

# SALL4 recruits NuRD to PTEN gene

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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

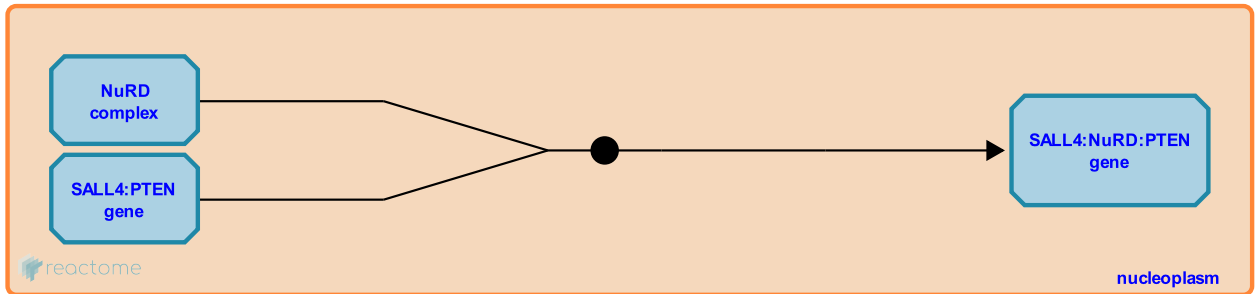
This document contains 1 reaction ([see Table of Contents](#))

SALL4 recruits NuRD to PTEN gene ↗

Stable identifier: R-HSA-8943780

Type: binding

Compartments: nucleoplasm



SALL4 recruits the transcriptional repressor complex NuRD, containing histone deacetylases HDAC1 and HDAC2, to the PTEN gene promoter (Lu et al 2009, Gao et al. 2013). SALL4 may also recruit DNA methyltransferases (DNMTs) to the PTEN promoter (Yang et al. 2012).

Literature references

Tatetsu, H., Dimitrov, T., Bradner, JE., Jeong, HW., Gao, C., Yong, KJ. et al. (2013). Targeting transcription factor SALL4 in acute myeloid leukemia by interrupting its interaction with an epigenetic complex. *Blood*, 121, 1413-21. ↗

Jeong, HW., Silberstein, LE., Carroll, J., Chai, L., Yang, Y., Kong, N. et al. (2009). Stem cell factor SALL4 represses the transcriptions of PTEN and SALL1 through an epigenetic repressor complex. *PLoS One*, 4, e5577. ↗

Editions

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