

K48 Tetra-Ubiquitin

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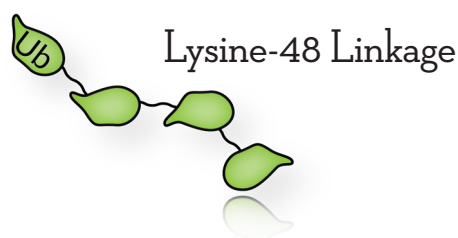


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K48 Tetra-Ubiquitin

The array of cellular processes initiated and regulated by ubiquitin has been partially explained by the structural diversity of differently linked ubiquitin chains. In a ubiquitin chain, ubiquitin moieties can be conjugated through one of their lysine residues (K6, K11, K27, K29, K33, K48 and K63) or the N-terminal methionine residue (M1), offering countless possibilities to assemble a specific polymer. Ubiquitin molecules can also be modified by other post-translational modifications, including acetylation and phosphorylation, adding another layer of ubiquitin signal regulation and diversification.

K48-polyubiquitin chains are the most abundant linkage in cells and thought to be the major signal for proteasome-mediated degradation. Quantitative MS analyses of intracellular ubiquitin linkages revealed K48-polyubiquitin linkages rapidly accumulate when cells are treated with the proteasome inhibitor MG132. This K48-linked tetra-ubiquitin was enzymatically conjugated, and purified via liquid chromatography.



References

- 1) Dikic, I., Wakatsuki, S., & Walters, K. J. (2009). Ubiquitin-binding domains – from structures to functions. *Nature Reviews Molecular Cell Biology*, 10(10), 659–671. <https://doi.org/10.1038/nrm2767>
- 2) Akutsu, M., Dikic, I., & Bremm, A. (2016). Ubiquitin chain diversity at a glance. *Journal of Cell Science*, 129(5), 875–880. <https://doi.org/10.1242/jcs.183954>

Product Information

Quantity: 25 µg **Molecular Weight:** 34 kDa

Concentration: 29 µM, 1 mg/mL

Purity: >95% by SDS-PAGE

Storage Buffer: 50 mM HEPES pH 7.5

Storage: -80°C, Avoid multiple freeze / thaw

Quality Control and Performance Data

98 kDa

62 kDa

49 kDa

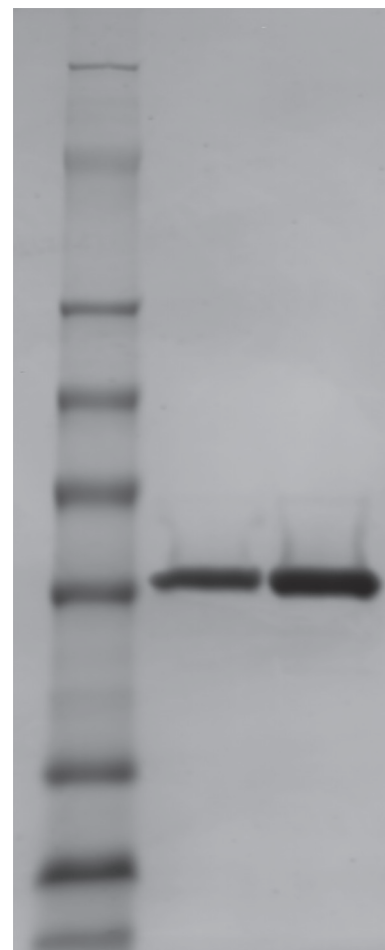
38 kDa

28 kDa

14 kDa

6 kDa

3 kDa



K48-Linked Tetra-Ubiquitin SDS-PAGE. From left to right, increasing amounts of tetra-ubiquitin were loaded onto a 10–20% SDS-PAGE gel, stained with Coomassie brilliant blue. Purity is > 95%.

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