MeSec is hydrolysed to MeSeH by PXLP-K212-CTH

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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. ↗

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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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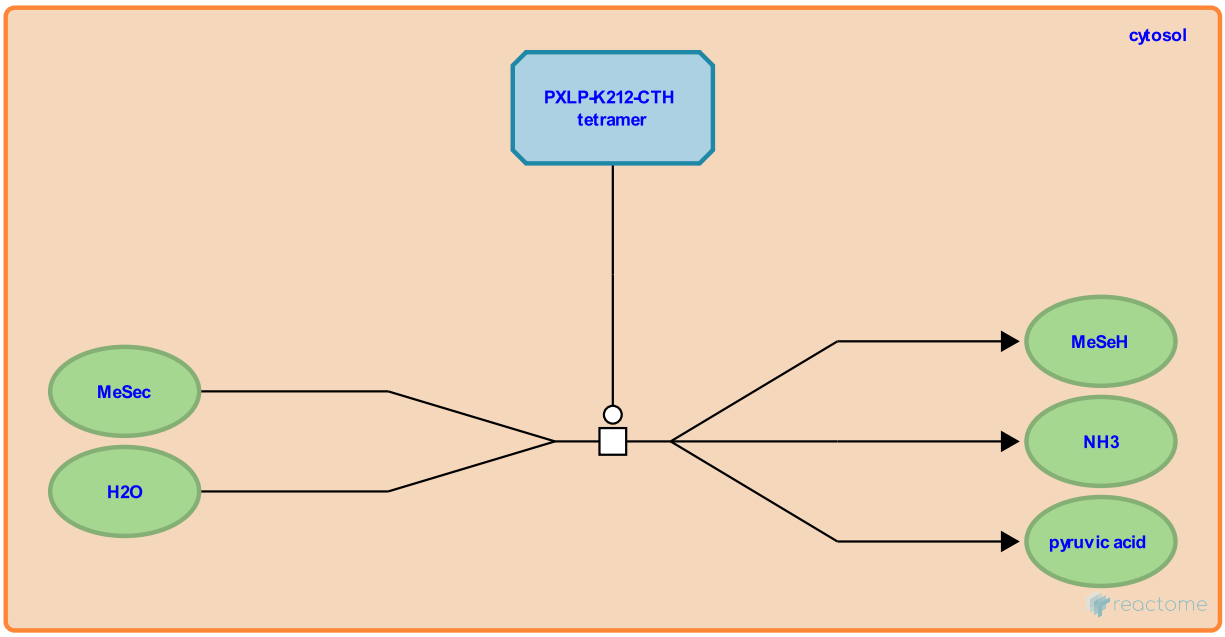
Stable identifier: R-HSA-2408539

Type: transition

Compartments: cytosol

Inferred from: MeSec is hydrolysed to MeSeH by PXLP-K211-Cth (Rattus norvegicus)



Methylselenocysteine (MeSec) undergoes an alpha,gamma-elimination reaction by cystathionine gamma-lyase (CTH) to produce methylselenol aka methaneselenol (MeSeH), ammonia, and pyruvic acid. This reaction is inferred from the event in rat involving the protein cystathionine gamma-lyase (Cth) (Pinto et al. 2011, Suzuki et al. 2007).

Literature references

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Editions

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