

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of UBE2L6

<u>Enzyme description:-</u>	UBE2L6
<u>Clone number:-</u>	DU32148
<u>Source:-</u>	BL21 recombinant
<u>Tag:-</u>	cleaved from N-terminal His ₆ -tag
<u>Purification method:-</u>	Ni ⁺⁺ -NTA-Sepharose, protease cleavage, SEC
<u>Expression level:-</u>	5mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	18055 Da
Average Mass	18066Da
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	8.72
<u>Purity:-</u>	90%
<u>Enzyme storage buffer:-</u>	
50mM HEPES pH 7.5, 150mM NaCl, 10% glycerol, 1mM DTT	
<u>Storage temperature:-</u>	-80°C
<u>Assay:-</u>	
Loading assay with ISG15 and UBA7 in the presence of Mg-ATP	

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Clone Data Sheet

UBE2L6

<u>Protein</u>	UBE2L6
<u>Synonyms</u>	UbcH6, RIG-B
<u>Clone Number</u>	DU32148
<u>Species</u>	Human
<u>Accession Number</u>	Protein: O14933 DNA: NM_004223
<u>Tags</u>	N-terminal His ₆ tag
Aminoacid sequence of the expressed protein	<u>G</u> <u>P</u> <u>G</u> <u>S</u> <u>M</u> <u>M</u> <u>A</u> <u>S</u> <u>M</u> <u>R</u> <u>V</u> <u>V</u> <u>K</u> <u>E</u> <u>L</u> <u>D</u> <u>L</u> <u>Q</u> <u>K</u> <u>K</u> <u>P</u> <u>P</u> <u>P</u> <u>Y</u> <u>L</u> <u>R</u> <u>N</u> <u>L</u> <u>S</u> <u>S</u> <u>D</u> <u>D</u> <u>A</u> <u>N</u> <u>V</u> <u>L</u> <u>V</u> <u>H</u> <u>A</u> <u>L</u> <u>L</u> <u>L</u> <u>P</u> <u>D</u> <u>Q</u> <u>P</u> <u>P</u> <u>Y</u> <u>H</u> <u>L</u> <u>K</u> <u>A</u> <u>F</u> <u>N</u> <u>L</u> <u>R</u> <u>I</u> <u>S</u> <u>F</u> <u>P</u> <u>P</u> <u>E</u> <u>Y</u> <u>P</u> <u>F</u> <u>K</u> <u>P</u> <u>P</u> <u>M</u> <u>I</u> <u>K</u> <u>F</u> <u>T</u> <u>T</u> <u>K</u> <u>I</u> <u>Y</u> <u>H</u> <u>P</u> <u>N</u> <u>V</u> <u>D</u> <u>E</u> <u>N</u> <u>G</u> <u>Q</u> <u>I</u> <u>C</u> <u>L</u> <u>P</u> <u>I</u> <u>I</u> <u>S</u> <u>S</u> <u>E</u> <u>N</u> <u>W</u> <u>K</u> <u>P</u> <u>C</u> <u>T</u> <u>T</u> <u>C</u> <u>Q</u> <u>V</u> <u>L</u> <u>E</u> <u>A</u> <u>L</u> <u>N</u> <u>V</u> <u>L</u> <u>V</u> <u>N</u> <u>R</u> <u>P</u> <u>N</u> <u>I</u> <u>R</u> <u>E</u> <u>P</u> <u>L</u> <u>R</u> <u>M</u> <u>D</u> <u>L</u> <u>A</u> <u>D</u> <u>L</u> <u>L</u> <u>T</u> <u>Q</u> <u>N</u> <u>P</u> <u>E</u> <u>L</u> <u>F</u> <u>R</u> <u>K</u> <u>N</u> <u>A</u> <u>E</u> <u>E</u> <u>F</u> <u>T</u> <u>L</u> <u>R</u> <u>F</u> <u>G</u> <u>V</u> <u>D</u> <u>R</u> <u>P</u> <u>S</u>
Native sequence	in bold
Protease cleavage	Prescission site underlined
Cloning sites	BamH1 / Not1
<u>DNA sequence of insert</u>	GGATCCATGATGGCGAGCATGCGAGTGGTGAAGGAGCTGGAGGATCTTCA GAAGAAGCCTCCCCATACCTGCGGAACCTGTCCAGCGATGATGCCAATG TCCTGGTGTGGCAGCTCTCCTCCTACCCGACCAACCTCCCTACCACCTG AAAGCCTTCAACCTGCGCATCAGCTTCCCGCCGAGTATCCGTTCAAGCC TCCCATGATCAAATTCACAACCAAGATCTACCACCCCAACGTGGACGAGA ACGGACAGATTTGCCTGCCCATCATCAGCAGTGAGAAGCTGGAAGCCTTGC ACCAAGACTTGCCAAGTCTGGAGGCCCTCAATGTGCTGGTGAATAGACC GAATATCAGGGAGCCCCTGCGGATGGACCTCGCTGACCTGCTGACACAGA ATCCGGAGCTGTTTCAGAAAGAATGCCGAAGAGTTCACCCTCCGATTCGGA GTGGACCGGCCCTCCTAAGCGGCCGC