

Product datasheet for **SC108945**

Aquaporin 4 (AQP4) (NM_001650) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Aquaporin 4 (AQP4) (NM_001650) Human Untagged Clone
Tag:	Tag Free
Symbol:	Aquaporin 4
Synonyms:	MIWC; WCH4
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL5</u>
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>OriGene ORF within SC108945 sequence for NM_001650 edited (data generated by NextGen Sequencing)

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ATGAGTGACAGACCCACAGCAAGCGGTGGGGTAAAGTGTGGACCTTTGTGTACCAGAGAG
AACATCATGGTGGCTTTCAAAGGGTCTGGACTCAAGCTTTCTGAAAGCAGTCACAGCG
GAATTTCTGGCCATGCTTATTTTGTTCCTCAGCCTGGGATCCACCATCAACTGGGGT
GGAACAGAAAAGCCTTTACCGGTCGACATGGTTCTCATCTCCCTTTGCTTTGGACTCAGC
ATTGCAACCATGGTGCAGTGCTTTGGCCATATCAGCGGTGGCCACATCAACCCTGCAGTG
ACTGTGGCCATGGTGTGCACCAGGAAGATCAGCATCGCCAAGTCTGTCTTCTACATCGCA
GCCAGTGCCTGGGGCCATCATTGGAGCAGGAATCCTCTATCTGGTCACACCTCCCAGT
GTGGTGGGAGGCCTGGGAGTCACCATGGTTCATGAAAATCTTACCCTGGTCATGGTCTC
CTGGTTGAGTTGATAATCACATTTCAATTGGTGTCTTACTATCTTTGCCAGCTGTGATTCC
AAACGGACTGATGTCACCTGGCTCAATAGCTTTAGCAATTGGATTTCTGTGCAATTGGA
CATTTATTTGCAATCAATTATACTGGTGCCAGCATGAATCCCGCCGATCCTTTGGACCT
GCAGTTATCATGGGAAATTGGGAAAACCATGGATATATTGGGTTGGGCCCATCATAGGA
GCTGTCTCGCTGGTGGCCTTTATGAGTATGTCTTCTGTCCAGATGTTGAATTCAAACGT
CGTTTTAAAGAAGCCTTCAGCAAAGCTGCCAGCAAACAAAAGGAAGCTACATGGAGGTG
GAGGACAACAGGAGTCAGGTAGAGACGGATGACCTGATTCTAAAACCTGGAGTGGTGCAT
GTGATTGACGTTGACCGGGGAGAGGAGAAGAAGGGGAAAGACCAATCTGGAGAGGTATTG
TCTTCAGTATGA

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Clone variation with respect to NM_001650.4



