

*Division of Signal Transduction Therapy*

**Standard Operation Procedure**

**Preparation of GST-UBE2L6**

<b><u>Enzyme description:-</u></b>	GST-UBE2L6
<b><u>Clone number:-</u></b>	DU32141
<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	44563 Da
Average Mass	44591 Da
[cysteines reduced, methionines have not been oxidised]	
<b><u>Theoretical pI:-</u></b>	6.49
<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 ISG15 and UBA7 in the presence of Mg-ATP	

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### Clone Data Sheet

#### GST-UBE2L6

<b><u>Protein</u></b>	UBE2L6
<b><u>Synonyms</u></b>	UbcH6, RIG-B
<b><u>Clone Number</u></b>	DU32148
<b><u>Species</u></b>	Human
<b><u>Accession Number</u></b>	Protein: O14933      DNA: NM_004223
<b><u>Tags</u></b>	N-terminal GST-tag
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAESMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGGDHPKSDLEVLFOGPLGSMASMRVVKELEDLQKKPPYLRNLSDDANVLVWHALLLPDQPPYHLKAFNLRISFPPEYPFKPPMIKFTTKIYHPNVDENGQICLPIISSENWKPCTKTCQVLEALNVLVNRPNIREPLRMDLADLLTQNPFLFRKNAEEFTLRFGVDRPS
Native sequence	in bold
Protease cleavage	Prescission site underlined
Cloning sites	BamH1 / NotI
<b><u>DNA sequence of insert</u></b>	GGATCCATGATGGCGAGCATGCGAGTGGTGAAGGAGCTGGAGGATCTTCA GAAGAAGCCTCCCCATACCTGCGGAACCTGTCCAGCGATGATGCCAATG TCCTGGTGTGGCAGCTCTCCTCCTACCCGACCAACCTCCCTACCACCTG AAAGCCTTCAACCTGCGCATCAGCTTCCCGCCGAGTATCCGTTCAGCC TCCCATGATCAAATTCACAACCAAGATCTACCACCCCAACGTGGACGAGA ACGGACAGATTTGCCTGCCCATCATCAGCAGTGAGAAGTGGAAAGCCTTGC ACCAAGACTTGCCAAGTCCTGGAGGCCCTCAATGTGCTGGTGAATAGACC GAATATCAGGGAGCCCCTGCGGATGGACCTCGCTGACCTGCTGACACAGA ATCCGGAGCTGTTTCAGAAAGAATGCCGAAGAGTTCACCCTCCGATTCGGA GTGGACCGGCCCTCCTAAGCGGCCGC