MAP2K mutants constitutively phosphorylate MAPKs

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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: 73

This document contains 1 reaction (see Table of Contents)
MAP2K mutants constitutively phosphorylate MAPKs

Stable identifier: R-HSA-9652165

Type: transition

Compartments: cytosol

Diseases: cardiofaciocutaneous syndrome, cancer

Although they occur at much lower frequently than mutations in upstream components of the RAS signaling pathway, activating mutations in MAP2K proteins, encoding MEK1 and MEK2, have been identified in a number of cancers and germline disorders (Marks et al, 2008; Murugan et al, 2009). These mutations cluster in the N-terminal autoinhibitory domain or in the catalytic domain and lead to constitutively active forms of the proteins that phosphorylate MAPK1 and MAPK2 (ERK2 and ERK1) independent of upstream signaling (Nikolaev et al, 2011; Rodriguez-Viciana and Rauen, 2008; Bortoff et al, 1995; Marks et al, 2008; Estep et al, 2007; Van Allen et al, 2014; Chen et al, 2014; Wagle et al, 2011; Waterfall et al, 2014; Rauen et al, 2010; reviewed in Samatar and Poulrikakos, 2014; Rauen, 2013; Bezniakow et al, 2014).

Literature references


