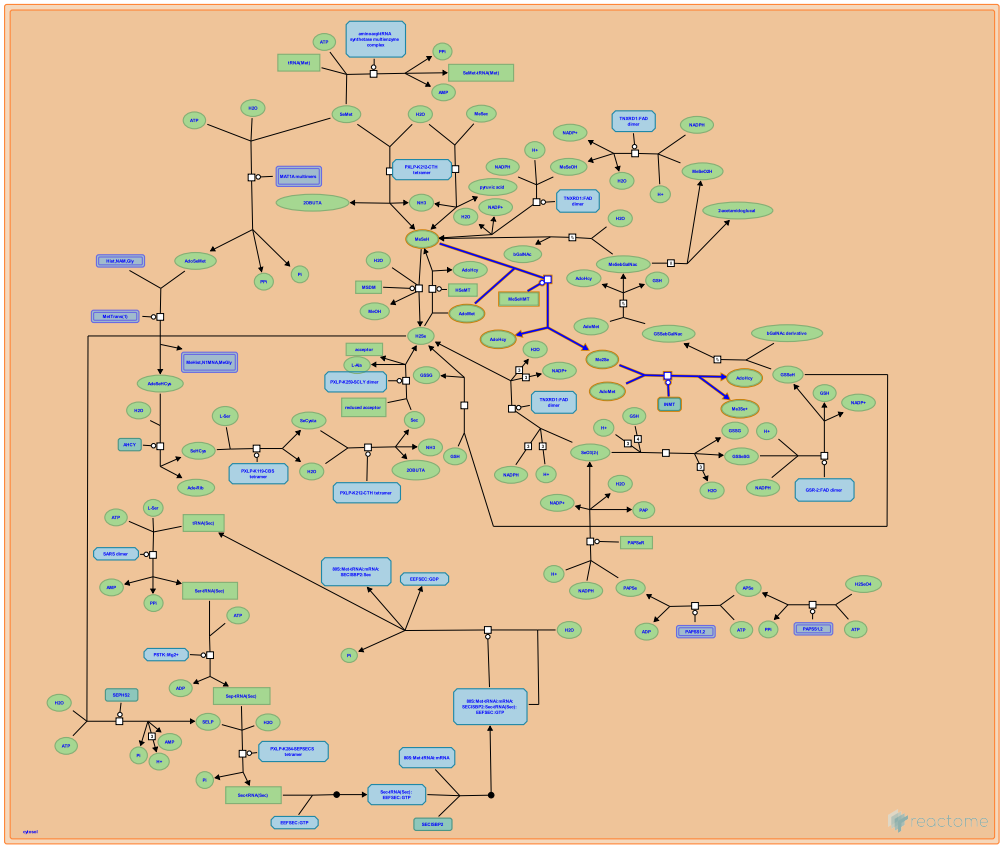
Methylation of MeSeH for excretion



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17/05/2024

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. ↗

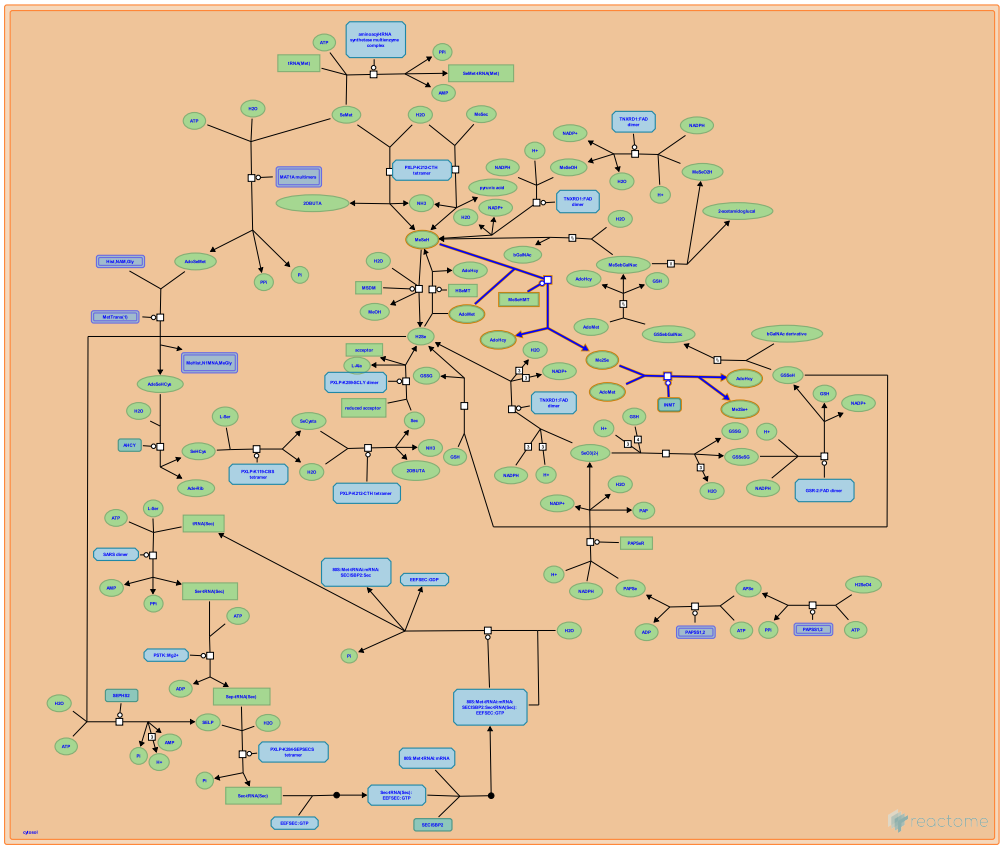
Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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. ↗

