

## Product datasheet for RN216132

### Aqp4 (NM\_001270559) Rat Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	Aqp4 (NM_001270559) Rat Untagged Clone
Tag:	Tag Free
Symbol:	Aqp4
Synonyms:	AQP-4; Miwc; WCH4
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>RN216132 representing NM_001270559 Red=Cloning site Blue=ORF Orange=Stop codon

TTTGTAAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
 GCC**CGATCGCC**

ATGGTGGCTTTCAAAGCGTCTGGACTCAAGCCTTCTGGAAGCGGTACAGCAGAGTTCCTGGCCATGC  
 TCATCTTTGTTCTGCTCAGCGTGGGATCCACCATTAACTGGGGTGGCTCAGAGAACCCCTACCTGTGGA  
 CATGGTCTCATCTCCCTCTGCTTTGGACTCAGCATTGCCACCATGGTTCAGTGTTCGGCCACATCAGC  
 GGTGGCCACATCAACCCAGCGGTGACAGTGGCCATGGTGTGCACACGAAAGATCAGCATCGCCAAGTCCG  
 TCTTCTACATCACTGCGCAGTGCCTGGGGGCCATCATCGGAGCTGGGATCCTCTACCTGGTCACACCCC  
 CAGCGTGGTGGGAGGATTGGGAGTCAACACGATCAATTATACCGAGCCAGCATGAATCCAGCTCGATCC  
 TTTGGCCCTGCAGTTATCATGGGAACTGGGAAAACCACTGGATATATTGGGTTGGACCAATCATAGGCG  
 CTGTGCTGGCAGGTGCACTTTACGAGTATGTCTTCTGTCTGACGTGGAGCTCAAACGTCGCCTAAAGGA  
 AGCCTTCAGCAAAGCTGCACAGCAGACGAAAGGGAGCTACATGGAGGTGGAGGACAACCGGAGCCAAGTG  
 GAGACAGAAGACTTGATCCTGAAGCCCGGGTGGTGCATGTGATCGACATTGACCGTGGAGACGAGAAGA  
 AGGGGAAGGACTCGTCTGGAGAGGTATTATCTTCTGTATGA

**ACGCGT**ACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT  
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites:	SgfI-MluI
ACCN:	NM_001270559
Insert Size:	741 bp


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<b>OTI Disclaimer:</b>	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).
<b>OTI Annotation:</b>	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
<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>Note:</b>	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
<b>RefSeq:</b>	<u>NM_001270559.2, NP_001257488.1</u>
<b>RefSeq Size:</b>	4853 bp
<b>RefSeq ORF:</b>	741 bp
<b>Locus ID:</b>	25293
<b>Cytogenetics:</b>	18p13
<b>Gene Summary:</b>	<p>This gene encodes a member of the aquaporin family of intrinsic membrane proteins that function as water-selective channels in the plasma membranes of many cells. This protein is the predominant aquaporin found in brain and has an important role in brain water homeostasis. Alternatively spliced transcript variants encoding different isoforms have been described for this gene. A recent study provided evidence for translational readthrough in this gene and expression of an additional C-terminally extended isoform via the use of an alternative in-frame translation termination codon. [provided by RefSeq, Dec 2015]</p> <p>Transcript Variant: This variant (4, also known as AQP4d) contains an alternate 5' terminal exon and lacks an in-frame coding exon compared to variant 1. These changes result in translation initiation from an in-frame, downstream start codon, and an isoform (4) with a shorter N-terminus and missing an internal protein segment compared to isoform M1.</p> <p>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>