

Product datasheet for **MC229405**

Bag6 (NM_001252468) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Bag6 (NM_001252468) 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: >MC229405 representing NM_001252468
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGGATCGCC**

ATGGAGCCGAGTGATAGTGCCAGTACCGCTATGGAGGAGCCTGACAGCCTGGAGGTACTGGTGAAGACCC
 TGGACTCTCAGACTCGGACTTTTATTGTGGGGCCAGATGAATGTAAGGAGTTAAGGAACACATAGC
 TGCTCTGTGAGCATCCCTCCGAGAAACAGCGGCTCATCTACCAGGGCCGGTCTACAAGACGACAAG
 AAGCTCCAGGAGTACAAGTTGGGGAAAGTTATTCACCTGGTGAACGGGCTCCTCCTCAGACTCAGC
 TTCTTCTGGAGCATCTTCTGGGACAGGCTCTGCCTCAGCAACTCATGGTGGGGCACCCCTGGCAGC
 TCGGGGCCCTGGGGCTTCTGTTTCATGACCGGAATGCCAACAGCTATGTCATGGTTGGAACCTTAATCTT
 CCTAGTGAGCCCCGGGTCGGCTGGTATGGCTCAGCACATGATTAGGGATATACAGACCTTACTGTCCC
 GGATGGAGTGTGAGGGGAACCAAGCTCAGGCCAGTCAGCCACCCCGCAGACACCGCAGACTGTGGC
 CTCAGAGACGGTAGCCTTGAACACAAACATCAGAACCAGTCGAAAGTGAAGCTCCTCCTCAGAGACCC
 ATGGAGTCAGAAGAAATGGAGGAACGTCCCCAACCCAGACTCCAGAGCTTGCGCCCTCAGGCCAGCTC
 CCGCAGGCCAGCTCCCGCAGGCCAGCTCCCGCGCCAGAGACAAATGCACCAACCCACCTTCCCCCGC
 AGAGCACGTGGAGGTGCTCCAGGAGCTTACGCGCTTGCAGCGCCGTCTTACGCTTCTACAGCGCTAC
 TGCAGGTCCTGGGCGCTGCTGCCACCACAGACTACAACAACAACCATGAGGGCCGTGAGGAGGACCAGA
 GTTGATCAACTTGGTTGGGAGAGCCTGCGGCTACTGGCAACACTTTCGTGGCATTGTCTGATCTGCG
 CTGCAATCTAGCCTGTGCACCCACCGCACCTGCACGTGGTTCGGCCTATGTCTCACTACAGACTCCC
 ATGGTGTCCAGCAGGCAGCCATCCCATTAGATCAATGTGGGACTACTGTGACCATGACAGGCAATG
 GGGCTCGGCTCCACCAGCTCCTGGTGGGAGGCAGCAACCCAGGTTCTGCCAGGCCACATCCCTGCC
 TCCCTCTCCACCACTGTTGATTCATCAACTGAAGGAGCTCCCCACCAGGGCCAGCACCACCAGCC
 TCCAGCCACCCAGGGTCATCCGATTTCCACCAGAGTGTGGAGCCCGTGGTCATGATGCACATGAACA
 TTCAAGATTCTGAGCACAGCCTGGTGGTGTGCCAAGTGCTCCCACTGGTCCACTGGGACCTCCTGGTCA
 TGGACAGACCCTGGGACAGCAGGTGCCCGGCTTCCAACAGCACCAACTCGGGTGGTGATTGCCCGGCA
 ACTCCTCCACAGGCTCGGCTTCCATCCTGGGGACCTCCAGTCTCTGGAGCTCTGAGGGCGCTGGG



View online »

