

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of FLAG-UBXD7

<u>Enzyme description:-</u>	FLAG-UBXD7 2-489
<u>Clone number:-</u>	DU21327
<u>Source:-</u>	BL21 Recombinant
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	cleaved from N-terminal GST
<u>Expression level:-</u>	1mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	56036
Average Mass	56069
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	4.88
<u>Purity:-</u>	80%
<u>Enzyme storage buffer:-</u>	
50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT	
<u>Storage temperature:-</u>	-80°C
<u>Assay:-</u>	

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Clone Data Sheet

Protein name FLAG-UBXD7

<u>Protein</u>	UBXD7 2-489
<u>Synonyms</u>	UBXN7
<u>Clone Number</u>	DU21327
<u>Species</u>	Human
<u>Accession Number</u>	Protein: O94888 DNA: NM_015562
<u>Tags</u>	N-terminal FLAG-tag, cleaved from N-terminal GST-tag
Aminoacid sequence of the purified protein	GGSDYKDDDDKGSAAHGGSAASSALKGLIQQFTTITGASESVGKHMLEACNNNL EMAVTMFLDGGGIAEEPSTSSASVSTVRPHTEEEVRAPIPQKQEILVEPEPLFG APKRRRPARSIFDGFRDFQTETIRQEQELRNNGAIDKKLTTLADLFRPPIDLMH KGSFETAKECGQMKNKWLMINIQNVQDFACQCLNRDVWSNEAVKNIIREHFIFW QVYHDSEEGQRYIQFYKLGDFPYVSILDPRTGQKLVEWHQLDVSSFLDQVTGFL GEHGQLDGLSSSPKKCARSESLIDASEDSQLEAAIRASLQETHFDSTQTKQDS RSDEESESELFSGSEEFISVCGSDEEEVENLAKSRKSPHKDLGHRKEENRRPL TEPPVRTDPGTATNHQGLPAVDSEIILEMPPEKADGVVEGIDVNGPKAQLMLRYP DGKREQITLPEQAKLLALVKHVQSKGYPNRFEELLTNFPRRKLSHLDYDITLQE AGLCPQETVVFVQERN
Native sequence	2-489 in bold
Protease cleavage	TEV protease site
Cloning sites	BamH1 / NotI
<u>DNA sequence of insert</u>	GGATCCGCTGCCCACGGGGGCTCCGCGGCGTCCTCGGCGCTGAAGGGGTAAATT CAACAGTTCACCACCATTAACGGGTGCAAGTGAAAGTGTAGGAAAACATATGCTT GAAGCGTGCAACAATAATCTGGAAATGGCAGTCACTATGTTTTTTGGATGGTGGA GGAATCGCTGAAGAGCCCAGTACCAGTTCAGCAAGTGTCTCTACTGTCAGACCA CACACAGAAGAAGAAGTTCGTGCCCCAATTCCTCAAAAGCAGGAAATACTGGTG GAACCAGAACCATTATTTGGTGCTCCTAAAAGACGACGGCCTGCACGTTCAATT TTTGATGGTTTTCCGGGATTTTCAGACTGAAACTATTCGGCAAGAACAAGAATTA AGAAATGGAGGAGCTATCGATAAGAAATTAACACCCTTGCAGATCTATTCGGG CCACCCATTGATTTGATGCATAAAGGCAGCTTTGAAACAGCCAAAGAGTGTGGC CAGATGCAAAATAAGTGGCTGATGATAAACATTCAAAATGTTCAAGACTTTGCA TGTCAGTGCCTCAACCGCGATGTGTGGAGCAACGAAGCTGTGAAGAATATTATC CGGGAACATTTTCATTTTCTGGCAGGTTTATCATGACAGTGAGGAAGGTCAGAGA TACATACAGTTTTATAAGTTAGGGGATTTCCCCTATGTTTCCATATTGGACCCA CGGACAGGTCAGAAGCTAGTAGAATGGCACCAGTTAGATGTATCTTCTTTCTTG GACCAAGTGACGGGATTTCTGGGTGAACATGGACAACCTGGATGGACTTTCTAGC AGTCCCCCAAAAAATGTGCCCGTTCCGAGAGCCTTATAGATGCAAGTGAAGAC AGCCAGCTAGAAGCTGCCATCAGAGCCTCCTTACAAGAAACACATTTTGATTCA ACACAGACAAAACAGGATAGCCGCTCAGATGAAGAATCTGAATCTGAACTTTTT TCTGGCAGTGAGGAGTTCATATCCGTTTGTGGCTCTGATGAAGAAGAAGAGGTA

GAGAACTTTGCCAAGTCCAGAAAGTCTCCCCACAAAGATTTGGGGCATAGAAAA
GAGGAGAATAGAAGGCCGCTGACTGAGCCACCAGTCAGAACTGATCCTGGAACA
GCCACAAACCACCAAGGATTGCCAGCTGTGGATTCAGAGATACTGGAGATGCCA
CCTGAAAAAGCAGATGGAGTAGTGGAGGGGATAGATGTAAATGGACCAAAAGCA
CAGCTGATGTTGCGGTATCCAGATGGAAAAAGGGAACAGATCACTCTTCCAGAG
CAAGCTAAACTGCTAGCTTTGGTGAAGCACGTGCAGTCTAAAGGATACCCAAAT
GAACGTTTTGAACTTCTCACCAACTTTCCTCGAAGGAAATTATCTCATCTGGAC
TATGATATTACATTGCAAGAGGCAGGCCTTTGTCCTCAAGAGACTGTCTTTGTA
CAGGAAAGAAATTAAGCGGCCGC