Methylation of MeSeH for excretion ↗

Stable identifier: R-HSA-2408552



Methylselenol (MeSeH) is further methylated to dimethylselenide (Me2Se) and trimethylselenonium (Me3Se+) for excretion.

Literature references

Suzuki, KT., Ohta, Y. (2008). Methylation and demethylation of intermediates selenide and methylselenol in the metabolism of selenium. *Toxicol. Appl. Pharmacol., 226*, 169-77. ↗

Editions

2014-05-06	Authored	Williams, MG.
2015-08-29	Edited	D'Eustachio, P.
2015-08-30	Reviewed	Rush, MG.

MeSeH is methylated to Me2Se by MeSeH methyltransferase ↗

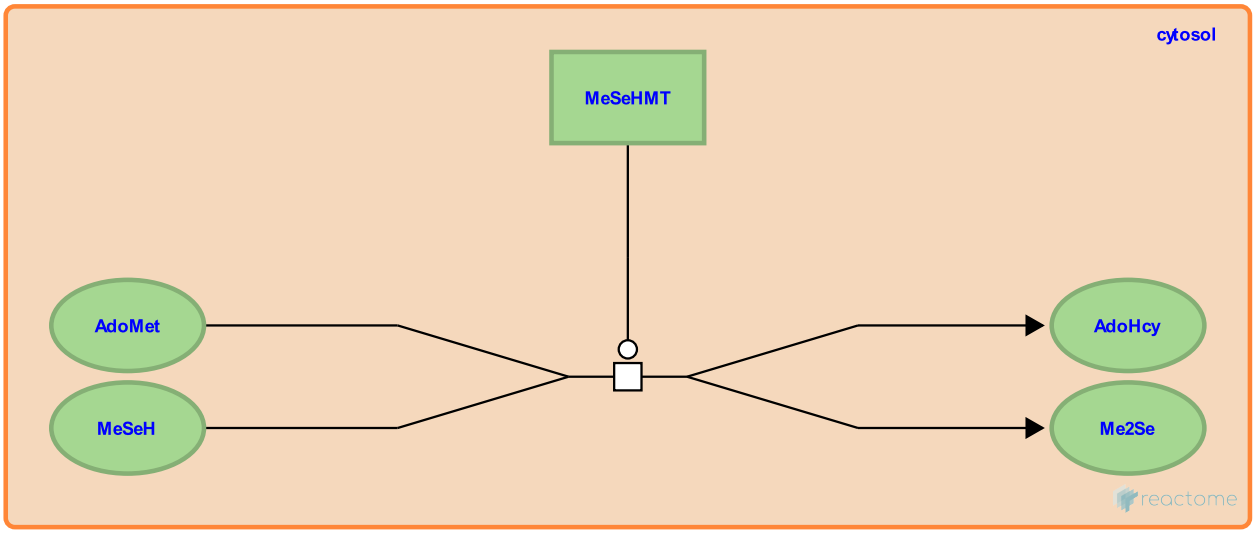
Location: Methylation of MeSeH for excretion

Stable identifier: R-HSA-2408541

Type: transition

Compartments: cytosol

Inferred from: MeSeH is methylated to Me2Se by MeSeH methyltransferase (Rattus norvegicus)



A yet to be identified enzyme with methylselenol methyltransferase (MeSeHMT) activity is involved in the methylation of methylselenol aka methaneselenol (MeSeH) into dimethyl selenide (Me2Se) in tandem with S-adenosylmethionine (AdoMet) transforming into S-adenosylhomocysteine (AdoHcy). This reaction is inferred from the event in rat (Ohta and Suzuki 2008, Hsieh and Ganther 1977).

