

Product datasheet for **MC215800**

P2rx7 (NM_001038845) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: P2rx7 (NM_001038845) Mouse Untagged Clone
Tag: Tag Free
Symbol: P2rx7
Synonyms: A1467586; P2X(7); P2X7R
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC215800 representing NM_001038845
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**GCGATCGCC**

ATGCCGGCTTGTGCAGCTGGAACGATGTCTTGCAGTATGAGACAAACAAAGTCACCCGGATCCAGAGCA
 CGAATTATGGCACCGTCAAGTGGGTCTTGCACATGATCGTCTTTTCTACATTAGCTTTGCTTTGGTGAG
 CGATAAGCTGTACCAGCGAAAGAGCCTGTTATCAGCTCCGTGCACACCAAGGTCAAAGGCATAGCAGAG
 GTGACGGAGAATGTCACAGAGGGTGGGGTGACGAAGTTAGGACACAGCATCTTTGACACTGCAGACTACA
 CCTTCCCTTTCAGGGGAACCTATTCTTTGTCATGACAACTATGTCAAGTCAGAAGGCCAAGTGCAGAC
 GCTGTGCTCCTGAGTATCCAGGGCGGGTGCACAGTGTCTTCTGACCGGGCTGTAAAAAGGGGTGGATG
 GACCCACAGAGCAAAGGAATCCAGACTGGCAGGTGTGTTCCATATGACAAGACAAGGAAGACCTGTGAAG
 TCTCTGCCTGGTGTCTACTGAGGAGGAGAAAGAGCTCCCCGACCTGCACTCTTGAGGAGCGCCGAAAA
 CTTACCGTACTCATCAAGAATAATATCCACTTCCCCGGCCACAATAACCACGAGAAACATCTTGCCA
 ACTATGAACGGCTCTTGTACCTTTCACAAGACTTGGGACCCTCAGTGTTCATCTTCCGACTAGGGGACA
 TCTCCAGGAAGCAGGAGAGAACCTTACAGAGGTGGCAGTTCAGGGAGGAATCATGGGTATCGGATCTA
 CTGGGATTGCAACCTAGACAGCTGGTCCCATCACTGCCGACCCAGGTACAGCTTCCGCCGCTGGATGAC
 AAGAACACGGATGAGTCCTTCGTCGCCGCTACAACCTCAGATATGCCAAGTACTATAAGGAGAACAATG
 TGGAAAAGCGGACGTTGATCAAAGCCTTCGGCATCCGTTTTGACATCCTGGTTTTCGGCACTGGAGGAAA
 ATTTGACATCATCCAGCTGGTTGTATACATTGGATCCACCCTGTCTACTTTGGCTTGGCCACTGTGTGC
 ATTGACTTGCTCATCAACACATACTCCAGTGCTTTCTGCAGGTGGGGGTTTACCCTACTGTAAGTGCT
 GTGAGCCCTGCACAGTGAACGAGTATTACTACAGAAAGAAGTGTGAGTCCATCATGGAACCAAGCCGAC
 GTTGAAGTATGTGCCTTTGTCGACGAGCCGCACATTTCGCATGGTGGACCAGCAGCTGCTGGGAAAAGT
 CTGCAAGTTGTCAAAGGCCAAGAAGTTCAGTACGGGTGCTTTGCCTGCATGTATGTATGCCACCTGA

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA



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Restriction Sites:	Sgfl-Mlul
ACCN:	NM_001038845
Insert Size:	1329 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_001038845.2</u> , <u>NP_001033934.1</u>
RefSeq Size:	1633 bp
RefSeq ORF:	1329 bp
Locus ID:	18439
Cytogenetics:	5 F
Gene Summary:	<p>Receptor for ATP that acts as a ligand-gated ion channel. Responsible for ATP-dependent lysis of macrophages through the formation of membrane pores permeable to large molecules. Could function in both fast synaptic transmission and the ATP-mediated lysis of antigen-presenting cells. In the absence of its natural ligand, ATP, functions as a scavenger receptor in the recognition and engulfment of apoptotic cells.[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (2) contains an alternate 3' terminal exon and differs in the 3' UTR and the 3' coding region, compared to variant 1. It encodes isoform b, which is shorter and has a distinct C-terminus, compared to isoform a. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.</p>