

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-OTUB1 [47-271]

Enzyme description:- GST-OTUB1 [47-271]

Clone number:- SC20855

Source:- BL21 Recombinant

Tag:- N-terminal GST tag

Purification method:- GSH sepharose

Expression level:- 1.4 mg/L

Calculated molecular mass:-

Monoisotopic 52989 Da

Average Mass 53022 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 5.74

Purity:- 90 %

Enzyme storage buffer:-

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

Storage temperature:- -80°C

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Clone Data Sheet

GST-OTUD1 [47-271]

<u>Protein</u>	GST-OTUD1 [47-271]
<u>Synonyms</u>	
<u>Clone Number</u>	SC20855
<u>Species</u>	Human
<u>Accession Number</u>	Protein: Q96FW1 DNA: NM017670
<u>Tags</u>	N-terminal GST tag
<u>Amino acid sequence of expressed protein</u>	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA WPLQGWQATFGGGDHPPKSDLEVLFOGPLGSLVSERLELSVLYKEYAEDD NIYQQKIKDLHKKYSYIRKTRPDGNCFYRAFGFSHLEALLDDSKELQRFK AVSAKSKEDLVSQGFTEFTIEDFHNTFMDLIEQVEKQTSVADLLASFNDQ STSDYLVVYLRLLTSGYLQRESKFFEHFIEGGRTVKEFCQQEVEPMCKES DHIHIALAQALSVSIOVEYMDRGEgggTTPHIFPEGSEPKVYLLYRPGH YDILYK
<u>Native sequence</u>	in bold
<u>Protease cleavage</u>	site underlined
<u>Cloning sites</u>	BglIII / NotI
<u>DNA sequence of insert</u>	GGATCCCTGGTGTCTCAGAGCGGCTGGAGCTCTCGGTCCTATACAAGGAGTA TGCTGAAGATGACAACATCTATCAACAGAAGATCAAGGACCTCCACAAAA AGTACTCGTACATCCGCAAGACCAGGCCTGACGGCAACTGTTTCTATCGG GCTTTCGGATTCTCCCACTTGGAGGCACTGCTGGATGACAGCAAGGAGTT GCAGCGGTTCAAGGCTGTGTCTGCCAAGAGCAAGGAAGACCTGGTGTCCC AGGGCTTCACTGAATTCACAATTGAGGATTTCCACAACACGTTTCATGGAC CTGATTGAGCAGGTGGAGAAGCAGACCTCTGTGCGCGACCTGCTGGCCTC CTTCAATGACCAGAGCACCTCCGACTACCTTGTGGTCTACCTGCGGCTGC TCACCTCGGGCTACCTGCAGCGCGAGAGCAAGTTCTTCGAGCACTTCATC GAGGGTGGACGGAAGTGTCAAGGAGTTCTGCCAGCAGGAGGTGGAGCCCAT GTGCAAGGAGAGCGACCACATCCACATCATTCGCGCTGGCCCAGGCCCTCA GCGTGTCCATCCAGGTGGAGTACATGGACCGCGGCGAGGGCGGCACCACC AATCCGCACATCTTCCCTGAGGGCTCCGAGCCCAAGGTCTACCTTCTCTA CCGGCCTGGACACTACGATATCCTCTACAAATAGGCGGCCGC