Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of His$_6$-TUBE
UBQL1 536-589 (UBA domain) tetramer = TUBE

Enzyme description:-	Ubiquilin 536-589 tetramer
Clone number:-	DU20100
Source:-	BL21 recombinant
Tag:-	N-terminal His$_6$;
Purification method:-	Ni^{++}-Sepharose
Expression level:-	15 mg/L
Calculated molecular mass:-	
Monoisotopic	27566 Da
Average Mass	27582 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:-	4.97
Purity:-	90%

Enzyme storage buffer:-

50mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT

Storage temperature:-	-80ºC

Assay:-

This protein binds to long K63 poly Ub chains.

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Clone Data Sheet

His-UBQL1 536-589 tetramer
His-TUBE Tandem Ubiquitin Binding Entity

Protein	UBQL1 536-589 (UBA-domain) tetramer
Synonyms	UBQL1, DA41, PLIC1
Clone Number	DU20108
Species	Human
Accession Number	Protein: Q9UMX0; DNA:NM_053067
Tags	N-terminal His$_6$
Aminoacid sequence of the expressed protein	MGSSHHHHHHSSGLEVLFQGPGS**GGGVNPQLQNPEVRFQQQLEQLSAMGFLNREANLQALIATGGDINAAIERLLGSQPS**GGGGSGGG**VNPQLQNPEVRFQQQLEQLSAMGFLNREANLQALIATGGDINAAIERLLGSQPS**GGGGSGGG**VNPQLQNPEVRFQQQLEQLSAMGFLNREANLQALIATGGDINAAIERLLGSQPS**GGGGSGGG**VNPQLQNPEVRFQQQLEQLSAMGFLNREANLQALIATGGDINAAIERLLGSQPS**
Native sequence	in bold
Protease cleavage	Prescission protease site underlined
Cloning sites	BglII/BamHI insert (cloned into BamHI site)

DNA sequence of the expression cassette

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ATGGGCAGCAGCCATCATCATCATCATCACAGCAGCGGCCTGGAAGTTCT
GTTCCAGGGGCCCGGATCTGGAGGTGGAGTAAATCCTCAGCTACAGAATC
CAGAAGTCAGATTTCAGCAACAACTGGAACAACTCAGTGCAATGGGATTT
TTGAACCGTGAAGCAAACTTGCAAGCTCTAATAGCAACAGGAGGTGATAT
CAATGCAGCTATTGAAAGGTTACTGGGCTCCCAGCCATCAGGAGGTGGAG
GATCTGGAGGTGGAGTAAATCCTCAGCTACAGAATCCAGAAGTCAGATTT
CAGCAACAACTGGAACAACTCAGTGCAATGGGATTTTTGAACCGTGAAGC
AAACTTGCAAGCTCTAATAGCAACAGGAGGTGATATCAATGCAGCTATTG
AAAGGTTACTGGGCTCCCAGCCATCAGGAGGTGGAGGATCTGGAGGTGGA
GTAAATCCTCAGCTACAGAATCCAGAAGTCAGATTTCAGCAACAACTGGA
ACAACTCAGTGCAATGGGATTTTTGAACCGTGAAGCAAACTTGCAAGCTC
TAATAGCAACAGGAGGTGATATCAATGCAGCTATTGAAAGGTTACTGGGC
TCCCAGCCATCAGGAGGTGGAGGATCTGGAGGTGGAGTAAATCCTCAGCT
ACAGAATCCAGAAGTCAGATTTCAGCAACAACTGGAACAACTCAGTGCAA
TGGGATTTTTGAACCGTGAAGCAAACTTGCAAGCTCTAATAGCAACAGGA
GGTGATATCAATGCAGCTATTGAAAGGTTACTGGGCTCCCAGCCATCATA
GGGAGGTGGAGGATCC
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