

Product datasheet for **SC321009**

AP1S2 (NM_003916) Human Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: AP1S2 (NM_003916) Human Untagged Clone
Tag: Tag Free
Symbol: AP1S2
Synonyms: DC22; MRX59; MRXS5; MRXS21; MRXSF; PGS; SIGMA1B
Mammalian Cell Selection: Neomycin
Vector: pCMV6-AC (PS100020)
E. coli Selection: Ampicillin (100 ug/mL)

Fully Sequenced ORF: >OriGene sequence for NM_003916.3
CGGCGACAGGGGCTTCCCCTTCGCCGCCGCCGCCGCCGCCAAGCTCCGCCCGCCCC
GCGGCCCGCGGCCCATGCAGTTTATGTTGCTTTTTAGTCAGGAAAGCTTCGACT
GCAAAAATGGTATGTCCACTATCAGACAAAGAGAAGAAAAGATCACAAGAGAAGCTTGT
TCAGACCGTTTTAGCACGAAACCTAAAATGTGCAGCTTCCTTGAGTGGCGAGATCTGAA
GATTGTTTACAAAAGATATGCTAGTCTGTATTTTTGCTGTGCTATTGAGGATCAGGACAA
TGAACATAATTACCCTGAAATAATTCATCGTTATGTGGAATTACTTGACAAGTATTTGCG
CAGTGTCTGTGAAGTATATCATCTTTAATTTGAGAAGGCTTATTTATTTGGATGA
GTTTCTTTGGGAGGGGAAGTTCAGGAAACATCCAAGAAAATGCCTTAAAGCAATTGA
GCAGGCTGATCTACTGCAGGAGGAAGCTGAAACCCACGTAGTGTCTTGAAGAAATTGG
ACTGACATAACTCTCCTCCTTGTGATGACTTCTTGTGGCATTTCACACTGTAGATG
GTCCTCCCTCATGTCCATGTTAGCTCATGGTGAAGATGATGCTTGTGAGTATTACT
GTTTTGCTAAGCCGCTTCATTCATGCCTACACAATTTTTTTAAAAGGGAAGCTTTAGTTA
ATTAAGTGATAAGGGACTTAAATATGAATTAGAATGGTGCAGAAAAGAGATACCTTTCTG
GATTTTTAAAGTTTAAAGGTCAGTTTCTCTTAATCTGATTATGTGCACATATGAAAATG
GCACATCATATACATGTAATAATCAGGCAGTATACATTTAATAATTACTGTATTTGACAAA
GGAAACTTTAATTATAATGTGAAACCTGGTTTTATGAAACCAAGACTAGTGCAGCAT
TTCAGCATATGTAACAAAAAAAAAAAAAAAAAAAA

Restriction Sites: Please inquire
ACCN: NM_003916
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).



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| 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: | <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: | NM_003916.3 , NP_003907.3 |
| RefSeq Size: | 2283 bp |
| RefSeq ORF: | 474 bp |
| Locus ID: | 8905 |
| UniProt ID: | P56377 |
| Cytogenetics: | Xp22.2 |
| Domains: | Clat_adaptor_s |
| Protein Families: | Druggable Genome |
| Protein Pathways: | Lysosome |
| Gene Summary: | <p>Adaptor protein complex 1 is found at the cytoplasmic face of coated vesicles located at the Golgi complex, where it mediates both the recruitment of clathrin to the membrane and the recognition of sorting signals within the cytosolic tails of transmembrane receptors. This complex is a heterotetramer composed of two large, one medium, and one small adaptin subunit. The protein encoded by this gene serves as the small subunit of this complex and is a member of the adaptin protein family. Transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jan 2013]</p> <p>Transcript Variant: This variant (2) lacks an alternate in-frame 3' exon compared to variant 1. The resulting isoform (2) has the same N- and C-termini but is shorter compared to isoform 1.</p> <p>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.</p> |