ESR1 binds to TGFA 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. ↗

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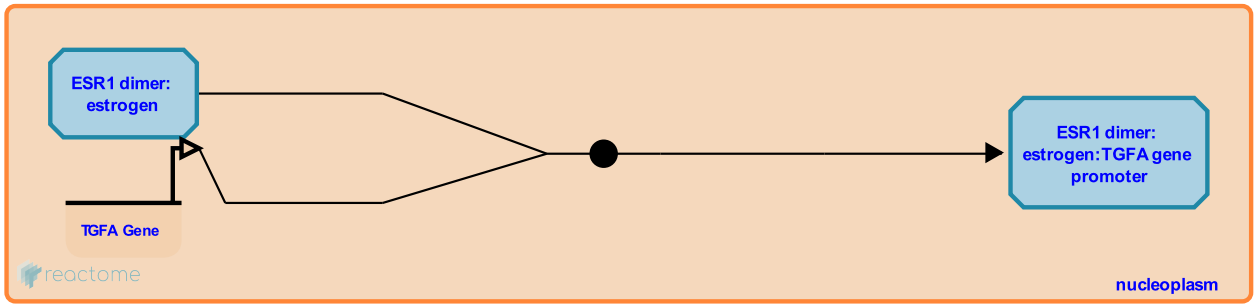
Stable identifier: R-HSA-9008267

Type: binding

Compartments: nucleoplasm



Hormone-activated estrogen receptor (ER) binds with high affinity to specific DNA sequences, estrogen response elements (EREs), found in the regulatory regions of estrogen-responsive genes (Klinge CM 2001). The majority of known estrogen responsive genes contain imperfect EREs that differ from the consensus ERE sequence, 5′-GGTCAnnnTGACC-3′, by one or more base pairs. The individual ERE sequences were found to differentially induce changes in ER conformation that may influence the recruitment of specific coactivator proteins (Wood JR et al. 2001). The promoter of the TGFA gene has two imperfect EREs between -252 to -200 and an additional upstream sequence between -623 and -549. These elements confer estrogen-responsiveness to the promoter and are bound by ESR1 as assessed by electrophoretic mobility shift assay (Vyhidal et al, 2000).

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Editions

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