

## *Division of Signal Transduction Therapy*

### **Standard Operation Procedure**

#### **Preparation of GST-TUBE UBQL1 536-589 (UBA domain) tetramer = TUBE**

**Enzyme description:-** GST-Ubiquilin 536-589 tetramer

**Clone number:-** DU20100

**Source:-** BL21 recombinant

**Tag:-** N-terminal GST;

**Purification method:-** GSH-Sepharose

**Expression level:-** 1 mg/L

**Calculated molecular mass:-**

Monoisotopic 51930 Da

Average Mass 51961 Da

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 5.03

**Purity:-** 90%

**Enzyme storage buffer:-**

50mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT

**Storage temperature:-** -80°C

**Assay:-**

This protein binds to long K63 poly Ub chains.

*Division of Signal Transduction Therapy*

**Clone Data Sheet**

**GST-UBQL1 536-589 tetramer  
GST-TUBE Tandem Ubiquitin Binding Entity**

<b><u>Protein</u></b>	GST-UBQL1 536-589 (UBA-domain) tetramer
<b><u>Synonyms</u></b>	UBQL1, DA41, PLIC1
<b><u>Clone Number</u></b>	DU20100
<b><u>Species</u></b>	Human
<b><u>Accession Number</u></b>	Protein: Q9UMX0; DNA:NM_053067
<b><u>Tags</u></b>	N-terminal GST
Amino acid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA WPLQGWQATFGGGDHPKSDLEVLFOGPLGSGGGVNPQLQNPEVRFQOQL <b>EQLSAMGFLNREANLQALIATGGDINAAIERLLGSQPSGGGGSGGGVNPQ LQNPEVRFQOQLEQLSAMGFLNREANLQALIATGGDINAAIERLLGSQPS GGGGSGGGVNPQLQNPEVRFQOQLEQLSAMGFLNREANLQALIATGGDIN AAIERLLGSQPSGGGGSGGGVNPQLQNPEVRFQOQLEQLSAMGFLNREAN LQALIATGGDINAAIERLLGSQPS</b>
Native sequence	in bold
Protease cleavage	Prescission protease site underlined
Cloning sites	BglIII/BamHI insert (cloned into BamHI site)
<b><u>DNA sequence of the expression cassette</u></b>	ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCAC TCGACTTCTTTTGGAAATATCTTGAAGAAAAATATGAAGAGCATTTGTATG AGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTGGGTTTG GAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAATTAACACA GTCTATGGCCATCATACTTATATAGCTGACAAGCACAACATGTTGGGTG GTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTTG GATATTAGATACGGTGTTCGAGAATTGCATATAGTAAAGACTTTGAAAC TCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTTCG AAGATCGTTTATGTCATAAAACATATTTAAATGGTGATCATGTAACCCAT CCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATACATGGACCC AATGTGCCTGGATGCGTTCCCAAATTAGTTTGTTTTTAAAAACGTATTG AAGCTATCCCACAAATTGATAAGTACTTGAAATCCAGCAAGTATATAGCA TGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACCATCCTCC AAAATCGGATCTGGAAGTTCTGTTCAGGGGCCCTGGGATCTGGAGGTG GAGTAAATCCTCAGCTACAGAATCCAGAAGTCAGATTTTCAGCAACAACCTG GAACAACCTCAGTGCAATGGGATTTTTGAACCGTGAAGCAAACCTTGAAGC TCTAATAGCAACAGGAGGTGATATCAATGCAGCTATTGAAAGGTTACTGG

GCTCCCAGCCATCAGGAGGTGGAGGATCTGGAGGTGGAGTAAATCCTCAG  
CTACAGAATCCAGAAGTCAGATTCAGCAACAACCTGGAACAACCTCAGTGC  
AATGGGATTTTTGAACCGTGAAGCAAACCTTGCAAGCTCTAATAGCAACAG  
GAGGTGATATCAATGCAGCTATTGAAAGGTTACTGGGCTCCCAGCCATCA  
GGAGGTGGAGGATCTGGAGGTGGAGTAAATCCTCAGCTACAGAATCCAGA  
AGTCAGATTCAGCAACAACCTGGAACAACCTCAGTGCAATGGGATTTTTGA  
ACCGTGAAGCAAACCTTGCAAGCTCTAATAGCAACAGGAGGTGATATCAAT  
GCAGCTATTGAAAGGTTACTGGGCTCCCAGCCATCAGGAGGTGGAGGATC  
TGGAGGTGGAGTAAATCCTCAGCTACAGAATCCAGAAGTCAGATTCAGC  
AACAACTGGAACAACCTCAGTGCAATGGGATTTTTGAACCGTGAAGCAAAC  
TTGCAAGCTCTAATAGCAACAGGAGGTGATATCAATGCAGCTATTGAAAG  
GTTACTGGGCTCCCAGCCATCATAGGGAGGTGGAGGATCC