TCF7L2/TCF7L1 bind CTBP1 to repress WNT target genes

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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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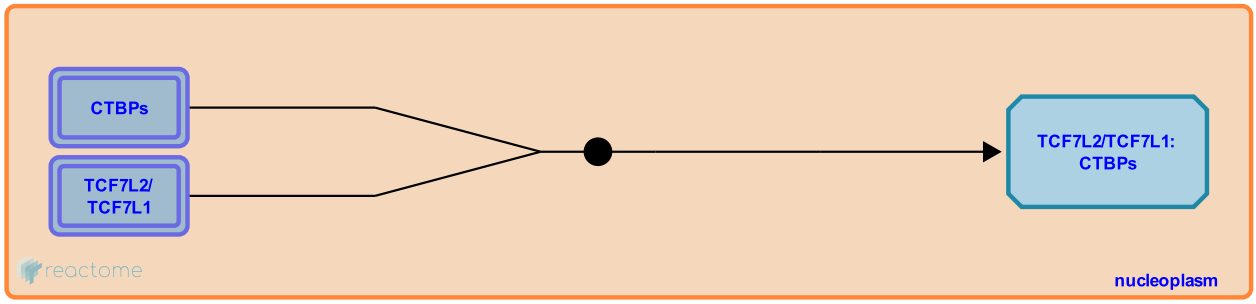
Stable identifier: R-HSA-5334050

Type: binding

Compartments: nucleoplasm



In addition to repressing WNT-dependent targets through Groucho/TLE proteins, some TCF/LEF transcription factors may also work by recruiting the CTBP1 and CTBP2 repressors (Duval et al, 2000). CTBP-binding regions are present in the 'E-form' splice variants of TCF7L2 and in TCF7L1 and in vitro interactions have been demonstrated in Xenopus and mammals, although the in vivo relevance of these interactions is unclear (Brannon et al, 1999; Valenta et al, 2003; Cuilliere-Dartigues et al, 2006; Tang et al, 2008; Hamada and Bienz, 2004). Abrogation of the interaction interface results in a loss of TCF-CTBP colocalization and increased expression of a TCF-dependent reporter gene (Cuilliere-Dartigues et al, 2006; Tang et al, 2008).

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Editions

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