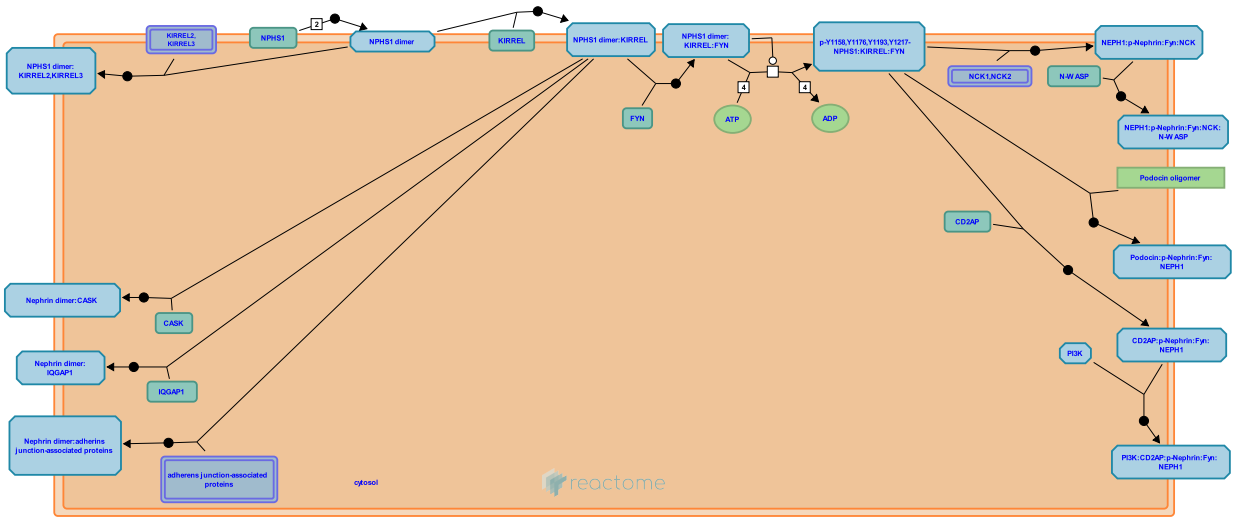
Nephrin family interactions



Garapati, P V., Grahammer, Florian., Huber, TB., Jupe, S., de Bono, B.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

20/04/2024

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. ↗

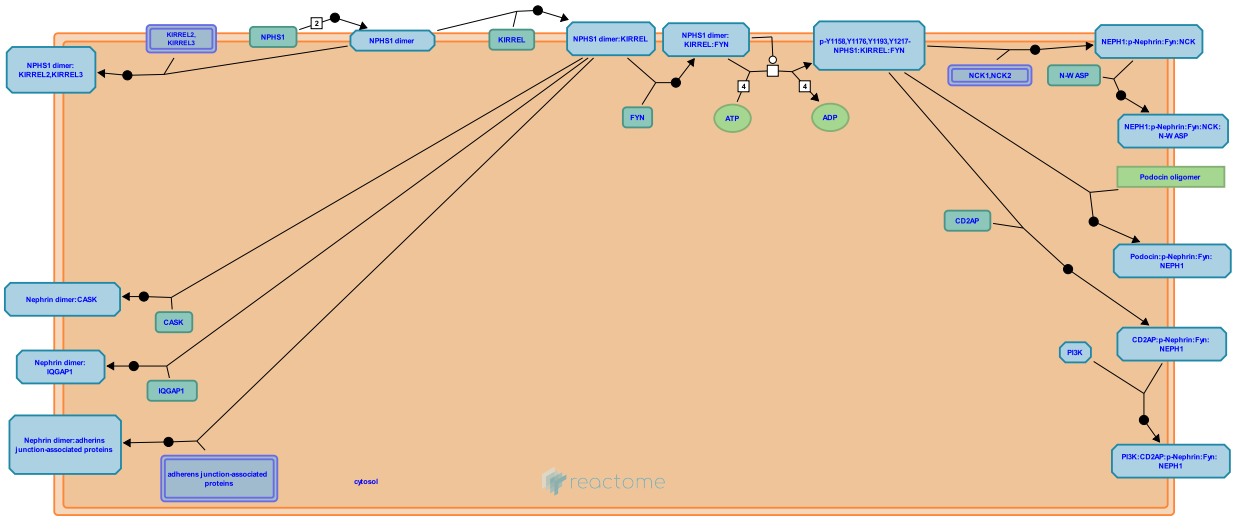
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Nephrin family interactions ↗

