

## *Division of Signal Transduction Therapy*

### **Standard Operating Procedure**

#### **Preparation of His-Ubiquitin [2 - 76]**

**Enzyme description:-** His-Ubiquitin [2 - 76]

**Clone number:-** DU 3351

**Source:-** Recombinant

**Expression system:-** *E.coli*

**Tag:-** N-terminal His(6)

**Purification method:-** Ni<sup>2+</sup> -NTA agarose

**Expression level:-** 0.5 mg/L

**Calculated molecular mass:-**

Monoisotopic            11,970.13 daltons  
Average Mass            11,977.55 daltons  
[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 9.16

**Purity:-** 85 %

**Enzyme storage buffer:-**

50 mM Tris-HCl pH 7.5, 270 mM Sucrose, 150 mM NaCl, 0.1 mM EGTA,  
0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 0.2 mM PMSF, 1 mM Benzamidine.

**Storage temperature:-** -70 °C

**Assay:-** Ubiquitin assay

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**Clone Data Sheet**

**Ubiquitin [2 - 76]**

|   |  |
|---|--|
| <b><u>Protein</u></b>                       | Ubiquitin [2 - 76]   |
| <b><u>Clone Number</u></b>                  | DU 3551  |
| <b><u>Species</u></b>                       | Human  |
| <b><u>Accession number</u></b>              | P62988   |
| <b><u>Tags</u></b>                          | N-terminal His(6)  |
| <b><u>Bacterially expressed protein</u></b> | <b>MGSSHHHHHSSGLVPRGSHMASMTGGQQMGRGSQIFVKTLTGKTITLE<br/>VEPSDTIENVKAKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYNIQKES<br/>TLHLVLRLLGG</b>  |
| <b><u>Native sequence</u></b>               | Amino acids Q2 – G76 (end) of human Ubiquitin.<br>Residue Q35 of the fusion protein is equivalent to Q2 of the native enzyme.<br>The His(6) tag is located at residues 5 – 10.   |
| <b><u>Protease cleavage</u></b>             | None   |
| <b><u>Cloning sites</u></b>                 | <i>Bam</i> H1 and <i>Not</i> 1 site of pET28a  |
| <b><u>Nucleotide Sequence</u></b>           | ggatccCAGATCTTCGTGAAGACCCTGACTGGTAAGACCATCACTCTCG<br>AAGTGGAGCCGAGTGACACCATTGAGAATGTCAAGGCAAAGATCCAAGA<br>CAAGGAAGGCATCCCTCCTGACCAGCAGAGGTTGATCTTTGCTGGGAAA<br>CAGCTGGAAGATGGACGCACCCTGTCTGACTACAACATCCAGAAAGAGT<br>CCACCCTGCACCTGGTCCCTCCGTCTCAGAGGTGGGtgataactcgag |