

Product datasheet for SC111697

Tapasin (TAPBP) (NM_003190) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Tapasin (TAPBP) (NM_003190) Human Untagged Clone
Tag:	Tag Free
Symbol:	Tapasin
Synonyms:	NGS17; TAPA; TPN; TPSN
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL4</u>
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>NCBI ORF sequence for NM_003190, the custom clone sequence may differ by one or more nucleotides

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ATGAAGTCCCTGTCTCTGCTCCTCGCTGTGGCTTTGGGCCTGGCGACCGCGTCTCAGCAGGACCCGCGG
TGATCGAGTGTGGTTTCGTGGAGGATGCGAGCGGAAAGGGCCTGGCCAAGAGACCCGGTGCCTGTGT
GCGCCAGGGACCGGGGAACCGCCGCCCGGACCTCGACCCTGAGCTCTATCTCAGTGTACACGAC
CCCGCGGGCGCCCTCCAGGCTGCCTTCAGGCGGTATCCCCGGGGCGCCCCGACCACACTGCGAGATGA
GCCGCTTCGTGCCTCTCCCCGCCTCTGCGAAATGGGCCAGCGGCCTGACCCCGCGCAGAAGTGCCTGCG
GGCCCTGGATGGGGCTTGGCTGATGGTCAGCATATCCAGCCAGTCTCAGCCTCTCCAGCCTCTTGCGA
CCACAGCCAGAGCCTCAGCAGGAGCCTGTCTCATCACCATGGCAACAGTGGTACTGACTGTCCTACCC
ACACCCCTGCCCTCGAGTGAGACTGGGACAAGATGCTCTGCTGGACTTGAGCTTTGCCTACATGCCCC
CACCTCCGAGGCCGCTCATCTCTGGCTCCGGTCCCCCTCCCTTTGGGCTAGAGTGGCGACGCCAGCAC
CTGGGTAAAGGGACATCTGCTCCTGGCTGCAACTCCTGGGCTGAATGGCCAGATGCCAGCAGCCAAAGAAG
GGGCCGTGGCATTGCTGCTTGGGATGATGATGAGCCATGGGGCCATGGACCGGAAATGGGACCTTCTG
GCTGCCTACAGTTCAACCCTTTCAGGAGGGCACCTATCTGGCCACCATACACCTGCCATACCTGCAAGGA
CAGGTACCCTGGAGCTTGTGTGTACAAACCCCAAGTGTCCCTGATGCCAGCAACCCTTGCACGGG
CCGCCCCAGGGGAGGCACCCCGGAATTGCTCTGCCTTGTGCCACTTCTACCTTCTGGGGCCCTGGA
GGTGGAGTGGAACTCCGGGTGGCCAGGGGGCCGCTCTCAGAAGGCCGAGGGGCGAGGTTGGCTCTCG
GCCCTGCGCCACCATCCGATGGCTCTGTGAGCCTCTCTGGGCACTTGCAGCCGCCCCAGTCACCACTG
AGCAGCATGGGGCAGCTATGCCTGTGCAATTCACCATCCAGCCTGCCTGCCTCGGGGCGCAGCGCTGA
GGTACCCTGGAGGTAGCAGGTCTTTCAGGGCCCTCCCTTGGAGCAGCGTAGGCCTTTTCTGTCTGCC
TTTCTTCTGCTTGGGCTCTCAAGGCACTGGGCTGGGCTGCTGTACCTGTCCACCTGCAAGGATTCAA
AGAAGAAAGCAGAGTGA