Stable identifier: R-HSA-373753

Compartments: plasma membrane



Nephrin (NPHS1) is a member of the Super-IgG-Molecule family and is most prominently expressed in kidney podocytes. It is a major if not the most important structural component of the slit diaphragm, a modified adherens junction in between these cells. NPHS1 has an extracellular domain that contains eight distal IgG like domains and one proximal fibronectin type III domain, a transmembrane domain and a short intracellular domain. NPHS1 molecules show both homophilic and heterophilic interactions. Among heterophilic interaction partners, slit diaphragm proteins such as Kin of IRRE-like protein 1 (KIRREL, Nephrin-like protein 1, NEPH1), KIRREL3 (NEPH2) and KIRREL2 (NEPH3) were shown to stabilize the slit diaphragm structure. Intracellularly Podocin (NPHS2), CD2 associated protein (CD2AP) and adherins junction associated proteins like IQGAP, MAGI, CASK and spectrins all interact with NPHS1. Hence it seems to play a major role in organizing the molecular structure of the slit diaphragm itself and via its binding partners links it to the actin cytoskeleton. NPHS1 tyrosine phosphorylation by the Src kinase FYN initiates the PI3K-AKT signaling cascade, which seems to promote antiapoptotic signals.

Literature references

Walz, G., Schermer, B., Kim, J., Borner, C., Keil, A., Egger, L. et al. (2003). Nephrin and CD2AP associate with phosphoinositide 3-OH kinase and stimulate AKT-dependent signaling. *Mol Cell Biol, 23*, 4917-28. ↗

Benzing, T., Huber, TB. (2005). The slit diaphragm: a signaling platform to regulate podocyte function. *Curr Opin Nephrol Hypertens, 14*, 211-6. ↗

Wartiovaara, J., Patrakka, J., Tryggvason, K. (2006). Hereditary proteinuria syndromes and mechanisms of proteinuria. *N Engl J Med, 354*, 1387-401. ↗

Holmberg, C., Wartiovaara, J., Ljungberg, P., Lenkkeri, U., Jalanko, H., Tryggvason, K. et al. (1999). Nephrin is specifically located at the slit diaphragm of glomerular podocytes. *Proc Natl Acad Sci U S A, 96*, 7962-7. ↗

Kudlicka, K., Zhou, H., Lehtonen, S., Farquhar, MG., Iino, N., Ryan, JJ. (2005). Cell junction-associated proteins IQGAP1, MAGI-2, CASK, spectrins, and alpha-actinin are components of the nephrin multiprotein complex. *Proc Natl Acad Sci U S A, 102*, 9814-9. ↗

Editions

2008-02-26	Authored	de Bono, B., Garapati, P V.
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2010-05-20	Reviewed	Huber, TB., Grahammer, Florian.

