

## *Division of Signal Transduction Therapy*

### **Standard Operation Procedure**

#### **Preparation of GST-RAP80 80-120 (UIM domain dimer)**

**Enzyme description:-** GST-RAP80 80-120 (UIM-domain dimer)

**Clone number:-** DU20750

**Source:-** BL21 recombinant

**Tag:-** N-terminal GST

**Purification method:-** GSH-Sepharose

**Expression level:-** 2 mg/L

**Calculated molecular mass:-**

Monoisotopic 31888 Da

Average Mass 31907 Da

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 4.85

**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 K63 poly Ub chains.

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### **Clone Data Sheet**

#### **GST-RAP80 80-120**

<b><u>Protein</u></b>	RAP80 80-120 (UIM domain dimer)
<b><u>Synonyms</u></b>	UIMC1, RXRIP110
<b><u>Clone Number</u></b>	DU20750
<b><u>Species</u></b>	Human
<b><u>Accession Number</u></b>	Protein: Q96RL1
<b><u>Tags</u></b>	N-terminal GST
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMATIRYIADKHNMLGGCPKERAIEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA WPLQGWQATFGGGDHPKSDLEVL <u>FQG</u> PLGSMVD <b>TEEEQFALALKMSEQE</b> <b>AREVNSQEEEEELLRKAIAESLNS</b>
Native sequence	the UIM dimer is in bold
Protease cleavage	Prescission protease site underlined
Cloning sites	BamH1 / Not1
<b><u>DNA sequence of the expression cassette</u></b>	ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCAC TCGACTTCTTTTGGAAATATCTTGAAGAAAAATATGAAGAGCATTTGTATG AGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTGGGTTTG GAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAATTAACACA GTCTATGGCCATCATACGTTATATAGCTGACAAGCACAACATGTTGGGTG GTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTG GATATTAGATACGGTGTTCGAGAATTGCATATAGTAAAGACTTTGAAAC TCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTTCG AAGATCGTTTATGTCATAAAACATATTTAAATGGTGATCATGTAACCCAT CCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATACATGGACCC AATGTGCCTGGATGCGTTCCCAAATTAGTTTGTTTTTAAAAACGTATTG AAGCTATCCCACAAATTGATAAGTACTTGAAATCCAGCAAGTATATAGCA TGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACCATCCTCC AAAATCGGATCTGGAAGTTCTGTTCCAGGGGCCCTGGGATCC <b>ATGGTTCG</b> <b>ACACAGAAGAAGAACAGTTTGCTCTGGCTCTCAAATGAGTGAGCAGGAA</b> <b>GCTAGGGAGGTGAACAGCCAGGAGGAGGAAGAAGAGGAGCTCTTGAGGAA</b> <b>AGCCATTGCTGAAAGCCTGAATAGTTGAGCGGCCGC</b>