

HDAC3 containing complexes deacetylate histone

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16/11/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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. [↗](#)

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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Reactome database release: 90

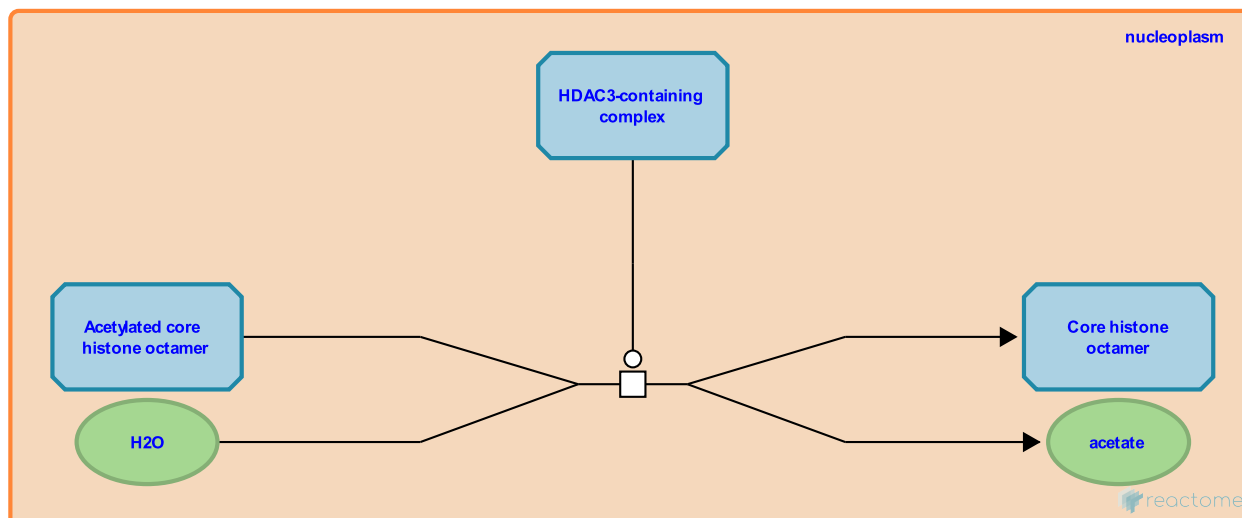
This document contains 1 reaction ([see Table of Contents](#))

HDAC3 containing complexes deacetylate histone ↗

Stable identifier: R-HSA-3777129

Type: transition

Compartments: nucleoplasm



HDAC3 mediates the gene silencing activity of Retinoic acid and thyroid hormone receptor (SMRT) complex or the homologous nuclear receptor corepressor (NCoR). These coregulators are involved in a wide range of developmental and homeostatic processes, including metabolism, inflammation, and circadian rhythms (Mottis et al. 2013). HDAC3 interacts with a conserved SANT-like domain known as the deacetylase activating domain (DAD) within NCOR2 (SMRT) or NCOR1 (Li et al. 2000, Wen et al. 2000, Zhang et al. 2002, Yoon et al. 2003, Oberoi et al. 2011). This interaction both recruits and activates HDAC3 (Wen et al. 2000, Guenther et al. 2001, Zhang et al. 2002). Recruitment of HDAC3 to the DAD is essential for repression by the nuclear thyroid hormone receptor and for the maintenance of normal circadian physiology (You et al. 2010, Yin et al. 2007). A second SANT-like domain has been reported to interact directly with histone tails and termed the histone interaction domain (HID) (Hartman et al. 2005, Yu et al. 2003). NCORs are largely unstructured platform proteins that act as a scaffold upon which the enzymatic machinery of the repression complex is built (Watson et al. 2012). They can recruit other deacetylases such as HDAC4 (Fischle et al. 2002), HDAC5, HDAC7 (Kao et al. 2000), Sirt1 (Picard et al. 2004), and via mSin3, HDAC1 (Heinzel et al. 1997, Nagy et al. 1997). The importance of these deacetylase enzymes is not yet established. It has been demonstrated HDAC3 was shown to be responsible for deacetylase activities associated with HDAC4 and HDAC7 (Fischle et al. 2002). Corepressor complexes are heterogeneous, context-specific and transient in nature, but in addition to HDAC3, some additional partners are regularly found in stoichiometric association with NCOR1/NCOR2 and are essential for repressive function. These partners include the G protein pathway suppressor (GPS2) and transducing beta-like 1 (TBL1) and its homologue, TBL-related 1 (TBLR1), which together form the core repression complex (Oberoi et al. 2011). Ins(1,4,5,6)P4 is a further component of the complex (Watson et al. 2012).

Literature references

Lazar, MA., Guenther, MG., Barak, O. (2001). The SMRT and N-CoR corepressors are activating cofactors for histone deacetylase 3. *Mol. Cell. Biol.*, 21, 6091-101. ↗

Editions

2013-03-12	Authored, Edited	Jupe, S.
2014-05-08	Reviewed	Yang, XJ.