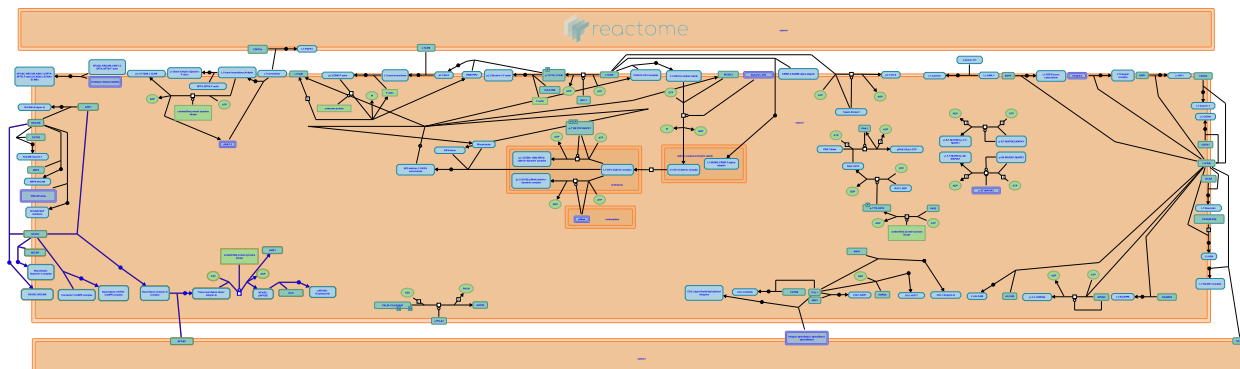


Neurofascin interactions



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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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- 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. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

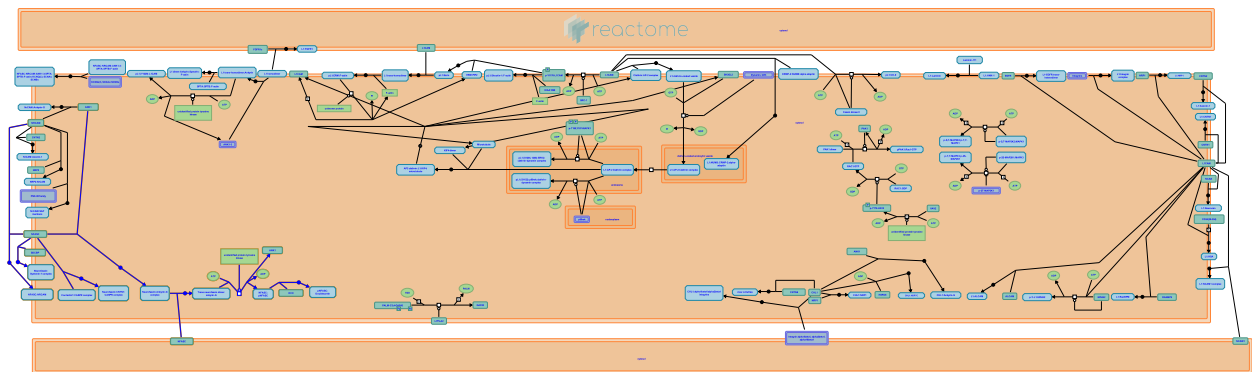
Reactome database release: 70

This document contains 1 pathway and 7 reactions ([see Table of Contents](#))

Neurofascin interactions [↗](#)

Stable identifier: R-HSA-447043

Compartments: plasma membrane



Neurofascin is an L1 family immunoglobulin cell adhesion molecule involved in axon subcellular targeting and synapse formation during neural development. There are a range of different isoforms identified in Neurofascin of which two of them are well studied the 186kDa commonly referred to as neuronal form and is present in node of Ranvier neurons and the 155kDa form known as a glial form present in schwann cells.

Neurofascin colocalizes with NrCAM and ankyrinG at the nodes of Ranvier. Neurofascin participates in transheterophilic adhesion with NrCAM and stimulates neurite outgrowth in chicken tectal neurons. The last few amino acids of neurofascin form the PDZ class I binding motif (SLA) and through these last few amino acids it associates with syntenin-1.