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5' Read Nucleotide Sequence:	<p>>OriGene 5' read for NM_001650 unedited</p> <pre> NNNNNNNNNNNGTTCAAATTTTGTNATACGACTCATATAGGCGGCCGCGNATTCGGCAC GAGGCCTCGTGCCGAATTCGGCACGAGGCTGCACTCTGGCTGGGGAAGGCATGAGTGACA GACCCACAGCAAGGCGGTGGGGTAAAGTGTGGACCTTTGTGTACCAGAGAGAACATCATGG TGGCTTCAAAGGGTCTGGACTCAAGCTTCTGGAAAGCAGTCACAGCGGAATTTCTGGC CATGCTTATTTTTGTTCTCCTCAGCCTGGGATCCACCATCAACTGGGGTGAACAGAAAA GCCTTACC GGTCGACATGGTTCTCATCTCCCTTGGCTTGGACTCAGCATTGCAACCAT GGTGCAGTGCTTTGGCCATATCAGCGGTGGCCACATCAACCCTGCAGTGACTGTGGCCAT GGTGTGCACCAGGAAGATCAGCATCGCCAAGTCTGTCTTCTACATCGCAGCCAGTGCCCT GGGGGCCATCATTGGAGCAGGAATCCTCTATCTGGTCACACCTCCAGTGTGGTGGGGAG GCCCTGNGAGTCACCATGGTTCATGGAAATCTTACCGCTGGTCATGGTCTCCTGGNNTGA GNTGATAATCACATTTCAATTGGGTGTTACTANTCTTGGCCAGCTGTGATTCCAAACGG ACTGATGCACTGGCTCAATAGCTNTAGCATTGGATTTCTGGGTGCATTGGACATTTT TATTTGCATCAATTATACTGGNTGCCAGCATGAATCCCGCCGATCCTTTTGACCTGCAG TTATCATGGGAAATTGGGAAAAACATTGATATATTGTGGGGTTGGGCCCATCATAGGG AGCTGTCCCTCCCTGGTGGGCTTATGGAAGTATGGTCTGTGCCAAAGTTGGATTCAA AACGTCGGTTTTAAAGAAACCCTTCAGCCAAGTGCC </pre>
3' Read Nucleotide Sequence:	<p>>OriGene 3' read for NM_001650 unedited</p> <pre> NAAATTGACTTGNNACCGCGCCGCTTNTANGATCGAGTTTTTTTTTTTTTTTTTTTACC TTTTAAAACATCCATGTTTATTTTCAACAAGCTTAGTAGTACAAGATGCAACATAATTCAA GAAAATCAACCACAGTGTAATACTTTAATATATTATTCCAAATATTAGACGTTACAGTT TAAATCTTTTTAACATTAGCTCTAATGTTGGAATAACATTTAAGTTAATAAATAACTGTG AATATAACCATATGTTTCAGTCTATTCTCCCGATTTATCCTAAATGACAATTTTATTGTG ATTTGGGTCATAAAAGTGATAAATAATTGTTTATATGTTTTTCATAAATTGCATGTTTATT TAATTAATCCTGAAGAGAACCTAGAAAATACATTCCAATGGGTTACATAAATTAGACGTAT TTTTTAGCTCTTCGATTTTTTTTTAAACATGAGTGAGTCACTGTAACCTGCTCTTAAATT TAGTGTTTCATTGCACATAACATTTTTTGAATGTATTTTACAGGCTATAGGTAGTCATT TGCAAAGATGGCCACAATTTTTGATCCTTGAATTAATGTCTTTCATTTATTTTCAGAGAA TTATGAGTTTCAAAGCTACTGCTCTTATGGGGCAATCTGTAGAGTACTAAACTCACAAA ATTTGTGGTAACAAAAGAGAGTTTTGTTACATTACACTTCCAAATAGTAACCACATCTT CCTACTAATTTTTCATGTTAAAAACACTTTAGGAAAGACAGAATTACTTTTAGGTAAAAA TGTTCTGAATTTGCAAATCTATAGTGCTTATGAGAAATTATATTGGGCTTTTATATTGT TTTGATAAAGTTGTCTGGTGCCCCCAAACCTTCCATCTTCAGTTGGCACCAAAGCAAATT CTCTGTGGATT </pre>
Restriction Sites:	NotI-NotI
ACCN:	NM_001650
Insert Size:	5000 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:

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_001650.4](#), [NP_001641.1](#)

RefSeq Size: 5216 bp

RefSeq ORF: 972 bp

Locus ID: 361

UniProt ID: [P55087](#)

Cytogenetics: 18q11.2

Domains: MIP

Protein Families: Druggable Genome, Transmembrane

Gene Summary: 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. Additional isoforms, resulting from the use of alternative in-frame translation initiation codons, have also been described. Recent studies provided evidence for translational readthrough in this gene, and expression of C-terminally extended isoforms via the use of an alternative in-frame translation termination codon. [provided by RefSeq, Jun 2018]

Transcript Variant: This variant (1, also known as hMIWC2) represents the predominant transcript and encodes four isoforms, resulting from the use of two alternative in-frame translation initiation codons and two alternative in-frame translation termination codons. This RefSeq represents isoform M1, which results from the use of the upstream AUG start codon and the upstream UGA stop codon. **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.