

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-ATG4a

<u>Enzyme description:-</u>	GST-ATG4a
<u>Clone number:-</u>	DU40089
<u>Source:-</u>	BL21 Recombinant
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH sepharose
<u>Expression level:-</u>	1.5 mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	72671 Da
Average Mass	72716 Da
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	5.20
<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

GST-ATG4a

<u>Protein</u>	GST-ATG4a
<u>Synonyms</u>	Autophagin-2, APG4a, AUTL2
<u>Clone Number</u>	DU40089
<u>Species</u>	Human
<u>Accession Number</u>	Protein: Q8WYN0 DNA: NM_052936.3
<u>Tags</u>	N-terminal GST
<u>Amino acid sequence of expressed protein</u>	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFP NLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGV SRIAYSKDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDHVTHPDFMLYDAL DVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLOGWQATFGG GDHPPKSDHPPKSDENLYFQGGSMESVLSKYEDQITIFTDYLEEYPDTDELVW ILGKQHLLKTEKSKLLSDISARLWFTYRRKFSPIGGTGPSSDAGWGCMLRCGQ MMLAQALICRHLGRDWSWEKQKEQPKEYQRILOCFDRKDCCYSIHQMAQMGV GEGKSIGEWFGPNTVAQVLKLLALFDEWNSLAVYVSMDNVTVIEDIKKMCRVL PLSADTAGDRPPDSL TASNQSKGTSAYCSAWKPLLLIVPLRLGINQINPVYVD AFKECFKMPQSLGALGGKPNNAYYFIGFLGDELIFLDPHTTQTFVDTEENGTV NDQTFHCLQSPQRMNILNLDPSVALGFFCKEEKDFDNWCSLVQKEILKENLRM FELVQKHPSHWPPFVPPAKPEVTTTGAEFIDSTEQLEEFDLEEDFEILSV
<u>Native sequence</u>	in bold
<u>Protease cleavage</u>	TEV site underlined
<u>Cloning sites</u>	BglII/NotI

**DNA sequence of
insert**

AGATCTATGGAGTCAGTTTTATCCAAGTATGAAGATCAGATTACTATTTTCACTGACT
ACCTAGAAGAATATCCAGATACAGATGAGCTGGTATGGATCTTAGGGAAGCAGCATCT
CCTTAAAAACAGAAAAATCTAAGCTGTTGCTGATATAAGTGCTCGTCTATGGTTTACA
TACAGAAGGAAATTTTCACCAATTGGTGGAACGGGCCCTTCATCAGATGCTGGTTGGG
GATGTATGCTACGCTGTGGACAGATGATGCTGGCTCAAGCCCTTATCTGTAGACACTT
GGGAAGGGACTGGAGCTGGGAGAAAACAAAAAGAACAACCCAAAGAATACCAACGCATC
CTACAGTGCTTCTTAGATAGAAAAGATTGTTGCTACTCTATCCATCAAATGGCACAAA
TGGGTGTAGGAGAAGGGAAATCAATTGGAGAAATGGTTTGGACCAAATACAGTTGCACA
GGTGTAAAAAAAATTGCTTTATTTGACGAATGGAATTCCCTGGCTGTTTATGTTTCA
ATGGATAACACAGTGGTCATTGAAGATATCAAAAAAATGTGCCGTGTCCTTCCCTTGA
GTGCTGACACAGCTGGTGACAGGCTCCCGATTCTTTAACTGCTTCAAACCAGAGTAA
GGGCACCTCTGCCTACTGCTCAGCCTGGAAACCCCTGCTGCTCATTGTGCCCTTCGC
CTGGGCATAAACCAAATCAATCCTGTCTATGTTGATGCATTCAAAGAGTGTTTTAAGA
TGCCACAGTCTTTAGGGGCATTAGGAGGAAAACCAAATAACCGTATTATTTTCATAGG
ATTCTTAGGTGACGAGCTCATCTTCTTGGACCCCTCATACAACCCAGACCTTTTGTGAC
ACTGAAGAGAATGGAACGGTTAATGACCAGACTTTCATTGCTTGCAGTCCCCACAGC
GAATGAACATCCTAAACCTGGATCCTTCAGTTGCATTGGGATTTTTCTGCAAAGAAGA
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AGGATGTTTGAATTAGTTCAGAAACATCCATCACACTGGCCTCCCTTTGTACCTCCAG
CCAAGCCAGAAGTGACAACCACTGGGGCAGAATTCATTGACTCTACTGAGCAACTGGA
GGAGTTTGATCTGGAGGAAGATTTTGAGATTCTGAGTGTGTAGCGGCCG