mycothione is reduced to mycothiol

Jassal, B., Stephan, R., Warner, D.

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

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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.

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Literature references

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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. ↗

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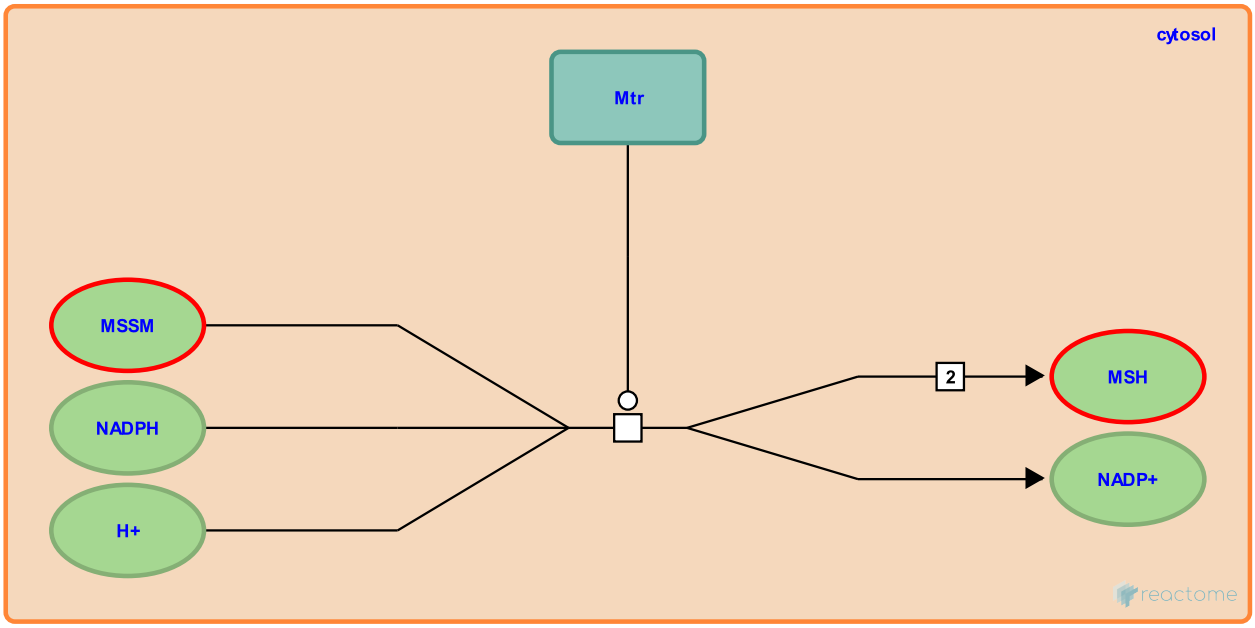
Stable identifier: R-MTU-879322

Type: transition

Compartments: cytosol



Mycothiol is recycled using a reduction equivalent (NADPH/H+) and the help of the mycothione reductase enzyme. Although a *mtr* null mutant was obtained by McAdam and coworkers in *M. tuberculosis*, another study by Sassetti suggests the enzyme is essential in the H37Rv strain. It appears possible that thioredoxin reductases can provide some enzymatic rest activity. (Patel and Blanchard, 1999; Rawat and Av-Gay, 2007)

Literature references

Patel, MP., Blanchard, JS. (1999). Expression, purification, and characterization of Mycobacterium tuberculosis mycothione reductase. *Biochemistry, 38*, 11827-33. ↗

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Editions

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