Cell redox homeostasis

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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


Reactome database release: 72

This document contains 1 pathway and 7 reactions (see Table of Contents)
The most important response of \textit{Mtb} to oxidative stress is provided by catalase and peroxiredoxins, both of which get their reducing equivalents through a network of disulfide proteins and, finally, from NAD(P)H. Multiple redundancies make choosing a good drug target difficult (Koul et al. 2011). Optimum efficacy can only be expected from inhibitors of the most upstream components of the redox cascades, i.e. the NAD(P)H-dependent reductases TrxB and Lpd (Jaeger & Flohe 2006).

**Literature references**


**Editions**

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AhpD reactivates AhpC

**Location:** Cell redox homeostasis

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