Literature references

- Hortsch, M. (2000). Structural and functional evolution of the L1 family: are four adhesion molecules better than one?. *Mol Cell Neurosci*, 15, 1-10. [↗](#)
- Herron, LR., Hill, M., Davey, F., Gunn-Moore, FJ. (2009). The intracellular interactions of the L1 family of cell adhesion molecules. *Biochem J*, 419, 519-31. [↗](#)

Editions

2008-07-30	Authored, Edited	Garapati, P V.
2010-02-16	Reviewed	Maness, PF.

Neurofascin binds Ankyrin-G ↗

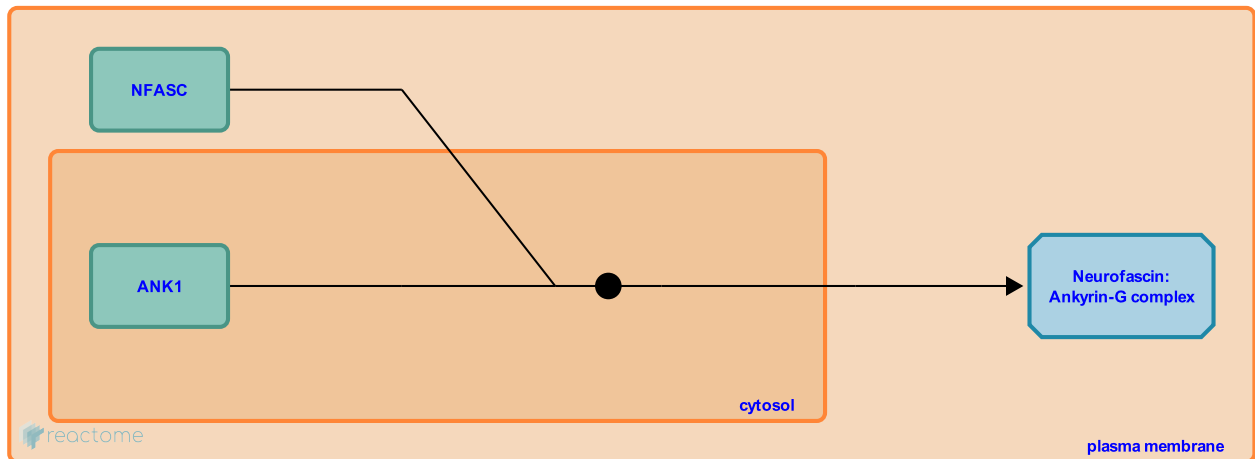
Location: [Neurofascin interactions](#)

Stable identifier: R-HSA-373729

Type: binding

Compartments: cytosol, plasma membrane

Inferred from: [Neurofascin binds Ankyrin-G \(Rattus norvegicus\)](#)



The cytoplasmic domains of neurofascin contains a highly conserved sequence (F1315IGQY) that binds ankyrin. The membrane binding domain of ankyrin has two distinct binding sites for neurofascin and is proposed to form lateral complexes between ion channels and cell adhesion molecules as well as to couple these proteins to the spectrin based membrane skeleton.

Followed by: [Trans-homodimerization of Neurofascin](#)

Editions

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2010-02-16	Reviewed	Maness, PF.

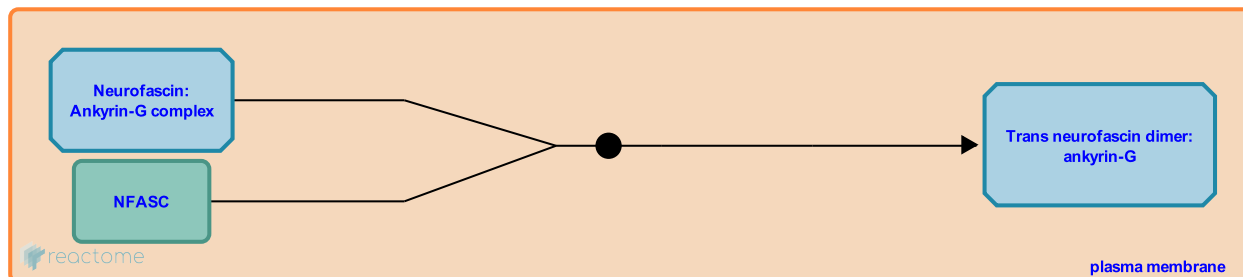
Trans-homodimerization of Neurofascin [↗](#)

Location: [Neurofascin interactions](#)

Stable identifier: R-HSA-443774

Type: binding

Compartments: plasma membrane



Interaction with ankyrins mediates the lateral oligomerization of neurofascin and this lateral oligomerization enhances its homophilic trans-adhesion.

