

# Expression of Amh 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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Reactome database release: 88

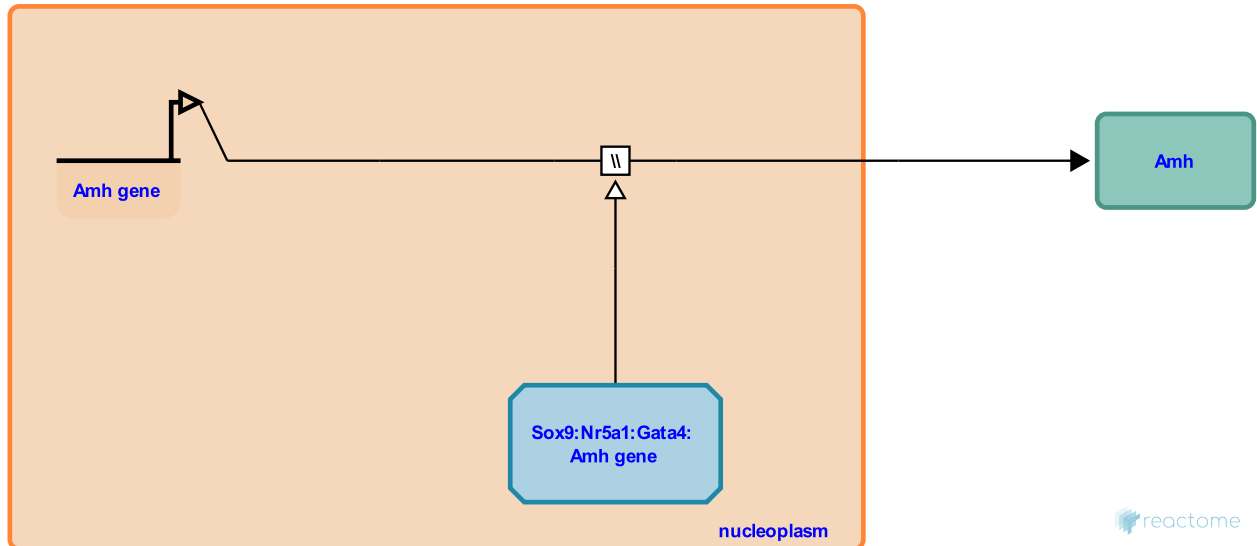
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## Expression of Amh in testis differentiation [↗](#)

**Stable identifier:** R-MMU-9692156

**Type:** omitted

**Compartments:** nucleoplasm, extracellular region



In differentiating Sertoli cells of the testis, the Amh gene is transcribed to yield mRNA and the mRNA is translated to yield Amh protein (Arango et al. 1999, Li et al. 2014). Sox9, Nr5a1 (SF1), and Gata4 bind the promoter of the Amh gene and activate transcription (Arango et al. 1999, Li et al. 2014).

### Literature references

Zheng, M., Lau, YF., Li, Y. (2014). The sex-determining factors SRY and SOX9 regulate similar target genes and promote testis cord formation during testicular differentiation. *Cell Rep*, 8, 723-33. [↗](#)

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### Editions

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