RAS mutants bind inactive RAF

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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: 83

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https://reactome.org
Downstream of oncogenic RAS, a number of pathways are activated in a cancer- and tissue-specific manner. Common effectors include the PI3K/AKT pathway, the RAL GDS pathway and the canonical RAF/MEK/ERK pathway (reviewed in Prior et al, 2012; Pylayeva-Gupta et al, 2011; Stephen et al, 2014). Activation of the RAF/MEK/ERK pathway depends on the recruitment and activation of RAF downstream of oncogenic RAS, although the extent of pathway activation and the importance of the different RAF genes varies among cancer types. For instance, RAF1 (also known as CRAF) is necessary for onset of RAS-driven non-small cell lung cancer and melanoma, but is dispensable in RAS-driven pancreatic ductal adenocarcinoma (Dumaz et al, 2006; Heidorn et al, 2010; Blasco et al, 2011; Karreth et al, 2011; Eser et al, 2013). Although BRAF activity is not required in RAS-driven melanoma as assessed by siRNA knockdown, in the presence of BRAF inhibitors, BRAF paradoxically contributes to pathway activation through dimerization-dependent activation of RAF1 (Dumaz et al, 2006; Heidorn et al, 2010; Poulikakos et al, 2010; Hatzivassiliou et al, 2010; reviewed in Dumaz, 2011; Lito et al, 2013).

**Literature references**


