

Product datasheet for MR206664

Baat (NM_007519) Mouse Tagged ORF Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Baat (NM_007519) Mouse Tagged ORF Clone
Tag:	Myc-DDK
Symbol:	Baat
Synonyms:	AI118337; AI158864; BAT
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
ORF Nucleotide Sequence:	>MR206664 representing NM_007519 Red=Cloning site Blue=ORF Green=Tags(s)

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGATCGCC**

ATGGCCAAGCTGACAGCTGTTCTCTCAGTGCTCTTGTGATGAGCCTGTGCACATCCAGGTCACAGGCC
TGGCCCCCTTTCAGGTGGTGTGCCTTCAGGCATCACTGAAAGATGAGAAGGAAACCTGTTTAGTCTCA
GGCCTTCTACAGGGCCAGTGAAGTGGGTAGGTAGATCTGGAGCATGACCCCTCACTTGGAGGAGACTAT
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AGTCGTCAGTCCCTTGGATAGCCTGACTCTGGAAAGGTGGTATGTGGCACCTGGGGTCAAGAGGATC
CAGGTAAGGAAAGCCGATCCGGGGAGCCCTGTTTCTGCCTCCAGGAGAAGGTCTTTTCCAGGGGTCA
TTGACTTGTGGAGGTGCTGGTGGATTGATGGAGTCCGGGCCAGTCTTCTGGCAAGTCGTGGCTTTGC
CACCTTAGCTCTGGCTTACTGGAATAATGATGACCTGCCTTCTCGACTGGAGAAGGTAGACTAGAATAT
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CAATGGGCCTAATTTTGTCTCAAAGTCCACATGTATATCATGGTCAGGTCTACCCACCTGTACCCAGT
AATGAAGAGTTTGTAGTACCAATGCCTTGGACTTGTAGAATTCTATCGAACCTTTCAGGAACTGCAG
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AATTGGACTCTGCTGTCTTACCCTGGGGCAGGTACCTGATTGAGCCTCCCTATACCCCACTGTGCCAAG
CCTCAAGGATGCCATTTTGTCCCAAGCCTCAGCTGGGGAGGAGAGTTATCCCCCATGCAGCTGCACA
GGAGCATCTTGGAAAGGATACAGAAATTTCTCAAGCAGCATCTCCTCCAGATTTGAGCAGTCAGCTC

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA



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Protein Sequence: >MR206664 representing NM_007519
 Red=Cloning site Green=Tags(s)

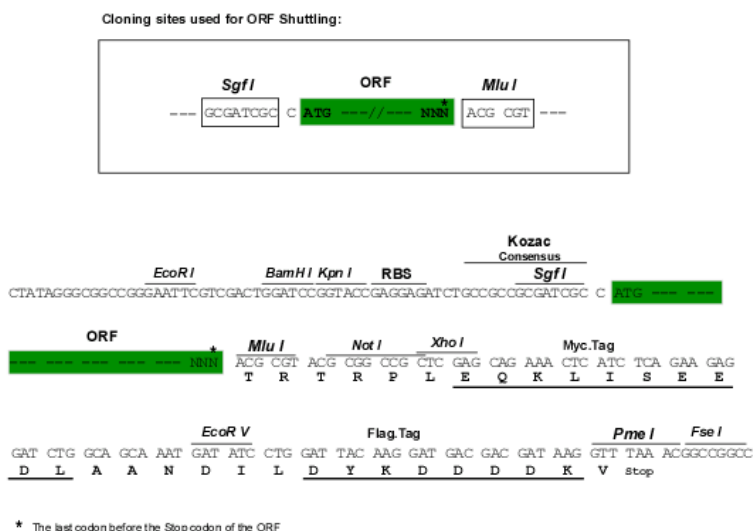
MAKLTAVPLSALVDEPVHIQVTGLAPFQVVCLQASLKDEKGNLFSSQAFYRASEVGEVDLEHDPSLGGDY
 MGVHPMGLFWSLKPEKLLGRLIKRDVMNSPYQIHIKACHPYFPLQDIVVSPPLDSLTLERWYVAPGVKRI
 QVKESRIRGALFLPPGEGPFPGVIDLFGGAGGLMEFRASLLASRGFATLALAYWNYDDLPSRLEKVDLEY
 FEEGVEFLLRHPKVLGPGVGILSVCIGAEIGLSMAINLKQIRATVLIINGPNFVSQSPHVYHGQVYPPVPS
 NEEFVVTNALGLVEFYRTFQETADKDSKYCFPIEKAHGHFLFVVGEDDKNLNSKVHANQAIQLMKNGKK
 NWTLLSYPGAGHLIEPPYTPLCQASRPILIPSLSWGGEVIPHAAAQEHWSKEIQKFLKQHLLPDLSSQL

TRTRPLEQKLISEEDLAANDILDYKDDDDKV

Chromatograms: https://cdn.origene.com/chromatograms/mm9057_c06.zip

Restriction Sites: SgfI-MluI

Cloning Scheme:



ACCN: NM_007519

ORF Size: 1260 bp

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_007519.3](#), [NP_031545.2](#)

RefSeq Size: 1961 bp

RefSeq ORF: 1263 bp

Locus ID: 12012

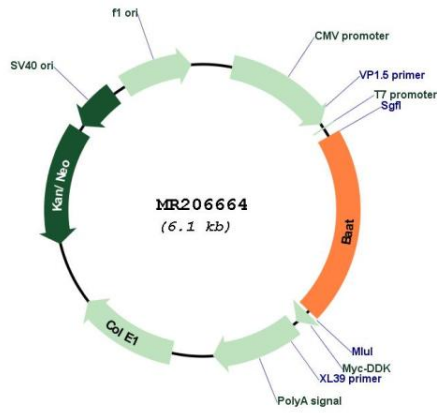
UniProt ID: [Q91X34](#)

Cytogenetics: 4 26.51 cM

MW: 46.5 kDa

Gene Summary: Involved in bile acid metabolism. In liver hepatocytes catalyzes the second step in the conjugation of C24 bile acids (choloneates) to taurine before excretion into bile canaliculi. The major components of bile are cholic acid and chenodeoxycholic acid. In a first step the bile acids are converted to an acyl-CoA thioester, either in peroxisomes (primary bile acids deriving from the cholesterol pathway), or cytoplasmic at the endoplasmic reticulum (secondary bile acids). May catalyze the conjugation of primary or secondary bile acids, or both. The conjugation increases the detergent properties of bile acids in the intestine, which facilitates lipid and fat-soluble vitamin absorption. In turn, bile acids are deconjugated by bacteria in the intestine and are recycled back to the liver for re-conjugation (secondary bile acids). May also act as an acyl-CoA thioesterase that regulates intracellular levels of free fatty acids. In vitro, catalyzes the hydrolysis of long- and very long-chain saturated acyl-CoAs to the free fatty acid and coenzyme A (CoASH), and conjugates glycine to these acyl-CoAs. [UniProtKB/Swiss-Prot Function]

Product images:



Circular map for MR206664