

High kinase activity BRAF mutants bind MAP2Ks and MAPKs

Rothfels, K., Stephens, RM.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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: 70

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

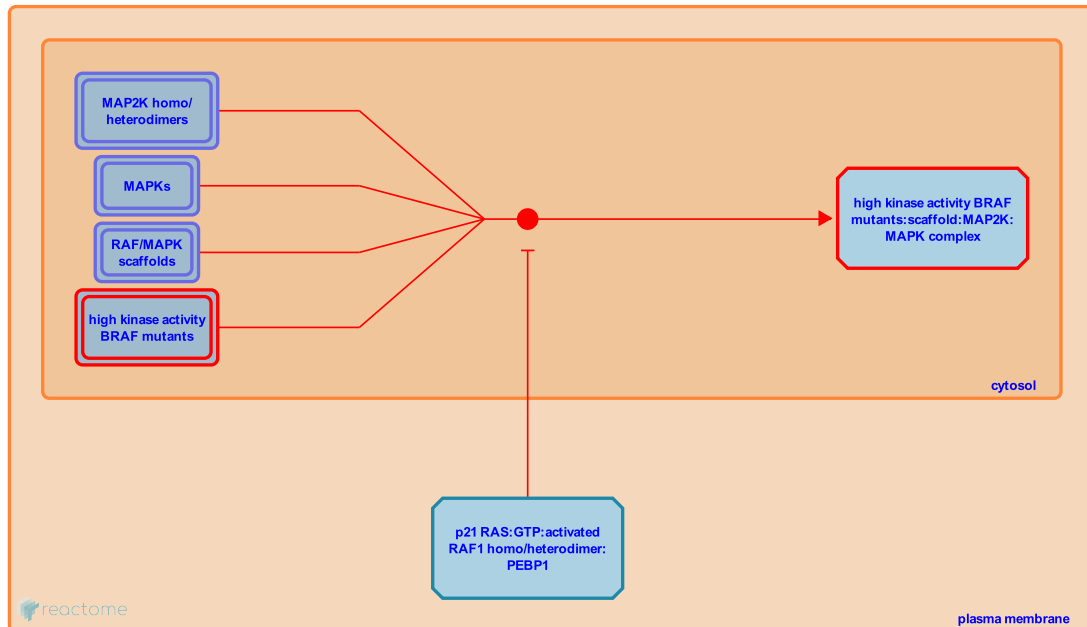
High kinase activity BRAF mutants bind MAP2Ks and MAPKs ↗

Stable identifier: R-HSA-6802912

Type: binding

Compartments: cytosol

Diseases: cardiofaciocutaneous syndrome, cancer



High-kinase activity BRAF mutants such as the prevalent V600E mutant bind MAP2K and MAPK proteins to activate signaling in a constitutive, RAS-independent manner (Wan et al, 2004; Garnett et al, 2005; Ritt et al, 2010; Roring et al, 2012; Freeman et al, 2013; reviewed in Lavoie and Therrien, 2015). These highly active BRAF mutations are thought to disrupt interactions between the DFG motif and the P loop that are required to hold RAF in the inactive, "DFG out" conformation. In this way, BRAF V600E and other highly active BRAF mutations render the protein constitutively active (Wan et al, 2004; reviewed in Lito et al, 2013; Lavoie and Therrien, 2015). Although highly active BRAF mutants can heterodimerize with and signal through RAF1, V600E BRAF is resistant to disruptions in the dimerization interface, has relaxed requirements for RAF1 activation loop phosphorylation, and is able to signal as a monomer (Garnett et al, 2005; Ritt et al, 2010; Roring et al, 2012; Freeman et al, 2013; reviewed in Lavoie and Therrien, 2015; Lito et al, 2013).

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Editions

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