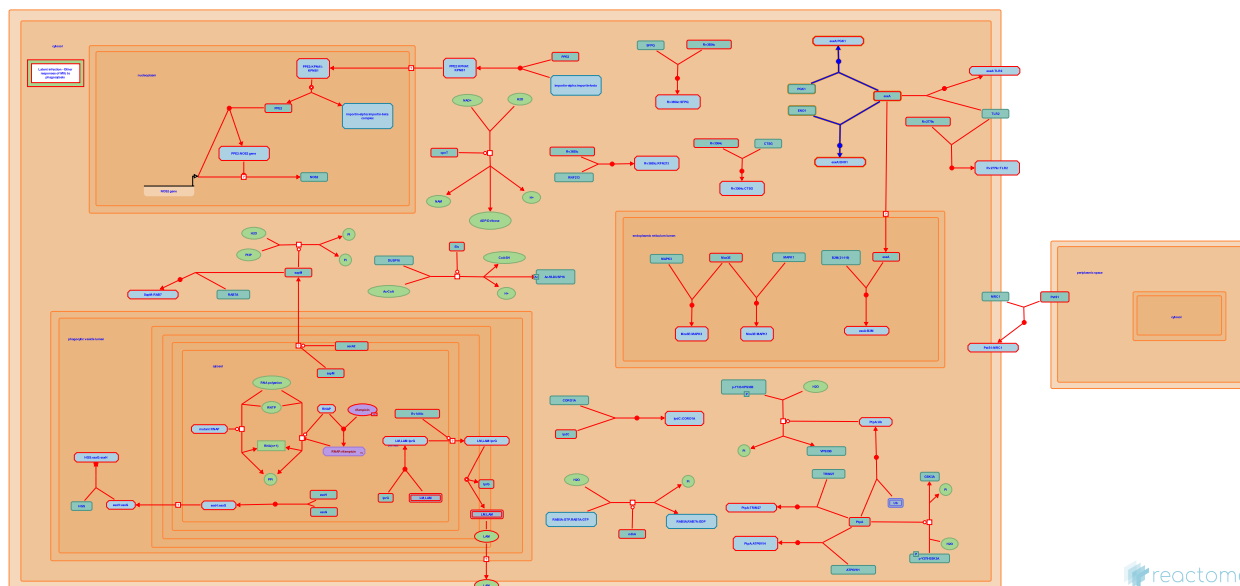


# Manipulation of host energy metabolism



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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the [Reactome Textbook](https://reactome.org/textbook/).

29/04/2024

## 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

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- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
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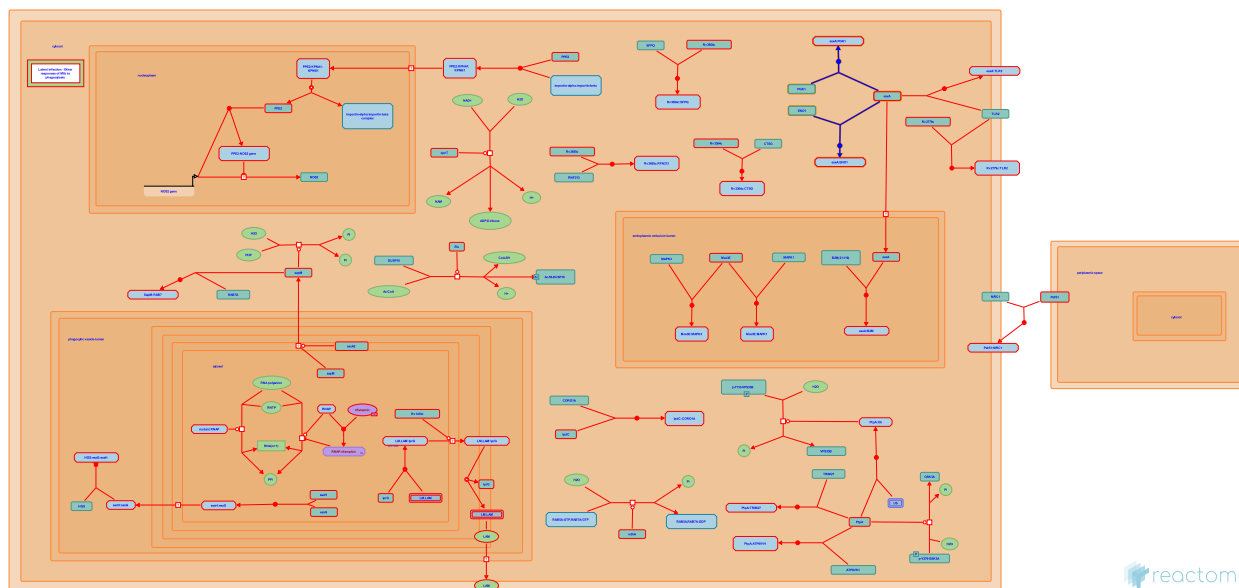
Reactome database release: 88

This document contains 1 pathway and 2 reactions ([see Table of Contents](#))

## Manipulation of host energy metabolism ↗

**Stable identifier:** R-HSA-9636667

**Diseases:** tuberculosis



Mtb secretes proteins that enhance enzymatic activity of glucose metabolism in the phagocyte. The same proteins also appear to increase glucose uptake and to cause accumulation of DHAP, ultimately increasing the host cell's lipid production (Singh et al. 2015).