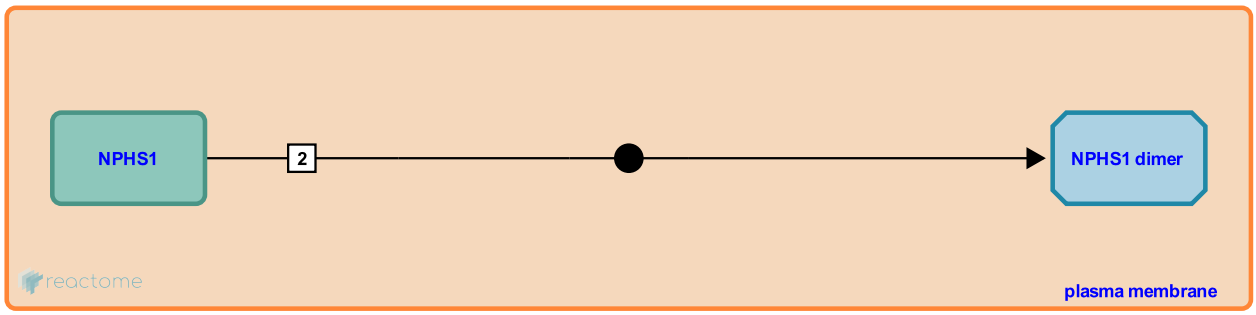
Nephrin trans-homophilic interaction ↗

Location: Nephrin family interactions

Stable identifier: R-HSA-373732

Type: binding

Compartments: plasma membrane



Foot processes are slender, actin rich protrusions of the cytoplasm that are anchored to the glomerular basement membrane. Adjacent foot processes are laterally interconnected by a highly specialized cell-cell junction, the slit diaphragm (SD). Nephrin (NPHS1) is the critical structural component within the slit diaphragm. Nephrin molecules of adjacent foot processes from neighboring podocytes interact with each other in the middle of the slit diaphragm forming a filter with a zipper like structure and with pores just the size of albumin on both sides of the midline density.

Followed by: Heterodimerization of nephrin and KIRREL2, KIRREL3, Cis-Heterodimerization of nephrin and KIRREL

Literature references

Sandin, S., Wartiovaara, J., Khoshnoodi, J., Cheng, RH., Mäkelä, E., Zhang, J. et al. (2004). Nephrin strands contribute to a porous slit diaphragm scaffold as revealed by electron tomography. *J Clin Invest, 114*, 1475-83. ↗

Holmberg, C., Wartiovaara, J., Ljungberg, P., Lenkkeri, U., Jalanko, H., Tryggvason, K. et al. (1999). Nephrin is specifically located at the slit diaphragm of glomerular podocytes. *Proc Natl Acad Sci U S A, 96*, 7962-7. ↗

Holthofer, H., Aaltonen, P. (2007). The nephrin-based slit diaphragm: new insight into the signalling platform identifies targets for therapy. *Nephrol Dial Transplant, 22*, 3408-10. ↗

Walz, G., Benzing, T., Gerke, P., Sellin, L., Huber, TB. (2003). Homodimerization and heterodimerization of the glomerular podocyte proteins nephrin and NEPH1. *J Am Soc Nephrol, 14*, 918-26. ↗

Sigmundsson, K., Wartiovaara, J., Khoshnoodi, J., Ofverstedt, LG., Skoglund, U., Tryggvason, K. et al. (2003). Nephrin promotes cell-cell adhesion through homophilic interactions. *Am J Pathol, 163*, 2337-46. ↗

Editions

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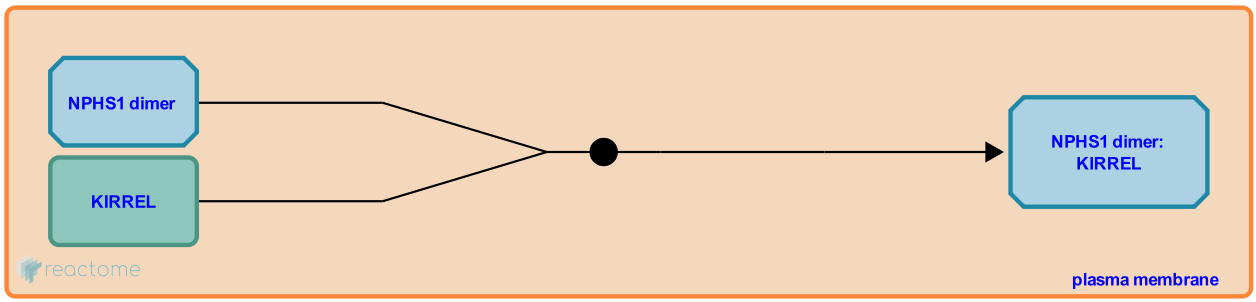
Cis-Heterodimerization of nephrin and KIRREL ↗

Location: Nephrin family interactions

Stable identifier: R-HSA-373714

Type: binding

Compartments: plasma membrane



Nephrin (NPHS1) forms heterodimers with KIRREL (NEPH1) molecules in a cis-configuration within the slit diaphram (SD). This heterologous protein protein interaction seems to be an important factor in maintaining the normal permeability characteristics of the slit diaphragm by relaying signals from the extracellular side into the podocyte. NPHS1:KIRREL heterodimer formation is highly conserved from C.elegans to human and serves different functions in different species and different tissues.

