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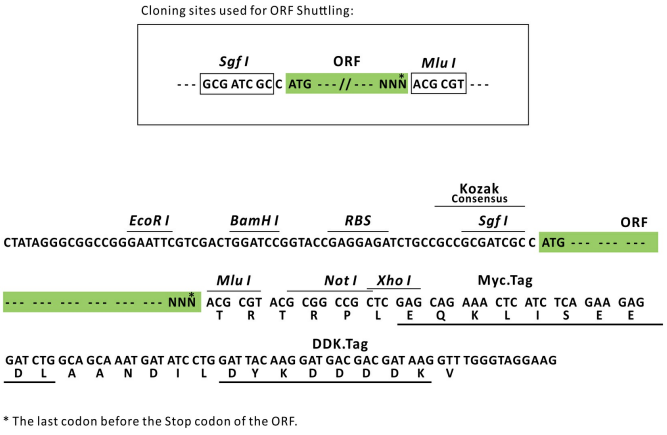
Product datasheet for RC202722L3

BAAT (NM_001701) Human Tagged Lenti ORF Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	BAAT (NM_001701) Human Tagged Lenti ORF Clone
Tag:	Myc-DDK
Symbol:	BAAT
Synonyms:	BACAT; BACD1; BAT; HCHO
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-Myc-DDK-P2A-Puro (PS100092)
E. coli Selection:	Chloramphenicol (34 ug/mL)
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC202722).
Restriction Sites:	SgfI-MluI
Cloning Scheme:	



ACCN:	NM_001701
ORF Size:	1254 bp

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OTI Disclaimer:	The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. More info
OTI Annotation:	This clone was engineered to express the complete ORF with an expression tag. Expression varies depending on the nature of the gene.
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_001701.2
RefSeq Size:	3478 bp
RefSeq ORF:	1257 bp
Locus ID:	570
UniProt ID:	Q14032
Cytogenetics:	9q31.1
Domains:	Bile_Hydr_Trans
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]