

Product datasheet for MC213929

Olfr915 (NM_146785) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Olfr915 (NM_146785) Mouse Untagged Clone
Tag: Tag Free
Symbol: Olfr915
Synonyms: MOR167-4
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC213929 representing NM_146785
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGGATCGCC**

ATGGGTTTCGGAAATGGCTCTTCAGTGACTGAGTTCATTCTGGTGGGATTAACCAAGGACCCTGATCTCC
 AATGCCCTCTTTTCGTCCTCTTTCTAGTGATGTATGTTCTCACTGTATTGGGAAATCTGAGTTTGATTAC
 CTTAATTGTAAGTGAATTCTCACCTTCATACCCCAATGTACTTTTTCTCTTTAACTTGCTACTAGTTGAC
 TTCTGGTACTCTCTGTGTTACACCAAAAATGCTAATGAGCTTTATATCAGAGAAGAACATTATTTCTCT
 ATAGAGGATGCATGACCAACTTTTCTTTTTAGTTTTTCTGCATTTCTGAATATTATGTGTGACTGT
 AATGGCCTATGATCGCTATGTGGCCATATGTAATCCACTCTTGTACAATATTGTCATGTCTCCTAAATTA
 TGTTTTGAACCTCATACTTGGCTCATATAATGGCATTCTAGTGCCATGGCTCACACGGGATGCATGC
 TGAGACTGACCTTCTGTGATGCAACACCATCAATCACTACTTCTGTGACATCCTCCCTTTGCTTCAGCT
 CTCCTGCACCAGCATCTATGTCAACGAGCTGGAGGTTTTGTTGTAATAGGCATCAACATTATTGTGCC
 ACCATCACCATCTTTATCTTTATGGTTTTATCATCTCAAGATTTTTTCGATCAGCTCCAAGGAGGGCA
 GGTCCAAGCCTTCAGCACCTGCAGTCCCACATAATTGCAGTTCTCTGTTCTTTGGATCAGGTGCATT
 TATGTATCTCAAACCATCTTCTGCTGAGTCAATGAATGAAAGTAAAGTCTCGTCTGCTTTTATACCAAT
 ACAGTTCTCTACTGAATCCCTTAATCTACAGCTTGGAGAACAAAGATGTTAAAATTGCCTTGATAAAGA
 CCTGAGTAAGAGAAAGTGTGA

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI
ACCN: NM_146785
Insert Size: 933 bp



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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:	NM_146785.2 , NP_666996.2
RefSeq Size:	933 bp
RefSeq ORF:	933 bp
Locus ID:	258781
Cytogenetics:	9 A5.1
Gene Summary:	<p>Olfactory receptors interact with odorant molecules in the nose, to initiate a neuronal response that triggers the perception of a smell. The olfactory receptor proteins are members of a large family of G-protein-coupled receptors (GPCR) arising from single coding-exon genes. Olfactory receptors share a 7-transmembrane domain structure with many neurotransmitter and hormone receptors and are responsible for the recognition and G protein-mediated transduction of odorant signals. The olfactory receptor gene family is the largest in the genome. The nomenclature assigned to the olfactory receptor genes and proteins for this organism is independent of other organisms. This olfactory receptor gene appears to represent a strain-specific polymorphic pseudogene in mouse, where some strains, including the C57BL/6 reference genome strain, have a non-functional allele, while other strains have a protein-coding allele. [provided by RefSeq, Jan 2019]</p> <p>Transcript Variant: This variant (1, coding) represents the non-reference strain functional allele and encodes the full-length protein. It is not present in some mouse strains, including the C57BL/6 strain of the reference genome. 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>