

# Di-ubiquitin (K11-linked) [untagged]

Ubiquitin/Ubiquitin-Like Protein Dimer



Cat. No. 60-0102-010

Lot. No. 30083

Quantity: 10 µg

Storage: -70°C

FOR RESEARCH USE ONLY

NOT FOR USE IN HUMANS

CERTIFICATE OF ANALYSIS Page 1 of 2

## Background

Ubiquitin (Ub) is a highly conserved 76 amino-acid protein found throughout eukaryotic cells. A vast number of cellular processes, including targeted protein degradation, cell cycle progression, DNA repair, protein trafficking, inflammatory response, virus budding, and receptor endocytosis, are regulated by Ub-mediated signalling; where the target protein is tagged by single or multi-monomeric Ub (monomeric Ub attached to multiple sites on the substrate) or a polymeric chain of Ubs (Fushman *et al.*, 2010). This post-translational modification is tightly controlled by an enzymatic cascade involving several enzymes (E1, E2, and E3) and occurs through either an isopeptide bond between the C-terminal Glycyl residue of Ub and the epsilon amino group of a Lysyl residue on a target protein or through a peptide bond between the C-terminal Glycyl residue of Ub and the N-terminal amine on a further Ub. In the former (isopeptide bond-linked) case the substrate protein may either be ubiquitin itself – thus leading to the generation of poly-ubiquitin chains – or another target protein (Fushman *et al.*, 2010). Thus, ubiquitin can be attached to a substrate either as a monomer or as a poly-ubiquitin chain. Further – depending on their linkage type (M1, K6, K11, K27, K29, K33, K48 and K63 linked) – the Ub chains can take different structural forms. Chains containing all eight possible Ub linkages have been found in living cells and different ubiquitin chain types may encode different biological signals, allowing this single protein to mediate many diverse functions (Komander 2009; Weeks *et al.*, 2009; Walczak *et al.*, 2012). The functionality of Ub chains is most commonly associated with their attachment to substrate proteins but there is also evidence that they may also play a role in cellular signalling as free chains (Braten *et al.*, 2012).

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## Physical Characteristics

### Protein Sequence:

```
MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYNIQKESTLHLVLRGG  
MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYNIQKESTLHLVLRGG  
K11
```

**Species:** human

**Molecular Weight:** 17.1 kDa

**Source:** synthetic/chemical ligation

**Purity:** >98% by InstantBlue™ SDS-PAGE

**Quantity:** 10 µg

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

**Concentration:** 0.5 mg/ml

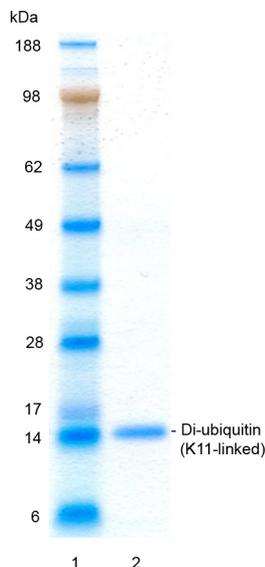
**Accession Number:** P62987

**Formulation:** 50 mM HEPES pH 7.5, 150 mM NaCl<sub>2</sub>, 2 mM DTT, 10% Glycerol

## Quality Assurance

### Purity:

4-12% gradient SDS-PAGE  
InstantBlue™ staining  
Lane 1: MW markers  
Lane 2: 1 µg Di-ubiquitin (K11-linked)

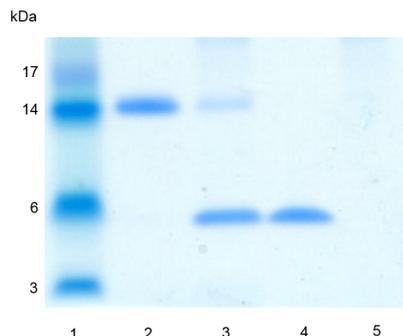


### Purity of the linkage type:

The linkage type (K11) was confirmed by tandem mass spectrometry.

### Di-ubiquitin cleavage assay:

The capacity of the di-ubiquitin substrate to be cleaved was tested using a promiscuous – with respect to ubiquitin linkage specificity – deubiquitylase (GST-USP2). Incubation of the di-ubiquitin for 1 hour at 37°C was compared either in the absence (Lane 2) or presence (Lane 3) of GST-USP2. The reaction products were compared alongside two control samples containing either mono-ubiquitin (Lane 4) or GST-USP2 (Lane 5) only. Cleavage of the di-ubiquitin and generation of mono-ubiquitin was determined by running reactions on a 4-12% SDS-PAGE gel and staining with InstantBlue™ (Lane 1; molecular weight markers).



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Lot-specific COA version tracker: v1.0.0

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A mass spectrometry-based study found that K11 linkages account for 28% of all yeast ubiquitin-ubiquitin linkages. The relative abundance of the other linkages were K6 (11%), K27 (9%), K29 (3%), K33 (4%), K48 (29%) and K63 (16%) (Xu *et al.*, 2009). Ubiquitin chains form distinct structures based on their linkage. K11- and K48-linked chains form compact, globular structures with significant ubiquitin-ubiquitin contact. In contrast, K63-linked chains adopt an extended conformation with little interaction between adjacent ubiquitins (Schaefer *et al.*, 2011). K11 linkages between ubiquitin molecules are as abundant as K48 linkages and data indicates that K11-linked chains are, like Lys48-linked chains, efficient proteasomal degradation signals. More recent data has indicated that K11-linked ubiquitin chains also play a vital role in the regulation of the cell cycle by regulating the substrates of the E3 ligase anaphase-promoting complex (APC/C) and controlling progression through mitosis (Bremm *et al.*, 2010; Wickliffe *et al.*, 2011). Cezanne has been identified as the first DUB with preference for K11 linkages, suggesting that K11-linked ubiquitin chains are independently regulated degradation signals within the ubiquitin system (Bremm *et al.*, 2010).

### References:

Braten O, Shabek N, Kravtsova-Ivantsiv Y, Ciechanover A (2012) Generation of free ubiquitin chains is upregulated in stress, and facilitated by the HECT domain ubiquitin ligases UFD4 and HUL5. *Biochem J* **444**, 611-617.

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Fushman D, Walker O (2010) Exploring the linkage dependence of polyubiquitin conformations using molecular modeling. *Journal of Molecular Biology* **395**, 803-814.

Komander D (2009) The emerging complexity of protein ubiquitination. *Biochem Soc Trans* **37**, 937-953.

Schaefer JB, Morgan DO (2011) Protein-linked ubiquitin chain structure restricts activity of deubiquitinating enzymes. *J Biol Chem* **286**, 45186-45196.

Walczak H, Iwai K, Dikic I (2012) Generation and physiological roles of linear ubiquitin chains. *BMC Biol* **10**, 23.

Weeks SD, Grasty KC, Hernandez-Cuebas L, Loll PJ (2009) Crystal structures of Lys-63-linked tri- and di-ubiquitin reveal a highly extended chain architecture. *Proteins* **77**, 753-759.

Wickliffe KE, Williamson A, Meyer HJ, Kelly A, Rape M (2011) K11-linked ubiquitin chains as novel regulators of cell division. *Trends in Cell Biology* **21**, 656-663.

Xu P, Duong DM, Seyfried NT, Cheng D, Xie Y, *et al.*, (2009) Quantitative proteomics reveals the function of unconventional ubiquitin chains in proteasomal degradation. *Cell* **137**, 133-145.



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