

# USP8 [untagged]

Deconjugating enzyme

**Alternate Names:** Ubiquitin carboxyl-terminal hydrolase 8, Ubiquitin thioesterase 8, Ubiquitin-specific-processing protease 8, Ubiquitin isopeptidase Y

**Cat. No.** 64-0053-050

**Lot. No.** 30212

**Quantity:** 50 µg

**Storage:** -70°C



FOR RESEARCH USE ONLY

NOT FOR USE IN HUMANS

CERTIFICATE OF ANALYSIS Page 1 of 2

## Background

Deconjugating enzymes (DCEs) are proteases that process ubiquitin or ubiquitin-like gene products, reverse the modification of proteins by a single ubiquitin or ubiquitin-like protein (UBL) and remodel polyubiquitin (or poly-UBL) chains on target proteins (Reyes-Turcu *et al.*, 2009). The deubiquitylating – or deubiquitinating – enzymes (DUBs) represent the largest family of DCEs and regulate ubiquitin dependent signalling pathways. The activities of the DUBs include the generation of free ubiquitin from precursor molecules, the recycling of ubiquitin following substrate degradation to maintain cellular ubiquitin homeostasis and the removal of ubiquitin or ubiquitin-like proteins (UBL) modifications through chain editing to rescue proteins from proteasomal degradation or to influence cell signalling events (Komander *et al.*, 2009). There are two main classes of DUB, cysteine proteases and metalloproteases. Ubiquitin specific protease 8 (USP8) is a member of the cysteine protease enzyme family and cloning of the gene was first described by Nomura *et al.* (1994). USP8 regulates the degradation of various transmembrane proteins at the sorting endosome by modulating the ubiquitin dynamics of both cargo and sorting proteins. USP8 interacts with signal transducing adaptor molecule (STAM) and stabilizes STAM and hepatocyte growth-factor-regulated substrate (Hrs), which together constitute the endosomal sorting complex required for transport (ESCRT) and govern the early steps of receptor trafficking en route to the lysosomes (De Ceuninck

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## Physical Characteristics

**Species:** human

**Source:** *E. coli*

**Quantity:** 50 µg

**Concentration:** 0.5 mg/ml

**Formulation:** 50 mM HEPES pH 7.5, 150 mM sodium chloride, 2 mM dithiothreitol, 10% glycerol

**Molecular Weight:** ~128 kDa

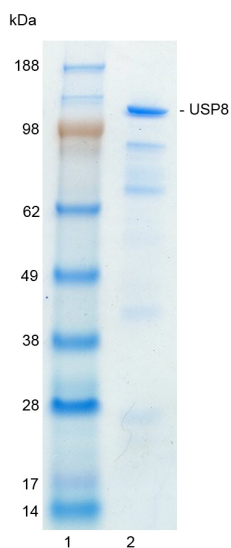
**Purity:** >66% by InstantBlue™ SDS-PAGE

**Stability/Storage:** 12 months at -70°C; aliquot as required

**Protein Sequence:** Please see page 2

## Quality Assurance

**Purity:** 4-12% gradient SDS-PAGE InstantBlue™ staining  
Lane 1: MW markers  
Lane 2: 1 µg USP8



**Protein Identification:** Confirmed by mass spectrometry.

**Deubiquitylase Enzyme Assay:** The activity of USP8 was validated by determining the increase in fluorescence measured as a result of the enzyme catalysed cleavage of the fluorogenic substrate Ubiquitin-Rhodamine110-Glycine generating Ubiquitin and Rhodamine110-Glycine. Incubation of the substrate in the presence or absence of USP8 was compared confirming the deubiquitylating activity of USP8.



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Lot-specific COA version tracker: v1.0.0

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## Background

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*et al.*, 2013). The E3 ubiquitin ligase IDOL (inducible degrader of the LDLR) employs ESCRT complexes to recognise and traffic low-density lipoprotein receptor (LDLR) to lysosomes. IDOL is recruited to the plasma membrane by LDLR, promoting LDLR internalisation and facilitating LDLR degradation by shuttling it into the multivesicular body (MVB) protein-sorting pathway. USP8 acts downstream of IDOL to deubiquitylate LDLR and is required for LDLR entry into the MVB pathway (Scotti *et al.*, 2013; Sorrentino *et al.*, 2013). USP8 has also been shown to interact with and stabilise another E3 ubiquitin ligase called Ring Finger Protein 41 (RNF41) which is also known to be involved in the trafficking of various transmembrane proteins. USP8 is a known substrate of RNF41 whereby RNF41 redistributes and ubiquitylates USP8, thus reducing USP8 levels. Balanced reciprocal cross-regulation between RNF41 and USP8 decides if receptors are sorted for lysosomal degradation or recycling, this way regulating basal cytokine receptor levels (De Ceuninck *et al.*, 2013). Recent cell-based and *in vivo* work has shown that the inhibition of USP8 activity or reduction in USP8 expression can selectively kill non-small cell lung cancer (NSCLC) cells. USP8 suppression leads to the downregulation of multiple oncogenic receptor tyrosine kinase (RTK) receptors; EGFR, ERBB2, ERBB3, and MET. Based on this work, USP8 has been proposed as a potential therapeutic target for both gefitinib-resistant and -sensitive NSCLC cells (Byun *et al.*, 2013).

