

# ESR dimerizes

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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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Reactome database release: 88

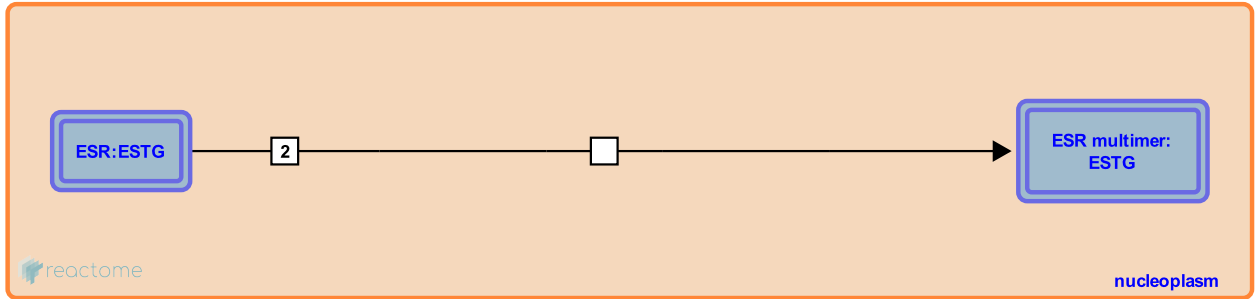
This document contains 1 reaction ([see Table of Contents](#))

**ESR dimerizes** ↗

**Stable identifier:** R-HSA-8939201

**Type:** transition

**Compartments:** nucleoplasm



Upon ligand binding, estrogen receptors form homo- or heterodimers mediated by dimerization domains in the DNA-binding and ligand-binding regions (White et al, 1991; Schwabe et al, 1993; Kuntz et al, 1997; Kumar and Chambon, 1998; Powell et al, 2010). Estrogen receptor dimers regulate transcription of estrogen-responsive genes either by direct binding to estrogen response elements (characterized by a palindromic consensus sequence AGGTCA separated by a 3bp spacer) or by interacting with other DNA binding transcriptional regulators (reviewed in Smith and Toft, 2008; Bai and Gust, 2009; Ikeda et al 2015; Liu and Cheung, 2014). Binding of estrogen receptors to the DNA promotes the assembly of higher order transcriptional complexes containing methyltransferases, histone acetyltransferases and other transcriptional activators, which promote transcription by establishing active chromatin marks and by recruiting general transcription factors and RNA polymerase II. ESR1- and estrogen-dependent recruitment of up to hundreds of coregulators has been demonstrated by varied co-immunoprecipitation and proteomic approaches (Kittler et al, 2013; Mohammed et al, 2013; Foulds et al, 2013; Mohammed et al, 2015; Liu et al, 2014; reviewed in Magnani and Lupien, 2014; Arnal, 2017).

**Literature references**

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**Editions**

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