

# Expression of DHH in testis differentiation

Imaimatsu, K., Kanai, Y., May, B.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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03/04/2024

## 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 reaction ([see Table of Contents](#))

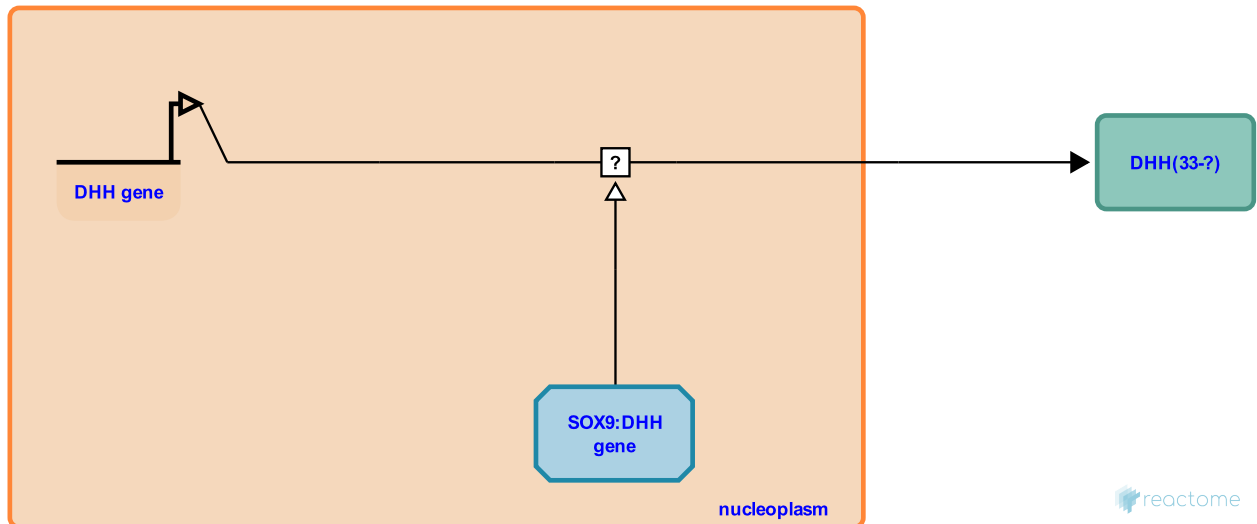
## Expression of DHH in testis differentiation [↗](#)

**Stable identifier:** R-HSA-9692146

**Type:** uncertain

**Compartments:** nucleoplasm, extracellular region

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



The DHH gene is transcribed to yield mRNA and the mRNA is translated to yield DHH protein (Rahmoun et al. 2017 and inferred from mouse homologs). Transcription of DHH is directly activated by SOX9 (inferred from mouse homologs). DHH is secreted from pre-Sertoli cells (Rahmoun et al. 2017 and inferred from mouse homologs) and acts via the PTCH1 receptor to regulate testis development.

### Literature references

Symon, A., Philip, GK., Chung, J., Clair, P., Boizet-Bonhoure, B., Bardwell, V. et al. (2017). In mammalian foetal testes, SOX9 regulates expression of its target genes by binding to genomic regions with conserved signatures. *Nucleic Acids Res.*, 45, 7191-7211. [↗](#)

### Editions

2020-06-15

Authored, Edited

May, B.

2020-10-29

Reviewed

Kanai, Y., Imaimatsu, K.