

# Mutant RAS:p-RAF complexes bind MAP2Ks and 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

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Reactome database release: 77

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

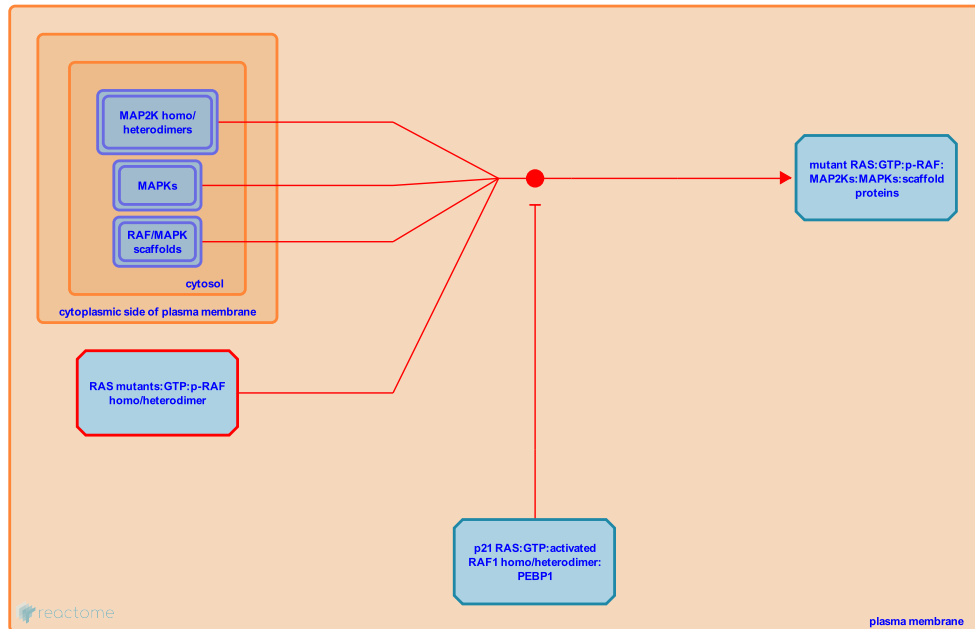
## Mutant RAS:p-RAF complexes bind MAP2Ks and MAPKs ↗

**Stable identifier:** R-HSA-6802925

**Type:** binding

**Compartments:** plasma membrane

**Diseases:** cancer



RAF dimerization and phosphorylation downstream of oncogenic RAS and RAF mutations is associated with increased MAP2K and MAPK phosphorylation (Wan et al, 2004; Garnett et al, 2005; reviewed in Holderfield et al, 2014). Although the interactions between oncogenic RAS or RAFs and downstream effectors hasn't been studied in detail, these disease pathways are presumed to recruit MAP2Ks and MAPKs in a scaffold-dependent manner similar to WT (reviewed in Matallanas et al, 2011).

### Literature references

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### Editions

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