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Product datasheet for MC217748

Slc10a1 (NM_001177561) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Slc10a1 (NM_001177561) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Slc10a1
Synonyms:	Ntcp
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Restriction Sites:	SgfI-MluI
ACCN:	NM_001177561
Insert Size:	1089 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_001177561.1, NP_001171032.1
RefSeq Size:	1674 bp
RefSeq ORF:	1089 bp

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Locus ID:	20493
UniProt ID:	O08705
Cytogenetics:	12 37.21 cM
Gene Summary:	The hepatic sodium/bile acid uptake system exhibits broad substrate specificity and transports various non-bile acid organic compounds as well. It is strictly dependent on the extracellular presence of sodium.[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (1) encodes the longer isoform (1). Variants 1 and 3 encode the same 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.