

*Division of Signal Transduction Therapy*

**Standard Operation Procedure**

**Preparation of GST-UBE2G2**

<b><u>Enzyme description:-</u></b>	UBE2G2
<b><u>Clone number:-</u></b>	DU4207
<b><u>Source:-</u></b>	BL21 recombinant
<b><u>Tag:-</u></b>	N-terminal GST-tag
<b><u>Purification method:-</u></b>	GSH-Sepharose
<b><u>Expression level:-</u></b>	5mg/L
<b><u>Calculated molecular mass:-</u></b>	
Monoisotopic	45229 Da
Average Mass	45258 Da
[cysteines reduced, methionines have not been oxidised]	
<b><u>Theoretical pI:-</u></b>	5.07
<b><u>Purity:-</u></b>	90%
<b><u>Enzyme storage buffer:-</u></b>	
50mM HEPES pH 7.5, 150mM NaCl, 10% glycerol, 1mM DTT	
<b><u>Storage temperature:-</u></b>	-80°C
<b><u>Assay:-</u></b>	
Loading assay with Ubiquitin and UBE1 in the presence of Mg-ATP	

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### **Clone Data Sheet**

#### **GST-UBE2G2**

<b><u>Protein</u></b>	GST-UBE2G2
<b><u>Synonyms</u></b>	
<b><u>Clone Number</u></b>	DU4207
<b><u>Species</u></b>	Human
<b><u>Accession Number</u></b>	Protein: NP_003334 DNA: NM_003343
<b><u>Tags</u></b>	N-terminal GST-tag
Aminoacid sequence of the expressed protein	<b>MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGVSR IAYSKDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFOGPLGS<b>AGTALKRLMAEYKQLTLNPEGIVAGPMNEENFFEW EALIMGPEDTCFEFGVFPAILSFP</b>LDYPLSPPK<b>MRFTCEMFHPNIYPDGRVCISILHAPGDDPMGYESSAERWSPVQSVEKILLSVVSMLAEPNDESGANVDASKMWRDDREQFYKIAKQIVQKSLGL</b></b>
Native sequence	in bold, Start Met is missing
Protease cleavage	Precision protease site underlined
Cloning sites	BamH1 / NotI
<b><u>DNA sequence of the expression cassette</u></b>	ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCAC TCGACTTCTTTTGGAAATATCTTGAAGAAAAATATGAAGAGCATTTGTATG AGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTGGGTTTG GAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAATTAACACA GTCTATGGCCATCATACGTTATATAGCTGACAAGCACAACATGTTGGGTG GTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTG GATATTAGATACGGTGTTCGAGAATTGCATATAGTAAAGACTTTGAAAC TCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTTCG AAGATCGTTTATGTCATAAAACATATTTAAATGGTGATCATGTAACCCAT CCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATAACATGGACCC AATGTGCCTGGATGCGTTCCCAAAATTAGTTTTGTTTTAAAAACGTATTG AAGCTATCCACAAATTGATAAGTACTTGAAATCCAGCAAGTATATAGCA TGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACCATCCTCC AAAATCGGATCTGGAAGTTCTGTTCCAGGGGCCCCCTGGGATCCGCGGGGA CCGCGCTCAAGAGGCTGATGGCCGAGTACAAACAATTAACACTGAATCCT CCGGAAGGAATTGTAGCAGGCCCATGAATGAAGAGAAGCTTTTTTGAATG GGAGGCATTGATCATGGGCCAGAAAGACACCTGCTTTGAGTTTGGTGT TTCTGCCATCCTGAGTTTCCCACTTGATTACCGTTAAGTCCCCCAAAG ATGAGATTTACCTGTGAGATGTTTCATCCCAACATCTACCCTGATGGGAG AGTCTGCATTTCCATCCTCCACGCGCCAGGCGATGACCCCATGGGCTACG AGAGCAGCGCGGAGCGGTGGAGTCTGTGCAGAGTGTGGAGAAGATCCTG CTGTCGGTGGTGGAGCATGCTGGCAGAGCCCAATGACGAAAGTGGAGCTAA

CGTGGATGCGTCCAAAATGTGGCGCGATGACCGGGAGCAGTTCTATAAGA  
TTGCCAAGCAGATCGTCCAGAAGTCTCTGGGACTGTGAGCGGCCGC