

TCF7L1/TCF7L2/LEF1:CTNNB1 promote transcription of the MYC gene

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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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Reactome database release: 77

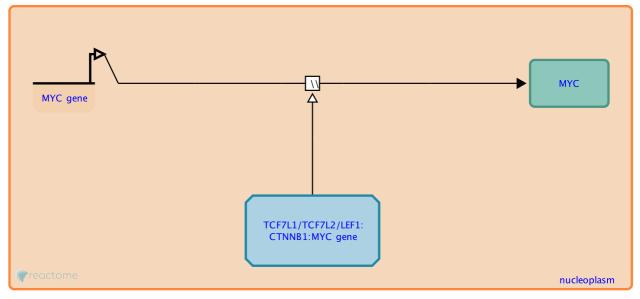
This document contains 1 reaction (see Table of Contents)

TCF7L1/TCF7L2/LEF1:CTNNB1 promote transcription of the MYC gene 7

Stable identifier: R-HSA-4411357

Type: omitted

Compartments: nucleoplasm



TCF7L1 (also known as TCF3), TCF7L3 (also known as LEF1) and TCF7L2 (also known as TCF4) have been demonstrated to bind to the MYC gene in vivo and in vitro and to mediate beta-catenin dependent transcription (Park et al, 2009; He et al, 1998; Sierra et al, 2006). Aberrant beta-catenin dependent activation of the MYC gene contributes to oncogenic signaling and cellular proliferation in colorectal and other cancers (see for instance Sansom et al, 2007; Moumen et al, 2013; reviewed in Wilkins and Sansom, 2008; Cairo et al, 2012).

Binding of RUNX3 to the CTNNB1:TCF7L2 and possibly to the CTNNB1:LEF1 and TCF7L1 complexes, prevents binding of CTNNB1 complexes to the MYC promoter, thus negatively regulating MYC transcription (Ito et al. 2008).

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