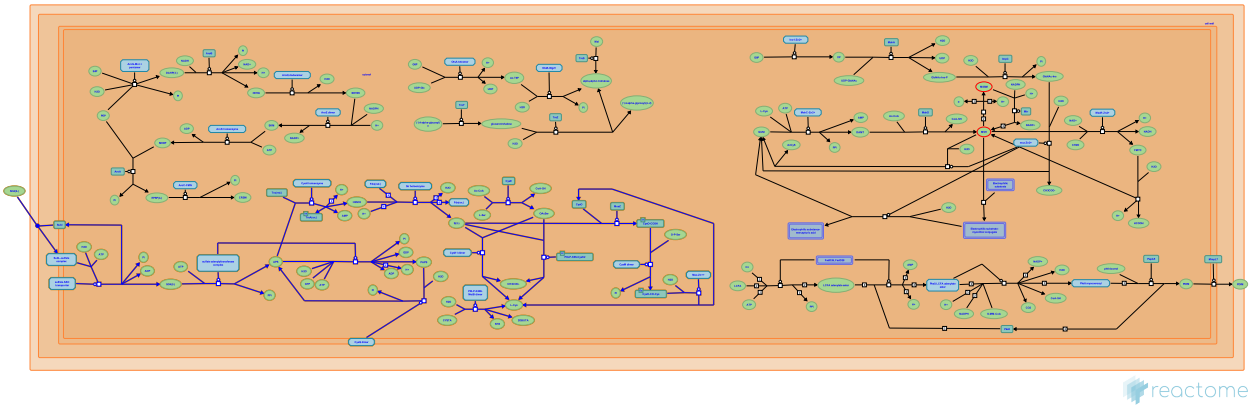
Sulfur compound metabolism



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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17/08/2021

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. ↗

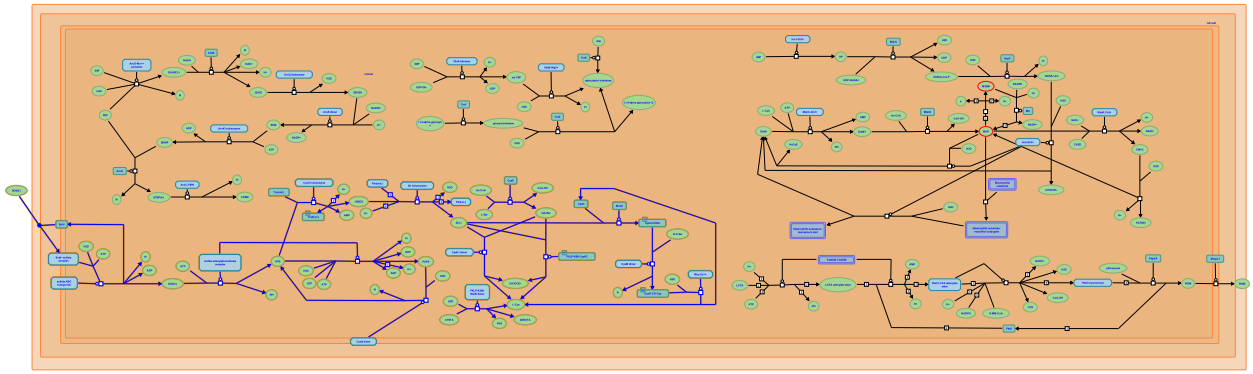
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Reactome database release: 77

This document contains 3 pathways (see Table of Contents)

Sulfur compound metabolism ↗

Stable identifier: R-MTU-936621



Unique small sulfur compounds, as well as unique pathways to sulfur amino acids are known in Mycobacteria. Sulfoglycolipids and mycothiols are an important part of the hardy pathogen nature of these organisms. Their pathways make interesting targets for drug designers (Bhave et al, 2007).

Literature references

Bhave, DP., Muse WB, 3rd., Carroll, KS. (2007). Drug targets in mycobacterial sulfur metabolism. *Infect Disord Drug Targets, 7*, 140-58. ↗

