reactome

Activated FGFR1 mutants phosphorylate FRS2

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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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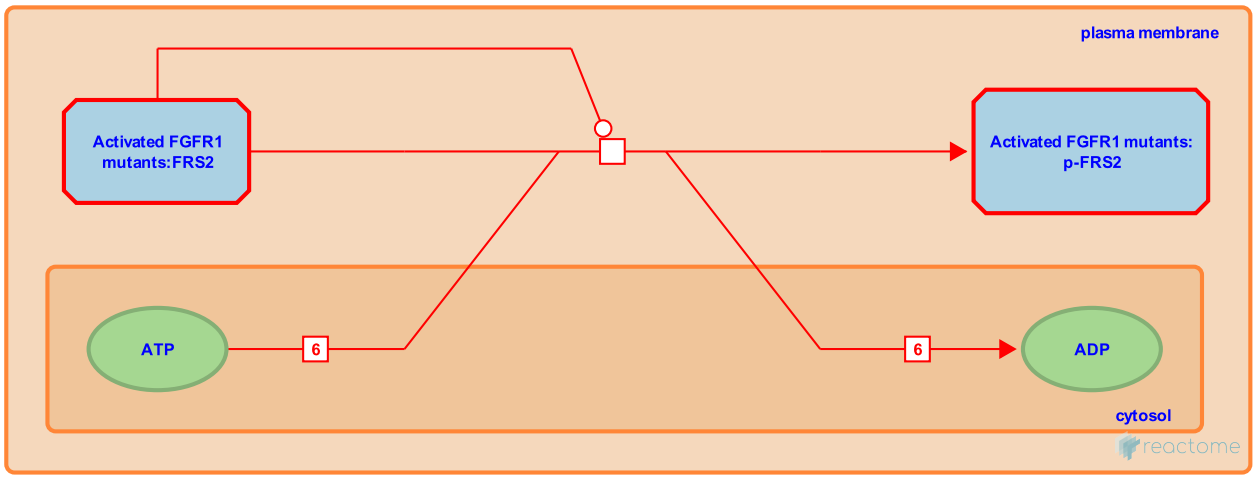
Activated FGFR1 mutants phosphorylate FRS2 ↗

Stable identifier: R-HSA-5655278

Type: transition

Compartments: plasma membrane, cytosol

Diseases: cancer, bone development disease



After recruitment to activated FGFR mutants, FRS2 is believed to be phosphorylated, potentially on all 6 of the tyrosines phosphorylated by wild-type FGFRs. Phosphorylation of FRS2 by FGFR has been demonstrated in some cases (see for instance Qing, 2009; Bai, 2010; Ahmed, 2008; Raffioni, 1998) and is inferred to occur in others based on activation of downstream signaling modules (reviewed in Wesche, 2011; Turner and Grose, 2010).

Literature references

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Editions

2012-02-09	Authored	Rothfels, K.
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