

## Product datasheet for **MC223500**

### Slc4a10 (NM\_033552) Mouse Untagged Clone

#### Product data:

**Product Type:** Expression Plasmids  
**Product Name:** Slc4a10 (NM\_033552) Mouse Untagged Clone  
**Tag:** Tag Free  
**Symbol:** Slc4a10  
**Synonyms:** mKIAA4136; NCBE  
**Vector:** pCMV6-Entry (PS100001)  
**E. coli Selection:** Kanamycin (25 ug/mL)  
**Cell Selection:** Neomycin  
**Fully Sequenced ORF:** >MC223500 representing NM\_033552  
**Red**=Cloning site **Blue**=ORF **Orange**=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
GCC**CGGATCGCC**

ATGGAGATTAAGACCAGGGAGCCCAAATGGAGCCGCTGCTGCCTACGAGAAATGATGAAGAAGCCGTTG  
TGGATAGAGGTGGAACACGCTCTATTCTCAAACACATTTTGAGAAAGAAGATTTAGAAGGTCATCGGAC  
ATTATTTATTGGAGTTCATGTGCCCTGGGTGGAAGAAAAGCCATCGTCGTACAGGCATCGTGGTCAT  
AAGCACAGAAAGAGGGACAGAGAGAGAGATTCCGGACTGGAGGATGGAAGAGAGTCCCCTCTTTTGACA  
CCCCATCGCAGAGGGTGCAGTTTATTCTTGAAGTGAAGGACGATGATGAGGAGCACCTCCCTCATGACCT  
TTTCACAGAGCTGGATGAGATTTGCTGGCGTGAAGGGGAAGATGCTGAGTGGCGAGAGACAGCCAGGTGG  
TTGAAATTTGAAGAGGATGTGGAAGATGGAGGAGAAAGATGGAGTAAGCCCTATGTGGCCACGCTTTCAT  
TACACAGCTTGTGGAGTTGAGAAGCTGCATCCTGAATGGAAGTGTGCTACTGGACATGCATGCCAACAC  
GATAGAAGAAATGCAGATATGGTCCTTGACCAGCAGGTCAGCTCAGGCCAGTGAATGAAGATGTTCCG  
CACAGGGTCCACGAAGCATTGATGAAGCAGCATCATCACCAGAATCAGAAAAAAGTGCCTAACAGGATTC  
CTATTGTCCGATCTTTGCTGATATTGGCAAGAAACAATCAGAACCAAATTCATGGATAAAAAAGCAGC  
TCAGTTGTTTCTCCTCAGTCTGCTCCAGCCTGTGCTGAGAATAAAAAATGATGTCAGCAGGGAAAAACAGC  
ACTGTAGACTTCAGCAAGTTGATCTGCATTTTATGAAAAAGATTCTCCGGGTGCTGAAGCTTCAAACA  
TCTTGGTAGGAGAACTGGAGTTCCTAGACAGAAGTGTGGTTCCTTTGTCAGGTTGTCTCCAGCTGTCTT  
GCTCCAAGGACTTGTGAAGTTCGAATCCCAAGCAGATTTCTGTTTCATCCTTCTGGGACCCCTGGGAAAG  
GGTCAACAGTACCACGAGATTGGCAGATCGATTGCGACCTTAATGACTGATGAGGTGTTTCATGATGTTG  
CTTACAAAGCTAAAGACCGCAATGACTTGGTATCAGGAATTGATGAGTTTCTGGATCAGGTTACCGTCT  
TCCTCCTGGAGAATGGGATCCAAGCATAACGAATAGAACCTCCAAAAATGTCCTTCCCAGGAGAAGAGG  
AAGATTCTGCTGTACCAATGGAACAGCAGCTCATGGCGAAGCTGAGCCACATGGAGGACACAGCGGAC  
CTGAACCTCAGCGAACTGGGAGGATTTTGGGGGACTTATATTAGATATCAAAGAAAGGCTCCATTCTT  
CTGGAGTGACTTCAGGGATGCTTTCAGCCTGCAGTGTAGCATGTTTCTGTTTCTACTGTGCATGC  
ATGTCTCCTGTATCACATTTGGAGGACTGTTGGGAGAAGCAACTGAAGTTCGTATAAGTGAATCGAAT



