

# *Division of Signal Transduction Therapy*

## **Standard Operating Procedure**

### **Preparation of RAB3IP [1 – 476]**

<b><u>Enzyme description:-</u></b>	RAB3IP [1 – 476]
<b><u>Clone number:-</u></b>	DU 21167
<b><u>Source:-</u></b>	Recombinant
<b><u>Expression system:-</u></b>	<i>E.coli</i> ,
<b><u>Tag:-</u></b>	N-terminal His(6) - SUMO
<b><u>Purification method:-</u></b>	Ni <sup>2+</sup> -NTA agarose, Cleavage of His6-SUMO and Gel filtration
<b><u>Calculated molecular mass:-</u></b>	
Monoisotopic	52, 987.71 daltons [After tag cleavage]
Average Mass	53, 021.21 daltons [After tag cleavage]
	[cysteines reduced, methionines have not been oxidised]
<b><u>Theoretical pI:-</u></b>	5.83
<b><u>Purity:-</u></b>	>80 %
<b><u>Activation Protocol:-</u></b>	Expressed in the presence of GroEL / GroES
<b><u>Enzyme storage buffer:-</u></b>	
50 mM Tris-HCl pH 7.5, 150 mM NaCl, 270 mM sucrose, 0.1 mM EGTA, 0.1 % 2-mercaptoethanol, 0.03 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF	
<b><u>Storage temperature:-</u></b>	-70 °C

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**Clone Data Sheet**

**RAB3IP [1 - 476]**

<b><u>Protein</u></b>	RAB31P [1 - 476]
<b><u>Clone number</u></b>	DU 21167
<b><u>Species</u></b>	Human
<b><u>Accession number</u></b>	NM_175623.3
<b><u>Tags</u></b>	N-terminal His(6) + SUMO
<b><u>Bacterially expressed RAB3IP protein</u></b>	MGHHHHHSDQEAKPSTEDLGDKKEGEYIKLKVGQDSSEIHFVVKMT THLKKLKESYCQRQGVPMSLRFLFEGQRIADNHTPKELGMEEEDVIE VYEQTGGMGLKKMKGLSYDEAFAMANDPLEGFHEVNLASPTSPDLLG VYESGTQEQTSPSVIYRPHPSALSSVPIQANALDVSELPTQPVYSSP RRLNCAEISSISFHVTDPAPCSTSGVTAGLTKLTRKDNYNAEREFLQ GATITEACDGSDDIFGLSTDLSRLRSPSVLEVREKGYERLKEELAKA QRELKLKDEECERLSKVRDQLGQELEELTASLFEEAHKMVREANIKQA TAEKQLKEAQGKIDVLQAEVAALKTLVLSSSPTSPQEPPLPGGKTPFK KGHTRNKSTSSAMSGSHQDLSVIQPIVKDCKEADLSLYNEFRWKDEP TMDRTCPFLDKIYQEDIFPCLTFSKSELASAVLEAVENNTLSIEPVGL QPIRFVKASAVECGGPKKCALTGQSCKHSRKLIKGDSSNNYYISPFCR YRITSVCNFFTYIRYIQQGLVKQQDVDQMFWEVMQLRKEMLAKLGYF KEEL
<b><u>Native sequence</u></b>	Amino acids M1 – L476 (end) of human RAB3IP. Residue M105 of the fusion protein is equivalent to M1 of the native enzyme. The His(6) tag is located at residues 2 – 7.
<b><u>Protease cleavage</u></b>	SENP1 cleavage of SUMO: (SDQEAKPSTEDLGDKKEGEYIKLKVGQDSSEIHFVVKMTT HLKKLKESYCQRQGVPMSLRFLFEGQRIADNHTPKELGMEE EEDVIEVYEQTGG) 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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<u>Nucleotide sequence of insert</u>	ggatccATGGGATTAAAAAAGATGAAAGGGTTATCTTATGATGAGGCTT TTGCTATGGCTAATGATCCCTGGAAAGGCTTCCATGAAGTAAACCTT GCTTCACCTACTTCTCCGGACCTTCTGGTGTATGAATCAGGAACCT CAAGAGCAGACTACCTCACCAAGTGTATCTACCGGCCACACCCTCA GCTTATCCTCTGTACCTATCCAGGCAAATGCATTAGATGTTCTGAA CTTCCTACACAACCCGTGTATTCATCCCCCAGACGTTAAATTGTGCG GAAATATCTAGTATCAGCTTCATGTTACAGACCCAGCCCCTGCTCT ACCTCTGGAGTCACAGCTGGATTAACTAAATTAACTACAAGAAAGGAC AACTATAATGCAGAGAGAGAGTTTACAGGGTGTACTATAACAGAG GCTTGCATGGCAGTGATGATATTTGGGTTGAGTACTGATAGTCTG TCTCGTTACGAAGCCCATCTGTTGGAAAGTTAGAGAAAAGGGCTAT GAACGATTAAGAAGAACCTCGCAAAGCTCAGAGGGAACTGAAGTTA AAAGATGAAGAATGTGAGAGGCTTCAAAAGTGCAGATCAACTTGGA CAGGAATTGGAAGAACTCACAGCTAGTCTATTGAGGAAGCTCATAAA ATGGTGAGAGAACAAATATCAAGCAGGCAACAGCAGAAAAACAGCTA AAAGAACACAAGGAAAATTGATGTACTTCAAGCTGAAGTAGCTGCA TTGAAGACACTTGTATTGTCAGTTCTCCAACATCACCTACGCAGGAG CCTTGCCAGGTGAAAGACACCTTTAAAAAGGGCATACAAGAAAT AAAAGCACAAGCAGTGCTATGAGTGGCAGTCATCAGGACCTCAGTGTG ATACAGCCAATTGTAAAAGACTGCAAAGAGGCTGACTTATCCTTGTAT AATGAATTCCGATTGTGGAAGGATGAGGCCACAATGGACAGGACGTGT CCTTCTTAGACAAAATCTACCAGGAAGATATCTTCCATGTTAACAA TTCTCAAAAGTGAAGTTGGCTTCAGCTGTTCTGGAGGCTGTGAAAAC AATACTCTAACGATTGAACCAGTGGGATTACAACCTATCCGGTTGTG AAAGCTTCTGCAGTTGAATGCGGAGGACCAAAAAATGTGCTCTCACT GGCCAGAGTAAGTCCGTAAACACAGAATTAAATTAGGGGACTCAAGC AACTATTATTATTTCTCCTTTGCAGATACAGGATCACTCTGTA TGTAACTTTTACATACATTGATACATTGAGCTGGGACTCGTGAA CAGCAGGATGTTGATCAGATGTTGGGAGTTATGAGTTGAGAAAA GAGATGTCATTGGCAAAGCTGGTTATTCAAAGAGGAACtgcg gccgc
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