

*Division of Signal Transduction Therapy*

**Standard Operation Procedure**

**Preparation of UBE2T**

<b><u>Enzyme description:-</u></b>	UBE2T 1-197 (full length)
<b><u>Clone number:-</u></b>	DU15711
<b><u>Source:-</u></b>	Recombinant
<b><u>Tag:-</u></b>	N-terminal GST
<b><u>Purification method:-</u></b>	GSH-Sepharose
<b><u>Expression level:-</u></b>	2 mg/L
<b><u>Calculated molecular mass:-</u></b>	
Monoisotopic	49313 Da
Average Mass	49343 Da
[cysteines reduced, methionines have not been oxidised]	
<b><u>Theoretical pI:-</u></b>	6.64
<b><u>Purity:-</u></b>	90 %
<b><u>Enzyme storage buffer:-</u></b>	
50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT	
<b><u>Storage temperature:-</u></b>	-80°C
<b><u>Assay:-</u></b>	

## *Division of Signal Transduction Therapy*

### **Clone Data Sheet**

#### **Protein name GST-UBE2T**

<b><u>Protein</u></b>	UBE2T 1-197 (full length)
<b><u>Synonyms</u></b>	HSPC150, PIG50
<b><u>Clone Number</u></b>	DU15711
<b><u>Species</u></b>	Human
<b><u>Accession Number</u></b>	Protein: Q9NPD8 or NP_054895
<b><u>Tag</u></b>	N-terminal GST
Aminoacid sequence of the expressed protein .	MSPILGYWKIKGLVQPTRLLEYLEEKYEELHYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA WPLQGWQATFGGGDHPKSD <u>LEVLFQGPLGSMQ</u> RASRLKRELHMLATEPP <b>PGITCWQDKDQMDLRAQILGGANTPYEKGVFKLEVIIPERYPFEPPOIR</b> <b>FLTPIYHPNIDSAGRICLDVLKLPKGAWRPSLNIATVLTISIQLLMSEPN</b> <b>PDDPLMADISSEFKYNKPAFLKNARQWTEKHARQKQKADEEEMLDNLPEA</b> <b>GDSRVHNSTQKRKASQLVGLIEKKFHPDV</b>
Native sequence	in bold
Protease cleavage	Precision Protease site underlined
Cloning sites	BamH1 / NotI
<b><u>DNA sequence of insert</u></b>	GGATCCATGCAGAGAGCTTCACGTCTGAAGAGAGAGCTGCACATGTTAGC CACAGAGCCACCCCAAGGCATCACATGTTGGCAAGATAAAGACCAAATGG ATGACCTGCGAGCTCAAATATTAGGTGGAGCCAACACACCTTATGAGAAA GGTGTTTTTAAGCTAGAAGTTATCATTCTGAGAGGTACCCATTTGAACC TCCTCAGATCCGATTTCTCACTCCAATTTATCATCCAAACATTGATTCTG CTGGAAGGATTTGTCTGGATGTTCTCAAATTGCCACCAAAAAGGTGCTTGG AGACCATCCCTCAACATCGCAACTGTGTTGACCTCTATTCAGCTGCTCAT GTCAGAACCAACCCTGATGACCCGCTCATGGCTGACATATCCTCAGAAT TTAAATATAATAAGCCAGCCTTCCTCAAGAAATGCCAGACAGTGGACAGAG AAGCATGCAAGACAGAAACAAAAGGCTGATGAGGAAGAGATGCTTGATAA TCTACCAGAGGCTGGTGACTCCAGAGTACACAACCTCAACACAGAAAAGGA AGGCCAGTCAGCTAGTAGGCATAGAAAAGAAATTCATCCTGATGTTTAG GCGGCCGC