

## Product datasheet for **RC211209L4V**

### **TAS2R38 (NM\_176817) Human Tagged ORF Clone Lentiviral Particle**

#### **Product data:**

Product Type:	Lentiviral Particles
Product Name:	TAS2R38 (NM_176817) Human Tagged ORF Clone Lentiviral Particle
Symbol:	TAS2R38
Synonyms:	PTC; T2R38; T2R61; THIOT
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-mGFP-P2A-Puro (PS100093)
Tag:	mGFP
ACCN:	NM_176817
ORF Size:	999 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC211209).
OTI Disclaimer:	The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. <a href="#">More info</a>
OTI Annotation:	This clone was engineered to express the complete ORF with an expression tag. Expression varies depending on the nature of the gene.
RefSeq:	<a href="#">NM_176817.2</a>
RefSeq Size:	1143 bp
RefSeq ORF:	1002 bp
Locus ID:	5726
UniProt ID:	<a href="#">P59533</a>
Cytogenetics:	7q34
Protein Families:	Druggable Genome, Transmembrane
Protein Pathways:	Taste transduction



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**MW:** 37.9 kDa

**Gene Summary:** This gene encodes a seven-transmembrane G protein-coupled receptor that controls the ability to taste glucosinolates, a family of bitter-tasting compounds found in plants of the Brassica sp. Synthetic compounds phenylthiocarbamide (PTC) and 6-n-propylthiouracil (PROP) have been identified as ligands for this receptor and have been used to test the genetic diversity of this gene. Although several allelic forms of this gene have been identified worldwide, there are two predominant common forms (taster and non-taster) found outside of Africa. These alleles differ at three nucleotide positions resulting in amino acid changes in the protein (A49P, A262V, and V296I) with the amino acid combination PAV identifying the taster variant (and AVI identifying the non-taster variant). [provided by RefSeq, Oct 2009]