

## Product datasheet for **SC332756**

### **P2RX4 (NM\_001261397) Human Untagged Clone**

#### Product data:

**Product Type:** Expression Plasmids  
**Product Name:** P2RX4 (NM\_001261397) Human Untagged Clone  
**Tag:** Tag Free  
**Symbol:** P2RX4  
**Synonyms:** P2X4; P2X4R  
**Vector:** pCMV6-Entry (PS100001)  
**Fully Sequenced ORF:** >SC332756 representing NM\_001261397.  
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

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ATGGCGGGCTGCTGCGCCGCGCTGGCGGCCTTCCTGTTTCGAGTACGACACGCCGCGCATCGTGCTCATC
CGCAGCCGCAAAGTGGGGCTCATGAACCGCGCCGTGCAACTGCTCATCCTGGCCTACGTCATCGGGTGG
GTGTTTGTGTGGAAAAGGGCTACCAGGAACTGACTCCGTGGTCAGCTCCGTTACGACCAAGGTCAAG
GGCGTGGCTGTGACCAACTTCTAACTTGGATTCCGGATCTGGGATGTGGCGGATTATGTGATACCA
GCTCAGGAGGAAAACCTCCTCTTCGTATGACCAACGTGATCCTCACCATGAACCAGACACAGGGCCTG
TGCCCCGAGATCCAGATGCGACCACTGTGTGTAATCAGATGCCAGCTGTACTGCCGGCTCTGCCGGC
ACCCACAGCAACGGAGTCTCAACAGGCAGACCTGCTTTTTAAAGGCTGCAGAAAACCTCACTCTTTTG
GTTAAGAACAACATCTGGTATCCCAAATTTAATTTTCAGCAAGAGGAATATCCTTCCCAACATCACCCT
ACTTACCTCAAGTCGTGCATTTATGATGCTAAAACAGATCCCTTCTGCCCATATTCCTGTTGGCAA
ATAGTGGAGAACGCAGGACACAGTTTCCAGGACATGGCCGTGGAGGGAGGCATCATGGGCATCCAGGTC
AACTGGGACTGCAACCTGGACAGAGCCGCTCCCTCTGCTTGCCAGGTAATCCTTCCGCCGCTCGAT
ACACGGGACGTTGAGCACAACGTATCTCCTGGCTACAATTTTCAGGTTTGCCAAGTACTACAGAGACCTG
GCTGGCAACGAGCAGCGCAGCTCATCAAGGCCTATGGCATCCGCTTCGACATCATTGTGTTTGGGAAG
GCAGGAAAATTTGACATCATCCCCTATGATCAACATCGGCTCTGGCCTGGCACTGCTAGGCATGGCG
ACCGTGTGTGTGACATCATAGTCTCTACTGCATGAAGAAAAGACTCTACTATCGGGAGAAGAAATAT
AAATATGTGGAAGATTACGAGCAGGGTCTTGTCTAGTGAGCTGGACCAGTGA
  
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**Restriction Sites:** SgfI-MluI  
**ACCN:** NM\_001261397  
**Insert Size:** 1086 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).



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<b>Components:</b>	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).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"><li>1. Centrifuge at 5,000xg for 5min.</li><li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li><li>3. Close the tube and incubate for 10 minutes at room temperature.</li><li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li><li>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.</li></ol>
<b>RefSeq:</b>	<u>NM_001261397.1</u>
<b>RefSeq Size:</b>	2023 bp
<b>RefSeq ORF:</b>	1086 bp
<b>Locus ID:</b>	5025
<b>UniProt ID:</b>	<u>Q99571</u>
<b>Cytogenetics:</b>	12q24.31
<b>Protein Families:</b>	Druggable Genome, Ion Channels: ATP Receptors, Transmembrane
<b>Protein Pathways:</b>	Calcium signaling pathway, Neuroactive ligand-receptor interaction
<b>MW:</b>	40.5 kDa
<b>Gene Summary:</b>	<p>The product of this gene belongs to the family of purinoceptors for ATP. This receptor functions as a ligand-gated ion channel with high calcium permeability. The main pharmacological distinction between the members of the purinoceptor family is the relative sensitivity to the antagonists suramin and PPADS. The product of this gene has the lowest sensitivity for these antagonists. Multiple alternatively spliced transcript variants, some protein-coding and some not protein-coding, have been found for this gene. [provided by RefSeq, Feb 2012]</p> <p>Transcript Variant: This variant (5) lacks an in-frame exon in the 5' coding region and an in-frame segment in the central coding region, compared to variant 1. The resulting isoform (3) lacks two internal segments, 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>