

Product datasheet for SC114117

Cytohesin 2 (CYTH2) (NM_017457) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Cytohesin 2 (CYTH2) (NM_017457) Human Untagged Clone
Tag:	Tag Free
Symbol:	Cytohesin 2
Synonyms:	ARNO; CTS18; CTS18.1; cytohesin-2; PSCD2; PSCD2L; SEC7L; Sec7p-L; Sec7p-like
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL6</u>
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>OriGene ORF within SC114117 sequence for NM_017457 edited (data generated by NextGen Sequencing)

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ATGGAGGACGGCGTCTATGAACCCCGACCTGACTCCGGAGGAGCGGATGGAGCTGGAG
AACATCCGGCGGGGAAGCAGGAGCTGCTGGTGGAGATTCAGCGCCTGCGGGAGGAGCTC
AGTGAAGCCATGAGCGAGGTGGAGGGGCTGGAGGCCAATGAGGGCAGTAAGACCTTGCAA
CGGAACCGGAAGATGGCAATGGGCAGGAAGAAGTTCAACATGGACCCCAAGAAGGGGATC
CAGTTCTTGGTGGAGAATGAACTGCTGCAGAACACCCGAGGAGATCGCCCGCTTCTCTG
TACAAGGGCGAGGGGCTGAACAAGACAGCCATCGGGGACTACCTGGGGGAGAGGAAGAA
CTGAACCTGGCAGTGCTCCATGCTTTTGTGGATCTGCATGAGTTCACCGACCTCAATCTG
GTGCAGGCCCTCAGGCAGTTTCTATGGAGCTTTCGCTACCCGGAGAGGCCAGAAAATT
GACCGGATGATGGAGGCCTTCGCCAGCGATACTGCCTGTGCAACCTGGGGTTTTCCAG
TCCACAGACACGTGCTATGTGCTGCTCCTTCGCCGTCATCATGCTCAACACAGTCTCCAC
AATCCCAATGTCCGGGACAAGCCGGGCCTGGAGCGCTTTGTGGCCATGAACCGGGGCATC
AACGAGGGCGGGGACCTGCCTGAGGAGCTGCTCAGGAACCTGTACGACAGCATCCGAAAT
GAGCCCTTCAAGATTCCTGAGGATGACGGGAATGACCTGACCCACACCTTCTTCAACCCG
GACCGGGAGGGCTGGCTCCTGAAGCTGGGAGGGGGCCGGGTGAAGACGTGGAAGCGGCGC
TGGTTTATCCTCACAGACAACCTGCCTCTACTACTTTGAGTACACCACGGACAAGGAGCCC
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AACTGCTTTGAACCTTACATCCCCAACAAGGGGCAGCTCATCAAAGCCTGCAAAACT
GAGGCGGACGGCCGAGTGGTGGAGGAAACACATGGTGTACCGGATCTCGGCCCCACG
CAGGAGGAGAAGGACGAGTGGATCAAGTCCATCCAGGCGGCTGTGAGTGTGGACCCCTTC
TATGAGATGCTGGCAGCGAGAAAGAAGCGGATTTAGTCAAGAAGAAGCAGGAGCAGCCC
TGA

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Clone variation with respect to NM_017457.5