Followed by: Me2Se is methylated to Me3Se+ by INMT

Literature references

Suzuki, KT., Ohta, Y. (2008). Methylation and demethylation of intermediates selenide and methylselenol in the metabolism of selenium. *Toxicol. Appl. Pharmacol., 226*, 169-77. ↗

Ganther, HE., Hsieh, HS. (1977). Biosynthesis of dimethyl selenide from sodium selenite in rat liver and kidney cell-free systems. *Biochim. Biophys. Acta, 497*, 205-17. ↗

Editions

2014-05-06	Authored	Williams, MG.
2015-08-29	Edited	D'Eustachio, P.
2015-08-30	Reviewed	Rush, MG.

Me2Se is methylated to Me3Se+ by INMT ↗

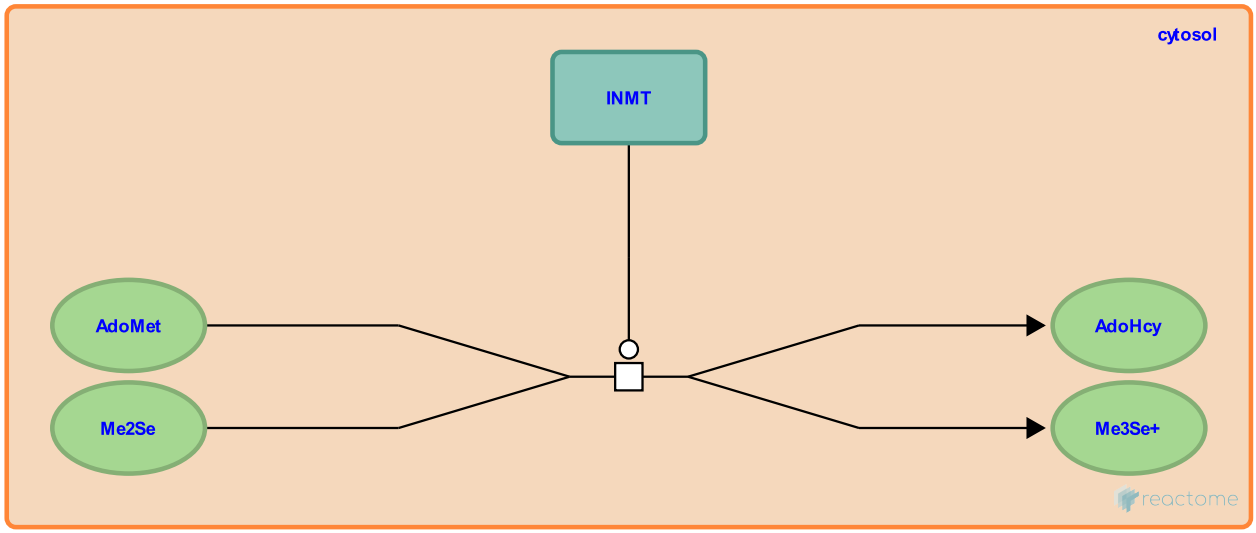
Location: Methylation of MeSeH for excretion

Stable identifier: R-HSA-2408554

Type: transition

Compartments: cytosol

Inferred from: Me2Se is methylated to Me3Se+ by Inmt (Mus musculus)



Indolethylamine N-methyltransferase (INMT) is involved in the methylation of dimethyl selenide (Me2Se) into trimethylselenonium (Me3Se+) in tandem with S-adenosylmethionine (AdoMet) transforming into S-adenosylhomocysteine (AdoHcy). This reaction is inferred from the event in mouse (Mozier et al. 1988).

Preceded by: MeSeH is methylated to Me2Se by MeSeH methyltransferase

Literature references

McConnell, KP., Mozier, NM., Hoffman, JL. (1988). S-adenosyl-L-methionine:thioether S-methyltransferase, a new enzyme in sulfur and selenium metabolism. *J. Biol. Chem., 263*, 4527-31. ↗

Editions

2014-05-06	Authored	Williams, MG.
2015-08-29	Edited	D'Eustachio, P.
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