

# TLE recruits HDAC1 to WNT promoters

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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

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

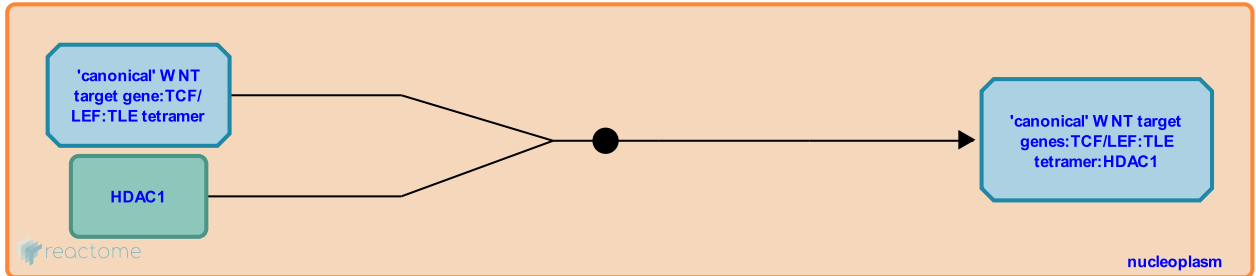
**TLE recruits HDAC1 to WNT promoters** ↗

**Stable identifier:** R-HSA-4641231

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [xTLE4 binds HDAC1 \(Homo sapiens\)](#)



Groucho/TLE mediates repression of WNT target genes in part by recruiting a histone deacetylase to the promoter. The weakly conserved central GP domain of Groucho/TLE has been shown to interact with the histone deacetylase RPD3/HDAC1 (Brantjes et al, 2001; Chen et al, 1999). Knockdown of rpd3 in *Drosophila* cells, or treatment of human or *Drosophila* cells with the histone deacetylase inhibitor Trichostatin A significantly decreases repression of a Groucho/TLE dependent reporter gene, and Groucho and RPD3 have been shown to co-localize to chromatin of target genes by ChIP leading to deacetylation of H3K9, H3K14, K4K5, H4K8 and H4K12 (Chen et al, 1999; Choi et al 1999; Winkler et al, 2010).

**Literature references**

Kim, Y., Choi, CY., Kwon, HJ., Kim, YH. (1999). The homeodomain protein NK-3 recruits Groucho and a histone deacetylase complex to repress transcription. *J. Biol. Chem.*, 274, 33194-7. ↗

Ponce, A., Courey, AJ., Winkler, CJ. (2010). Groucho-mediated repression may result from a histone deacetylase-dependent increase in nucleosome density. *PLoS ONE*, 5, e10166. ↗

van De Wetering, M., Clevers, HC., Brantjes, H., Roose, J. (2001). All Tcf HMG box transcription factors interact with Groucho-related co-repressors. *Nucleic Acids Res.*, 29, 1410-9. ↗

Chen, G., Mische, S., Fernandez, J., Courey, AJ. (1999). A functional interaction between the histone deacetylase Rpd3 and the corepressor groucho in *Drosophila* development. *Genes Dev.*, 13, 2218-30. ↗

**Editions**

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