

Product datasheet for **MC223776**

Bag6 (NM_057171) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Bag6 (NM_057171) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Bag6
Synonyms:	2410045D21Rik; AA408914; BAG-6; Bat3; D17H6S52E; G3; Scythe
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin
Fully Sequenced ORF:	>MC223776 representing NM_057171 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGGATCGCC**

ATGGAGCCGAGTGATAGTGCCAGTACCGCTATGGAGGAGCCTGACAGCCTGGAGGTACTGGTGAAGACCC
TGGACTCTCAGACTCGGACTTTTATTGTGGGGCCAGATGAATGTAAGGAGTTAAGGAACACATAGC
TGCTCTGTGAGCATCCCTTCCGAGAAACAGCGGCTCATCTACCAGGGCCGGTCTACAAGACGACAAG
AAGCTCCAGGAGTACAAGTTGGGGAAAGTTATTCACCTGGTGAACGGGCTCCTCCTCAGACTCAGC
TTCTTCTGGAGCATCTTCTGGGACAGGCTCTGCCTCAGCAACTCATGGTGGGGCACCCCTGGCTGGCAC
TCGGGGCCCTGGGGCTTCTGTTTCATGACCGGAATGCCAACAGCTATGTCATGGTTGGAACCTTAACTCTT
CCTAGTGACGGCTCTGCTGTGGATGTTACATCAACATGGAACAGGCCCAATTCAGAGTGAGCCCCGGG
TCCGGCTGGTGTGGCTCAGCACATGATTAGGGATATACAGACCTTACTGTCCCGGATGGAGTGTGAGG
GGGAACCAAGCTCAGGCCAGTCAGCCACCCCGCAGACACCGCAGACTGTGGCCTCAGAGACGGTAGCC
TTGAACTCACAACATCAGAACCAGTCGAAAGTGAAGTCCTCCTCGAGAGCCCATGGAGTCAGAAGAAA
TGGAGGAACGTCCCCAACCAGACTCCAGAGCTTGCCTCAGGCCAGCTCCCGCAGGCCAGCTCC
CGCAGGCCAGCTCCCGGCCAGAGACAAATGCACCAACCACCTTCCCGCAGAGCACGTGGAGGTG
CTCCAGGAGCTTCAAGCCTTGCAGCGCTTTCAGCCTTTCCTACAGCGCTACTGCGAGGTCTGGGCG
CTGCTGCCACCACAGACTACAACAACAACCATGAGGGCCGTGAGGAGGACCAGAGTTGATCAACTTGGT
TGGGGAGAGCCTGCGGCTACTGGCAACACTTTCGTGGCATTGTCTGATCTGCGTGCAATCTAGCCTGT
GCACCCACGACCTGCACGTGGTTCGGCCTATGTCTACTACAGACTCCCATGGTGTCCAGCAGG
CAGCCATCCCATTCAGATCAATGTGGGACTACTGTGACCATGACAGGCAATGGGGCTCGGCCTCCACC
AGCTCCTGGTGGGAGGAGCAACCCAGGTTCTGCCAGGCCACATCCCTGCCTCCTCTCCACCACT
GTTGATTCATCAACTGAAGGAGTCCCCACCAGGGCCAGCACCACCAGCCTCCAGCCACCCACGGG
TCATCCGATTTCCACCAAGAGTGTGGAGCCCGTGGTTCATGATGCACATGAACATTCAAGATTCTGGAGC
ACAGCCTGGTGGTGTGCAAGTGTCCCACTGGTCCACTGGGACCTCCTGGTTCATGGACAGACCCTGGGA
CAGCAGGTGCCGGCTTCCCAACAGCACCACCTCGGGTGGTGATTGCCGGCCAACCTCCTCCACAGGCTC



