HP1 alpha binds Histone H3K9(me)3

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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. ↗

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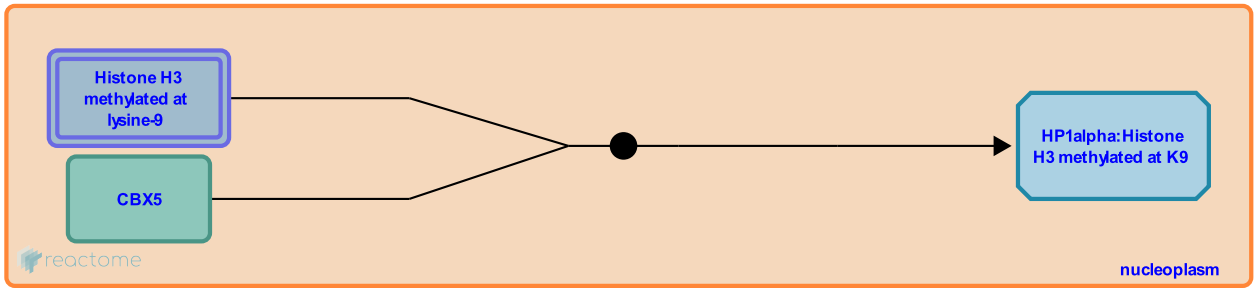
Stable identifier: R-HSA-994106

Type: binding

Compartments: nucleoplasm



Chromobox (CBX) genes encode members of the Heterochromatin Protein (HP) family. HP1 was discovered in Drosophila as a dominant suppressor of position-effect variegation and a major component of heterochromatin. The HP1 family is evolutionarily conserved, with members in fungi, plants and animals. Most animal species have several HP1 isoforms; humans have HP alpha, beta and gamme encoded by the genes CBX5, CBX1 and CBX3 respectively.
The HP1 amino-terminal chromodomain binds methylated lysine-9 of histone H3, causing transcriptional repression (Lachner et al. 2001). A crystal structure of human HP1 alpha in complex with H3K9(me)3 peptide is available (Amaya et al. 2008). The highly-conserved carboxy-terminal chromoshadow domain enables dimerization and also serves as a docking site for proteins involved in a wide variety of nuclear functions, from transcription to nuclear architecture.

Literature references

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Editions

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