Preceded by: Nephrin trans-homophilic interaction

Followed by: Nephrin binds CASK, Interaction of IQGAP1 with nephrin, Interaction of nephrin with adherens junction-associated proteins, Nephrin dimer:KIRREL binds FYN

Literature references

Holzman, LB., Verma, R., Garg, P., Johnstone, DB., Nihalani, D. (2007). Neph1 cooperates with nephrin to transduce a signal that induces actin polymerization. *Mol Cell Biol, 27*, 8698-712. ↗

Kurfis, J., Kaw, B., Chugh, SS., Kanwar, YS., Rahmanuddin, S., Liu, G. (2003). Neph1 and nephrin interaction in the slit diaphragm is an important determinant of glomerular permeability. *J Clin Invest, 112*, 209-21. ↗

Walz, G., Gödel, M., Martin, K., Kramer-Zucker, A., Noutsou, F., Wanner, N. et al. (2010). A model organism approach: defining the role of Neph proteins as regulators of neuron and kidney morphogenesis. *Hum Mol Genet, 19*, 2347-59. ↗

Walz, G., Benzing, T., Gerke, P., Sellin, L., Huber, TB. (2003). Homodimerization and heterodimerization of the glomerular podocyte proteins nephrin and NEPH1. *J Am Soc Nephrol, 14*, 918-26. ↗

Editions

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2010-05-20	Reviewed	Huber, TB., Grahammer, Florian.

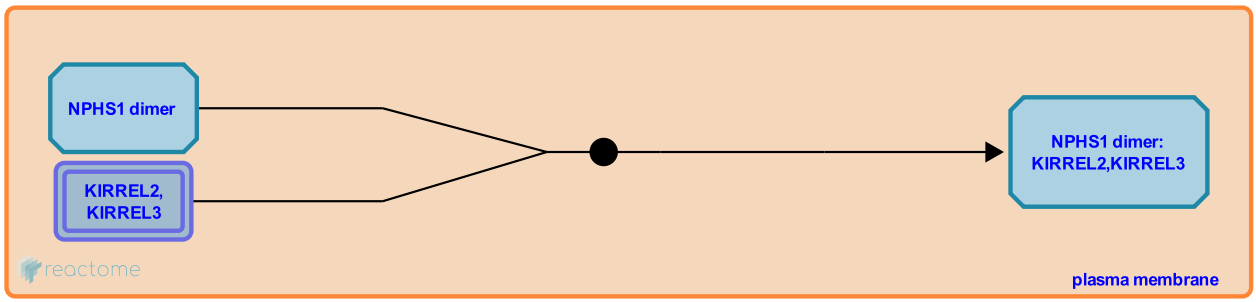
Heterodimerization of nephrin and KIRREL2, KIRREL3 ↗

Location: Nephrin family interactions

Stable identifier: R-HSA-451757

Type: binding

Compartments: plasma membrane



NEPH2 and NEPH3 specifically interact with the extracellular domains of nephrin in the slit diaphragm of podocytes and potentially other tissues as well (eg. brain). The functional significance of these interactions is unknown.

Preceded by: Nephrin trans-homophilic interaction

Literature references

Walz, G., Gödel, M., Martin, K., Kramer-Zucker, A., Noutsou, F., Wanner, N. et al. (2010). A model organism approach: defining the role of Neph proteins as regulators of neuron and kidney morphogenesis. *Hum Mol Genet, 19*, 2347-59. ↗

Walz, G., Petraschka, D., Kretz, O., Benzing, T., Zentgraf, H., Gerke, P. et al. (2005). NEPH2 is located at the glomerular slit diaphragm, interacts with nephrin and is cleaved from podocytes by metalloproteinases. *J Am Soc Nephrol, 16*, 1693-702. ↗

