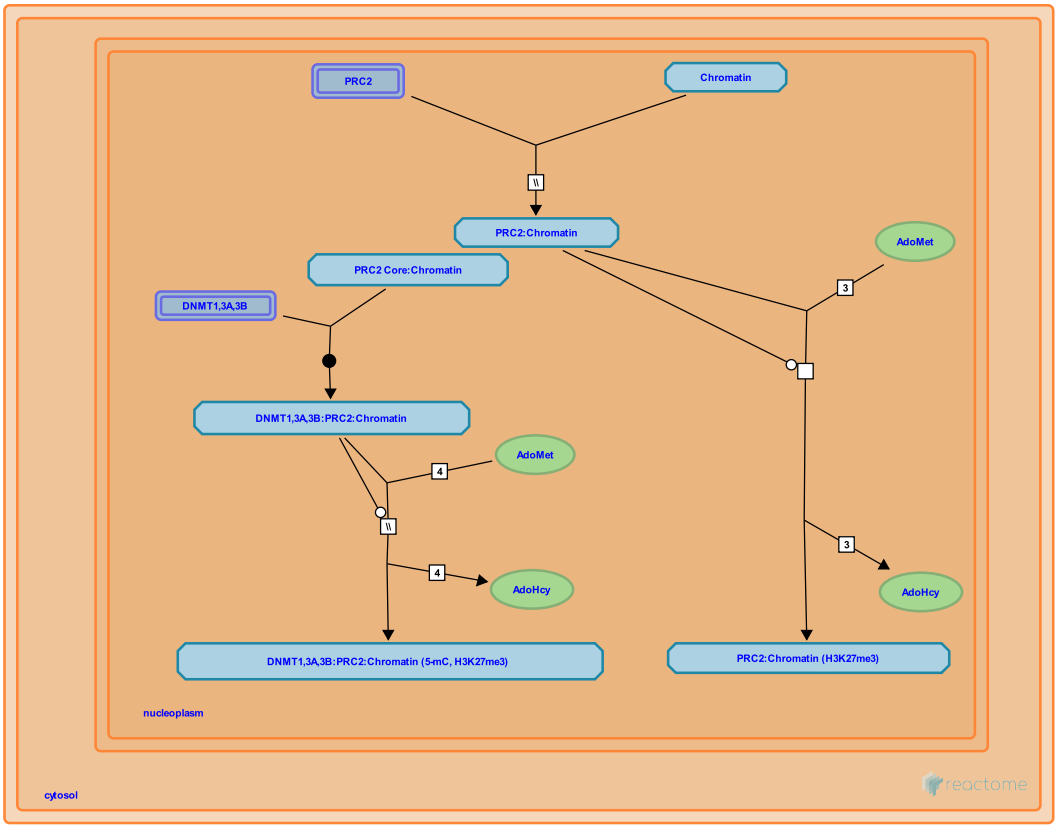
PRC2 methylates histones and DNA



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

05/05/2024

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

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. ↗

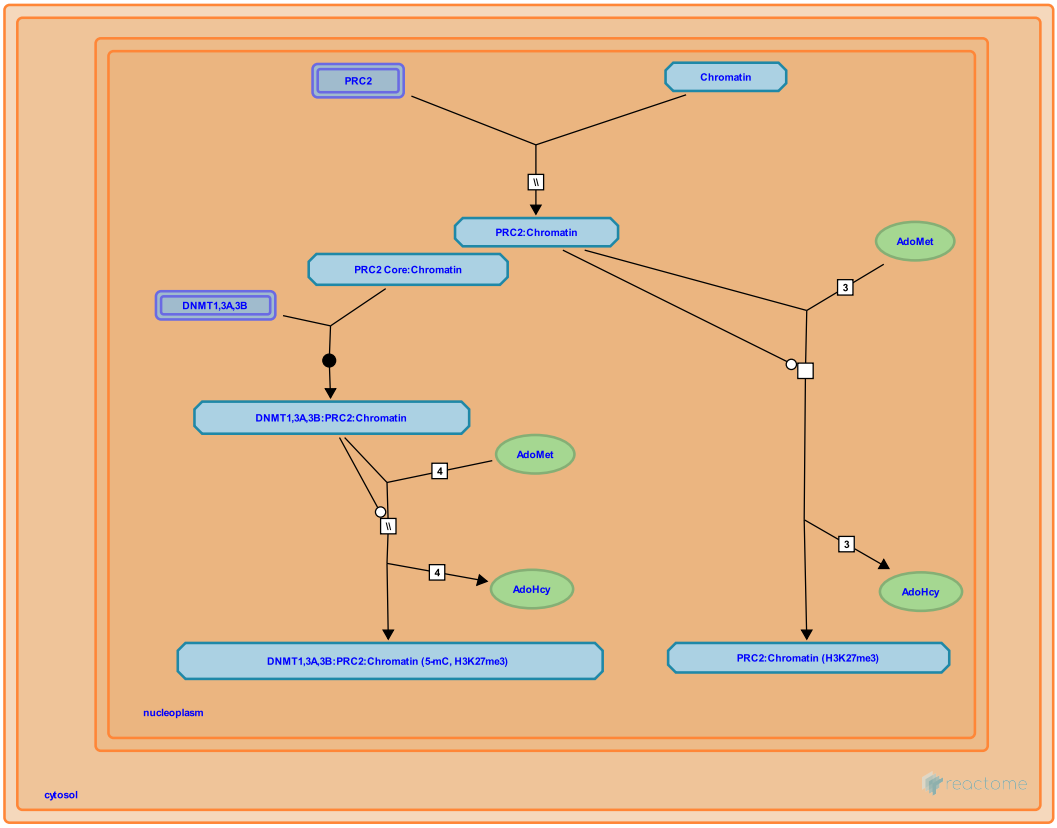
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

PRC2 methylates histones and DNA ↗

Stable identifier: R-CFA-212300

Compartments: nucleoplasm

Inferred from: PRC2 methylates histones and DNA (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Polycomb Repressive Complex 2 (PRC2) Is recruited to chromatin ↗

