

BAG2 cDNA

Catalog Number: ATGD0088

PRODUCT INFORMATION

Catalog number

ATGD0088

Product type

cDNA

Species

Human

NCBI Accession No.

NP_004273.1

Alternative Names

BAG-2, dJ417I1.2

mRNA Refseq

NM_004282.3

OMIM

603882

Chromosome location

6p12.1-p11.2

PRODUCT SPECIFICATION

Formulation

Lyophilized

Storage

Store the plasmid at -20C.

cDNA Size

636bp

Preparation before usage

1. Centrifuge at 7000rpm for 1 minute.
2. Carefully open the vial and add 100ul of sterile water to dissolve the DNA. Each tube contains approximately 10ug of lyophilized plasmid.

Vector description

This shuttle vector contains the complete ORF. It is inseted BamH I to Xho I. The gene insert contains multiple cloning sites which can be used to easily cut and transfer the gene and recombination site into your expression vector.

Cloning Vector

pATGen (puc19-derived cloning vector)

General Description

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BCL2-associated athanogene 2, also known as BAG2, is a member of the Bag family of proteins. BAG proteins compete with Hip for binding to the Hsc70/Hsp70 ATPase domain. BAG2 is a major component of the HSC 70/CHIP chaperone-dependent ubiquitin ligase complex and acts to disrupt CHIP-mediated ubiquitylation.

DATA

Sequence nucleotides

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ATGGCTCAGG CGAAGATCAA CGCTAAAGCC AACGAGGGGC GCTTCTGCCG CTCCTCCTCC ATGGCTGACC
GCTCCAGCCG CCTGCTGGAG AGCCTGGACC AGCTGGAGCT CAGGGTTGAA GCTTTGAGAG AAGCAGCAAC
TGCTGTTGAG CAAGAGAAAG AAATCCTTCT GGAAATGATC CACAGTATCC AAAATAGCCA GGACATGAGG
CAGATCAGTG ACGGAGAAAG AGAAGAATTA AATCTGACTG CAAACCGTTT GATGGGAAGA ACTCTCACCG
TTGAAGTGTC AGTAGAAACA ATTAGAAACC CCCAGCAGCA AGAATCCCTA AAGCATGCCA CAAGGATTAT
TGATGAGGTG GTCAATAAGT TTCTGGATGA TTTGGGAAAT GCCAAGAGTC ATTTAATGTC GCTCTACAGT
GCATGTTTAT CTGAGGTGCC ACATGGGCCA GTTGATCAGA AGTTTCAATC CATAGTAATT GGCTGTGCTC
TTGAAGATCA GAAGAAAATT AAGAGAAGAT TAGAGACTCT GCTTAGAAAT ATTGAAAACCT CTGACAAGGC
CATCAAGCTA TTAGAGCATT CTAAGGAGC TGGTTCCAAA ACTCTGCAAC AAAATGCTGA AAGCAGATTC AATTAG
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Transaction Sequence

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MAQAKINAKA NEGRFCRSSH MADRSSRLLE SLDQLELRVE ALREAATAVE QEKEILLEMI HSIQNSQDMR QISDGEREEL
NLTANRLMGR TLTVEVSVET IRNPQQQESL KHATRIIDEV VNKFLDDLGN AKSHLMSLYS ACSSEVPHGP VDQKFQSIIV
GCALEDQKKI KRRLETLLRN IENSDKAIKL LEHSGAGGSK TLQQNAESRF N
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