### References:

Byun S, Lee SY, Lee J, Jeong CH, Farrand L, Lim S, *et al.* (2013) USP8 Is a Novel Target for Overcoming Gefitinib Resistance in Lung Cancer. *Clinical cancer research: an official journal of the American Association for Cancer Research* **19**, 3894-3904.

De Ceuninck L, Wauman J, Masschaele D, Peelman F and Tavernier J (2013) Reciprocal cross-regulation between RNF41 and USP8 controls cytokine receptor sorting and processing. *J Cell Sci* **126**, 3770-3781.

Komander D, Clague MJ and Urbe S (2009) Breaking the chains: structure and function of the deubiquitinases. *Nat Rev Mol Cell Biol* **10**, 550-563.

Nomura N, Nagase T, Miyajima N, Sazuka T, Tanaka A, Sato S, *et al.* (1994) Prediction of the coding sequences of unidentified human genes. II. The coding sequences of 40 new genes (KI-AA0041-KI-AA0080) deduced by analysis of cDNA clones from human cell line KG-1. *DNA research: an international journal for rapid publication of reports on genes and genomes* **1**, 223-229.

Reyes-Turcu FE, Ventii KH and Wilkinson KD (2009) Regulation and cellular roles of ubiquitin-specific deubiquitinating enzymes. *Ann Rev Biochem* **78**, 363-397.

Scotti E, Calamai M, Goulbourne CN, Zhang L, Hong C, Lin RR, *et al.* (2013) IDOL stimulates clathrin-independent endocytosis and multivesicular body-mediated lysosomal degradation of the low-density lipoprotein receptor. *Mol Cell Biol* **33**, 1503-1514.

Sorrentino V, Nelson JK, Maspero E, Marques AR, Scheer L, Polo S, *et al.* (2013) The LXR-IDOL axis defines a clathrin-, caveolae-, and dynamin-independent endocytic route for LDLR internalization and lysosomal degradation. *J Lipid Res* **54**, 2174-2184.

## Physical Characteristics

Continued from page 1

### Protein Sequence:

GPLGSMPAVASVPKELYLSSSLKDLNK  
KTEVKPEKISTKSYVHSALKIFKTAE  
CRLDRDEERAYVLVMKYVTVYNLIKRPD  
FKQQQDYFHSILGPGNIKKAVEEAERLS  
ESLKLRYEEAEVRKKLEEKDRQEEAQR  
LQOKRQETGREDDGTLAKGSLNVLDSKDK  
TQKSNGEKNEKCEKTKGAIKAKELYTMMTD  
KNISLIIMDARRMQDYQDSCILHSLVPEE  
AISP GVTASWIEAHL PDDSKDTWK  
KRGNVEYVLLDWFSSAKDLQIGTTL  
RSLKDALFKWESKTVLRNEPLVLEGGYEN  
WLLCYPQYTTNAKVTPRRQNEEVSISLD  
FTYPSLEESI PSKPAAQTPPASIEVDEN  
IELISGQNERMGLNISTPVEPVAASKSD  
VSP I IQVPVSIKNVPOIDRTKKPAVKLPEEH  
RIKSESTNHEQQSPQSGKVI PDRSTKPVVF  
SPTLMLTDEEKARIHAETALLMEKNQEKEL  
RERQEEEQEKLKREEQEQA KKKQEAEE  
NEITEKQOKAGKEEMKKESEQAKKEDKET  
SAKRKGTIVKVRQSKSEHETSADAKKSVE  
DRGKRCPTEIQKKS TGDVPHTSVTGDSGS  
GKPFKIKGQPE SGI LRTGT FREDTD  
DTERNKAQREPLTRARSEEMGRIVPGLPS  
GWAKFLDPITGTFRYHSPNTVHMYPPE  
MAPSSAPPSTPP THKAKPQI PAERDREP  
SKLKRYSYSPDITQAIQEEERKPTVTPVN  
RENKPTCYPKAEISRLSASQIRNLNPFVFGS  
GPALTLGLRNLGNTCYMNSILQCLCNAPHLA  
DYFNRCYQDDINRNLGLGHKGEVAEEFGI  
IMKALWTGQYRISP KDFKITIGKINDQF  
AGYSQQDSQELLLFLMDGLHEDLNKAD  
NRKRYKEENNDHLLDDFKAAEHAWQKHKQL  
NESIIVALFQGFKSTVQCLTCHKKSRT  
FEAFMYLSLPLASTSKCTLQDCLRLFSKEE  
KLTDDNRFYCSHCRARRDSLKKIEIWKLP  
PVLVHLKRFYSYDGRWKQLQTSVDFPLEN  
LDLSQYVIGPKNNLKKYNLFSVSNHYGLDG  
GHYTA YCKNAARQRWFKFD DHEVSDISVSS  
VKSSAAYILFYTSLGRVTDVAT

The residues underlined remain after cleavage and removal of the purification tag.

USP8 (regular text): Start ***bold italics*** (amino acid residues 1-1118)

Accession number: NP\_005145



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