Editions

2008-02-26	Authored	de Bono, B., Garapati, P V.
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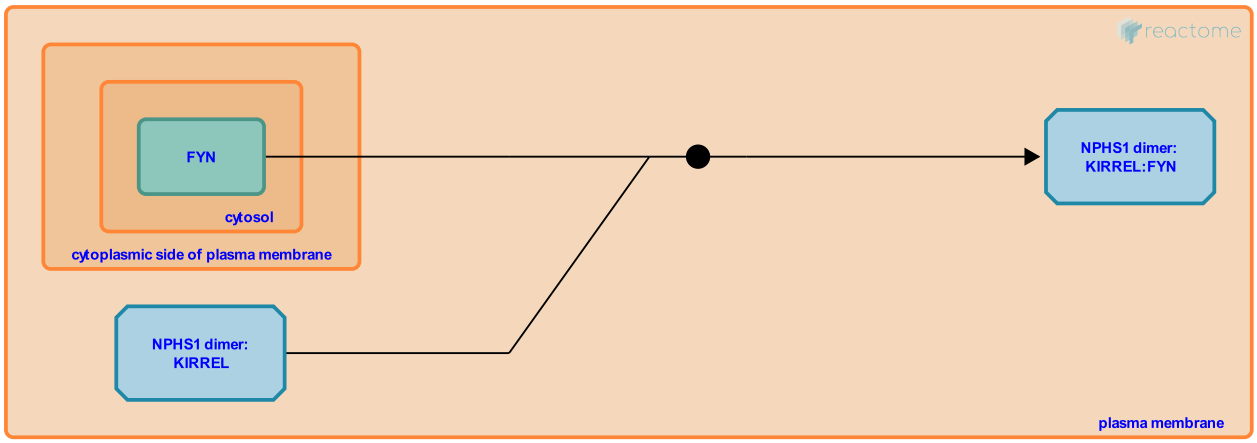
Nephrin dimer:KIRREL binds FYN ↗

Location: Nephrin family interactions

Stable identifier: R-HSA-8981534

Type: binding

Compartments: plasma membrane



Nephrin (NPHS1) is tyrosine phosphorylated by the Src family tyrosine kinase FYN in developing and injured podocytes. Phosphorylation of three tyrosines (1176, 1193 and 1217) results in the formation of a preferred binding motif (YDXV) for the SH2 domain of the adaptor protein NCK, which links Nephrin to the cytoskeleton. Phosphorylation of NPHS1 tyrosine 1158 results in a binding motif for the p85 regulatory subunit of PI3K.

Preceded by: Cis-Heterodimerization of nephrin and KIRREL

Followed by: Phosphorylation of nephrin by FYN

Literature references

Kunkel, R., Wharram, B., Holzman, LB., Verma, R., Kovari, I., Killen, P. et al. (2003). Fyn binds to and phosphorylates the kidney slit diaphragm component Nephrin. *J Biol Chem, 278*, 20716-23. ↗

Editions

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2017-03-09	Edited	Jupe, S.

