

Expression of SRY in testis differentiation

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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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Reactome database release: 88

This document contains 1 reaction ([see Table of Contents](#))

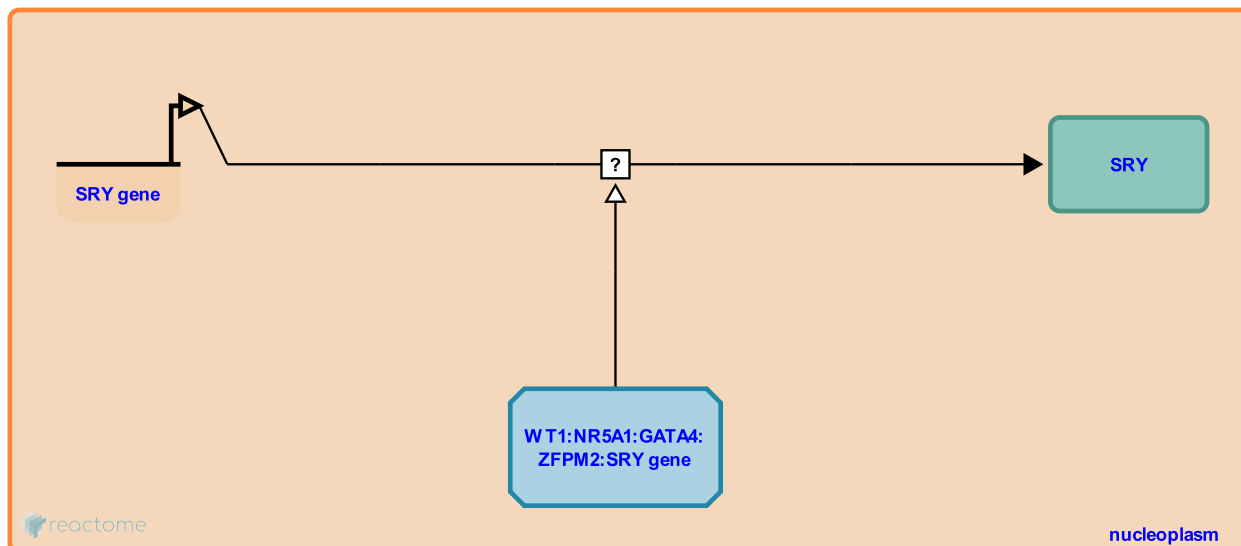
Expression of SRY in testis differentiation [↗](#)

Stable identifier: R-HSA-9692241

Type: uncertain

Compartments: nucleoplasm

Inferred from: [Expression of Sry in testis differentiation \(Mus musculus\)](#)



In the gonadal ridge (genital ridge), the SRY gene is transcribed to yield mRNA and the mRNA is translated to yield SRY protein (De Santa Barbara et al. 2001, Hossain and Saunders 2001, Miyamoto et al. 2008, also inferred from mouse homologs). Transcription of SRY is activated by WT1 (Hossain and Saunders 2001, Miyamoto et al. 2008), GATA4:ZFPM2 (also called GATA4:FOG2) (Miyamoto et al. 2008), and NR5A1 (also called SF1) (De Santa Barbara et al. 2001).

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Editions

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