

# Mt1 binds cadmium

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22/11/2019

## 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: 70

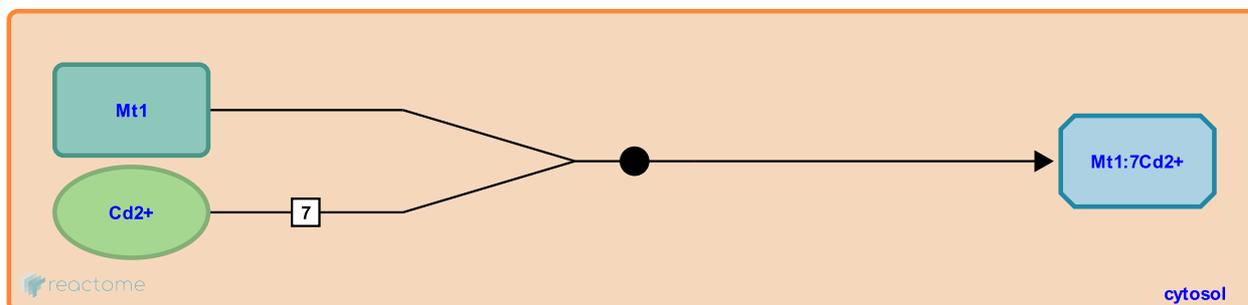
This document contains 1 reaction ([see Table of Contents](#))

## Mt1 binds cadmium ↗

**Stable identifier:** R-MMU-6798570

**Type:** binding

**Compartments:** cytosol



Mouse Mt1 binds 7 atoms of divalent cadmium (Zangger et al. 1999, Tio et al. 2004, Artells et al. 2013). The mMt1 isoform exhibits metal ion binding abilities distinct from those of mMt2, with mMt2 showing a clear preference for Zn(II) coordination, if compared to Cu(I) or even to Cd(II). This is in full agreement with the gene expression regulation pattern for the Mt1 and Mt2 genes, as well as with the hypothesized preferential role of mMt2 in Zn(II) homeostasis mechanisms, while Mt1, possibly differentiated from a most recent duplication event in the mammalian metallothionein gene cluster, would have evolved to detoxify Cd(II), and probably other divalent metal ions (Artells et al, 2013).

## Literature references

Tío, L., Villarreal, L., Atrian, S., Capdevila, M. (2004). Functional differentiation in the mammalian metallothionein gene family: metal binding features of mouse MT4 and comparison with its paralog MT1. *J. Biol. Chem.*, 279, 24403-13. ↗

Artells, E., Palacios, Ò., Capdevila, M., Atrian, S. (2013). Mammalian MT1 and MT2 metallothioneins differ in their metal binding abilities. *Metallomics*, 5, 1397-410. ↗

Zangger, K., Oz, G., Otvos, JD., Armitage, IM. (1999). Three-dimensional solution structure of mouse [Cd7]-metallothionein-1 by homonuclear and heteronuclear NMR spectroscopy. *Protein Sci.*, 8, 2630-8. ↗

## Editions

2015-09-19	Reviewed	Atrian, S.
2015-09-19	Authored, Edited	May, B.