

Division of Signal Transduction Therapy

Standard Operation Procedure

GST-A20 [1-366]

<u>Enzyme description:-</u>	GST-A20 [1-366]
<u>Clone number:-</u>	DU32912
<u>Source:-</u>	BL21 Recombinant
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH Sepharose
<u>Expression level:-</u>	6 mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	70779 Da
Average Mass	70843 Da
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	6.84
<u>Purity:-</u>	90%
<u>Enzyme storage buffer:-</u>	
50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT	
<u>Storage temperature:-</u>	-80°C
<u>Assay:-</u>	
Ub-Rho110-Gly cleavage assay monitored by Ex/Em 485/535 nm	
<u>Assay buffer:-</u>	
40 mM Tris pH 7.5, 100 mM NaCl, 5 mM DTT, 0.01% Triton X-100, 0.005% Ovalbumin, 0.5 µM Ub-Rho110-Gly	

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Clone Data Sheet

GST-A20 [1-366]

<u>Protein</u>	GST-A20 [1-366]
<u>Synonyms</u>	TNAP3, TNFAIP3, OTUD7C
<u>Clone Number</u>	DU32912
<u>Species</u>	Human
<u>Accession Number</u>	Protein: P21580 DNA: BC114480
<u>Tags</u>	N-terminal GST tag
<u>Amino acid sequence of expressed protein</u>	MSPIILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSR IAYS KDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA WPLQGWQATFGGGDHPPKSDLEVLFOGPLGSPGIPGSTRAAAMAEQVLPO ALYLSNMRKAVKIRERTPEDIFKPTNGIIHHFKTMHRYTLEMFRTCQFCP QFREIIHKALIDRNIQATLESQKKNWCREVRKLVALKTNGDGNCLMHAT SQYMWGVQDSDLVLRKALFSTLKETDTRNFKFRWQLESLSKSQEFVETGLC YDTRNWNDEWDNLIKMASTDTPMARSGLQYNSLEEIHIFVLCNILRRPII VISDKMLRSLESGSNFAPLKVGGIYLPLHWP AQECYRYP IVLGYDSSH FV PLVTLKDSGPEIRAVPLVNRDRGRFEDLKVHFLTDPENEMKEKLLKEYLM VIEIPVQGDHGTTHLINA AKLDEANLPKEINLVDDYFELVQHEYKKWQE NSEQGRRE
<u>Native sequence</u>	in bold
<u>Protease cleavage</u>	Precision site underlined
<u>Cloning sites</u>	NotI

**DNA sequence of
insert**

CGGCGCGATGGCTGAACAAGTCCTTCCTCAGGCTTTGTATTTGAGCAA
TATGCGGAAAGCTGTGAAGATACGGGAGAGAAGCTCCAGAAGACATTTTTA
AACCTACTAATGGGATCATTTCATCATTTTTAAAACCATGCACCGATACACA
CTGGAAATGTTTCAGAACTTGCCAGTTTTTGTCCCTCAGTTTCGGGAGATCAT
CCACAAAGCCCTCATCGACAGAAACATCCAGGCCACCCCTGGAAAGCCAGA
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AACGGTGACGGCAATTGCCTCATGCATGCCACTTCTCAGTACATGTGGGG
CGTTCAGGACACAGACTTGGTACTGAGGAAGGCGCTGTTTCAGCACGCTCA
AGGAAACAGACACACGCAACTTTAAATTCCGCTGGCAACTGGAGTCTCTC
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CATTTAATGGGATCTGCAGTACTTGCTTCAAAGGACTACAGCAGAGGCC
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