

ESRRA:PPARG1CB binds the RUNX2 gene promoter

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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

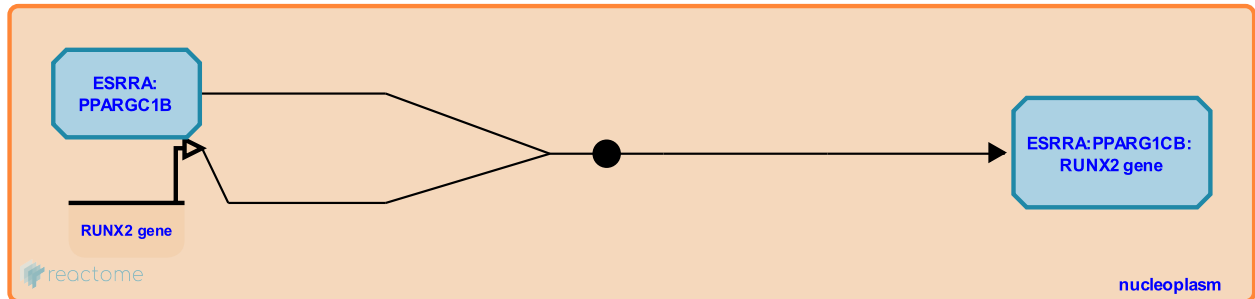
This document contains 1 reaction ([see Table of Contents](#))

ESRRA:PPARG1CB binds the RUNX2 gene promoter [↗](#)

Stable identifier: R-HSA-8939938

Type: binding

Compartments: nucleoplasm



Estrogen-related receptor alpha (ESRRA), in complex with its co-activator PPARG1CB (PGC1B), binds estrogen response elements (EREs) and/or estrogen-related response elements (ERREs) in the proximal P2 promoter of the RUNX2 gene (Kammerer et al. 2013).

Literature references

Gutzwiller, S., Kammerer, M., Fournier, B., Stauffer, D., Delhon, I., Seltenmeyer, Y. (2013). Estrogen Receptor α (ER α) and Estrogen Related Receptor α (ERR α) are both transcriptional regulators of the Runx2-I isoform. *Mol. Cell. Endocrinol.*, 369, 150-60. [↗](#)

Editions

2016-09-21	Authored	Orlic-Milacic, M.
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