

Product datasheet for MC209738

Homer2 (NM_001164086) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Homer2 (NM_001164086) Mouse Untagged Clone
Tag: Tag Free
Symbol: Homer2
Synonyms: 9330120H11Rik; AW539445; CPD; Vesl-2
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC209738 representing NM_001164086
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGATCGCC**

ATGGGAGAACAGCCCATCTTCACCACGCGAGCGCAGTCTTCCAGATTGACCCAGCACCAAGAAGAACT
 GGGTGCCGGCAAGCAAGCAGGCCGTACGGTTTCTACTTCTATGATGTCACCAGGAACAGCTATCGGAT
 CATCAGTGTGGATGGAGCCAAGGTGATCATAAACAGCACTATCACCCGAACATGACTTTCACAAAACG
 TCACAGAAGTTCCGGCAGTGGGCTGACAGCAGAGCCAACACCGTGTTCGGTTTGGGATTCTCCTCCGAGC
 TGCAGCTCACGAAGTTTCAGAGAAGTTCCAGGAGGTAAGAGAAGCTGCCAGGCTAGCCAGAGACAAGTC
 CCAGGAGAAAACCGAGACCTCCAGCAATCATTCCCAAGCATCCAGCGTCAATGGCACAGACGACGAAAAG
 GCCTCTCACGCGAGCCCAGCCGACACTCACCTCAAGTCTGAGAATGACAAGCTGAAGATCGCGCTGACAC
 AGAGTGTGCCAATGTGAAGAAGTGGGAGATGGAGCTGCAGACCTGCGGGAGAGCAACGCCCGGCTGAC
 CACGGCACTGCAGGAGTCGGCGCCAGCGTGGAGCAGTGGAAAGCGGCAGTTCTCCATCTGCAGGGACGAG
 AATGACAGGCTCCGCAGCAAGATCGAGGAGCTGGAAGAAGTGCAGCGAGATAAACAGGGAGAAGGAGA
 AGAACACACAGCTGAAGAGGAGGATCGAGGAGCTGGAGTCAAGGTCAGAGGTCGAGACAAGGAGATGGAGTTGAA
 AGATCTCCGAAAACAGAGTGAATCATACCTCAGCTCATGTCCGAGTGTGAATATGTCTCTGAGAAGTTA
 GAGGCGGCCGAAAAGAGACAATCAAACTTGAAGACAAAGTGCAGTCTCTAAAGACAGACATCGAGGAGA
 GTAATAACCGACAGCGCCACCTGAAGGGGAGCTGAAGAGCTTCTTGAGGTGCTGGATGAAAAGATCGA
 CGACCTCCATGACTTCCGTAGAGGACTCTCAAGTTAGGCACAGATAACTAG

ACGGTACGGCGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI
ACCN: NM_001164086



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Insert Size:	1032 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:	<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:	<u>NM_001164086.1</u> , <u>NP_001157558.1</u>
RefSeq Size:	10966 bp
RefSeq ORF:	1032 bp
Locus ID:	26557
UniProt ID:	<u>Q9QWW1</u>
Cytogenetics:	7 D3
Gene Summary:	<p>Postsynaptic density scaffolding protein. Binds and cross-links cytoplasmic regions of GRM1, GRM5, ITPR1, DNMT3, RYR1, RYR2, SHANK1 and SHANK3. By physically linking GRM1 and GRM5 with ER-associated ITPR1 receptors, it aids the coupling of surface receptors to intracellular calcium release. May also couple GRM1 to PI3 kinase through its interaction with AGAP2 (By similarity). Isoforms can be differently regulated and may play an important role in maintaining the plasticity at glutamatergic synapses (By similarity) Required for normal hearing (PubMed:25816005). Negatively regulates T cell activation by inhibiting the calcineurin-NFAT pathway. Acts by competing with calcineurin/PPP3CA for NFAT protein binding, hence preventing NFAT activation by PPP3CA (By similarity).[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (2) uses an alternate in-frame splice site in the central coding region, compared to variant 1. The resulting isoform (2) lacks an internal 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.</p>