- termini but lacks an internal protein segment compared to isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.