

Formation of DSIF complex

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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.

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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Reactome database release: 74

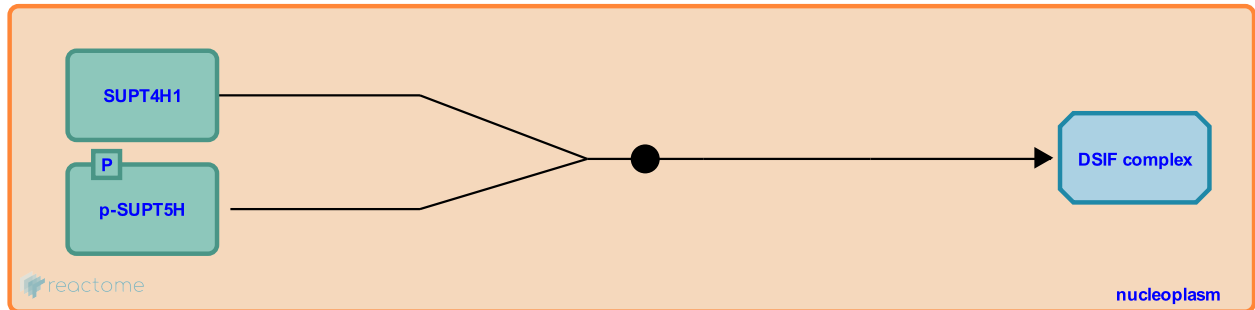
This document contains 1 reaction ([see Table of Contents](#))

Formation of DSIF complex [↗](#)

Stable identifier: R-HSA-112434

Type: binding

Compartments: nucleoplasm



At the beginning of this reaction, 1 molecule of 'SUPT5H protein', and 1 molecule of 'SPT4H1 protein' are present. At the end of this reaction, 1 molecule of 'DSIF complex' is present (Wada et al. 1998).

This reaction takes place in the 'nucleus'.

Literature references

Wada, T., Takagi, T., Yamaguchi, Y., Ferdous, A., Imai, T., Hirose, S. et al. (1998). DSIF, a novel transcription elongation factor that regulates RNA polymerase II processivity, is composed of human Spt4 and Spt5 homologs. *Genes Dev*, 12, 343-56. [↗](#)