# Activated MAP2Ks phosphorylate MAPKs downstream of oncogenic RAS

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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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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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Reactome database release: 88
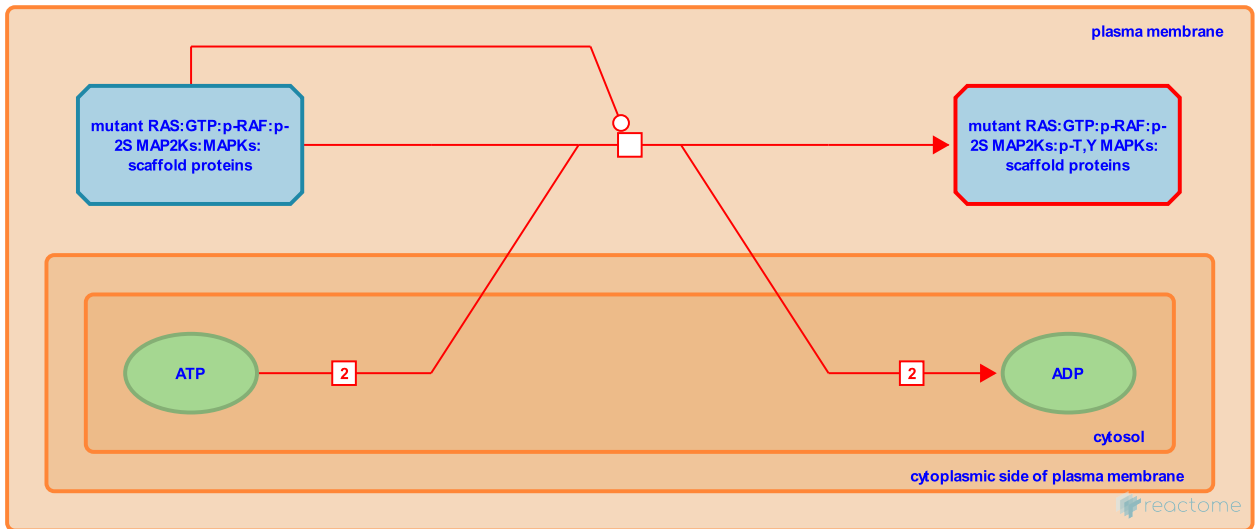
This document contains 1 reaction (see Table of Contents)

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**Stable identifier:** R-HSA-6802922

**Type:** transition

**Compartments:** plasma membrane

**Diseases:** cancer



MAPK proteins are phosphorylated downstream of oncogenic RAS mutants; somewhat surprisingly, however, steady state levels of phospho-MAP2K and phospho-MAPKs are not always elevated in cancer cells (reviewed in Ramos, 2008; Neuzillet et al, 2014; Stephen et al, 2014).

## Literature references

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McCormick, F., Stephen, AG., Bagni, RK., Esposito, D. (2014). Dragging ras back in the ring. *Cancer Cell, 25,* 272-81. ↗

## Editions

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| 2015-05-18 | Authored, Edited | Rothfels, K. |
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