BRD7 promotes EP300-mediated acetylation of TP53

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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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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. ↗

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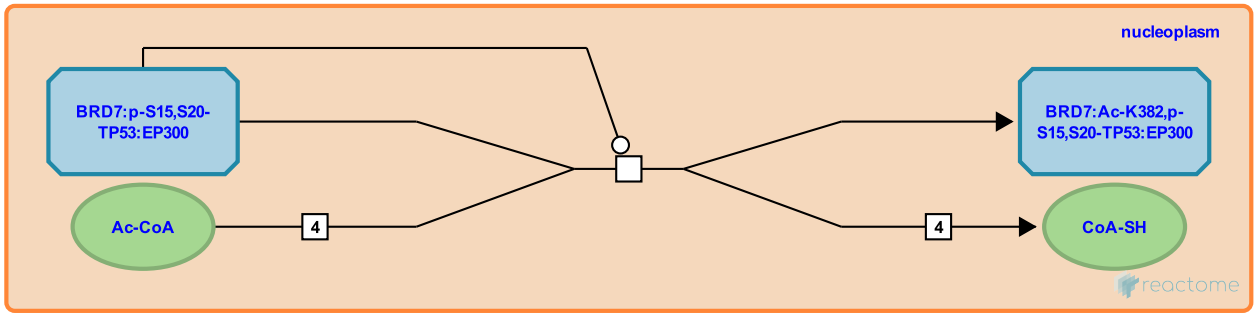
Stable identifier: R-HSA-5628871

Type: transition

Compartments: nucleoplasm



BRD7 promotes EP300 (p300)-mediated acetylation of TP53 on lysine residue K382, which enhances binding of TP53 to its target promoters. Also, BRD7 induces EP300-mediated acetylation of histone 3 on lysine residue K10 (also labeled in literature as K9), creating the H3K9 active chromatin mark at CDKN1A and MDM2 promoters (Drost et al. 2010), and possibly other TP53 promoters co-regulated by BRD7, such as SERPINE1, TIGAR, TNFRSF10C and NDRG1.

Literature references

Drost, J., Mantovani, F., Tocco, F., Elkon, R., Comel, A., Holstege, H. et al. (2010). BRD7 is a candidate tumour suppressor gene required for p53 function. *Nat. Cell Biol., 12*, 380-9. ↗

Editions

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