reactome

HOXB2 chromatin is activated

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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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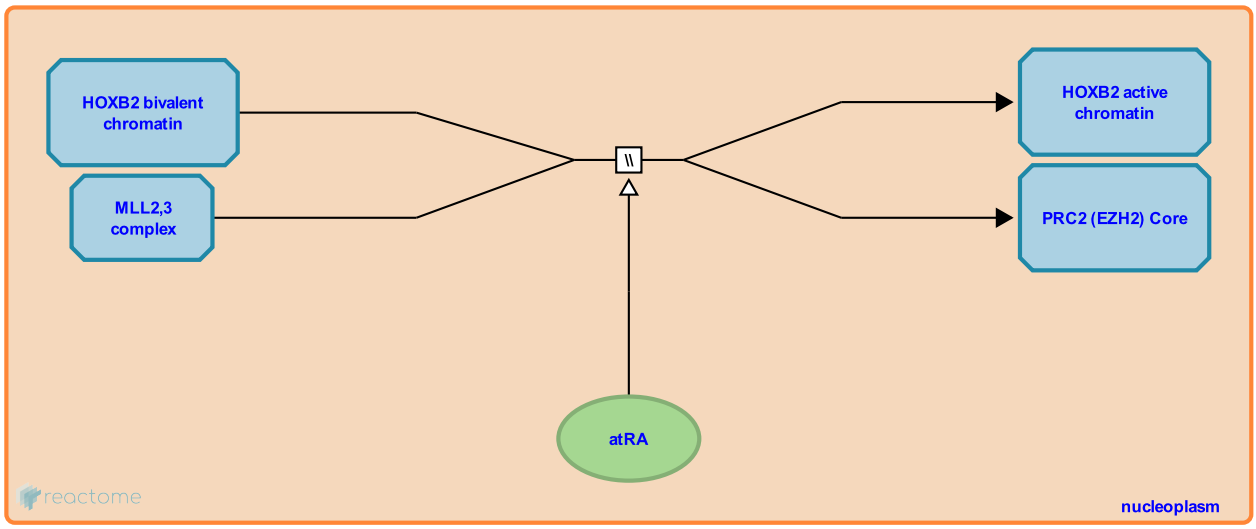
HOXB2 chromatin is activated ↗

Stable identifier: R-HSA-6810159

Type: omitted

Compartments: nucleoplasm

Inferred from: Hoxb2 chromatin is activated (Mus musculus)



During activation of HOXB1 by retinoic acid in human embryonal carcinoma cells, methylation at lysine-27 of histone H3 (H3K27me3) is lost and methylation at lysine-4 (H3K4me3) is gained (Lan et al. 2007, Lee et al. 2007). The histone demethylase KDM6A (UTX) binds HOXB2 chromatin and may demethylate H3K27me3 (Lee et al. 2007). Other factors may also participate in demethylation. Loss of H3K27me3 is associated with loss of polycomb repressive complex 2 (PRC2) (Lan et al. 2007, Lee et al. 2007). KDM6A forms complexes with the histone methyltransferases KMT2C,D (MLL2,3) which may participate in methylating H3K4 (Lee et al. 2007). The activation of HOXB1 chromatin may be produced by euchromatin spreading from distant 3' retinoic acid response elements.

Literature references

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Editions

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