

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of His-ATG4b

<u>Enzyme description:-</u>	His-ATG4b
<u>Clone number:-</u>	DU40027
<u>Source:-</u>	BL21 Recombinant
<u>Tag:-</u>	N-terminal His ₆ tag
<u>Purification method:-</u>	Ni ⁺⁺ -Sephrose
<u>Expression level:-</u>	5 mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	47072 Da
Average Mass	47101 Da
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	5.42
<u>Purity:-</u>	80%
<u>Enzyme storage buffer:-</u>	
50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT	
<u>Storage temperature:-</u>	-80°C

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Clone Data Sheet

His-ATG4b

<u>Protein</u>	His-ATG4b
<u>Synonyms</u>	APG4B, AUT1L
<u>Clone Number</u>	DU40027
<u>Species</u>	Human
<u>Accession Number</u>	Protein: Q9Y4P1 DNA: NM013325.4
<u>Tags</u>	N-terminal His tag
<u>Amino acid sequence of expressed protein</u>	MGSSHHHHHSSGENLYFQGHMLGSMDAATLTYDTLRFAEFEDFPETSEPVI LGRKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGCMLRCQM IFAQALVCRHLGRDWRWTQRKRQPSYF SVLNAF IDRKDSYYSIHQIAQMGVG EGKSIGQWYGPNTVAQVLKKLAVFDTWSSLAVHIAMDNTVVMEEIRRLCRTSV PCAGATAFPADSDRHCNGFPAGAEVTNRPSWRPLVLLIPLRLGLTDINEAYV ETLKHCMMPOSLGVI GGKPN SAHYF IGYVGEELIYLDPHTTQPAVEPTDGC IPDEFHCQHPPCRMSIAELDPSIAVGFFCKTEDDFNDWCQOVKKLSLLGGAL PMFELVEQOPSHLACPDVLNLSLDSSDVERLERFFDSEDEDFEILSL
<u>Native sequence</u>	in bold
<u>Protease cleavage</u>	TEV site underlined
<u>Cloning sites</u>	BamH1 / Not1

**DNA sequence of
insert**

GGATCCATGGACGCAGCTACTCTGACCTACGACACTCTCCGGTTTGCTGAGTT
TGAAGATTTTCCTGAGACCTCAGAGCCCGTTTGGATACTGGGTAGAAAATACA
GCATTTTTCACAGAAAAGGACGAGATCTTGTCTGATGTGGCATCTAGACTTTGG
TTTACATACAGGAAAACTTCCAGCCATTGGGGGGACAGGCCCCACCTCGGA
CACAGGCTGGGGCTGCATGCTGCGGTGTGGACAGATGATCTTTGCCCAAGCCC
TGGTGTGCCGGCACCTAGGCCGAGATTGGAGGTGGACACAAAGGAAGAGGCAG
CCAGACAGCTACTTCAGCGTCCCTCAACGCATTCATCGACAGGAAGGACAGTTA
CTACTCCATTACACAGATAGCGCAAATGGGAGTTGGCGAAGGCAAGTCCATAG
GCCAGTGGTACGGGCCCAACACTGTCGCCCAGGTCCTGAAGAAGCTTGCTGTC
TTCGATACGTGGAGCTCCTTGGCGGTCCACATTGCAATGGACAACACTGTTGT
GATGGAGGAAATCAGAAGGTTGTGCAGGACCAGCGTTCCCTGTGCAGGCGCCA
CTGCGTTTTCCTGCAGATTCCGACCGGCACTGCAACGGATTCCCTGCCGGAGCT
GAGGTCACCAACAGGCCGTCGCCATGGAGACCCCTGGTACTTCTCATTCCCCT
GCGCCTGGGGCTCACGGACATCAACGAGGCCCTACGTGGAGACGCTGAAGCACT
GCTTCATGATGCCCCAGTCCCTGGGCGTCATCGGAGGGAAGCCCAACAGCGCC
CACTACTTCATCGGCTACGTTGGTGAGGAGCTCATCTACCTGGACCCCCACAC
CACGCAGCCAGCCGTGGAGCCCACTGATGGCTGCTTCATCCCGGACGAGAGCT
TCCACTGCCAGCACCCGCCGTGCCGCATGAGCATCGCGGAGCTTGACCCGTCC
ATCGCTGTGGGGTTTTTCTGTAAGACTGAAGATGACTTCAATGATTGGTGCCA
GCAAGTCAAAAAGCTGTCTCTGCTCGGAGGTGCCCTGCCCATGTTTGGAGCTGG
TGGAGCAGCAGCCTTACATCTGGCCTGCCCGACGTCCTGAACCTGTCCCTA
GATTCTTCTGATGTAGAGCGACTGGAAAGATTCTTCGACTCAGAAGATGAAGA
CTTTGAAATCCTGTCCCTTTGAGCGGCCGC