

MRSBs reduce L-methyl-(R)-S-oxide to L-methionine

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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

- 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

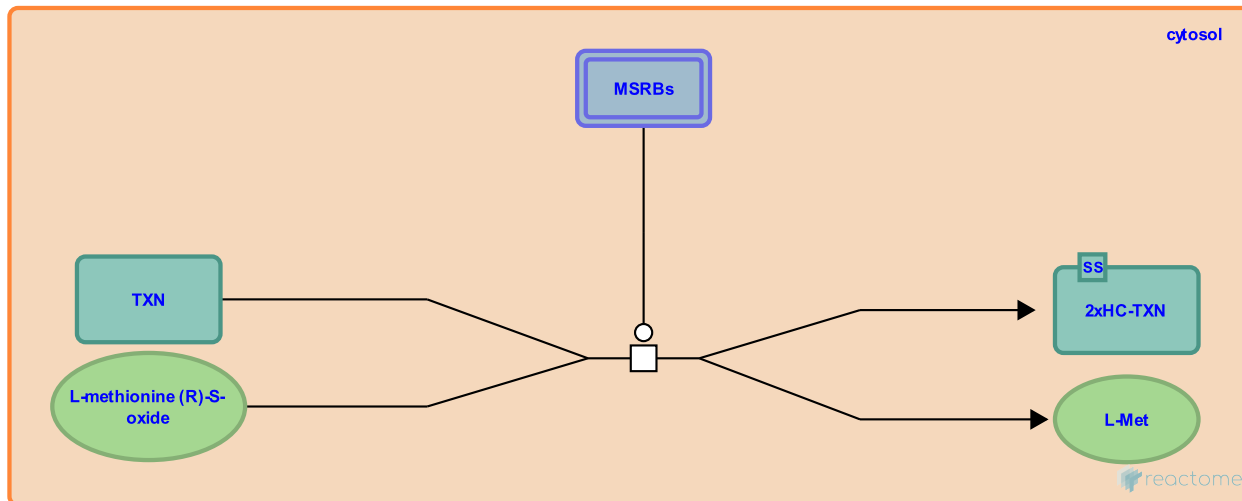
This document contains 1 reaction ([see Table of Contents](#))

MRSBs reduce L-methyl-(R)-S-oxide to L-methionine [↗](#)

Stable identifier: R-HSA-5676917

Type: transition

Compartments: cytosol



Methionine Sulfoxide Reductase B (MSRBs) are able to reduce methyl-(R)-S-oxide to methionine (Grimaud et al. 2001). They are specific for the reduction of protein-based methyl-(R)-S-oxide, reducing free methyl-(R)-S-oxide with very low efficiency (Lee et al. 2009). Mammals have at least 3 MSRB genes (Kryukov et al. 1999, Huang et al. 1999, Jung et al. 2002, Kim & Gladyshev 2004). They are ubiquitously expressed, no clear substrate specificities are known, all three contain a zinc atom and can use thioredoxin as an in vivo reducing agent (Kim & Gladyshev 2007).

Literature references

Coca-Prados, M., Huang, W., Sarfarazi, M., Escribano, J. (1999). Identification, expression and chromosome localization of a human gene encoding a novel protein with similarity to the pilB family of transcriptional factors (pilin) and to bacterial peptide methionine sulfoxide reductases. *Gene*, 233, 233-40. [↗](#)

Kryukov, VM., Kryukov, GV., Gladyshev, VN. (1999). New mammalian selenocysteine-containing proteins identified with an algorithm that searches for selenocysteine insertion sequence elements. *J. Biol. Chem.*, 274, 33888-97. [↗](#)

Heinemann, SH., Hansel, A., Hoshi, T., Jung, S., Kasperczyk, H. (2002). Activity, tissue distribution and site-directed mutagenesis of a human peptide methionine sulfoxide reductase of type B: hCBS1. *FEBS Lett.*, 527, 91-4. [↗](#)

Editions

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