Activated ESR1 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

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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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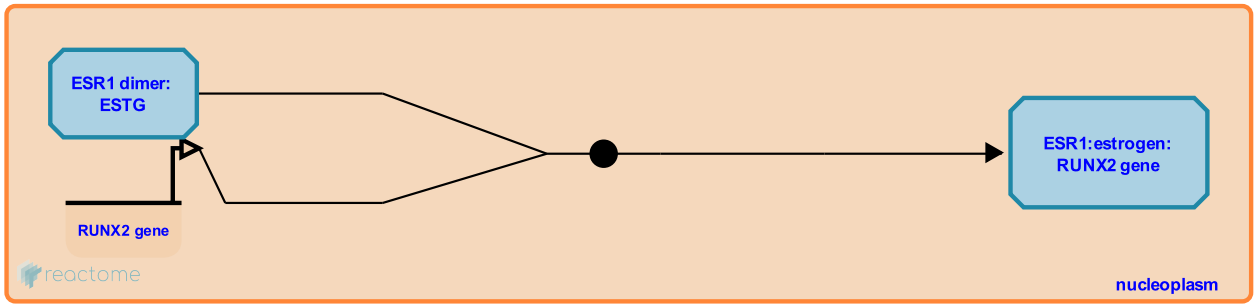
Stable identifier: R-HSA-8939904

Type: binding

Compartments: nucleoplasm



Activated estrogen receptor alpha (ESR1) binds estrogen response elements 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 (ERα) and Estrogen Related Receptor α (ERRα) are both transcriptional regulators of the Runx2-I isoform. *Mol. Cell. Endocrinol., 369*, 150-60. ↗

Editions

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