

# TUBB binds colchicine

Jassal, B., Shoichet, BK.

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](#). For more information see our [license](#).

02/04/2024

## 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: 88

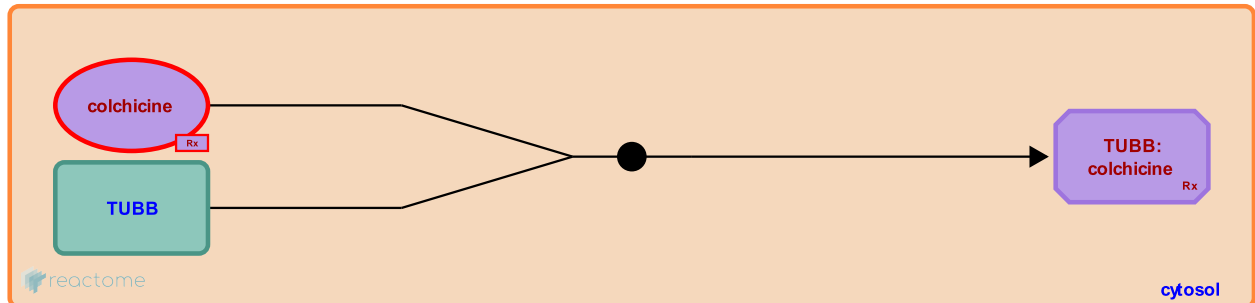
This document contains 1 reaction ([see Table of Contents](#))

## TUBB binds colchicine [↗](#)

**Stable identifier:** R-HSA-9685830

**Type:** binding

**Compartments:** cytosol



Colchicine is an antimitotic agent used to treat gout and Behçet's disease (Cerquaglia et al. 2005, Saleh & Arayssi 2014, Angelidis et al. 2018). It works by decreasing inflammation. Colchicine primarily inhibits tubulin (TUBB) (Lu et al. 2012), preventing microtubule polymerization and thereby disrupts inflammasome activation, microtubule-based inflammatory cell chemotaxis, generation of leukotrienes and cytokines, and phagocytosis.

The COLCORONA trial conducted by the Montreal Heart Institute (MHI) (<https://clinicaltrials.gov/ct2/show/NCT04322682>) showed that the use of colchicine was associated with statistically significant reductions in the risk of death or hospitalization in patients with Covid-19 compared to placebo. Colchicine showed efficacy in preventing the 'cytokine storm' and other complications associated with Covid-19.

### Literature references

Lu, Y., Li, W., Xiao, M., Chen, J., Miller, DD. (2012). An overview of tubulin inhibitors that interact with the colchicine binding site. *Pharm. Res.*, 29, 2943-71. [↗](#)

### Editions

|            |                  |               |
|------------|------------------|---------------|
| 2020-04-27 | Authored, Edited | Jassal, B.    |
| 2020-05-14 | Reviewed         | Shoichet, BK. |