

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

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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: 88

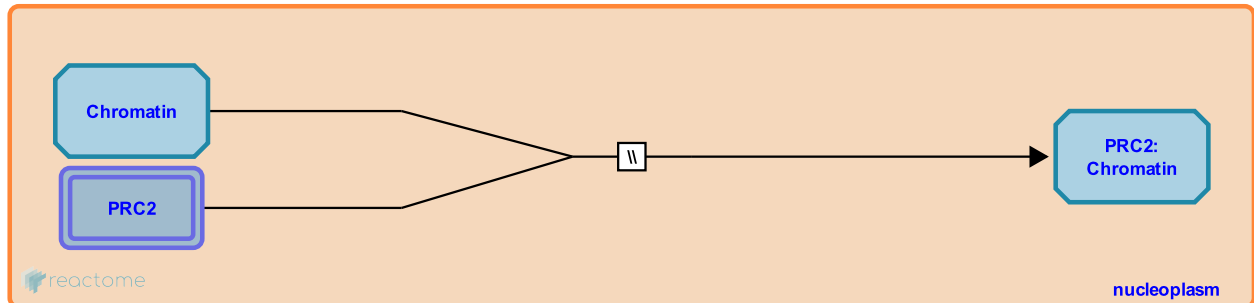
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## Polycomb Repressive Complex 2 (PRC2) Is recruited to chromatin [↗](#)

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The core of the Polycomb Repressor Complex 2 (PRC2) contains EZH2, EED, SUV12, RpAp46, and RpAp48 (Kuzzmichev et al. 2002, Cao et al. 2002). PRC2 complexes at different sites in the genome contain the core subunits plus different accessory subunits. In *Drosophila* PRC2 is recruited to chromatin by specific DNA sequences. In vertebrates PRC2 appears to be recruited to chromatin through several mechanisms: some (about 20%) of noncoding RNAs tethered to the locus of origin recruit PRC2 via the RNA-binding activity of EZH2 (Zhao et al. 2008, Khalil et al. 2009), GC-rich sequence elements in DNA (Mendenhall et al. 2010) and poly(ADP-ribose) polymerase at sites of DNA damage (Chou et al. 2010) can also recruit polycomb components, The DNA-binding proteins JARID2, AEBP2, and YY1 recruit PRC2 (Pasini et al. 2010, Li et al. 2010, reviewed in Kim and Kim 2012). The EED subunit of PRC2 can bind existing trimethylated lysine-27 on histone H3 of PRC2 which may provide a mechanism for propagation of trimethylated lysine-27 during DNA replication (Xu et al. 2010).

### Literature references

- Nottke, AC., Elledge, SJ., Chou, DM., Adamson, B., Gygi, SP., Dephoure, NE. et al. (2010). A chromatin localization screen reveals poly (ADP ribose)-regulated recruitment of the repressive polycomb and NuRD complexes to sites of DNA damage. *Proc. Natl. Acad. Sci. U.S.A.*, 107, 18475-80. [↗](#)
- Zhou, VW., Ku, M., Chi, AS., Bernstein, BE., Mendenhall, EM., Koche, RP. et al. (2010). GC-rich sequence elements recruit PRC2 in mammalian ES cells. *PLoS Genet.*, 6, e1001244. [↗](#)
- Khalil, AM., van Oudenaarden, A., Guttman, M., Regev, A., Presser, A., Thomas, K. et al. (2009). Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. *Proc. Natl. Acad. Sci. U.S.A.*, 106, 11667-72. [↗](#)
- Chambon, P., Reinberg, D., Ku, M., Bernstein, BE., Margueron, R., Li, G. (2010). Jarid2 and PRC2, partners in regulating gene expression. *Genes Dev.*, 24, 368-80. [↗](#)
- Zhao, J., Sun, BK., Erwin, JA., Song, JJ., Lee, JT. (2008). Polycomb proteins targeted by a short repeat RNA to the mouse X chromosome. *Science*, 322, 750-6. [↗](#)

### Editions

2008-02-09	Authored	Gopinathrao, G., May, B.
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