

*Division of Signal Transduction Therapy*

**Standard Operation Procedure**

**Preparation of GST-UBE2Q2**

<b><u>Enzyme description:-</u></b>	GST-UBE2Q2
<b><u>Clone number:-</u></b>	DU20524
<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>	0.8 mg/L
<b><u>Calculated molecular mass:-</u></b>	
Monoisotopic	69598 Da
Average Mass	69641 Da
[cysteines reduced, methionines have not been oxidised]	
<b><u>Theoretical pI:-</u></b>	5.04
<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 with Ubiquitin and UBE1 in the presence of Mg-ATP	

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### Clone Data Sheet

#### GST-UBE2Q2

**Protein** UBE2Q2  
**Synonyms**  
**Clone Number** DU20524  
**Species** Human  
**Accession Number** Protein: Q8WVN8      DNA: NM\_173469  
**Tags** N-terminal GST tag

Aminoacid sequence of the expressed protein

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGL  
EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGAVL  
DIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTH  
PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA  
WPLQGWQATFGGGDHPKSDLEVLFOGPLGSMSV**SGLKAEKFLASIFDK**  
**NHERFRIVSWKLDLHCQFLVPQQGSPHSLPPPLTLHCNITESYPSSSPI**  
**WFVDS**EDPNLTSVLERLEDTKNNLL**RQQLKWLICELCSLYNLPKHL**DVE  
MLDQPLPTG**QNGTTE**EV**TSEEEEEEE**MAEDIEDLDHYEMKEEEPISGKK  
SEDEGIEKENLAILEKIRKT**QRQD**HLNGAVSGSVQASDRMKELRDIYRS  
QSYKTGIYSVELINDSLYDWHVKLQKVDPDSPLHSDLOILKEKEGIEYIL  
LNFSFKDNFPDPPFVRVVLVLSGGYVLGGGALC**MELLTKQ**WSSAYS**IESVIMQ**INATLVKGKARV**QFGANKNQYNLARAQQSYNSIVQI**HEKNGWYT  
PPKEDG

Native sequence in bold  
Protease cleavage Precission site underlined  
Cloning sites BamH1 / NotI

**DNA sequence of the insert**

GGATCCATGTCCGTGTCAGGGCTCAAGGCCGAGCTGAAGTTCCTGGCGTC  
CATCTTCGACAAGAACCACGAGCGATTCCGCATCGTCAGTTGGAAGCTGG  
ACGAGCTGCACTGCCAGTTCCTGGTGCCGCAGCAGGGCAGCCCCGCACTCG  
CTGCCGCCGCCACTCACGCTCCACTGCAACATCACGGAATCCTATCCATC  
TTCTTCACCGATATGGTTTGTGGATTCTGAAGACCCAAATCTGACATCAG  
TTCTGGAACGTCTAGAAGATACTAAGAACAACAATTTGCTTCGTCCAGCAA  
TTGAAGTGGTTGATATGTGAACCTCTGCAGTTTATATAACCTTCCTAAGCA  
CCTGGATGTTGAGATGCTAGATCAACCACTACCCACGGGTCAGAATGGGA  
CAACAGAAGAAGTGACTTCAGAAGAAGAGGAAGAAGAAGAAGAGATGGCT  
GAAGATATAGAAGACTTAGATCACTATGAGATGAAGGAAGAAGAGCCTAT  
TAGTGGGAAAAAGTCAGAGGATGAAGGAATTGAAAAAGAAAATTTGGCAA  
TATTAGAGAAAATTAGGAAGACTCAAAGGCAAGACCATTTAAATGGTGCA  
GTGCTGGGTCAGTGCAAGCTTCAGATAGACTTATGAAAGAGCTCAGGGA  
CATATACAGATCACAGAGTTATAAAACAGGGATTTATTCAGTGGAACTCA  
TAAATGACAGTTTATATGACTGGCATGTTAAACTGCAGAAGGTTGACCCT  
GATAGTCCTTTGCACAGTGATCTTCAGATCTTAAAGAAAAAGAAGGCAT

AGAATATATTTTGCTTAACTTCTCTTTTAAGGATAACTTTCCATTTGATC  
CTCCATTTGTTTCGAGTGGTGTACCTGTTCTCTCAGGAGGGTATGTATTG  
GGTGGAGGAGCATTATGTATGGAACCTCTCACAAAACAGGGCTGGAGCAG  
TGCCTACTCAATAGAATCGGTCATCATGCAAATAAATGCCACCTTAGTCA  
AAGGCAAAGCCAGAGTGCAGTTTGGAGCAAATAAGAATCAATATAATCTA  
GCAAGAGCCCAACAATCCTATAATTCCATTGTACAGATACATGAGAAAAA  
TGGCTGGTACACCCCTCCAAAGGAAGATGGCTAAGCGGCCGC