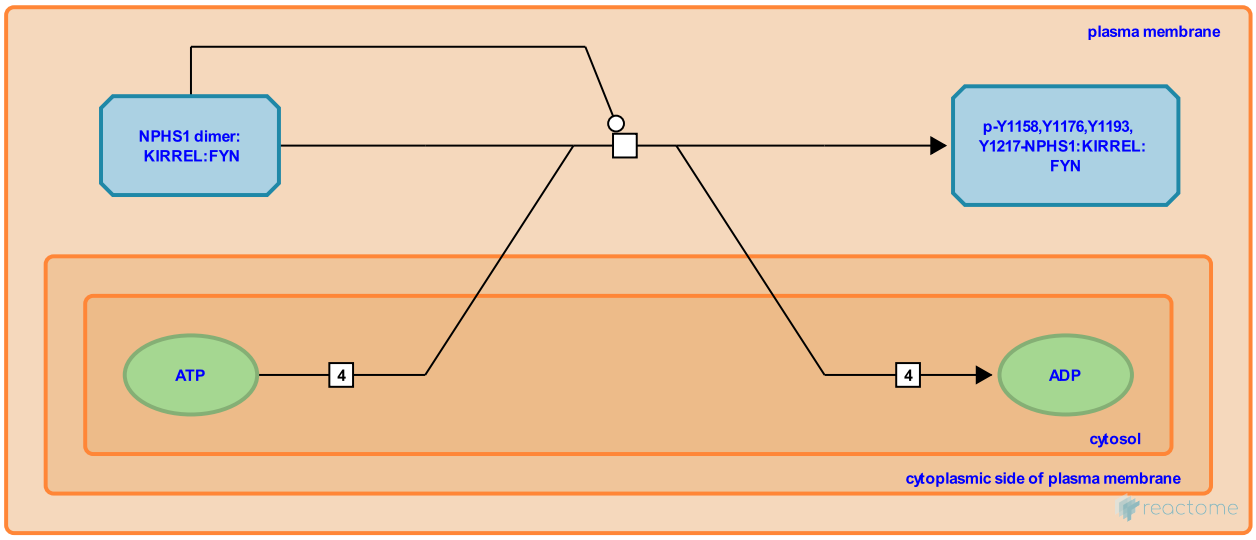
Phosphorylation of nephrin by FYN ↗

Location: Nephrin family interactions

Stable identifier: R-HSA-373747

Type: transition

Compartments: plasma membrane



Nephrin has eight putative phosphorylation sites, which nicely match with substrate sites for the Src kinase family. Nephrin, is tyrosine phosphorylated by the Src family tyrosine kinase, Fyn in developing and injured podocytes. Phosphorylation of three of these tyrosines (1176, 1193 and 1217) results in the formation of a preferred binding motif (YDXV) for the SH2 domain of the adaptor protein NCK, which is one of the bricks linking Nephrin to the cytoskeleton. Phosphorylation of tyrosine 1158 results in a binding motif for the p85 regulatory subunit of PI3K.

Preceded by: Nephrin dimer:KIRREL binds FYN

Followed by: Nephrin binds NCK, Nephrin binds CD2AP, Nephrin interacts with Podocin

Literature references

Kawachi, H., Li, H., Zhu, J., Lemay, S., Aoudjit, L., Takano, T. et al. (2008). Nephrin mediates actin reorganization via phosphoinositide 3-kinase in podocytes. *Kidney Int, 73*, 556-66. ↗

Pikkarainen, T., Liu, XL., Reponen, P., Kilpelainen, P., Tryggvason, K., Ruotsalainen, V. et al. (2003). Clustering-induced tyrosine phosphorylation of nephrin by Src family kinases. *Kidney Int, 64*, 404-13. ↗

Soofi, A., Holzman, LB., Patrie, K., Verma, R., Kovari, I., Nihalani, D. (2006). Nephrin ectodomain engagement results in Src kinase activation, nephrin phosphorylation, Nck recruitment, and actin polymerization. *J Clin Invest, 116*, 1346-59. ↗

Kawachi, H., Li, H., Lemay, S., Aoudjit, L., Takano, T. (2004). SRC-family kinase Fyn phosphorylates the cytoplasmic domain of nephrin and modulates its interaction with podocin. *J Am Soc Nephrol, 15*, 3006-15. ↗

Kunkel, R., Wharram, B., Holzman, LB., Verma, R., Kovari, I., Killen, P. et al. (2003). Fyn binds to and phosphorylates the kidney slit diaphragm component Nephrin. *J Biol Chem, 278*, 20716-23. ↗