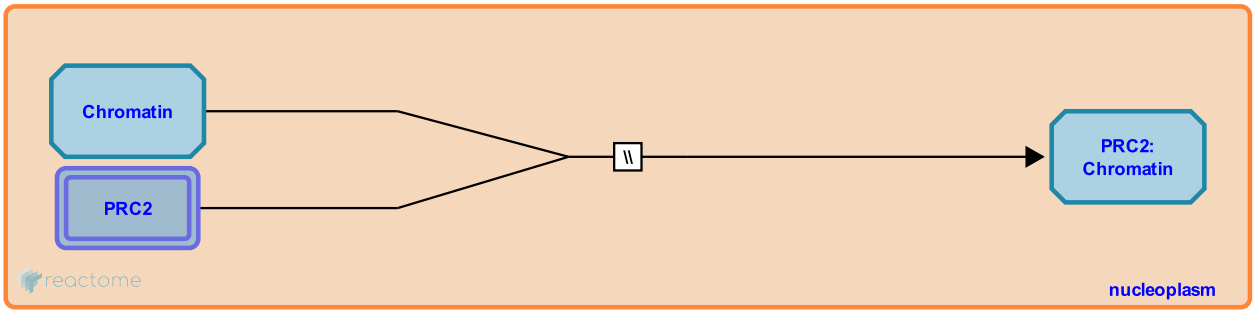
Location: PRC2 methylates histones and DNA

Stable identifier: R-CFA-212252

Type: omitted

Compartments: nucleoplasm

Inferred from: Polycomb Repressive Complex 2 (PRC2) Is recruited to chromatin (Homo sapiens)



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Followed by: PRC2 trimethylates histone H3 at lysine-27, PRC2 recruits DNA methyltransferases

PRC2 trimethylates histone H3 at lysine-27 ↗

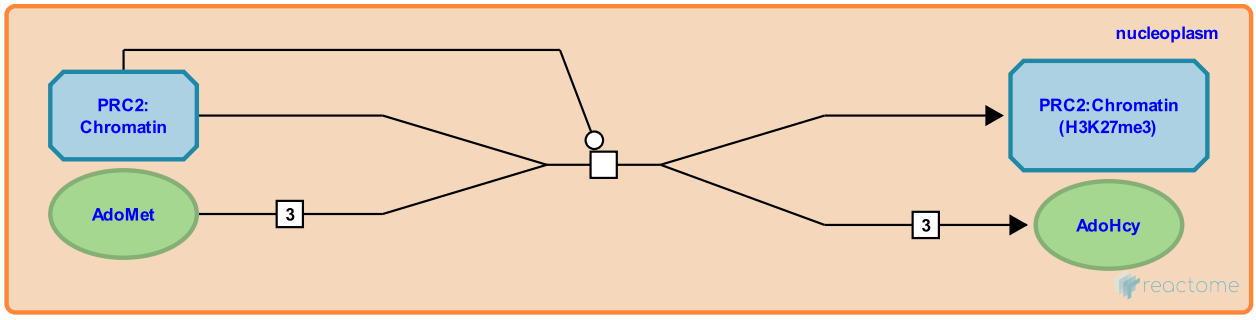
Location: PRC2 methylates histones and DNA

