Positive epigenetic regulation of rRNA expression

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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**


Reactome database release: 71

This document contains 3 pathways (see Table of Contents)
Positive epigenetic regulation of rRNA expression

Stable identifier: R-HSA-5250913

Compartments: nucleoplasm

Transcription of rRNA genes is controlled by epigenetic activation and repression according to the metabolic requirements of the cell (reviewed in Percipalle and Farrants 2006, McStay and Grummt 2008, Goodfellow and Zomerdijk 2012, Grummt and Langst 2013). Depending on the growth state of the cell, about half of the approximately 400 rRNA genes are expressed and these have the modifications characteristic of active chromatin: unmethylated DNA and acetylated histones. Repressed genes generally have methylated DNA and histone H3 methylated at lysine-9. Regulators of activation include ERCC6 (CSB), histone acetylases such as KAT2B (PCAF), and the B-WICH complex. Dysregulation of RNA polymerase I transcription plays a role in disease (reviewed in Hannan et al. 2013).

The B-WICH complex positively regulates rRNA expression by remodeling chromatin and recruiting histone acetyltransferases that modify histones to transcriptionally active states

ERCC6 (CSB) and EHMT2(G9a) positively regulate rRNA expression by ERCC6 recruiting the histone methyltransferase EHMT2 (also known as G9a) which dimethylates histone H3 at lysine-9 within the transcribed regions of rRNA genes.

ERCC6 (CSB) and KAT2B (PCAF) positively regulate rRNA expression by ERCC6 recruiting the histone acetyltransferase KAT2B to the promoter where KAT2B acetylates histone H4 at several lysine residues and histone H3 at lysine-9. The acetylated chromatin facilitates the assembly of RNA polymerase I initiation complex.

Literature references


**Editions**

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<td>2015-11-07</td>
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B-WICH complex positively regulates rRNA expression

Location: Positive epigenetic regulation of rRNA expression

Stable identifier: R-HSA-5250924

Compartments: nucleoplasm

The B-WICH complex is a large 3 Mdalton complex containing SMARCA5 (SNF2H), BAZ1B (WSTF), ERCC6 (CSB), MYO1C (Nuclear myosin 1c), SF3B1, DEK, MYBBP1A, and DDX21 (Cavellán et al. 2006, Percipalle et al. 2006, Vintermist et al. 2001, Sarshad et al. 2013, Shen et al. 2013, reviewed in Percipalle and Farrants 2006). B-WICH is found at active rRNA genes as well as at 5S rRNA and 7SL RNA genes. B-WICH appears to remodel chromatin and recruit histone acetyltransferases that modify histones to transcriptionally active states.

Literature references


ERCC6 (CSB) and EHMT2 (G9a) positively regulate rRNA expression

**Location:** Positive epigenetic regulation of rRNA expression

**Stable identifier:** R-HSA-427389

**Compartments:** nucleoplasm

About half of the rRNA genes in the genome are actively expressed, being transcribed by RNA polymerase I (reviewed in Nemeth and Langst 2008, Bartova et al. 2010, Goodfellow and Zomerdijk 2012, Grummt and Langst 2013). As inferred from mouse, those genes that are expressed are activated by ERCC6 (also known as Cockayne Syndrome protein, CSB) which interacts with TTF-I bound to the T0 terminator region (also know as the Sal Box) of rRNA genes (Yuan et al. 2007, reviewed in Birch and Zomerdijk 2008, Grummt and Langst 2013). ERCC6 recruits the histone methyltransferase EHMT2 (also known as G9a) which dimethylates histone H3 at lysine-9 in the coding region of rRNA genes. The dimethylated lysine is bound by CBX3 (also known as Heterochromatic Protein-1gamma, HP1gamma) and increases expression of the rRNA gene. Continuing dimethylation depends on continuing transcription. Mutations in CSB result in dysregulation of RNA polymerase I transcription, which plays a role in the symptoms of Cockayne Syndrome (reviewed in Hannan et al. 2013).

**Literature references**


**Editions**

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<td>2016-02-12</td>
<td>Reviewed</td>
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