

Formation of FACT 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.

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Literature references

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Reactome database release: 73

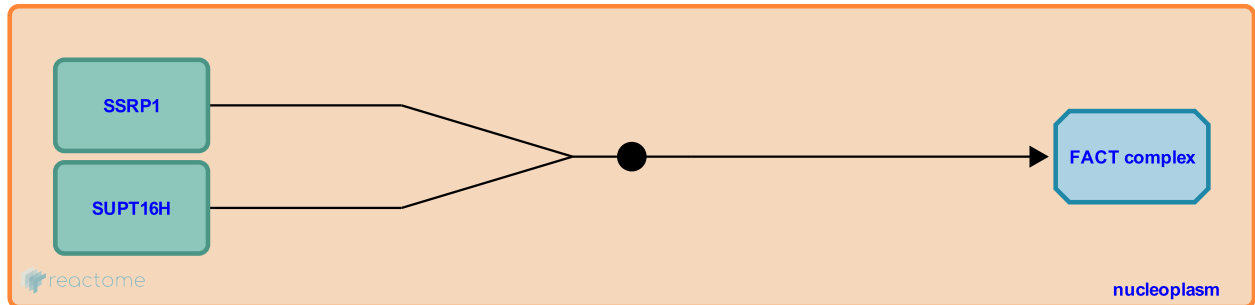
This document contains 1 reaction ([see Table of Contents](#))

Formation of FACT complex [↗](#)

Stable identifier: R-HSA-112429

Type: binding

Compartments: nucleoplasm



At the beginning of this reaction, 1 molecule of 'FACT 140 kDa subunit', and 1 molecule of 'FACT 80 kDa subunit' are present. At the end of this reaction, 1 molecule of 'FACT complex' is present.

This reaction takes place in the 'nucleus' (Kamakaka et al.1993, Orphanides et al.1998).

Literature references

Kamakaka, RT., Bulger, M., Kadonaga, JT. (1993). Potentiation of RNA polymerase II transcription by Gal4-VP16 during but not after DNA replication and chromatin assembly. *Genes Dev.*, 7, 1779-95. [↗](#)

Orphanides, G., LeRoy, G., Chang, CH., Luse, DS., Reinberg, D. (1998). FACT, a factor that facilitates transcript elongation through nucleosomes. *Cell*, 92, 105-16. [↗](#)