

# SFKs phosphorylate NGEF

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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: 88

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

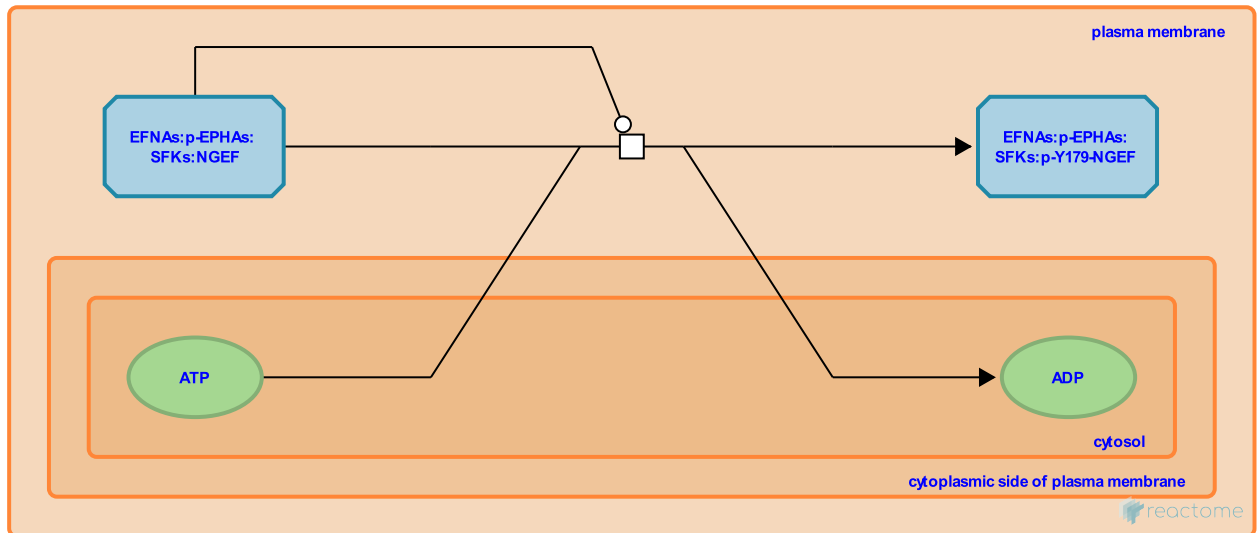
## SFKs phosphorylate NGEF ↗

**Stable identifier:** R-HSA-3928648

**Type:** transition

**Compartments:** plasma membrane, cytosol

**Inferred from:** Phosphorylation of ephexin1 (Gallus gallus)



Activation of EPHAs leads to phosphorylation of ephexin1 (NGEF) on conserved tyrosine (Y) 179 (Y87 in isoform3) by Src family kinases (SFKs). This phosphorylation preferentially activates NGEF's GDP/GTP exchange activity specifically towards RHOA but not RAC1 and CDC42, thus switching the substrate preference of NGEF and leading to actin cytoskeletal changes that result in growth cone collapse (Sahin et al. 2005, Knoll and Drescher 2004).

### Editions

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