Preceded by: [Neurofascin binds Ankyrin-G](#)

Literature references

Zhang, X., Davis, JQ., Carpenter, S., Bennett, V. (1998). Structural requirements for association of neurofascin with ankyrin. *J Biol Chem*, 273, 30785-94. [↗](#)

Tuvia, S., Garver, TD., Bennett, V. (1997). The phosphorylation state of the FIGQY tyrosine of neurofascin determines ankyrin-binding activity and patterns of cell segregation. *Proc Natl Acad Sci U S A*, 94, 12957-62. [↗](#)

Editions

2008-07-30	Authored, Edited	Garapati, P V.
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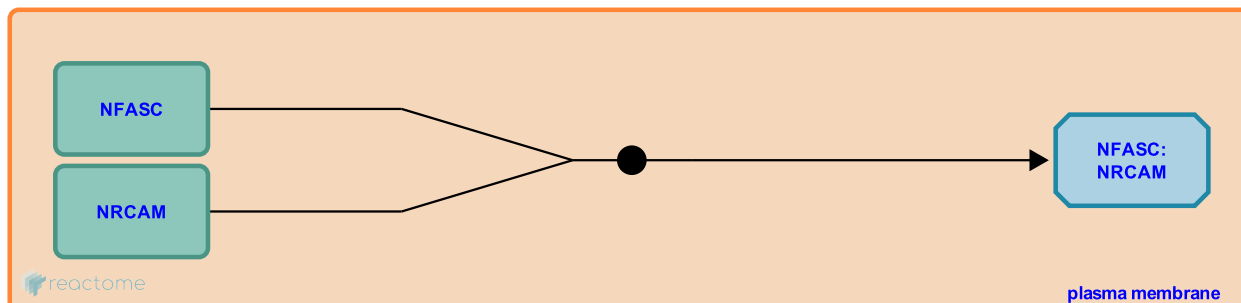
Neurofascin and NrCAM heterodimerization [↗](#)

Location: [Neurofascin interactions](#)

Stable identifier: R-HSA-373730

Type: binding

Compartments: plasma membrane



Neurofascin and NrCAM proteins undergo heterophilic interaction with one another with their extracellular Ig like domains and promote axon outgrowth.

Literature references

Volkmer, H., Leuschner, R., Zacharias, U., Rathjen, FG. (1996). Neurofascin induces neurites by heterophilic interactions with axonal NrCAM while NrCAM requires F11 on the axonal surface to extend neurites. *J Cell Biol*, 135, 1059-69. [↗](#)

Editions

2008-07-30	Authored, Edited	Garapati, P V.
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Phosphorylation of Neurofascin ↗

