TP53 stimulates GLS2 transcription

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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

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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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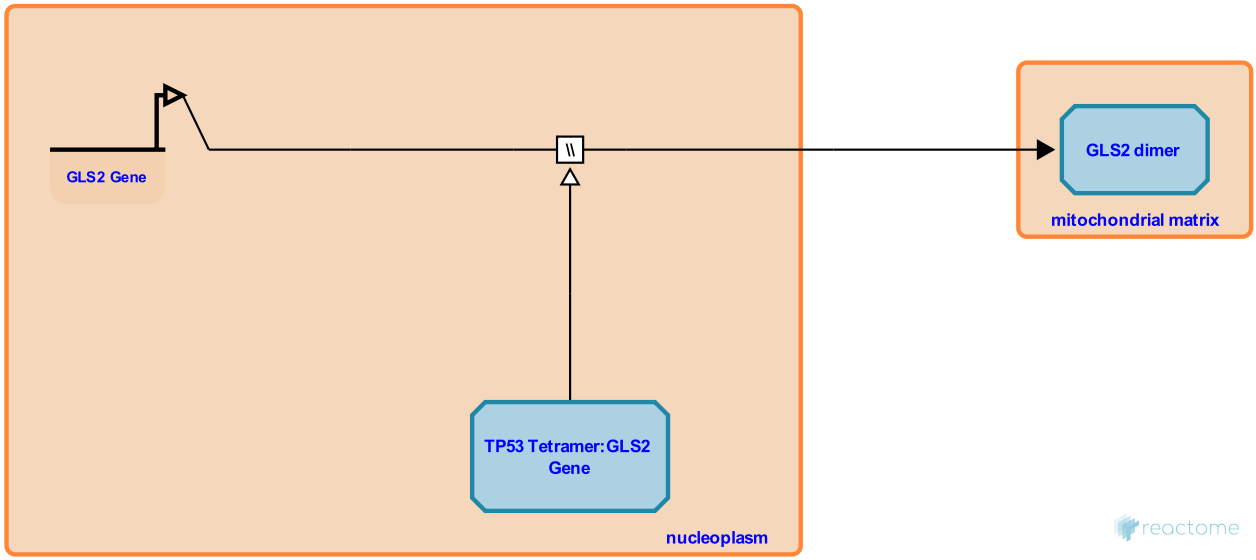
Stable identifier: R-HSA-5632924

Type: omitted

Compartments: mitochondrial matrix, nucleoplasm



TP53 (p53) directly stimulates transcription of mitochondrial glutaminase GLS2 under non-stress and stress conditions. Increased GLS2 levels lead to increased production of glutamate and alpha-ketoglutarate, increased mitochondrial respiration rate, and reduced ROS (reactive oxygen species) load through enhanced glutathione reduction (Hu et al. 2010).

Elevated GLS2 was associated with lower levels of intracellular ROS and a decrease in DNA oxidation. GLS2 knockdown resulted in higher ROS levels and was associated with stimulation of p53-induced cell death (Suzuki et al. 2010).

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Editions

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