

Product datasheet for **SC116691**

BCAT1 (NM_005504) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	BCAT1 (NM_005504) Human Untagged Clone
Tag:	Tag Free
Symbol:	BCAT1
Synonyms:	BCATC; BCT1; ECA39; MECA39; PNAS121; PP18
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL6</u>
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>OriGene ORF within SC116691 sequence for NM_005504 edited (data generated by NextGen Sequencing)

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ATGAAGGATTGCAGTAACGGATGCTCCGCAGAGTGTACCGGAGAAGGAGGATCAAAGAG  
GTGGTGGGGACTTTTAAAGCTAAAGACCTAATAGTCACACCAGCTACCATTTTAAAGGAA  
AAACCAGACCCCAATAATCTGGTTTTTGGAACTGTGTTACCGGATCATATGCTGACGGTG  
GAGTGGTCTCAGAGTTGGATGGGAGAAAACCTCATATCAAGCCTCTTCAGAACCTGTCA  
TTGCACCCCTGGCTCATCAGCTTTGCACTATGCAGTGGAATTTTGAAGGATTGAAGGCA  
TTTCGAGGAGTAGATAATAAAATTCGACTGTTTCAGCCAAACCTCAACATGGATAGAATG  
TATCGCTCTGCTGTGAGGGCAACTCTGCCGGTATTTGACAAAGAAGAGCTCTTAGAGTGT  
ATTCAACAGCTTGTGAAATTGGATCAAGAATGGGTCCCATATTCAACATCTGCTAGTCTG  
TATATTCGTCCTACATTCATTGGAAGTGAAGCTTCTCTTGGAGTCAAGAAGCCTACCAA  
GCCCTGCTCTTTGACTCTTGGAGCCAGTGGGACCTTATTTTTCAAGTGGAACTTTAAT  
CCAGTGTCCCTGTGGGCAATCCCAAGTATGTAAGAGCCTGGAAAAGTGGAACTGGGGAC  
TGCAAGATGGGAGGGAATTACGGCTCATCTTTTTGCCCAATGTGAAGCAGTAGATAAT  
GGGTGTCAGCAGGTCCTGTGGCTCTATGGAGAGGACCATCAGATCACTGAAGTGGGAACT  
ATGAATCTTTTTCTTTACTGGATAAATGAAGATGGAGAAGAAGAACTGGCAACTCCTCCA  
CTAGATGGCATCATTCTCCAGGAGTGACAAGGCGGTGCATTCTGGACCTGGCACATCAG  
TGGGGTGAATTTAAGGTGTCAGAGAGATACCTCACCATGGATGACTTGACAACAGCCCTG  
GAGGGGAACAGAGTGAGAGAGATGTTTGGCTCTGGTACAGCCTGTGTTGTTTGGCCAGTT  
TCTGATATACTGTACAAAGCGAGACAATACACATTCCAACATATGGAGAATGGTCCTAAG  
CTGGCAAGCCGCATCTTGGAGCAATTAAGTATCCAGTATGGAAGAGAAGAGAGCGCAC  
TGGACAATTGTGCTATCCTGA
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Clone variation with respect to NM_005504.6



