Switching of origins to a post-replicative state
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


Reactome database release: 79

This document contains 3 pathways and 2 reactions (see Table of Contents)
Switching of origins to a post-replicative state

Stable identifier: R-HSA-69052

Compartments: nucleoplasm, cytosol

Switching of origins to a post-replicative state involves the removal of Orc1 from chromatin, CDK-mediated phosphorylation and removal of Cdc6, and the rearrangement and mobilization of Mcm2-7.
Orc1 removal from chromatin

Location: Switching of origins to a post-replicative state

Stable identifier: R-HSA-68949

Compartments: nucleoplasm, cytosol

Mammalian Orc1 protein is phosphorylated and selectively released from chromatin and ubiquitinated during the S-to-M transition in the cell division cycle.

Literature references


CDK-mediated phosphorylation and removal of Cdc6

Location: Switching of origins to a post-replicative state

Stable identifier: R-HSA-69017

Compartments: nucleoplasm, cytosol

As cells enter S phase, HsCdc6p is phosphorylated by CDK promoting its export from the nucleus (see Bell and Dutta 2002).

Literature references


Mcm4,6,7 trimer forms and associates with the replication fork

Location: Switching of origins to a post-replicative state

Stable identifier: R-HSA-69019