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CACTCTTTGGAGCATCTATGACCGGGATAGCCTATTCTCTTTTTGGTGGACAGCCCCTGACCATATTAGG  
 CAGCACAGGACCTGTTTTGGTGTGTTGAAAAGATCTTGTTAAGTTTTGCAAGGAATACGGCCTGTGCTAC  
 TTGTCTTACGGGCCAGCATTGGGCTCTGGACTGCAACACTGTGCATCATCTTGTGGCCACGGACGCGA  
 GCTCACTCGTCTGCTACATCACCCGGTTTACCGAAGAGGCTTTTCTCTCTCATTTGCATCATTTTTAT  
 CTATGAAGCCCTGGAGAAGTTGTTTGGCTCAGTGAAACCTATCCAATCAATATGCACAATGATTTGGAA  
 CTGCTGACACAATACTCATGTAAGTGTATGGAGCCACATAGTCCCAGCAATGACACACTGAAGGAATGGC  
 GGGAGTCCAACCTTTCTGCCTCTGACATAATCTGGGGAACTAACTGTGTCAGAGTGCAGATCACTGCA  
 CGGGGAGTATGTCGGGCCAGCCTGTGGCCATGGCCACCCCTACGTGCCAGATGTTCTCTTCTGGTCGGTG  
 ATCCTGTTCTTCTCCACAGTTACCATGTGAGCCACCCTGAAGCAGTTCAAGACCAGCCGCTATTTCCCAA  
 CCAAGGTCGATCCATAGTGAGTGATTTTGGGTTTTTCTTACAATTCTGTGTATGGTTTTAATTGACTA  
 TGCCATTGGGATCCCATCACAAAACACTACAAGTACCAAGCGTTTTCAAGCCGACCAGAGACGACCGTGGC  
 TGGTTTTGTACACCTTTGGTCCAAACCCATGGTGGACAATCATAGTGCATCATCCCAGCTTTACTCT  
 GTACTATTCTGATTTTCTGACCAGCAGATTACAGCTGCATCATCAACAGAAAAGAGCACAAGCTAAA  
 GAAAGTTGTGGCTATCACCTGGATCTGTTAATGGTGGCAGTCTGCTCGGGTCTGCTCCATTATGGC  
 CTGCCATGGTTTGTGGTCCACAGTTCTCCATCACTCATGTCAACAGCCTCAAGCTCGAATCAGAGT  
 GCTCTGCTCCAGGAGAACAACCAAGTTTCTCGGCATTCCGGAGCAGAGGGTACCCGGGCTCATGATTTT  
 TATTCTTATGGGTTTATCCGTTTTTCTGACCAGCATTCTGAAGTTTATCCCCATGCCAGTGTATACGGA  
 GTGTTTCTTTATATGGGTGCTTCGTCTCTCAAAGGAATTCAGTTATTTGATAGAATAAAGCTCTTCTGGA  
 TGCCAGCCAAACATCAACCAGATTTTCTATCTAATGAGCAGTGGCCCTCCGGAAAGTCCATCTCTTAC  
 AGTCATTAGATGAGTTGCTCGGCCTTCTGTGGATAATCAAAGTTTTCGAGAGCTGCTATTGTCTTTCT  
 ATGATGGTGTGGCACTAGTGTGTTGTGAGAAAGTTGATGGACTTCTGTTTACCAAACGGGAACTCAGT  
 GGCTTGATGATTTAATGCCTGAGAGTAAAAGAAGAACTTGAAGATGCTGAGAAAAGAAGAACAAG  
 TATGCTAGCCATGGAGGACGAGGGCACAGTACAACCTCCACTGGAGGGACACTACAGAGACGACCCGTCT  
 GTGATCAATATTCTGATGAAATGTCAAAGACTGCCATGTGGGGAACTTCTAGTTACTGCTGACAACT  
 CAAAAGAAAAGGAGTACGCTTTCTTCTAAAAGCTCCCTTCTAA

**ACGCGT**ACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT  
 ACAAGGATGACGACGATAAGGTTTAA

**Restriction Sites:**

SgfI-MluI

**ACCN:**

NM\_033552

**Insert Size:**

3267 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\\_033552.3](#), [NP\\_291030.2](#)

RefSeq Size: 5463 bp

RefSeq ORF: 3267 bp

Locus ID: 94229

Cytogenetics: 2 C1.3

**Gene Summary:** Sodium/bicarbonate cotransporter which plays an important role in regulating intracellular pH (PubMed:10993873, PubMed:20566632). Has been shown to act as a sodium/bicarbonate cotransporter in exchange for intracellular chloride (PubMed:10993873, PubMed:20566632). Has also been shown to act as a sodium/bicarbonate cotransporter which is not responsible for net efflux of chloride, with the observed chloride efflux being due to chloride self-exchange (By similarity). Controls neuronal pH and may contribute to the secretion of cerebrospinal fluid (PubMed:18165320). Reduces the excitability of CA1 pyramidal neurons and modulates short-term synaptic plasticity (PubMed:26136660). Required in retinal cells to maintain normal pH which is necessary for normal vision (PubMed:23056253). In the kidney, likely to mediate bicarbonate reclamation in the apical membrane of the proximal tubules (By similarity).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (2) lacks an alternate in-frame exon and differs in the 3' UTR and coding sequence compared to variant 1. The resulting isoform (2) lacks an alternate internal segment and has a shorter and distinct C-terminus 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.