TGGGTACAAACACTTCATTGGCCAGATGGTGAGCGGCCTTGTGGGGCAACTTCTTATGCAGCCTGTTCT
TGTGGCTCAGGGGACTCCAGGAATGGCTCAGGCTCAGGCCAGGCCAGGCTCAGGCCAGGCCAGGCC
CAGGCTCCAGCTCCGGCTCCGGCTCCAGCTCCAGCTCCTGCCACTGCTTCAGCTAGTGCTGGTACTACCA
ACACAGCTACCACAGCTGGCCCTGCTCCTGGGGTCTGCCAGCCTCCACCTCCTCAGCCCTCTGCAGC
TGATCTTCAGTTCTCAGCTCCTGGGAAATCTGCTGGGGCTGCAGGGCCAGGGGCTGGGGGCCAGGC
ATGGCTTCTCCACCATCACTGTGGCAATGCCTGGTGTCCCTGCTTTTCTCCAGGGCATGACTGATTTTT
TGCAGGCATCACAGACTGCCCCCACCCTCCACCTCCTCCACCCCACTCCACCCCACTCCAGAGCAGCA
GAGCACACCCCAACCAGGGTCTCCTTCTGGTGGAAACAGCAAGCCCTGGAGGCTTAGGTCCTGAGAGCCTG
CCACCAGAGTTTTTACCTCAGTGGTGCAGGGCGTGTGAGCTCCCTCCTGGGCTCCTTGGGGGCTCGAG
CTGGCAGCAGTGAGAGTATCGTGCCTTCAACACGCCTCAGTGGATCCAGCAACATCTTTGAGCCTGG
GGCTGATGGCGCCTTGGATTCTCGGAGCTCTGCTCTCTCCTGTGCCAGAATTTCTCCATGGTGGAT
GTGGTGTGCTTCTCCATGGCCATTTCCAGCCACTGCAGCGGCTCCAGCCACAGCTGCGATCTTTCTTCC
ACCAGCACTACCTGGGTGGCCAGGAGCCACGCCTAGCAACATCCGGATGGCGACCCACACACTGATCAC
TGGGCTGGAAGAGTATGTAAGGGAGAGTTTTTCTTTGGTACAGGTTACAGCCAGGTGGATATCATCCGG
ACAAATTTAGAATTTCTCAAGAGCAGTTAACAGCATTGCTGCTCATGTGCTGCACTGTACAGACAGTG
GATTTGGAGCCCGTTGCTGGAGCTGTGTAACAGGGCCTGTTTGAATGCTTGGCCCTGAACCTCCACTG
CTTGGGGGACAGCAAATGGAGCTTGTGCTGTCAATGGTGAATTCGCCGCATGTCTCGCGGGGTG
AATCCATCCTTGGTGAGCTGGTGACAACCATGATGGGACTGAGGCTTACGGTGGTCTTGGAGCACATGC
CTGTGGGTCCCGACGCCATCCTCAGATATGTTCTGAGGGTTGGTATCCTCCTCAGACACTTCTGAAGA
GCCGATGGAAGTTCAGGGAGCAGAAAGAACTTCCCCTGAACCTCAGAGAGAGAATGCTTCCCCAGCCCT
GGAACAACAGCAGAAGAAGCCATGTCCCGAGGCCCGCCCTGCTCCTGAAGGAGGTTCCCGAGATGAAC
AGGATGGAGCTTCAGCTGATGCAGAACCCTGGGAGCTGCAGTCCCCCTGAATGGTCCCTATTATCCA
GCAGGACATTAGAGCCAGCGGAAGGTGAAACCTCAGCCGCCCTGAGTGTGCTACCTCAGTGGCATG
CCTGCCAAGAGACGAAAGACAATGCAGGGTGAAGGCCCCAGCTGCTACTCTCAGAGGCAGTGAGCCGGG
CAGCTAAGGCAGCCGGAGCTCGGCCCTGACAAGCCCGAGAGCCTGAGCCGGGACCTGGAGGCACCAGA
GGTTACAGGAGAGCTACAGGCAGCAGCTCCGGTCTGATATCCAAAAACGACTGCAGGAAGATCCCACTAC
AGCCCCAGCGCTTCCCTAATGCCATCGGGCATTGCTGATGACCCCTAG

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

- Restriction Sites:** SgfI-MluI
- ACCN:** NM_001252468
- Insert Size:** 3411 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).
- OTI Annotation:** Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
- 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_001252468.1](#), [NP_001239397.1](#)

RefSeq Size: 3804 bp

RefSeq ORF: 3411 bp

Locus ID: 224727

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 (2) lacks an exon in the 5' coding region, but maintains the reading frame, compared to variant 1. The encoded isoform (2) is shorter than 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.