RUNX1 binds PRC1 complexes

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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

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

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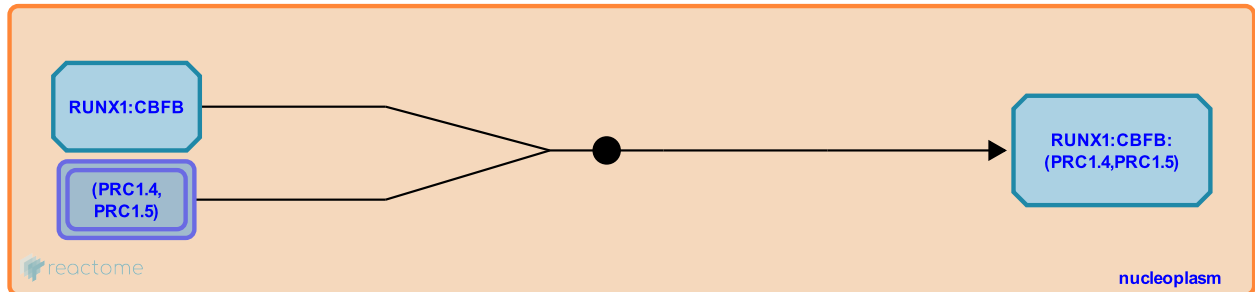
Reactome database release: 74

This document contains 1 reaction (see Table of Contents)

RUNX1 binds PRC1 complexes ↗

Stable identifier: R-HSA-8937989

Type: binding

Compartments: nucleoplasm

The RUNX1:CBFB complex associates with the polycomb repressor complex 1 (PRC1), including components of the PRC1.4 complex (the defining subunit being BMI1) and the PRC1.5 complex (the defining subunit being PCGF5). It is possible that the RUNX1:CBFB can also associate with other PRC1 complexes. PRC1 complexes are recruited to many RUNX1:CBFB target promoters and they either positively or negatively affect the transcription of RUNX1 target genes. The definitive composition of RUNX1:CBFB:PRC1 complexes at different RUNX1 target promoters has not been determined (Yu et al. 2011).

Literature references

Yu, M., Mazor, T., Huang, H., Huang, HT., Kathrein, KL., Woo, AJ. et al. (2012). Direct recruitment of polycomb repressive complex 1 to chromatin by core binding transcription factors. *Mol. Cell, 45*, 330-43. ↗

Editions

2016-09-14	Authored	Orlic-Milacic, M.
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