### Literature references

Rao, KV., Kaur, C., Chatterjee, S., Chaudhary, VK., Singh, V. (2015). M. tuberculosis Secretory Protein ESAT-6 Induces Metabolic Flux Perturbations to Drive Foamy Macrophage Differentiation. *Sci Rep*, 5, 12906. ↗

### Editions

2019-02-06	Authored	Stephan, R.
2019-02-13	Edited	Pardo, AM.
2019-10-23	Reviewed	Wilkinson, RJ., Deffur, A.

## esxA binds ENO1 [↗](#)

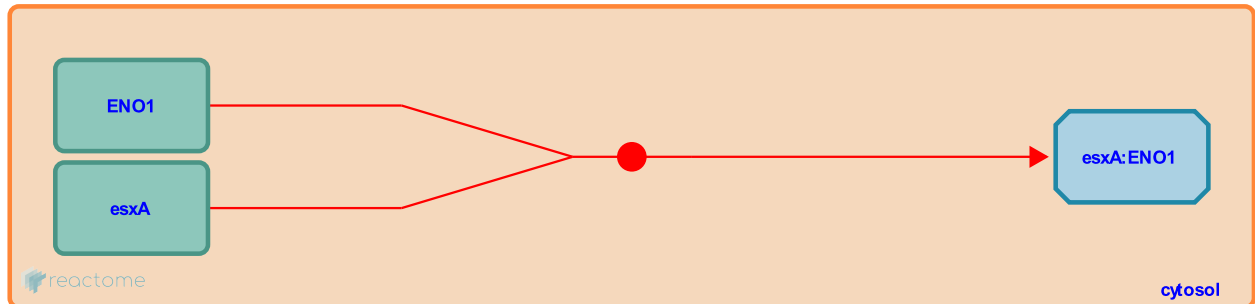
**Location:** [Manipulation of host energy metabolism](#)

**Stable identifier:** R-HSA-963669

**Type:** binding

**Compartments:** cytosol

**Diseases:** tuberculosis



Mtb secreted 6 kDa early secretory antigenic target (esxA) binds to human enolase-1 protein (ENO1) (Singh et al. 2015).

### Literature references

Rao, KV., Kaur, C., Chatterjee, S., Chaudhary, VK., Singh, V. (2015). M. tuberculosis Secretory Protein ESAT-6 Induces Metabolic Flux Perturbations to Drive Foamy Macrophage Differentiation. *Sci Rep*, 5, 12906. [↗](#)

### Editions

2019-02-06	Authored	Stephan, R.
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2019-10-23	Reviewed	Wilkinson, RJ., Deffur, A.

## esxA binds PGK1 [↗](#)

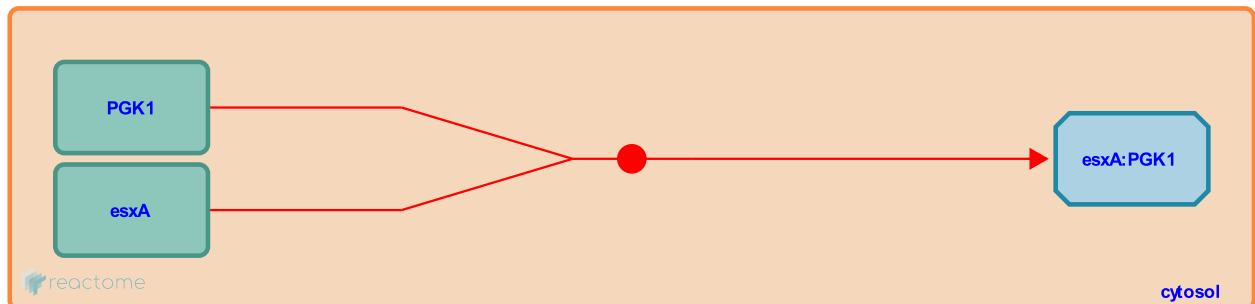
**Location:** [Manipulation of host energy metabolism](#)

**Stable identifier:** R-HSA-9636658

**Type:** binding

**Compartments:** cytosol

**Diseases:** tuberculosis



Mtb secreted 6 kDa early secretory antigenic target (esxA) binds to human phosphoglycerate kinase-1 (PGK1) (Singh et al. 2015).

### Literature references

Rao, KV., Kaur, C., Chatterjee, S., Chaudhary, VK., Singh, V. (2015). M. tuberculosis Secretory Protein ESAT-6 Induces Metabolic Flux Perturbations to Drive Foamy Macrophage Differentiation. *Sci Rep*, 5, 12906. [↗](#)

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# Table of Contents

- Introduction 1
- ☒ Manipulation of host energy metabolism 2
  - ☞ esxA binds ENO1 3
  - ☞ esxA binds PGK1 4
- Table of Contents 5