

## Product datasheet for **MC228313**

### **Eps8 (NM\_001271589) Mouse Untagged Clone**

#### **Product data:**

Product Type:	Expression Plasmids
Product Name:	Eps8 (NM_001271589) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Eps8
Synonyms:	AW261790
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



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**Fully Sequenced ORF:** >MC228313 representing NM\_001271589  
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
 GCC**CGCATCGC**

ATGATGGCAGCCCGGATCGACAGGGATGTGCAATCTTAAACCATATTTTGGATGACATTGAATTTTTTA  
 TCACAAACTCCAAAAGCCGCCGAAGCGTTTTCTGAGCTTTCTAAAAGGAAGAAAAGTAAGAAAAGTAA  
 AAGGAAAGGACCTGGAGAGGGCGTTTTAACTAGAGGAAAACCGCACCTCCTGATGAATTTGTTGAC  
 TGTTTCCAGAAGTTAAACATGGATTCAACCTTCTGGCCAAGTTGAAGTCCCATATCCAGAACCCGAGTG  
 CTTGAGATCTGGTTCAATTTTTTTTACTCCACTAAATATGGTGGTCCAGGCAACAGGTGGCCCCGAAT  
 GGCCAGTTCGGTACTCAGCCACTGTTGACAAAAGACACAGTTGATTTCTTAACTACACAGCCACTGCG  
 GAGGAACGGAAGCTGTGGATGTCACTGGGAGATAGTTGGGTGAAAGTGAGAGCAGAGTGGCCGAAAGAAC  
 AGTTCATCCACCTTACGTCCCGAGGTTCCGCAACGGCTGGGAGCCCCGATGCTGAATTCATGGGCGC  
 GCCACAGAGCAAGACATGTATCAACTGGCCGAGTCCGTGGCCAACGCAGAACACCAGCGCAAACAGGAC  
 AGCAAGAGGCTGTCCACAGAGCATTCCAATGTGTCCGACTATCCTCCAGCCGACGGATATGCGTACAGTA  
 GCAGCATGTACCACAGAGGACCACATGCAGACCACGGGAGGCTGCCATGCCTTTCAAGTCAACTCCTAA  
 TCACCAAGTAGATAGGAATTATGACGCAGTCAAAACACAACCCAGAAATACGCCAAATCCAAGTACGAC  
 TTTGTGGCGAGGAACAGCAGCGAGCTCTCGGTTATGAAAGATGATGTCTTAGAGATACTCGACGATCGAA  
 GGCAGTGGTGGAAAGTCCGGAATGCCAGTGGAGACTCTGGGTTTGTGCCAAATAACATTCTGGATATCAT  
 GAGAACTCCGGAATCTGGAGTGGGGCGCGCTGACCCCCATACACATACCATAAGAAACAAAGGACG  
 GAATACGGCCTGAGATCAGCTGACACTCCTTCTGCCCCATACCCCTCCAACGCCAGCACCCGTTCCGG  
 TCCCCCTCCACCTTCTGTACCAGCACCGTTTCTGTGCCAAGGTCCCAGCCAATGTCAACCCGCCAGAA  
 CAGCAGCTCCAGTGACAGTGGGGCGAGCATTGTGCGGGACAGCCAGAGATACAAACAACCTCCAGTGGAC  
 CGAAGGAAGTCCAGATGGAAGAGGTTCAAGATGAGCTCTTCCAGAGGCTGACCATCGGGCGCAGTGCTG  
 CACAGAGGAAGTCCACGTGCCACGCGAGAACGTTCCAGTGATCAATATCACTTATGACTCCTCACCGGA  
 AGAAGTAAAGACTTGGCTGCAGTCAAAGGGATTCAACCCGCTGACTGTCAATAGCCTCGGGGTGTTGAAC  
 GGAGCACAACTCTTTCTCTCAACAAAGACGAAGTGGAGTCTGTCTGCCGGAAGGTGCCAGAGTCTTTA  
 ACCAAATCACTGTTTCAAGAGCTGCTTTGGAGGACAGTAATGGAAGCTCCGAGTTACAAGAGATCATGCG  
 GAGACGGCAGGAGAAGATCAGCGCCGCTGCGAGCGACTCGGGAGTGGAGTCTTTCGATGAAGGGAGCAGC  
 CACTGA

**ACGCGT**ACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT  
 ACAAGGATGACGACGATAAGGTTTAA

**Restriction Sites:** Sgfl-MluI

**ACCN:** NM\_001271589

**Insert Size:** 1686 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).

**OTI Annotation:** Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.

**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.

**Note:** Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.

**RefSeq:** NM\_001271589.1, NP\_001258518.1

**RefSeq Size:** 3562 bp

**RefSeq ORF:** 1686 bp

**Locus ID:** 13860

**UniProt ID:** Q08509

**Cytogenetics:** 6 66.78 cM

**Gene Summary:**

Signaling adapter that controls various cellular protrusions by regulating actin cytoskeleton dynamics and architecture. Depending on its association with other signal transducers, can regulate different processes. Together with SOS1 and ABI1, forms a trimeric complex that participates in transduction of signals from Ras to Rac by activating the Rac-specific guanine nucleotide exchange factor (GEF) activity. Acts as a direct regulator of actin dynamics by binding actin filaments and has both barbed-end actin filament capping and actin bundling activities depending on the context. Displays barbed-end actin capping activity when associated with ABI1, thereby regulating actin-based motility process: capping activity is auto-inhibited and inhibition is relieved upon ABI1 interaction. Also shows actin bundling activity when associated with BAIAP2, enhancing BAIAP2-dependent membrane extensions and promoting filopodial protrusions. Involved in the regulation of processes such as axonal filopodia growth, stereocilia length, dendritic cell migration and cancer cell migration and invasion. Acts as a regulator of axonal filopodia formation in neurons: in the absence of neurotrophic factors, negatively regulates axonal filopodia formation via actin-capping activity. In contrast, it is phosphorylated in the presence of BDNF leading to inhibition of its actin-capping activity and stimulation of filopodia formation. Component of a complex with WHRN and MYO15A that localizes at stereocilia tips and is required for elongation of the stereocilia actin core. Indirectly involved in cell cycle progression; its degradation following ubiquitination being required during G2 phase to promote cell shape changes.

[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (5) contains a distinct 5' UTR, initiates translation at a downstream start codon and lacks an in-frame portion of the 5' coding region, compared to variant 1. The resulting isoform (3) has a shorter N-terminus, 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.