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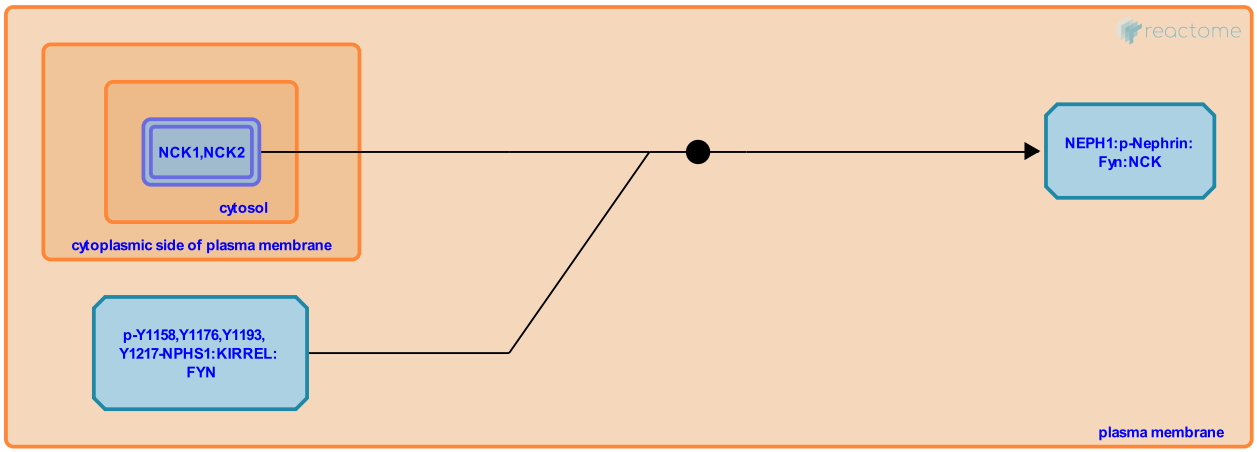
Nephrin binds NCK ↗

Location: Nephrin family interactions

Stable identifier: R-HSA-373724

Type: binding

Compartments: plasma membrane



Nephrin tyrosine phosphorylation regulates podocyte cell morphology via NCK adaptor proteins. NCK via its SH2 domain interacts with the three phosphotyrosines (1176, 1193 and 1217) on nephrin, and through its SH3 domain can recruit several other proteins involved in the regulation of the actin cytoskeleton such as N WASP, WIP, ARP2/3 and PAK to the slit diaphragm. The importance of this mechanism is the maintenance of the filtration barrier. When rapid actin polymerization and cytoskeletal reorganization is needed, for example during development or injury and repair, the level of nephrin phosphorylation increases and leads to recruitment of NCK and its downstream effectors to the cytoplasmic side of the slit diaphragm.

Preceded by: Phosphorylation of nephrin by FYN

Followed by: Nephrin mediated activation of N-WASP

Literature references

Pawson, T., Larose, L., Bladt, F., Eremina, V., Li, H., Li, SS. et al. (2006). Nck adaptor proteins link nephrin to the actin cytoskeleton of kidney podocytes. *Nature, 440*, 818-23. ↗

Pikkarainen, T., Patrakka, J., Tryggvason, K. (2006). Nck links nephrin to actin in kidney podocytes. *Cell, 125*, 221-4. ↗

Pawson, T., Liu, X., Eremina, V., New, LA., Zou, Y., Aoudjit, L. et al. (2009). Nck proteins maintain the adult glomerular filtration barrier. *J Am Soc Nephrol, 20*, 1533-43. ↗

Editions

2008-02-26	Authored	de Bono, B., Garapati, P V.
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2010-05-20	Reviewed	Huber, TB., Grahammer, Florian.