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5' Read Nucleotide Sequence:	<p>>OriGene 5' read for NM_003190 unedited ATCCCCCGCCCGTTGNCGCAAAGGGCGGTAGGCGGTACGGTGGGAGGTCTATATAAGCA GAGCTCGTTTAGTGAACCGTCAGAAATTTTGAATACGACTCACTATAGGGCGGCCGCGAA TTCGGCACCAGGCAGCGCCATGAAGTCCCTGTCTCTGCTCCTCGCTGTGGCTTTGGGCT GGGCACCGCCGTCTCAGCAGGACCCGCGGTGATCGAGTGTGGTTCGTGGAGGATGCGAG CGGAAAGGGCCTGGCCAAGAGACCCGGTGCCTGCTGTTGCGCCAGGGACCGGGGAACC GCCGCCCGGCCGACCTCGACCTGAGCTCTATCTCAGTGTACACGACCCCGGGGCGC CCTCCAGGCTGCCTTACGGCGGTATCCCCGGGGCGCCCCGACACACTGCGAGATGAG CCGCTTCGTGCCTCTCCCCGCTCTGCGAAATGGGCCAGCGCCTGACCCCGCGCAGAA CTGCCCGCGGCCCTGGATGGGGCTTGGCTGATGGTCAGCATATCCAGCCAGTCCCTCAG CCTCTCCAGCCTTTGCGACCACAGCCAGAGCCTCAGCAGGAGCCTGTTCTCATCACCAT GGCAACAGTGGTACTGACTGTCTCACCCACACCCCTGCCCTCGAGTGAGACTGGGACA AGATGCTCTGCTGGACTTGAAGTTGCCTACATGCCCCACCTCCGAAGCCGCTCATC TCTGGCTCCGGTCCCCCTCTTTGGGCTAGAGTGGCGACGCCAGCACCTGGGTAAAGGG ACATCTGCTCCTGCTGACTCCTGGGCTGAATGGCCAGATGCCAGCAGCCCAAGAGGG GCCGTGGGCATTGCTGCTTGGGATGATGATGAGCCATGGGGCCATGGGACCGGGAATGG GACNTCTGGCTGNCTAGAGTTCAACCTTTTCAGGAGGGNCACTATCTGCCACCATACAC C</p>
3' Read Nucleotide Sequence:	<p>>OriGene 3' read for NM_003190 unedited TAAAAGCGCTACTATGTACGCGCCGCTTTTTANNGTCGAGTTTTTTTTTTTTTTTTTTT TTAGGAGCAGATGATAGGTATTATTTTAGGGAGCTACTACAGAAGCTTGGGCCAGAGAT GATGGTGGCTTCCACAGGATGGCAGTGAAGTGCCTCACTCTGCTTTCTTCTTTGAATCCT TGCAGGTGGACAGGTAGACAGCAGCCAGCCAGTGCCTTGAAGAGCCCAAGCAGAAGAA AGGCAGACAGGAAAAGGCTACGCTGTCCTCAAGGGAGGGCCCTGAAAGACCTGCTACCT CCAGGGTGACCTCAGCGCTGCGCCCCGAGGCAGGCAGGCTGGGATGGTGAATTCGACAGG CATAGCGTGCCCCATGCTGCTCAGTGGTGAAGTGGGGCGGCTGCAAGTGGCCAGAGAGGC TGACAGAGCCATCGGAATGGTGGCGCAGGGCCGAGAGCCACCTCTGCCCTCGGCCTTCT GAGAGCGGCCCTGGGCCACCCCGAGTTCCTCACTCCACCTCCAGGCCCCAGAATGGT AGAAGTGGGACACAAAGCAGAGCAATTCGGGGGTGCCTCCCCGGGGCGGCCGTGCAA GGGTTGCTGGCATCAAGGACACTTTGGGGGTTTGTACACAGCAAGCTCCAGGTGACCTG TCCTTGACAGTTTGGCAGGTGTTGGTGGCCANATAGGTGCCCTCCTGAAGGGTTGAAACT CTAGGCAGCCAGAAAAGTCCCATTTTCGGGCATTGGGCCCATGGCTCATCTTTCTCCC AAGCAGGCAATGCCCGGGCCCTTTCTTGGGCTGCTGGGCATTTGGGCTTTCAAGCC CAGGAAT</p>
Restriction Sites:	NotI-NotI
ACCN:	NM_003190
Insert Size:	1500 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_003190.3](#), [NP_003181.3](#)

RefSeq Size: 3629 bp

RefSeq ORF: 1347 bp

Locus ID: 6892

UniProt ID: [O15533](#)

Cytogenetics: 6p21.32

Protein Families: Druggable Genome, Transmembrane

Protein Pathways: Antigen processing and presentation

Gene Summary: This gene encodes a transmembrane glycoprotein which mediates interaction between newly assembled major histocompatibility complex (MHC) class I molecules and the transporter associated with antigen processing (TAP), which is required for the transport of antigenic peptides across the endoplasmic reticulum membrane. This interaction is essential for optimal peptide loading on the MHC class I molecule. Up to four complexes of MHC class I and this protein may be bound to a single TAP molecule. This protein contains a C-terminal double-lysine motif (KKKAE) known to maintain membrane proteins in the endoplasmic reticulum. This gene lies within the major histocompatibility complex on chromosome 6. Alternative splicing results in three transcript variants encoding different isoforms. [provided by RefSeq, Jul 2008]

Transcript Variant: This variant (1) represents the longest transcript and encodes the longest isoform (1). 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.