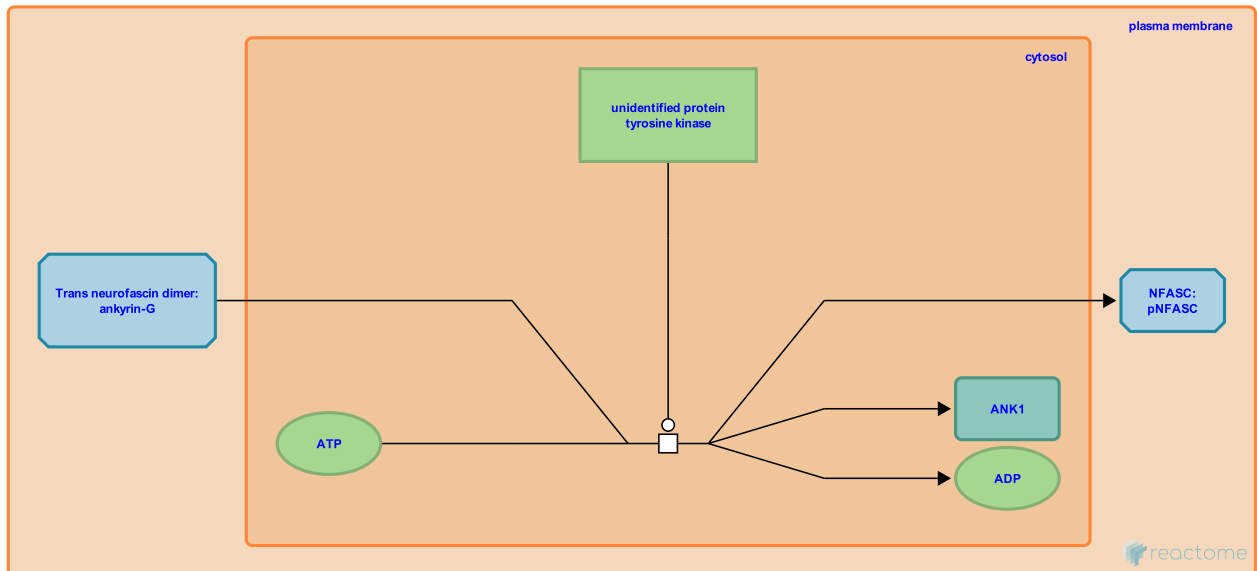
Location: [Neurofascin interactions](#)

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

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Doublecortin binds phosphorylated neurofascin [↗](#)

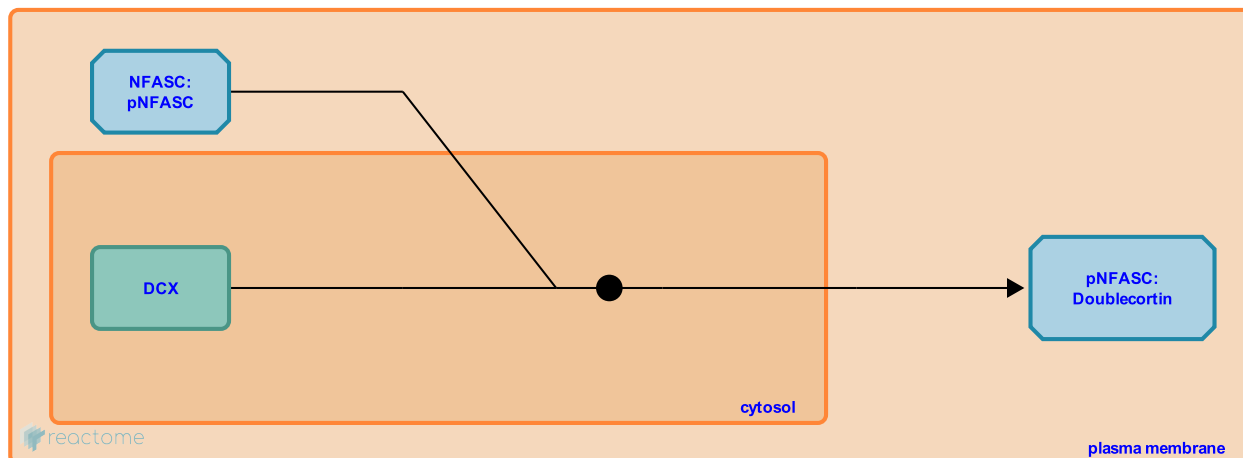
Location: [Neurofascin interactions](#)

Stable identifier: R-HSA-437243

Type: binding

Compartments: cytosol, plasma membrane

Inferred from: [Doublecortin binds phosphorylated neurofascin \(Homo sapiens\)](#)



Doublecortin is a microtubule associated protein expressed in neurons. Mutated doublecortin has been linked to the neuronal migration disorder X linked subcortical laminar heterotopia (double cortex)/lissencephaly. It binds neurofascin when the FIGQY motif of the latter protein is phosphorylated.

