STAT binds to the mutant PDGFRA receptor

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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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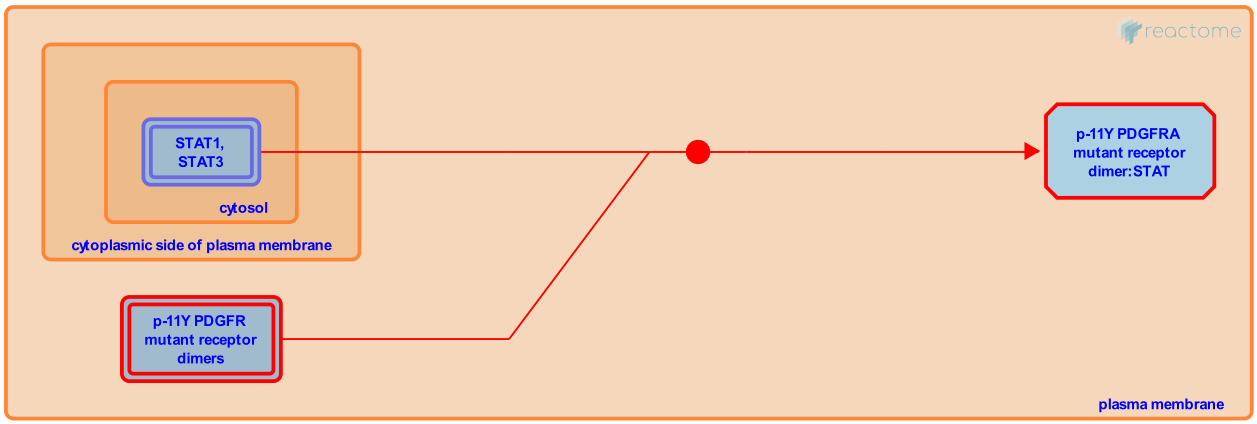
Stable identifier: R-HSA-9672176

Type: binding

Compartments: cytosol, plasma membrane

Diseases: cancer



Like the WT receptor, gain-of-function missense and in-frame deletion mutants of PDGFRA appear to act through the STAT signaling pathway. Binding and phosphorylation of SRC and subsequently STAT1 and 3 has been demonstrated for the activation loop D842V mutant, the juxtamembrane domain V561D mutant and for a small number of short in-frame deletion mutants in the kinase and juxtamembrane domain region. Specificity for interaction with different STAT family members is likely to vary depending on the PDGFRA mutation (Heinrich et al, 2003; Velghe et al, 2014; reviewed in Klug et al, 2018; Wang et al, 2016; Corless et al, 2011).

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Editions

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