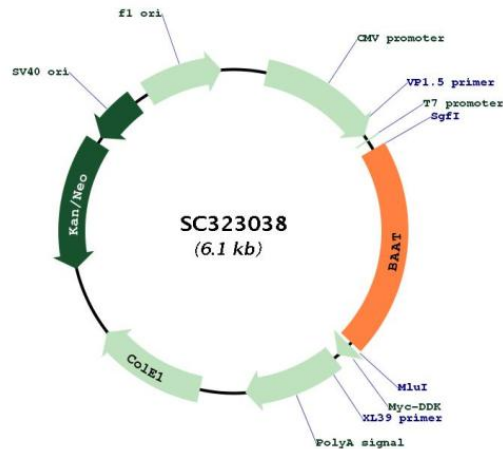




Restriction Sites: SgfI-MluI

Plasmid Map:



ACCN: NM\_001127610

Insert Size: 1257 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).

**OTI Annotation:** This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

**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\\_001127610.1](#)

RefSeq Size: 3377 bp

RefSeq ORF: 1257 bp

Locus ID: 570

UniProt ID: [Q14032](#)

Cytogenetics: 9q31.1

Protein Pathways: Biosynthesis of unsaturated fatty acids, Metabolic pathways, Primary bile acid biosynthesis, Taurine and hypotaurine metabolism

MW: 46.3 kDa

Gene Summary: The protein encoded by this gene is a liver enzyme that catalyzes the transfer of C24 bile acids from the acyl-CoA thioester to either glycine or taurine, the second step in the formation of bile acid-amino acid conjugates. The bile acid conjugates then act as a detergent in the gastrointestinal tract, which enhances lipid and fat-soluble vitamin absorption. Defects in this gene are a cause of familial hypercholanemia (FHCA). Two transcript variants encoding the same protein have been found for this gene. [provided by RefSeq, Jul 2008]  
Transcript Variant: This variant (2) differs in the 5' UTR compared to variant 1. Variants 1 and 2 both encode the same protein. Sequence Note: This RefSeq record was created from transcript and genomic sequence data because no single transcript was available for the full length of the gene. The extent of this transcript is supported by transcript alignments.