

MT2A binds zinc

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21/10/2019

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

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Reactome database release: 70

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

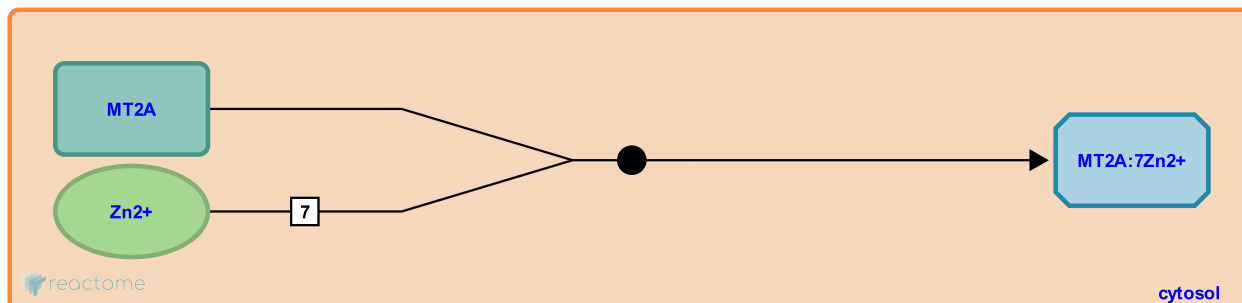
MT2A binds zinc ↗

Stable identifier: R-HSA-5662598

Type: binding

Compartments: cytosol

Inferred from: [Mt2 binds zinc \(Mus musculus\)](#)



The metallothionein MT2A binds 7 atoms of zinc(II) in two clusters, one at the N-terminal beta domain and one at the C-terminal alpha domain (Stillman et al. 2000, Yang et al. 2007). The cluster at the alpha domain is more stable than the cluster at the beta domain, making the beta domain a better zinc donor (Jiang et al. 2000). Each cluster assembles independently (Jiang et al. 2000).

Literature references

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Jiang, LJ., Vasák, M., Vallee, BL., Maret, W. (2000). Zinc transfer potentials of the alpha - and beta-clusters of metallothionein are affected by domain interactions in the whole molecule. *Proc. Natl. Acad. Sci. U.S.A.*, 97, 2503-8. ↗

Stillman, MJ., Thomas, D., Trevithick, C., Guo, X., Siu, M. (2000). Circular dichroism, kinetic and mass spectrometric studies of copper(I) and mercury(II) binding to metallothionein. *J. Inorg. Biochem.*, 79, 11-9. ↗

Editions

2015-01-09	Authored, Edited	May, B.
2015-09-19	Reviewed	Atrian, S.