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Product datasheet for MC213152

Cldn19 (NM_153105) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Cldn19 (NM_153105) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Cldn19
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC213152 representing NM_153105 Red=Cloning site Blue=ORF Orange=Stop codon TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCCGCGATCGCC ATGGCCAACTCGGGCCTCCAGCTCCTGGGCTACTTCCTAGCCTTGGGCGGCTGGGTGGGCATCATCGCCA GCACTGCCCTGCCACAGTGGAAGCAGTCTTCCTATGCAGGCGATGCCATCATCACTGCCGTGGGCCTCTA CGAAGGGCTGTGGATGTCTTGCGCCTCTCAGAGCACCGGGCAGGTGCAATGCAAACTCTACGATTCACTC CTGGCCCTGGACGGTCATATCCAGTCAGCACGAGCCCTGATGGTCGTGGCTGTGCTCCTGGGCTTTGTGG CCATGGTGCTCAGTGTCGTGGGCATGAAGTGCACTCGGGTTGGAGACAGTAACCCCACTGCCAAGAGCCG TGTGGCCATCTCCGGAGGTGCTCTCTTCCTCTTGGCAGGTCTCTGTACTTTGACTGCTGTCTCCTGGTAT GCTACCCTGGTAACACAGGAATTCTTCAACCCCAGCACTCCTGTCAATGCCAGGTACGAATTTGGCCCAG CTCTGTTCGTCGGCTGGGCCTCGGCCGGCCTGGCCATGCTGGGCGGTTCCTTTCTCTGCTGCACATGCCC AGAGCCGGAGAGGGCGAACAGCATCCCACAGCCCTATCGCTCTGGACCCTCAACTGCTGCCAGAGAGTAC GTCTGA ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT ACAAGGATGACGACGATAAGGTTTAA
Restriction Sites:	SgfI-MluI
ACCN:	NM_153105
Insert Size:	636 bp

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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.
Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	NM_153105.7, NP_694745.1
RefSeq Size:	4236 bp
RefSeq ORF:	636 bp
Locus ID:	242653
UniProt ID:	Q9ET38
Cytogenetics:	4 D2.1
Gene Summary:	This gene encodes a member of the claudin family. Claudins are integral membrane proteins and components of tight junction strands. Tight junction strands serve as a physical barrier to prevent solutes and water from passing freely through the paracellular space between epithelial or endothelial cell sheets, and also play critical roles in maintaining cell polarity and signal transductions. siRNA knockdown of this gene in mice develops the FHHNC (familial hypomagnesemia with hypercalciuria and nephrocalcinosis) symptoms of chronic renal wasting of magnesium and calcium together with defective renal salt handling. The protein encoded by this gene interacts with another family member, Claudin 16, and their interaction is required for their assembly into tight junctions and for renal reabsorption of magnesium. This protein is a constituent of tight junctions in the Schwann cells of peripheral myelinated nerves and the gene deficiency affects the nerve conduction of peripheral myelinated fibers. Alternatively spliced transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Aug 2010] Transcript Variant: This variant (2) has an additional segment in the last splice junction, as compared to variant 1. The transcript is longer but the resulting isoform (2) is shorter at the C-terminus, as compared to isoform 1. 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.