

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of His-SUMO2 (1-93 = mature full length)

| | |
|-------------------------------------|---------------------------------|
| <u>Enzyme description:-</u> | SUMO2 1-93 |
| <u>Clone number:-</u> | DU32081 |
| <u>Source:-</u> | human recombinant |
| <u>Tag:-</u> | His- |
| <u>Purification method:-</u> | Ni ²⁺ -NTA-Sepharose |
| <u>Expression system:-</u> | E.coli |

Calculated molecular mass:-

| | |
|---|----------|
| Monoisotopic | 13045 Da |
| Average Mass | 13053 Da |
| [cysteines reduced, methionines have not been oxidised] | |

Theoretical pI:- 6.4

Purity:- 90%

Enzyme storage buffer:-

10mM Ammonium bicarbonate

Storage temperature:- -80°C

Assay:-

Loading of UBE2I.

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Clone Data Sheet

His-SUMO2 1-93

| | |
|---|---|
| <u>Protein</u> | SUMO2 (1-93 = mature full length) |
| <u>Synonyms</u> | (SMT3 suppressor of mif two 3 homolog 2) |
| <u>Clone Number</u> | DU32081 |
| <u>Species</u> | Human |
| <u>Accession Number</u> | Protein: NP_008868 DNA AK311837.1 |
| <u>Tags</u> | His- |
| <u>Aminoacid sequence of the expressed protein</u> | MGSSHHHHHHSSGLEVL<u>FQ</u>GP<u>GSM</u>AD<u>EKP</u>KE<u>G</u>V<u>K</u>T<u>EN</u>NDHINLKVAG QD<u>G</u>S<u>V</u>V<u>Q</u>F<u>K</u>I<u>K</u>R<u>H</u>T<u>P</u>L<u>S</u>K<u>L</u>M<u>K</u>A<u>Y</u>C<u>E</u>R<u>Q</u>G<u>L</u>S<u>M</u>R<u>Q</u>I<u>R</u>F<u>R</u>D<u>G</u>Q<u>P</u>I<u>N</u>E<u>T</u>D TP<u>A</u>Q<u>L</u>E<u>M</u>E<u>D</u>E<u>D</u>T<u>I</u>D<u>V</u>F<u>Q</u>Q<u>T</u>G<u>G</u> |
| <u>Native sequence</u> | The native sequence is a little longer and normally processed to this mature form by SENP1. |
| <u>Protease cleavage</u> | Precession protease site underlined |
| <u>Cloning sites</u> | BamHI / NotI |
| <u>DNA sequence of insert</u> | GGATCCATGGCCGACGAAAAGCCCAAGGAAGGAGTCAAGACTGAGAACAA CGATCATATTAATTTGAAGGTGGCGGGGCAGGATGGTTCTGTGGTGCAGT TTAAGATTAAGAGGCATACACCACTTAGTAACTAATGAAAGCCTATTGT GAACGACAGGGATTGTCAATGAGGCAGATCAGATTCCGATTTGACGGGCA ACCAATCAATGAAACAGACACACCTGCACAGTTGGAAATGGAGGATGAAG ATACAATTGATGTGTTCCAACAGCAGACGGGAGGTTAATACTGAGTCGAC TCGAAAGCGGCCGC |