Editions

2008-07-30	Authored, Edited	Garapati, P V.
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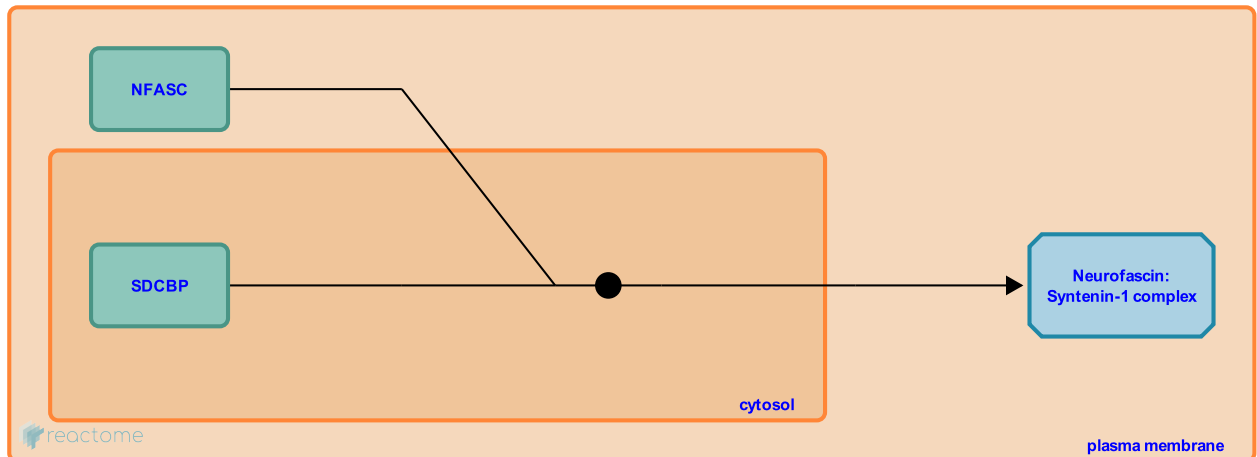
Neurofascin interacts with syntenin-1 [↗](#)

Location: [Neurofascin interactions](#)

Stable identifier: R-HSA-373738

Type: binding

Compartments: cytosol, plasma membrane



Syntenin-1 is an intracellular binding partner of neurofascin. Syntenin-1 contains two PDZ domains; the second one is a binding site for the COOH terminus of neurofascin.

Literature references

Koroll, M., Rathjen, FG., Volkmer, H. (2001). The neural cell recognition molecule neurofascin interacts with syntenin-1 but not with syntenin-2, both of which reveal self-associating activity. *J Biol Chem*, 276, 10646-54. [↗](#)

Editions

2008-07-30	Authored, Edited	Garapati, P V.
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Neurofascin binds contactin-1:CASPR complex ↗

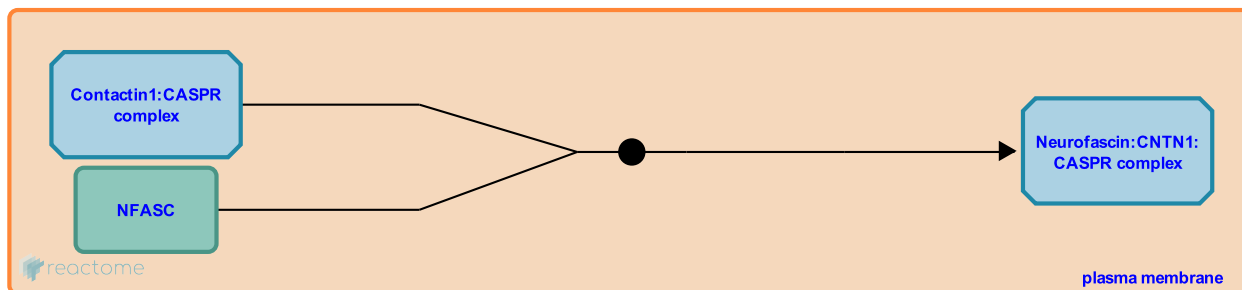
Location: [Neurofascin interactions](#)

Stable identifier: R-HSA-373733

Type: binding

Compartments: plasma membrane

Inferred from: [Neurofascin binds contactin-1:CASPR complex \(Mus musculus\)](#)



Neurofascin, expressed at the paranodal loop might be the glial receptor for the paranodin/Caspr-contactin complex. Neurofascin-Caspr-contactin complex forms the core structure of paranodal junctions.

Editions

2008-07-30	Authored, Edited	Garapati, P V.
2010-02-16	Reviewed	Maness, PF.

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