Stable identifier: R-CFA-212263

Type: transition

Compartments: nucleoplasm

Inferred from: PRC2 trimethylates histone H3 at lysine-27 (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Polycomb Repressive Complex 2 (PRC2) Is recruited to chromatin

PRC2 recruits DNA methyltransferases ↗

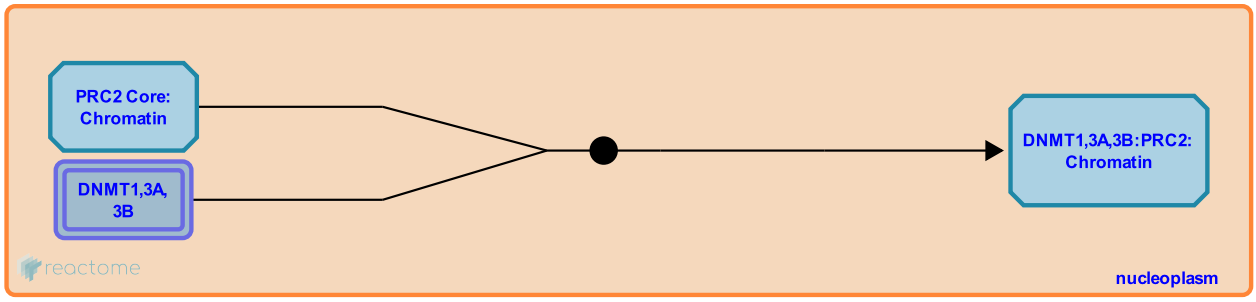
Location: PRC2 methylates histones and DNA

Stable identifier: R-CFA-212222

Type: binding

Compartments: nucleoplasm

Inferred from: PRC2 recruits DNA methyltransferases (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Polycomb Repressive Complex 2 (PRC2) Is recruited to chromatin

Followed by: DNMT1,3A,3B:PRC2 methylates cytosine and histone H3

DNMT1,3A,3B:PRC2 methylates cytosine and histone H3 ↗

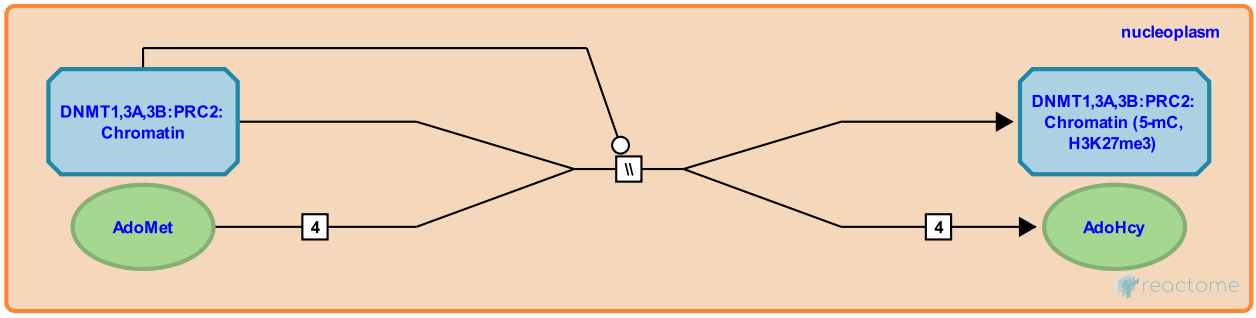
Location: PRC2 methylates histones and DNA

Stable identifier: R-CFA-212269

Type: omitted

Compartments: nucleoplasm

Inferred from: DNMT1,3A,3B:PRC2 methylates cytosine and histone H3 (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: PRC2 recruits DNA methyltransferases

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