

Product datasheet for **SC325590**

IMPA1 (NM_001144879) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	IMPA1 (NM_001144879) Human Untagged Clone
Tag:	Tag Free
Symbol:	IMPA1
Synonyms:	IMP; IMPA; MRT59
Vector:	<u>pCMV6 series</u>
Fully Sequenced ORF:	>NCBI ORF sequence for NM_001144879, the custom clone sequence may differ by one or more nucleotides ATGGCTGATCCTTGGCAGGAATGCATGGATTATGCAGTA ACTCTAGCAAGACAAGCTGGA GAGGTAGTTTGTGAAGCTATAAAAAATGAAATGAATGTTATGCTGAAAAGTTCTCCAGTT GATTTGGTAACTGCTACGGACCAAAAAGTTGAAAAATGCTTATCTCTCCATAAAGGAA AAGTATCCATCTCACAGTTTCATTGGTGAAGAATCTGTGGCAGCTGGGGAAAAAAGTATC TTAACCGACAACCCACATGGATCATTGACCCTATTGATGGAACA ACTA ACTTTGTACAT AGATTTCTTTTGTAGCTGTTTCAATTGGCTTTGCTGTAATAAAAAGATAGAATTTGGA GTTGTGTACAGTTGTGTGGAAGCAAGATGTACTGCTGCCAGAAAAGGAAAAGGTGCCTTT TGTAATGGTCAAAA ACTACAAGTTTCACAACAAGAAGGATCCGGAGTGTTGGAACAGCAG CTGTTAATATGTGCCTTGTGGCAACTGGCGGAGCAGATGCATATTATGAAATGGGAATTC ACTGCTGGGATGTTGCAGGAGCTGGCATTATTGTTACTGAAGCTGGTGGCGTGC
Restriction Sites:	Please inquire
ACCN:	NM_001144879
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).



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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_001144879.1](#), [NP_001138351.1](#)

RefSeq Size: 3287 bp

RefSeq ORF: 597 bp

Locus ID: 3612

UniProt ID: [P29218](#)

Cytogenetics: 8q21.13

Protein Families: Druggable Genome

Protein Pathways: Inositol phosphate metabolism, Metabolic pathways, Phosphatidylinositol signaling system

Gene Summary: This gene encodes an enzyme that dephosphorylates myo-inositol monophosphate to generate free myo-inositol, a precursor of phosphatidylinositol, and is therefore an important modulator of intracellular signal transduction via the production of the second messengers myo-inositol 1,4,5-trisphosphate and diacylglycerol. This enzyme can also use myo-inositol-1,3-diphosphate, myo-inositol-1,4-diphosphate, scyllo-inositol-phosphate, glucose-1-phosphate, glucose-6-phosphate, fructose-1-phosphate, beta-glycerophosphate, and 2'-AMP as substrates. This enzyme shows magnesium-dependent phosphatase activity and is inhibited by therapeutic concentrations of lithium. Inhibition of inositol monophosphate hydrolysis and subsequent depletion of inositol for phosphatidylinositol synthesis may explain the anti-manic and anti-depressive effects of lithium administered to treat bipolar disorder. Alternative splicing results in multiple transcript variants encoding distinct isoforms. A pseudogene of this gene is also present on chromosome 8q21.13. [provided by RefSeq, Dec 2014]

Transcript Variant: This variant (3) is missing an internal coding exon compared to transcript variant 1. This results in a frame-shift and a shorter isoform (3) with a novel C-terminus compared to isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data because no quality transcript was available for the full length of the gene. The extent of this transcript is supported by transcript alignments.