

Nucleolar Remodelling Complex (NoRC)

binds intergenic region of rDNA

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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.

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Literature references

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)

Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)

Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 90

This document contains 1 reaction ([see Table of Contents](#))

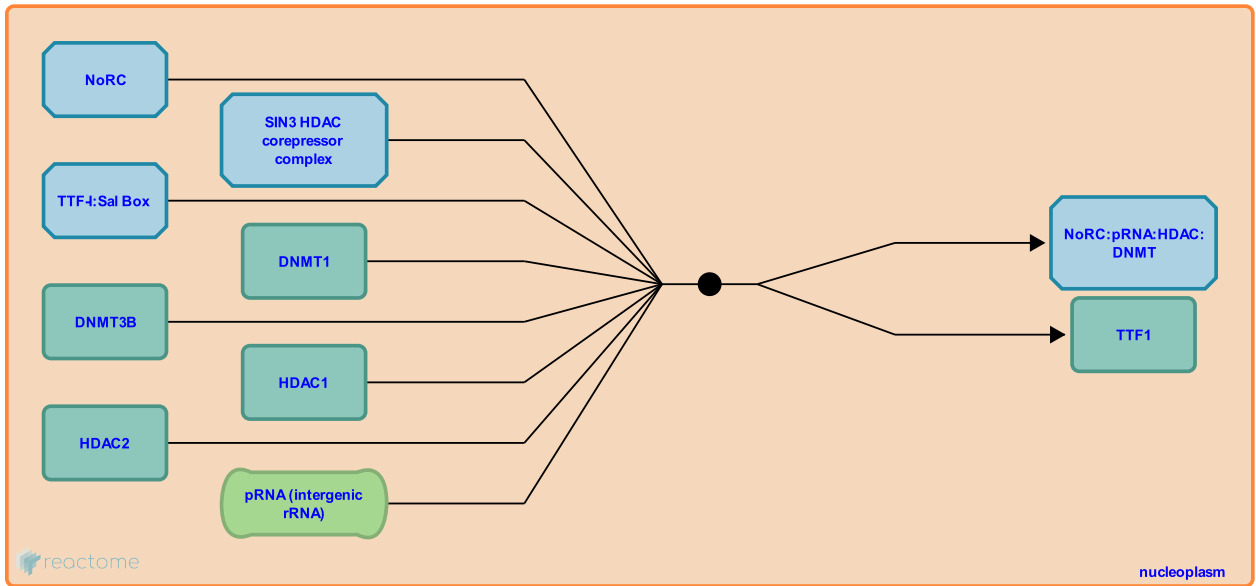
Nucleolar Remodelling Complex (NoRC) binds intergenic region of rDNA ↗

Stable identifier: R-HSA-427409

Type: binding

Compartments: nucleoplasm

Inferred from: Nucleolar Chromatin Remodeling Complex (NoRC) binds intergenic spacer of rRNA gene (Mus musculus)



As inferred from mouse cell models, the Nucleolar Remodeling Complex (NoRC) comprises TIP5 (BAZ2A) and the chromatin remodeller SNF2H (SMARCA5). The TAM domain of TIP5 (BAZ2A) binds promoter-associated RNA (pRNA) transcribed from the intergenic spacer region of rDNA (Anosova et al. 2015). Binding is not sequence-specific but depends on the secondary structure of the RNA. The pRNA bound by TIP5 is required to direct the complex to the main promoter of the rRNA gene possibly by triple helix formation between pRNA and the rDNA. The PHD domain of TIP5 binds histone H4 acetylated at lysine-16. Transcription Termination Factor-I (TTF-I) binds to a promoter-proximal terminator (T0 site) in the rDNA and interacts with the TIP5 subunit of NoRC. NoRC also interacts with the SIN3-HDAC complex, HDAC1, HDAC2, DNMT1, and DNMT3B. DNMT3B interacts with a triple helix formed by pRNA and the rDNA. HDAC1 and DNMT1 have been shown to be required for proper DNA methylation of silenced rRNA gene copies (Espada et al. 2007).

Literature references

Sattler, M., Anosova, I., Melnik, S., Grummt, I., Kateb, F., Tripsianes, K. (2015). A novel RNA binding surface of the TAM domain of TIP5/BAZ2A mediates epigenetic regulation of rRNA genes. *Nucleic Acids Res.*, 43, 5208-20. ↗

Längst, G., Fraga, MF., Villar-Garea, A., Esteller, M., Santoro, R., Ballestar, E. et al. (2007). Epigenetic disruption of ribosomal RNA genes and nucleolar architecture in DNA methyltransferase 1 (Dnmt1) deficient cells. *Nucleic Acids Res.*, 35, 2191-8. ↗

Editions

2009-06-19	Authored, Edited	May, B.
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