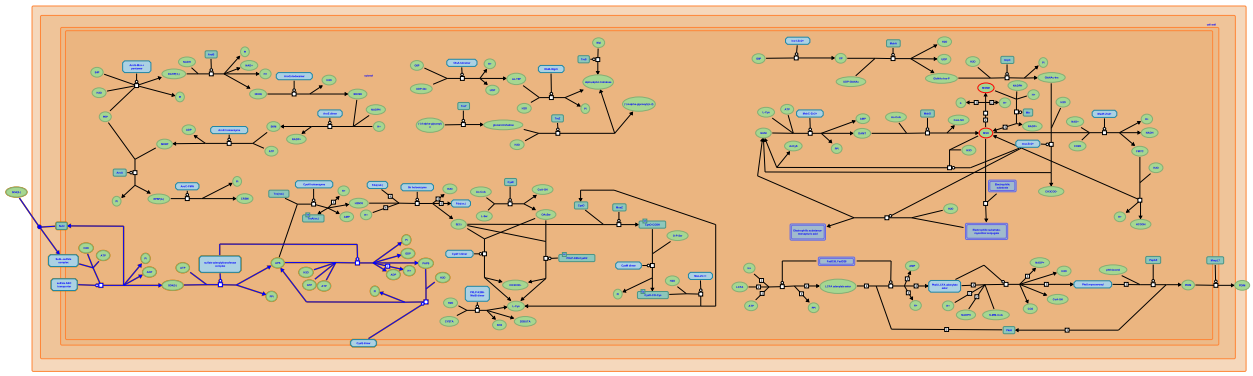
Editions

2010-06-17	Authored	Stephan, R.
2010-11-25	Reviewed	Warner, D.
2011-02-16	Edited	Jassal, B.

Sulfate assimilation ↗

Location: Sulfur compound metabolism

Stable identifier: R-MTU-936635



Uptake of sulfur in *Mycobacterium tuberculosis* happens exclusively through sulfate assimiliation, an abundant molecule in the bacterium's environment. All enzymes participating in this process are non-redundant ie they are essential enzymes. Sulfate is first taken up via an ABC transporter and appended to AMP giving APS and PAPS, which can be considered the activated forms of sulfate and are used in cysteine and sulfolipid biosynthesis (Bhave et al, 2007).

Literature references

Bhave, DP., Muse WB, 3rd., Carroll, KS. (2007). Drug targets in mycobacterial sulfur metabolism. *Infect Disord Drug Targets, 7*, 140-58. ↗

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2010-06-17	Authored	Stephan, R.
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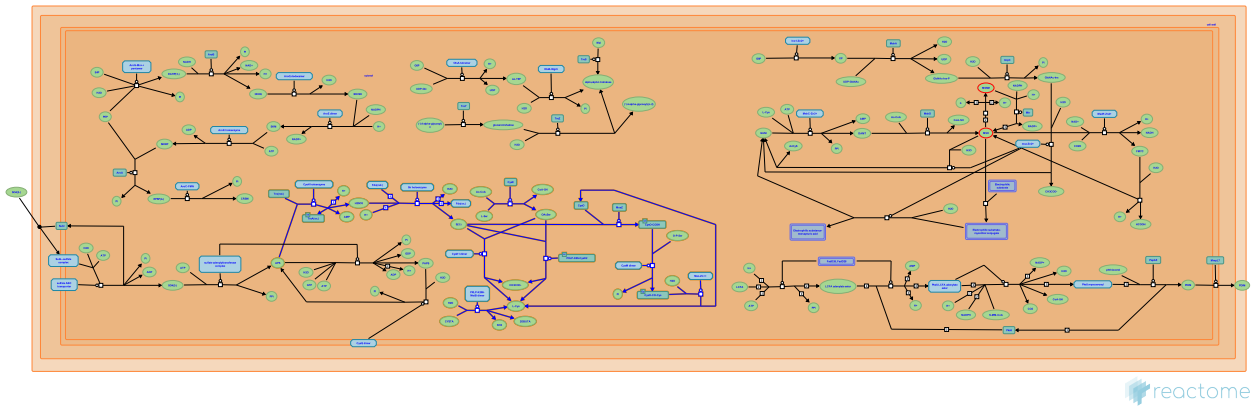
Sulfur amino acid metabolism ↗

Location: Sulfur compound metabolism

Stable identifier: R-MTU-937250



No cysteine auxotrophs of *Mycobacterium tuberculosis* are known. This suggests redundant pathways for sulfur uptake and cysteine biosynthesis. Indeed, there is full interconversion between taken up sulfate/sulfide, cysteine, and methionine via cystathionine. (Schnell and Schneider, 2010)

Literature references

Schnell, R., Schneider, G. (2010). Structural enzymology of sulphur metabolism in Mycobacterium tuberculosis. *Biochem Biophys Res Commun, 396*, 33-8. ↗

Editions

2010-06-20	Authored	Stephan, R.
2010-11-25	Reviewed	Warner, D.
2011-02-16	Edited	Jassal, B.

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