

Phosphorylation of Neurofascin

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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. [↗](#)
- Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)
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Reactome database release: 88

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

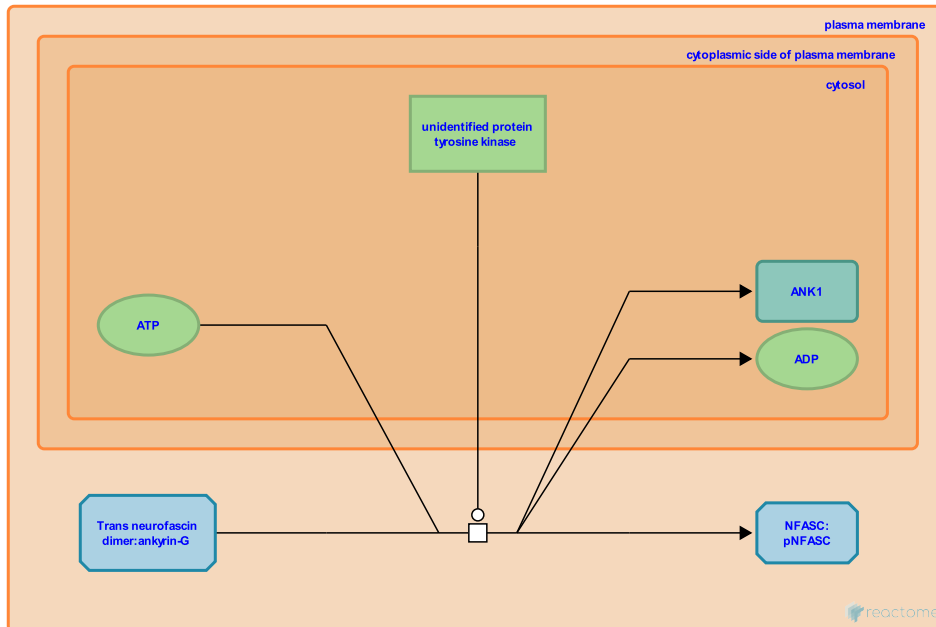
Phosphorylation of Neurofascin [↗](#)

Stable identifier: R-HSA-445091

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: [Phosphorylation of Neurofascin \(Rattus norvegicus\)](#)



The highly conserved FIGQY motif in the cytoplasmic domain of neurofascin is phosphorylated by tyrosine kinases in response to external signals. Phosphorylation of the tyrosine in the FIGQY motif inhibits ankyrin binding.

Editions

2008-07-30

Authored, Edited

Garapati, P V.

2010-02-16

Reviewed

Maness, PF.