

## *Division of Signal Transduction Therapy*

### **Standard Operating Procedure**

#### **Preparation of RILPL2 [1 - 120]**

**Enzyme description:-** RILPL2 [1 - 120]

**Clone number:-** DU 27504

**Source:-** Recombinant

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

**Tag:-** N-terminal His6-SUMO

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

**Calculated molecular mass:-**

Monoisotopic 25, 512.59 daltons

Average Mass 25, 528.50 daltons

[cysteines reduced, methionines have not been oxidised

**Theoretical pI:-** 4.84

**Purity:-** >80 %

**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, 1 mM benzamidine, 0.2 mM PMSF

**Storage temperature:-** -70 °C

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**Clone Data Sheet**

**RILPL2 [1 - 120]**

|   |  |
|---|--|
| <b><u>Protein</u></b>                       | RILPL2 [1 - 120]   |
| <b><u>Clone number</u></b>                  | DU 27504   |
| <b><u>Species</u></b>                       | Human  |
| <b><u>Accession number</u></b>              | NM_145058.2  |
| <b><u>Tags</u></b>                          | N-terminal His-SUMO  |
| <b><u>Bacterially expressed protein</u></b> | MGHHHHHHSDQEAKPSTEDLGDKKEGEYIKLKVIQDSSEIHFKVKMTT<br>HLKKLKESYCQRQGVPMNSLRFLFEGQRIADNHTPKELGMEEEDVIEVY<br>QEQTGGMEEPPVREEEEEEEDEERDEVGPEGALGKSPFQLTAEDVYD<br><b>I SYLLGRELMALGSDPRVTQLQFKVVRLLEMLEALVNEGSLALEELKME</b><br><b>RDHLRKVEGLRRQSPPASGEVNLPNK</b> |
| <b><u>Native sequence</u></b>               | Amino acids M1 – K120 (end residue T211) of human RILPL2.<br>Residue M105 of the fusion protein is equivalent to M1 of the native enzyme. The His6 tag is located at residues 3 – 8.   |
| <b><u>Protease cleavage</u></b>             | SENP1 cleavage of SUMO:<br>(SDQEAKPSTEDLGDKKEGEYIKLKVIQDSSEIHFKVKMTT<br>HLKKLKESYCQRQGVPMNSLRFLFEGQRIADNHTPKELGMEEEDVIEVYQEQTGG) residues 9 - 104  |
| <b><u>Cloning sites</u></b>                 | <i>Bam</i> H1 and <i>Not</i> 1 sites of pET15b His6-SUMO   |

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Nucleotide  
Sequence Of  
Insert

ggatccATGGAGGAGCCCCCTGTGCGAGAAGAGGAAGAGGAGGGAG  
AGGAGGACGAGGGAGGGACGAGGTTGGGCCGAGGGGGCGCTGGCAA  
GAGCCCCTTCCAGCTGACCGCCGAGGACGTGTATGACATCTCCTACCTG  
TTGGGCCGCGAGCTTATGCCCTGGGCAGCGACCCCCGGGTGACGCAGC  
TGCAGTTCAAAGTCGTCCCGTCCTGGAGATGCTGGAGGCGCTGGTGAA  
TGAGGGCAGCCTGGCGCTGGAGGAGCTGAAGATGGAGAGGGACCACCTC  
AGGAAGGAGGTGGAGGGCTCGGGAGACAGAGCCCTCCGGCCAGCGGGG  
AGGTGAACCTGGGCCAACAAAtaggcggccgc