Condensation of Prophase Chromosomes

Gallie, BL., Longworth, MS., Matthews, L., Orlic-Milacic, M.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of Creative Commons Attribution 4.0 International (CC BY 4.0) License. For more information see our license.

01/06/2020
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: 72

This document contains 1 pathway and 10 reactions (see Table of Contents)
Condensation of Prophase Chromosomes

Stable identifier: R-HSA-2299718

Compartments: nucleoplasm

In mitotic prophase, the action of the condensin II complex enables initial chromosome condensation.

The condensin II complex subunit NCAPD3 binds monomethylated histone H4 (H4K20me1), thereby associating with chromatin (Liu et al. 2010). Binding of the condensin II complex to chromatin is partially controlled by the presence of RB1 (Longworth et al. 2008).

Two mechanisms contribute to the accumulation of H4K20me1 at mitotic entry. First, the activity of SETD8 histone methyltransferase peaks at G2/M transition (Nishioka et al. 2002, Rice et al. 2002, Wu et al. 2010). Second, the complex of CDK1 and cyclin B1 (CDK1:CCNB1) phosphorylates PHF8 histone demethylase at the start of mitosis, removing it from chromatin (Liu et al. 2010).

Condensin II complex needs to be phosphorylated by the CDK1:CCNB1 complex, and then phosphorylated by PLK1, in order to efficiently condense prophase chromosomes (Abe et al. 2011).

Literature references


**Editions**

<table>
<thead>
<tr>
<th>Date</th>
<th>Action</th>
<th>Author</th>
</tr>
</thead>
<tbody>
<tr>
<td>2013-04-11</td>
<td>Authored</td>
<td>Gallie, BL.</td>
</tr>
<tr>
<td>2013-04-23</td>
<td>Edited</td>
<td>Matthews, L.</td>
</tr>
<tr>
<td>2013-04-23</td>
<td>Authored</td>
<td>Orlic-Milacic, M.</td>
</tr>
<tr>
<td>2013-10-14</td>
<td>Reviewed</td>
<td>Longworth, MS.</td>
</tr>
</tbody>
</table>

https://www.reactome.org
SETD8 monomethylates histone H4

Location: Condensation of Prophase Chromosomes

Stable identifier: R-HSA-2301205