

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of UBE2Q2

<u>Enzyme description:-</u>	UBE2Q2
<u>Clone number:-</u>	DU12801
<u>Source:-</u>	BL21 recombinant
<u>Tag:-</u>	cleaved from N-terminal His ₆ -tag
<u>Purification method:-</u>	Ni ⁺⁺ -NTA-Sepharose, protease treatment
<u>Expression level:-</u>	6 mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	43089 Da
Average Mass	43115 Da
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	4.77
<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 with Ubiquitin and UBE1 in the presence of Mg-ATP	

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Clone Data Sheet

UBE2Q2

Protein UBE2Q2
Synonyms
Clone Number DU12801
Species Human
Accession Number Protein: Q8WVN8 DNA: NM_173469
Tags N-terminal His₆ tag (cleaved)

Aminoacid sequence of the expressed protein **GPGSMSVSGLKAELKFLASIFDKNHERFRIVSWKLDLHCQFLVPQOGSP
HSLPPPLTLHCNITESYPSSSPIWFDSEDPNLTSVLERLEDTKNNLLR
QQLKWLICELCSLYNLPKHLDVEMLDQPLPTGQNGTTEEVTTSEEEEEEE
MAEDIEDLDHYEMKEEPI SGKKSEDEGIEKENLAILEKIRKTQRQDHLN
GAVSGSVQASDRMKELRDIYRSQSYKTGIYSVELINDSLYDWHVKLOKV
DPDSPLHSDLQILKEKEGIEYILLNFSFKDNFPFDPPFVRVLPVLSGGY
VLGGGALCMELLTKQGWSSAYSIESVIMQINATLVK GKARVOFGANKNOY
NLARAQQSYNSIVQIHEKNGWYTPPKEDG**

Native sequence in bold
Protease cleavage Precission site underlined
Cloning sites BamH1 / NotI

DNA sequence of the insert **GGATCCATGTCCGTGTCAGGGCTCAAGGCCGAGCTGAAGTTCTGGCGTC
CATCTTCGACAAGAACCACGAGCGATTCCGCATCGTCAGTTGGAAGCTGG
ACGAGCTGCACTGCCAGTTCTCTGGTGCCGCAGCAGGGCAGCCCGCACTCG
CTGCCGCCGCACTCACGCTCCACTGCAACATCACGGAATCCTATCCATC
TTCTTACCAGATATGGTTTGTGGATTCTGAAGACCCAAATCTGACATCAG
TTCTGGAACGTCTAGAAGATACTAAGAACAACAATTTGCTTCGTCAGCAA
TTGAAGTGGTTGATATGTGAACCTGTCAGTTTATATAACCTTCTTAAGCA
CCTGGATGTTGAGATGCTAGATCAACCACTACCCACGGGTCAGAATGGGA
CAACAGAAGAAGTGACTTCAGAAGAAGAGGAAGAAGAAGAAGAGATGGCT
GAAGATATAGAAGACTTAGATCACTATGAGATGAAGGAAGAAGAGCCTAT
TAGTGGGAAAAAGTCAGAGGATGAAGGAATTGAAAAAGAAAATTTGGCAA
TATTAGAGAAAATTAGGAAGACTCAAAGGCAAGACCATTTAAATGGTGCA
GTGTCTGGGTCAGTGCAAGCTTCAGATAGACTTATGAAAGAGCTCAGGGA
CATATACAGATCACAGAGTTATAAAACAGGGATTTATTCAGTGGAACTCA
TAAATGACAGTTTATATGACTGGCATGTTAAACTGCAGAAGGTTGACCCT
GATAGTCCTTTGCACAGTGATCTTCAGATCTTAAAAGAAAAAGAAGGCAT
AGAATATATTTTGCCTTAACCTTCTCTTTTAAAGGATAACTTTCCATTTGATC
CTCCATTTGTTTCGAGTGGTGTACCTGTTCTCTCAGGAGGGTATGTATTG
GGTGGAGGAGCATTATGTATGGAACCTTCTCACAAAACAGGGCTGGAGCAG
TGCCACTCAATAGAATCGGTCATCATGCAAATAAATGCCACCTTAGTCA
AAGGCAAAGCCAGAGTGCAGTTTGGAGCAAATAAGAATCAATATAATCTA**

GCAAGAGCCCAACAATCCTATAATTCCATTGTACAGATACATGAGAAAA
TGGCTGGTACACCCTCCAAAGGAAGATGGCTAAGCGGCCGC