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5' Read Nucleotide Sequence:	<p>>OriGene 5' read for NM_005504 unedited CGCCCCGTTGCCCAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCT TATTTAGGTGACACTATAGAATACAAGCTACTTGTTCCTTTTGCAGCGGCCGCAATTCG GCACGAGGGGACCGCGCTCTGCAGCCGACAGCCGGTCCACACGGCCAGGGGCTACGACC CTTGGGATCTGCCCTCCGCTCAGCTCGAGCTTCCCTCGTGGCCGACGGAACAATGAAGGA TTGCAGTAACGGATGCTCCGACAGTGTACCGGAGAAGGAGGATCAAAAGAGGTGGTGGG GACTTTTAAGGCTAAAGACCTAATAGTCACACCAGCTACCATTTTAAAGGAAAAACCAGA CCCAATAATCTGGTTTTTGGAACTGTGTTACCGGATCATATGCTGACGGTGGAGTGGTC CTCAGAGTTTGGATGGGAGAAACCTCATATCAAGCCTCTTCAGAACCTGTCATTGCAACC TGGCTCATCAGCTTTCAGCTATGCAAGTGAATTATTTGAAGGATTGAAGGCATTCGAGG AGTAGATAATAAAATTCGACTGTTTCAGCCAAACCTCAACATGGATAGAATGTATCGCTC TGCTGTGAGGGCAACTCTGCCGGTATTTGACANAGAAGAGCTCTTAGAGTGTATTCAACA GCTTGTGAAATTTGGATCAAGAATGGGTCCCATATCAACATCTGCTAGTGTATATTTCG TCCTACATTCATTGGAAGTGAAGCTTCTCTTGGNAGTCAGAGCCTACCCAGCCCTGCTCT TTGTAAGTCTTGGAGCCAGTGGACCTTATTTTNCAGTGGACCTTNATNCAGTGTCCCTGT GGCCATCCNAGTATGTAGAGCCTGGAAAGTGNACTGNNACTGCAGATGGGNAGGNAAT ACCGCTCATCTCTTTGCCCATGTGAGCAGTAATNAATGGTGGTACCAGGTCCTGTGGC TTTATGGAGAGGACATCAGATCACTGAGTGGAACTA</p>
3' Read Nucleotide Sequence:	<p>>OriGene 3' read for NM_005504 unedited GTCTACTATGNACCGCGCCGAATCTANGATCGAGTTTTTTTTTTTTTTTTTTTGTCTTAC ATTTTTTCTTACAACAATCTTTTGAAGAAAGAAAGAGAATGTTTACCAGGTAGAAAAAC CTGATTCCTTAACAAGACTTCTCAGTCACTTGTCTCTTCCCTTTCACCTTTCCCTTTG TGCTTTTGAAGCAAAAGGCTAAAGCAGGTGTTATAAATTTATTTCCTGTGCTAGAGA GCATGGAACACATCTCTGAAGTCAACTCTCTTTTGGTGTATCACGAGTTGAATCCTTAA TAAATGACTGCCCAAAGAAAATTTCTAACAGCAAATCTTTTAGGAACTGCTCAGGTTT TGCCCTCGTCTTGACACTTCATTTTAAAATCTTGGTTTCTACTGATGTGTTTTCAAAAA GCTGACAAACTCGGTCTGAAATGTAGACACTGAAAAAGTGAAGGAAGAGAATGCAA TATAAGTTAATCATTATCATTAAAGTCCACCAGTCTGTTTATATTAATGCACCTGTG AATTGTGAATCTCATTGTGATCAACCCATTAAACATTAATAATTGCAGCCAATTATGC CAATATCAGCCACAATATTAATTTGTGATCTTTTTGAGCAGTTAGCTTCACATGTCTCT AAAGCTAGACCATCTTATGCCTTTAAACGATCAATTAGTGTGACAATAACCTAATCCTTG AAGAATGGATAATTGCCTAGTTATAATGTTGGCACTCCTGCTGTATTAACCCTGGCAT TAAACCAATAGTGCACACAGAAAAAAGGGCCAAAGTTCCTGTTAAATCTTTTAAAC AAGAAAACGTCCAGGGCAATTTCCGGGGCTATTACCTAAAGGACAAGGTGGGATTGGGGT CTCCTTTTAAAGGAGAACCTCCCGTTTTTAAACACTCTTC</p>
Restriction Sites:	NotI-NotI
ACCN:	NM_005504
Insert Size:	4700 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:	<ol style="list-style-type: none">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_005504.4 , NP_005495.2
RefSeq Size:	8191 bp
RefSeq ORF:	1161 bp
Locus ID:	586
UniProt ID:	P54687
Cytogenetics:	12p12.1
Domains:	aminotran_4
Protein Families:	Druggable Genome
Protein Pathways:	Metabolic pathways, Pantothenate and CoA biosynthesis, Valine, leucine and isoleucine biosynthesis, Valine, leucine and isoleucine degradation
Gene Summary:	<p>This gene encodes the cytosolic form of the enzyme branched-chain amino acid transaminase. This enzyme catalyzes the reversible transamination of branched-chain alpha-keto acids to branched-chain L-amino acids essential for cell growth. Two different clinical disorders have been attributed to a defect of branched-chain amino acid transamination: hypervalinemia and hyperleucine-isoleucinemia. As there is also a gene encoding a mitochondrial form of this enzyme, mutations in either gene may contribute to these disorders. Alternatively spliced transcript variants have been described. [provided by RefSeq, May 2010]</p> <p>Transcript Variant: This variant (1) represents the longest transcript and encodes isoform 1.</p> <p>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.</p>