FOXM1 stimulates PLK1 transcription

Bruinsma, W., Orlic-Milacic, M.

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

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20/11/2021
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


Reactome database release: 78

This document contains 1 reaction (see Table of Contents)
FOXM1 stimulates PLK1 transcription

Stable identifier: R-HSA-4088305

Type: omitted

Compartments: cytosol, nucleoplasm

FOXM1 bound to the MuvB complex (consisting of LIN9, LIN37, LIN52, LIN54 and RBBP4) and MYBL2 (B-MYB) stimulates PLK1 transcription. This creates a positive feedback loop, where PLK1 phosphorylates and activates FOXM1 (Fu et al. 2008), while FOXM1 transcriptional activity results in increased PLK1 levels. MuvB and FOXM1 may persist on the PLK1 promoter throughout G2, while MYBL2 may gradually dissociate from the PLK1 promoter due to proteasome-mediated degradation initiated when MYBL2 is phosphorylated by CCNA (cyclin A)-associated CDKs (Sadasivam et al. 2012).

Literature references


Editions

<table>
<thead>
<tr>
<th>Date</th>
<th>Action</th>
<th>Author</th>
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<tbody>
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<td>Orlic-Milacic, M.</td>
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<tr>
<td>2013-08-14</td>
<td>Authored</td>
<td>Orlic-Milacic, M.</td>
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<tr>
<td>2013-08-21</td>
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<td>Bruinsma, W.</td>
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