

Recombinant Human BAG3, His-tagged

Cat. No. BAG3-26064TH **Lot. No.** (See product label)

SPECIFICATION

Product Overview	Recombinant full length Human Bag3 with an N-terminal His tag; 595 amino acids with tag, MWt 63.7kDa.
Species	Human
Source	E.coli
Description	BAG proteins compete with Hip for binding to the Hsc70/Hsp70 ATPase domain and promote substrate release. All the BAG proteins have an approximately 45-amino acid BAG domain near the C terminus but differ markedly in their N-terminal regions. The protein encoded by this gene contains a WW domain in the N-terminal region and a BAG domain in the C-terminal region. The BAG domains of BAG1, BAG2, and BAG3 interact specifically with the Hsc70 ATPase domain in vitro and in mammalian cells. All 3 proteins bind with high affinity to the ATPase domain of Hsc70 and inhibit its chaperone activity in a Hip-repressible manner.
Conjugation	HIS
Form	Liquid
Purity	>90% by SDS-PAGE
Storage buffer	Preservative: None Constituents: 10% Glycerol, 20mM Tris HCl, 1mM EDTA, 0.1mM PMSF, pH 8.0

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Storage	Shipped at 4°C. Upon delivery aliquot and store at -20°C or -80°C. Avoid repeated freeze / thaw cycles.
Sequences of amino acids	MGSSHHHHHH SSGLVPRGSH MSAATHSPMM QVASGNGDRD PLPPGWEIKI DPQTGWPFV DHNSRTTWN DPRVPSEGPK ETPSSANGPS REGSRLPPAR EGHPVYPQLR PGYIPIVLH EGAENRQVHP FHVYPQPGMQ RFRTEAAAAA PQRSQSPLRG MPETTQPKQ CGQVAAAAA QPPASHGPER SQSPAASDCS SSSSASLPS SGRSSLGSHQ LPRGYISIPV IHEQNVTRPA AQPSFHQAQK THYPAQQGEY QTHQPVYHKI QGDDWEPRPL RAASPFRSSV QGASSREGSP ARSSTPLHSP SPIRVHTVVD RPQQPMTHRE TAPVSQPENK PESKPGPVGP ELPPGHIPIQ VIRKEVDSKP VSQKPPPPSE KVEVKVPPAP VPCPPSPGP SAVPSSPKSV ATEERAAPST APAEATPPKP GEAEAPPKHP GVLKVEAILE KVQGLEQAVD NFEGKKTDKK YLMIEEYLT KELLALDSVDP EGRADVRRQAR RDGVRKVQTI LEKLEQKAID VPGQVQVYEL QPSNLEADQP LQAIMEMGAV AADKGKKNAG NAEDPHTETQ QPEATAAATS NPSSMTDTPG NPAAP
Sequence Similarities	Contains 1 BAG domain.Contains 2 WW domains.
Full Length	Full L.
GENE INFORMATION	
Gene Name	BAG3 BCL2-associated athanogene 3 [Homo sapiens]
Official Symbol	BAG3
Synonyms	BAG3; BCL2-associated athanogene 3; BAG family molecular chaperone regulator 3;
Gene ID	9531

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mRNA Refseq	NM_004281
Protein Refseq	NP_004272
MIM	603883
Uniprot ID	O95817
Chromosome Location	10q25.2-q26.2
Function	chaperone binding;

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