Phosphorylation of MEF2 proteins by p38

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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


Reactome database release: 78

This document contains 1 reaction (see Table of Contents)

[https://reactome.org](https://reactome.org)
The family of transcription factors myocyte enhancer factor-2 (MEF2) regulate myogenesis through combinatorial interactions with other transcription factors to the MEF2 site found in the promoter regions of numerous muscle specific genes. There are four members of the MEF2 family, MEF2A to D.

p38 MAPK plays a role in the regulation of the MEF2 family members and this is mediated by the phosphorylation of two or three (Thr312 and 319 in MEF2A and Thr 293, 300 and ser387 in MEF2C) amino acids in the C-terminal activation domain of MEF2 factors. MEF2A and MEF2C are preferred substrates for p38 compared with MEF2B and MEF2D. The phosphorylation of MEF2 members results in their increased transcriptional activity.

**Literature references**


**Editions**

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