Cohesin binding to decondensed chromatin is facilitated by NIPBL:MAU2

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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. ↗

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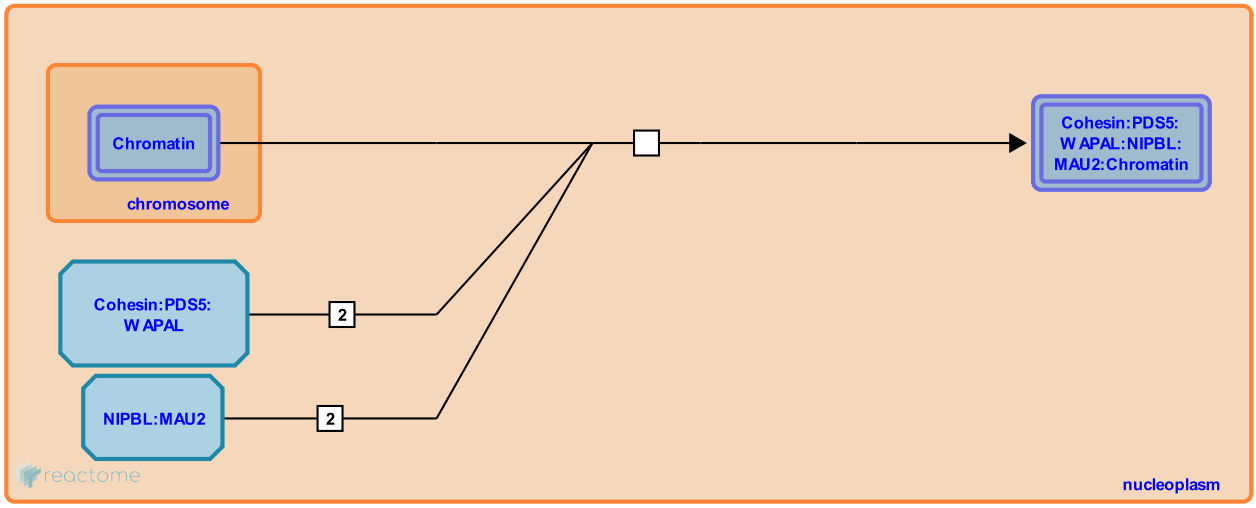
Stable identifier: R-HSA-2470935

Type: transition

Compartments: chromosome, nucleoplasm



Cohesin, in complex with WAPAL and PDS5 (PDS5A or PDS5B) binds decondensed chromatin in telophase (Kueng et al. 2006). This binding is facilitated by the NIPBL:MAU2 complex, also known as the 'cohesin loading complex'. NIPBL:MAU2 complex is associated with chromatin from telophase until prophase (Watrin et al. 2006) but seems to form a transient rather than stable complex with cohesin.

Literature references

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Editions

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