

## Product datasheet for **MC216883**

### **Slc39a14 (NM\_144808) Mouse Untagged Clone**

#### **Product data:**

Product Type:	Expression Plasmids
Product Name:	Slc39a14 (NM_144808) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Slc39a14
Synonyms:	FAD-123; fad123; ZIP-14; Zip14
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin



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**Fully Sequenced ORF:** >MC216883 representing NM\_144808  
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
 GCC**CGGATCGCC**

ATGAAGCGGCTGCACCCAGCCCTTCCAAGCTGCCTCCTGTTGGTGTGTTTGGTATATGGAGAAGTCCCC  
 CCCAGACTCATGCCTCGTCTGCTGGCCTGCCGCCCTCAGTGCCACCTCCTTCTGGAAGATCTCATGGA  
 CCGCTATGGAAAGAATGACAGCCTTACCCTGACACAGCTGAAGTCCCTGCTCGACCACCTGCATGTGGGA  
 GTGGGCGGGATAATGTTTCCCAGCCAAAGGAAGGACCCAGAACCTCTCCACGTGCTTTAGCTCTGGAG  
 ACCTCTTTGCGGCGCACAACTTGAGCGAGCGATCTCAGATCGGGGCGAGTGAGTTCCAGGAGTTCTGCC  
 CACCATTCTCCAGCAGCTGGATTCCCAGGCCTGCACCTCAGAAAACCAGAACTCTGAGGAGAATGAACAG  
 ACAGAGGAGGGGAAGCCAAGCGCCATTGAAGTATGGGGTACGGTTTCTCTGCGTTACCGTCATCTCCC  
 TCTGCTCCCTCATGGGGCCAGCGTGGTCCCTTCATGAAGAAGACTTTTACAAGAGGCTCCTGCTCTA  
 CTTCATAGCCTTGCGGATTGGAACCTCTACTCCAACGCCCTTCCAGCTCATCCAGAGGCTTTTGGC  
 TTCAACCCTCAGGACAATTACGTCTCCAAGTCTGCAGTGGTGTGGGGGTTTCTACCTTTCTTTTCA  
 CAGAAAAGATCCTGAAGATGCTCTTGAAGCAGAAAAACGAGCACCATCACGGGCATAACCATTTTACCTC  
 CGAGACTTCTTCCAAGAAGGACCAGGAGGAGGTGTACCGAGAAGCTACAGAACGGGGACCTGGAT  
 CACATGATCCCTCAGCACTGCAACAGCGAGCTGGATGGCAAGGCGCTGGCACGGACGAGAAGGTCATTG  
 TCAACTCCATGTCTGTGCAGGACCTGCAGGCATCCCAGAGTGTGCTACTGGCTCAAGGGGTCGGCTA  
 CTCTGATATCGGGACCTTGGCCTGGATGATCACCTGAGCGATGGGCTCCACAATTTTCATCGATGGCCTG  
 GCTATTGGTGCCTCCTTCACTGTGTCTGCTTCCAAGGCATCAGCACGTGAGTGGCCATTCTCTGTGAGG  
 AATTCCTCATGAGCTGGGAGACTTCGTATCCTGCTCAATGCTGGCATGAGCATCCAGCAGGCTCTTT  
 CTTCAACTTCTCTGCTGCTGCTGCTATTTGGGTCTGGCCTTTGGCATCCTGGCTGGCAGCCACTTC  
 TCTGCAAAGTGGATTTTGCAGTGGCTGGAGGAATGTTCTGTATATTGCCCTAGCCGATATGTTCCCTG  
 AGATGAATGAAGTCTGCCAGGAGGATGAGAAGAACGACAGCTTTCTGGTCCCCTTTGTCATCCAGAATCT  
 TGGCCTCTAACCGGCTTCTCCATTATGCTGGTCTCACAATGTATTCAGGGCAGATTAGATCGGG**TAG**

**ACGGT**ACGGCGGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT  
 ACAAGGATGACGACGATAAGGTTTAA

**Restriction Sites:** Sgfl-Mlul

**ACCN:** NM\_144808

**Insert Size:** 1470 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\\_144808.4](#), [NP\\_659057.2](#)

RefSeq Size: 4927 bp

RefSeq ORF: 1470 bp

Locus ID: 213053

UniProt ID: [Q75N73](#)

Cytogenetics: 14 D2

**Gene Summary:** Broad-scope metal ion transporter with a preference for zinc uptake. Also mediates cellular uptake of nontransferrin-bound iron.[UniProtKB/Swiss-Prot Function]  
Transcript Variant: This variant (3) lacks an in-frame exon and contains an alternate in-frame exon in the central coding region, compared to variant 1. The encoded isoform (b) is the same length as isoform a, but contains a distinct internal segment. 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.