Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-ATG3

Enzyme description:- GST-ATG3 1-314 (full length)

Clone number:- DU31143

Source:- BL21 recombinant

Tag:- N-terminal GST-tag

Purification method:- GSH-Sepharose

Expression level:- 1mg/L

Calculated molecular mass:-

Monoisotopic 62648 Da
Average Mass 62686 Da
[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 4.83

Purity:- 90%

Enzyme storage buffer:-

50mM HEPES pH 7.5, 150mM NaCl, 10% glycerol, 1mM DTT

Storage temperature:- -80ºC

Assay:-

Not tested yet.

Division of Signal Transduction Therapy

Clone Data Sheet

GST-ATG3

Protein	ATG3
Synonyms	Apg3, APG3L
Clone Number	DU31143
Species	Human
Accession Number	Protein: NP_071933 DNA: NM_ 022488
Tags	N-terminal GST-tag
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIA WPLQGWQATFGGGDHPPKSDLEVLFQGPLGS**MQNVINTVKGKALEVAEYL** **TPVLKESKFKETGVITPEEFVAAGDHLVHHCPTWQWATGEELKVKAYLPT** **GKQFLVTKNVPCYKRCKQMEYSDELEAIIEEDDGDGGWVDTYHNTGITGI** **TEAVKEITLENKDNIRLQDCSALCEEEEDEDEGEAADMEEYEESGLLETD** **EATLDTRKIVEACKAKTDAGGEDAILQTRTYDLYITYDKYYQTPRLWLFG** **YDEQRQPLTVEHMYEDISQDHVKKTVTIENHPHLPPPPMCSVHPCRHAEV** **MKKIIETVAEGGGELGVHMYLLIFLKFVQAVIPTIEYDYTRHFTM**
Native sequence	in bold
Protease cleavage	Prescission protease site underlined
Cloning sites	BamH1 / Not1
DNA sequence of insert	GGATCCATGCAGAATGTGATTAATACTGTGAAGGGAAAGGCACTGGAAGT GGCTGAGTACCTGACCCCGGTCCTCAAGGAATCAAAGTTTAAGGAAACAG GTGTAATTACCCCAGAAGAGTTTGTGGCAGCTGGAGATCACCTAGTCCAC CACTGTCCAACATGGCAATGGGCTACAGGGGAAGAATTGAAAGTGAAGGC ATACCTACCAACAGGCAAACAATTTTTGGTAACCAAAAATGTGCCGTGCT ATAAGCGGTGCAAACAGATGGAATATTCAGATGAATTGGAAGCTATCATT GAAGAAGATGATGGTGATGGCGGATGGGTAGATACATATCACAACACAGG TATTACAGGAATAACGGAAGCCGTTAAAGAGATCACACTGGAAAATAAGG ACAATATAAGGCTTCAAGATTGCTCAGCACTATGTGAAGAGGAAGAAGAT GAAGATGAAGGAGAAGCTGCAGATATGGAAGAATATGAAGAGAGTGGATT GTTGGAAACAGATGAGGCTACCCTAGATACAAGGAAAATAGTAGAAGCTT GTAAAGCCAAAACTGATGCTGGCGGTGAAGATGCTATTTTGCAAACCAGA ACTTATGACCTTTACATCACTTATGATAAATATTACCAGACTCCACGATT ATGGTTGTTTGGCTATGATGAGCAACGGCAGCCTTTAACAGTTGAGCACA TGTATGAAGACATCAGTCAGGATCATGTGAAGAAAACAGTGACCATTGAA AATCACCCTCATCTGCCACCACCTCCCATGTGTTCAGTTCACCCATGCAG GCATGCTGAGGTGATGAAGAAAATCATTGAGACTGTTGCAGAAGGAGGGG GAGAACTTGGAGTTCATATGTATCTTCTTATTTTCTTGAAATTTGTACAA GCTGTCATTCCAACAATAGAATATGACTACACAAGACACTTCACAATGTA

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AGCGGCCGC
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