

# CCPs deglutamylate tubulin

D'Eustachio, P., Jassal, B., Jupe, S.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org).

02/10/2024

## Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

## Literature references

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)

Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)

Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 90

This document contains 1 reaction ([see Table of Contents](#))

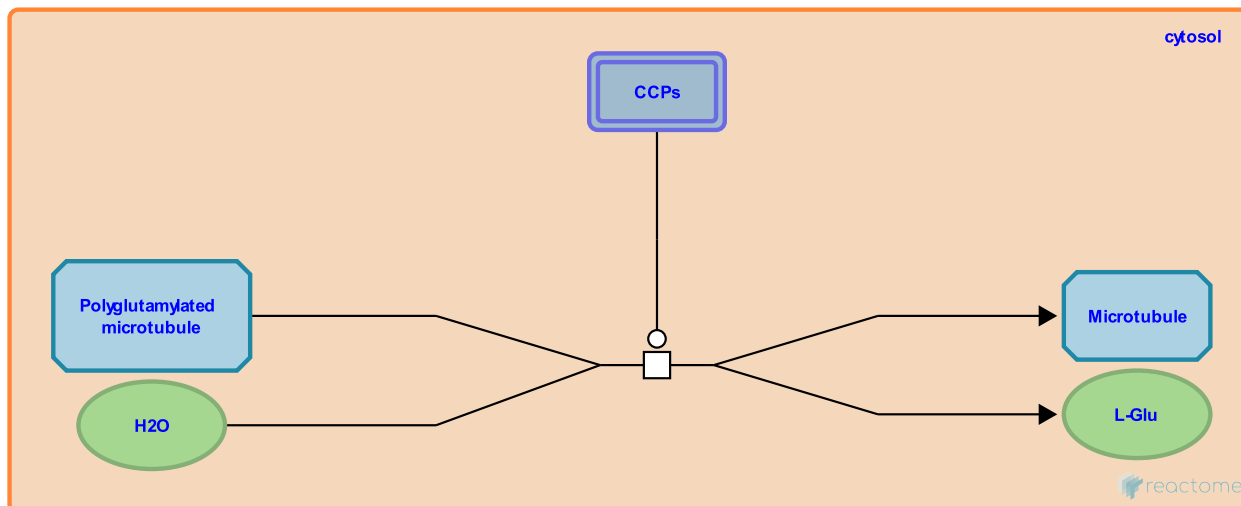
## CCPs deglutamylate tubulin ↗

**Stable identifier:** R-HSA-8866105

**Type:** transition

**Compartments:** cytosol

**Inferred from:** Ccps deglutamylate tubulin (Homo sapiens)



Cytosolic carboxypeptidases (CCPs) catalyze the removal of glutamate residues from the C-terminal tails of both alpha- and beta-tubulin. These glutamate residues are either enzymatically added in the polyglutamylation reaction, or gene-encoded glutamate residues are removed from alpha-tubulin after detyrosination to generate delta2-tubulin (Kimura et al. 2010, Rogowski et al. 2010). CCPs are members of the MC clan, M14 family, subfamily M14D of metallopeptidases (Kalinina et al. 2007, Rodriguez de la Vega et al. 2007). Mouse Ccp1, 2, 3, 4, and 6 are functionally homologous and remove linearly added glutamates from tubulin (alpha-peptide bonds), while Ccp5 specifically removes branching-point glutamates (gamma-peptide bonds) which are generated as first step of the polyglutamylation reaction (Rogowski et al. 2010; Tort et al. 2014). The catalytic activities of the human proteins are inferred from the properties of their mouse homologues and limited studies of human proteins expressed in cultured cells (Rogowski et al. 2010). In this event polyglutamylation is arbitrarily shown on only one tubulin protofilament within the polyglutamylated microtubule.

### Literature references

- Desagher, S., Bosson, A., Rogowski, K., van Dijk, J., Bosc, C., Larroque, C. et al. (2010). A family of protein-deglutamylating enzymes associated with neurodegeneration. *Cell*, 143, 564-78. ↗
- Avilés, FX., Berezniuk, I., Biswas, R., Fricker, LD., Kalinina, E., Hermoso, A. (2007). A novel subfamily of mouse cytosolic carboxypeptidases. *FASEB J.*, 21, 836-50. ↗
- Avilés, FX., Diez, A., Bautista, JM., Sevilla, RG., Lorenzo, J., Rodriguez de la Vega, M. et al. (2007). Nna1-like proteins are active metallocarboxypeptidases of a new and diverse M14 subfamily. *FASEB J.*, 21, 851-65. ↗
- Setou, M., Kurabe, N., Kimura, Y., Konishi, Y., Iino, Y., Kaplan, OI. et al. (2010). Identification of tubulin deglutamylase among *Caenorhabditis elegans* and mammalian cytosolic carboxypeptidases (CCPs). *J. Biol. Chem.*, 285, 22936-41. ↗
- Avilés, FX., Rocha, C., Tort, O., Lorenzo, J., Seixas, C., Bièche, I. et al. (2014). The cytosolic carboxypeptidases CCP2 and CCP3 catalyze posttranslational removal of acidic amino acids. *Mol. Biol. Cell*, 25, 3017-27. ↗

### Editions

2017-01-07	Edited	D'Eustachio, P.
2017-01-19	Reviewed	Jassal, B.
2017-01-19	Authored	Jupe, S.