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5' Read Nucleotide Sequence:	<p>>OriGene 5' read for NM_017457 unedited CCCGCCCGTTGACGCAATTGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAG TTTATTTAGGTGACACTATAGAATAACAAGCTACTTGTTCTTTTTGCAGCGGCCGCGAATT CGGCACGAGGTGAGGAGGCGGCGGTGGCTCCCGGGCGTTTGAGCGGGCTCACCCGAGCC CGCGGGCAACCGGATCCAGGCCGACTGGCGGGACCGCCCGGATTCCCGCGGGCT TCCTAGCCGCATGGAGGACGGCGTCTATGAACCCAGACCTGACTCCGAGGAGCGGA TGGAGCTGGAGAACATCCGGCGGCGGAAGCAGGAGCTGCTGGTGGAGATTACGCGCTGC GGGAGGAGCTCAGTGAAGCCATGAGCGAGGTGGAGGGGCTGGAGGCCAATGAGGGCAGTA AGACCTTGCAACGGAACCGGAAGATGGCAATGGGCAGGAAGAAGTTCAACATGGACCCCA AGAAGGGGATCCAGTTCTTGGTGGAGAATGAACTGCTGCAGAACACACCCGAGGAGATCG CCCGCTTCTGTACAAGGGCGAGGGGCTGAACAAGACAGCCATCGGGGACTACCTTGGGG AGAGGGAAGAAGTGAACCTGGCAGTGTCCATGCTTTTGTGGATGTCATGAGTTCACCG ACCTCAATCTGGTGCAGGCCCTCAGGCAGTTTCTATGGAGCTTTCGCCTACCCGGAGAGG CCCCAGAAATTGACCGGATGATGGAGGCCTTTCGCCAGCGATACTGCCTGTGCACCCNTG GGTTTTNCAGTCACAGACTGCTATGTGCTGTCTTTCGCGNATCATGCTCACACCAGT CTNCACATCCNATGTNCGNACANGCGNCCTGNAGCGCTTGTGGCATGACCGNCATC ACGAGGGCCGGGACTGCTGAGAGCTGTGAGAACCTGTCACAGCATCGATGAGCCTTAGA TCTGAGTTGACAGGATGACTGACACC</p>
3' Read Nucleotide Sequence:	<p>>OriGene 3' read for NM_017457 unedited TTTTTGGATTTAGCTATGNNACCGCGCCGCTTNTANGATCGAGTTTTTTTTTTTTTTTT TTTGCTGGGGTTAGGATTTTAATAAAGTTTTTTGTGGGGTGGGGGAGACACAATTT GATCCGTGCTGAGTCCATTTTGTGTTGCTGACAGAAGACCTGAGGCTGGGTCTTTATA AAGGAAGAGGTTGATTTGGCTCAGATTCTGATGGCTGGAAGGTTCAAGACTGGGCAGGTG CACTCACTGAGGACCTCCCTCATCCCTGAGGCTGCTGCTCTTCTGGGGGAGGGCAGAAG GATGCAGCTGTGTGCACAGAGATCACATGGTGTGAAGGAAGCAAGGGAGAGAAAACAA ATTCCCAAATCCCAAGGGTGAAGCACTCACTCACCCCTTAAGGCAGGCATTAATCTATCC ATGAGGACTCCACCTCCAAGACCACACAGCTCCTATGAGGCCCCACATCCCAACACTGC CACTGGGGGCTCGAATCTCAACATGAATTTAGTGAAGACAACGATATCCAAACCAT TGCCACCCAAAAGAAGTGGGGCTGAAGCCTGGCGGGTGGCTCACACCTGTAATCCCAAC ACTTTTGGGAGGCTGAAACAAATGGGTCCCTTGAAGTCAAGAATTTCCAGACCAGCTTG GGCCATATGGGGAAACCCCTCTTTTCTAAAATCCCAAATTTGCTGGGTACGGGGCTCCC ATCTTTAATCCCACTTCCCGGAAACTTAGCCAGGAAATCCTTTGCCCTCGGGAGTGGA GGGTTACATAAACCCAAATGGCCCTTTGCCCTCCCGTTTTAGGCACAAATGGTGACCT CCTTTCAAAAAAAAAAAAAAAAAAAAAA</p>
Restriction Sites:	NotI-NotI
ACCN:	NM_017457
Insert Size:	4700 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:

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_017457.3](#), [NP_059431.1](#)

RefSeq Size: 1545 bp

RefSeq ORF: 1203 bp

Locus ID: 9266

UniProt ID: [Q99418](#)

Cytogenetics: 19q13.33

Domains: Sec7, PH

Protein Families: Druggable Genome

Gene Summary: The protein encoded by this gene is a member of the PSCD family. Members of this family have identical structural organization that consists of an N-terminal coiled-coil motif, a central Sec7 domain, and a C-terminal pleckstrin homology (PH) domain. The coiled-coil motif is involved in homodimerization, the Sec7 domain contains guanine-nucleotide exchange protein (GEP) activity, and the PH domain interacts with phospholipids and is responsible for association of PSCDs with membranes. Members of this family appear to mediate the regulation of protein sorting and membrane trafficking. The encoded protein exhibits GEP activity in vitro with ARF1, ARF3, and ARF6 and is 83% homologous to CYTH1. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Aug 2008]

Transcript Variant: This variant (1) represents the longer transcript and encodes the longer 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.