Recruitment of ERCC6 (CSB), EHMT2 (G9a), and NuRD to the promoter of rRNA gene

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29/04/2024

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

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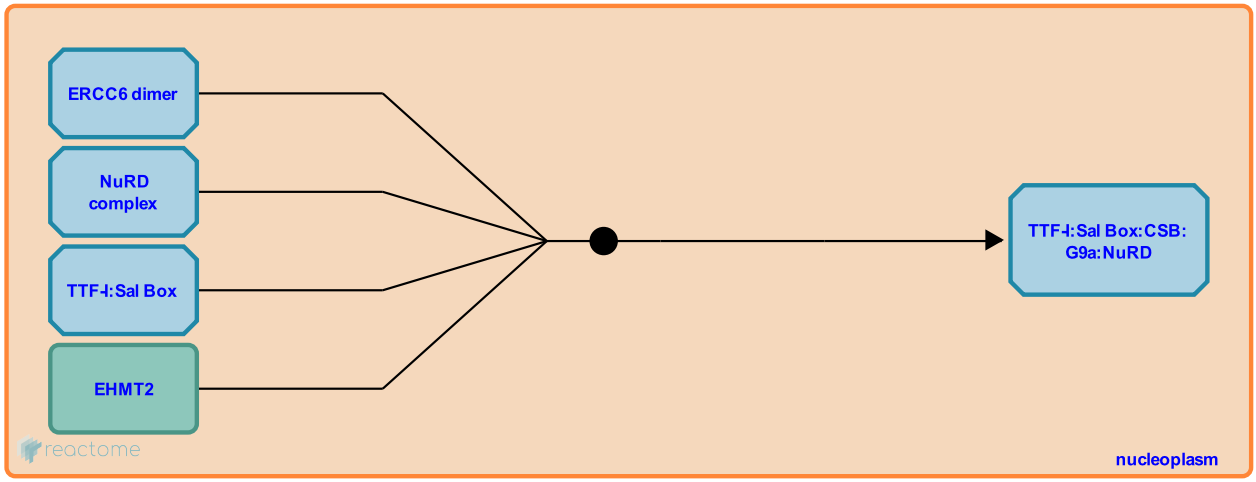
Stable identifier: R-HSA-427404

Type: binding

Compartments: nucleoplasm

Inferred from: Recruitment of CSB, G9a, and NuRD to the rRNA promoter (Homo sapiens)



Transcription Termination Factor-I (TTF-I) is a sequence-specific binding protein that binds sites 5' (Tsp and T0 sites) and 3' (T1-10 site) of rRNA genes. As inferred from mouse, when TTF-I is bound to the promoter-proximal T0 site TTF-I either recruits ERCC6 (also known as Cockayne Syndrome Protein, CSB), EHMT2 (also known as histone methyltransferase G9a), and NuRD to activate expression (Shimono et al. 2005, Lebedev et al. 2008) or recruits the Nucleolar Remodeling Complex (NoRC) to repress expression. How one is selected over the other is unknown.
CHD4 and presumably the rest of the NuRD complex is associated with bivalent domains containing H3K4me3 (active chromatin mark) and H3K27me3 (inactive chromatin mark). ERCC6 and EHMT2 appear to cooperate to regulate activation of rRNA expression with ERCC6 mediating the transition to permissive chromatin (Lebedev et al. 2008) and EHMT2 mediating the transition to active chromatin, which involves the positional shift of one nucleosome at the promoter.

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Editions

2009-06-19	Edited	May, B.
2009-06-21	Authored	May, B.
2016-02-12	Reviewed	Iben, S.