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GGCCTTCCCATCCTGGGGACCTCCAGTCTCTGGAGCTCTGCAGGGCGCTGGGCTGGGTACAAACTTC
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CCAGGAATGGCTCAGGCTCAGGCCAGGCCAGGCTCAGGCCAGGCCAGGCCAGGCTCCAGTCCGG
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ATGGAGCTTGCTGCTGTCAATGGTCAATTCGCCGATGTCTCGCGGGTGAATCCATCCTTGGTGA
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CATCCTCAGATATGTTTCGTAGGGTTGGTGTATCCTCCTCAGACACTTCTGAAGAGCCGATGGAAGTTCAG
GGAGCAGAAAGAATTTCCCTGAACCTCAGAGAGAGAATGCTTCCCAGCCCTGGAACAACAGCAGAAG
AAGCCATGTCCCAGGCCCGCCCTGCTCCTGAAGGAGGTTCCCGAGATGAACAGGATGGAGCTTCCAGC
TGATGCAGAACCCTGGGAGCTGCAGTCCCCCTGAATGGTCCCTATTATCCAGCAGGACATTCAGAGC
CAGCGGAAGGTGAAACCTCAGCCGCCCTGAGTGATGCCTACCTCAGTGGCATGCCTGCCAAGAGACGAA
AGACAATGCAGGGTGGAGGCCCCAGCTGCTACTCTCAGAGGCAGTGAGCCGGGAGCTAAGGCAGCCGG
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ACGGCTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

- Restriction Sites:** SgfI-MluI
- ACCN:** NM_057171
- Insert Size:** 3465 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_057171.2](#), [NP_476512.1](#)

RefSeq Size: 3858 bp

RefSeq ORF: 3465 bp

Locus ID: 224727

UniProt ID: [Q9Z1R2](#)

Cytogenetics: 17 18.59 cM

Gene Summary:

ATP-independent molecular chaperone preventing the aggregation of misfolded and hydrophobic patches-containing proteins (PubMed:18056262, PubMed:18678708, PubMed:20713601). Functions as part of a cytosolic protein quality control complex, the BAG6/BAT3 complex, which maintains these client proteins in a soluble state and participates to their proper delivery to the endoplasmic reticulum or alternatively can promote their sorting to the proteasome where they undergo degradation (PubMed:20713601). The BAG6/BAT3 complex is involved in the post-translational delivery of tail-anchored/type II transmembrane proteins to the endoplasmic reticulum membrane. Recruited to ribosomes, it interacts with the transmembrane region of newly synthesized tail-anchored proteins and together with SGTA and ASNA1 mediates their delivery to the endoplasmic reticulum. Client proteins that cannot be properly delivered to the endoplasmic reticulum are ubiquitinated by RNF126, an E3 ubiquitin-protein ligase associated with BAG6 and are sorted to the proteasome. SGTA which prevents the recruitment of RNF126 to BAG6 may negatively regulate the ubiquitination and the proteasomal degradation of client proteins. Similarly, the BAG6/BAT3 complex also functions as a sorting platform for proteins of the secretory pathway that are mislocalized to the cytosol either delivering them to the proteasome for degradation or to the endoplasmic reticulum. The BAG6/BAT3 complex also plays a role in the endoplasmic reticulum-associated degradation (ERAD), a quality control mechanism that eliminates unwanted proteins of the endoplasmic reticulum through their retrotranslocation to the cytosol and their targeting to the proteasome. It maintains these retrotranslocated proteins in an unfolded yet soluble state condition in the cytosol to ensure their proper delivery to the proteasome (By similarity). BAG6 is also required for selective ubiquitin-mediated degradation of defective nascent chain polypeptides by the proteasome. In this context, it may participate to the production of antigenic peptides and play a role in antigen presentation in immune response (PubMed:20713601). BAG6 is also involved in endoplasmic reticulum stress-induced pre-emptive quality control, a mechanism that selectively attenuates the translocation of newly synthesized proteins into the endoplasmic reticulum and reroutes them to the cytosol for proteasomal degradation. BAG6 may ensure the proper degradation of these proteins and thereby protects the endoplasmic reticulum from protein overload upon stress (By similarity). By inhibiting the polyubiquitination and subsequent proteasomal degradation of HSPA2 it may also play a role in the assembly of the synaptonemal complex during spermatogenesis (PubMed:18678708). Also positively regulates apoptosis by interacting with and stabilizing the proapoptotic factor AIFM1 (PubMed:18056262). By controlling the steady-state expression of the IGF1R receptor, indirectly regulates the insulin-like growth factor receptor signaling pathway (By similarity).[UniProtKB/Swiss-Prot Function]

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.