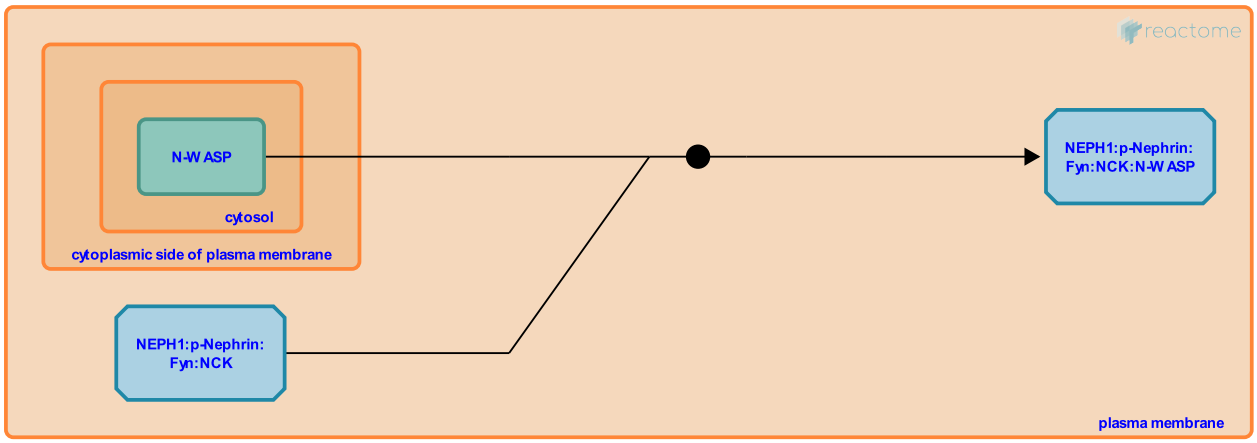
Nephrin mediated activation of N-WASP ↗

Location: Nephrin family interactions

Stable identifier: R-HSA-532603

Type: binding

Compartments: plasma membrane



The NCK adaptor protein binds to a proline rich region on WASP and N-WASP through its SH3 domains and has been implicated in the recruitment of WASP/N-WASP to sites of tyrosine phosphorylation. NCK stimulates actin nucleation by N WASP:Arp2/3 complexes. Recruitment of NCK to phosphorylated YDxV sites on nephrin could therefore directly control the cytoskeletal actin architecture of podocytes.

Preceded by: Nephrin binds NCK

Literature references

Kirschner, MW., Nollau, P., Mayer, BJ., Ho, HY., Rohatgi, R. (2001). Nck and phosphatidylinositol 4,5-bisphosphate synergistically activate actin polymerization through the N-WASP-Arp2/3 pathway. *J Biol Chem, 276*, 26448-52. ↗

Pawson, T., Larose, L., Bladt, F., Eremina, V., Li, H., Li, SS. et al. (2006). Nck adaptor proteins link nephrin to the actin cytoskeleton of kidney podocytes. *Nature, 440*, 818-23. ↗

Editions

2008-02-26	Authored	de Bono, B., Garapati, P V.
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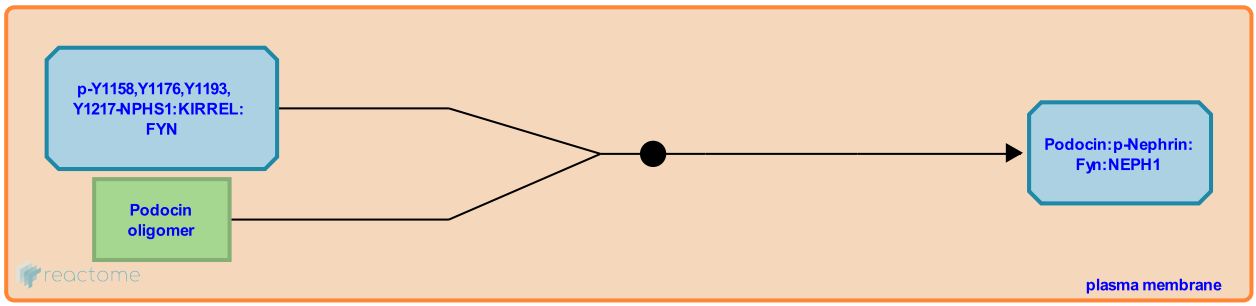
Nephrin interacts with Podocin ↗

Location: Nephrin family interactions

Stable identifier: R-HSA-373734

Type: binding

Compartments: plasma membrane



NPHS2 encodes podocin, a protein exclusively expressed in podocytes in developing and mature glomeruli. Podocin is a member of the stomatin protein family with a short N terminal domain, a membrane-anchoring region, and a cytosolic C-terminal domain. Podocin accumulates in an oligomeric form in lipid rafts of the slit diaphragm. The C-terminal domain of Podocin binds to the cytoplasmic domain of nephrin thus it may function as a scaffolding protein connecting nephrin with the actin cytoskeleton. Beside nephrin it was shown that podocin also interacts with several other SD proteins, hence forming functional microdomains

Preceded by: Phosphorylation of nephrin by FYN

Literature references

Walz, G., Schilling, B., Benzing, T., Kottgen, M., Huber, TB. (2001). Interaction with podocin facilitates nephrin signaling. *J Biol Chem, 276*, 41543-6. ↗

Walz, G., Sernetz, L., Saleem, MA., Simons, M., Hartleben, B., Benzing, T. et al. (2003). Molecular basis of the functional podocin-nephrin complex: mutations in the NPHS2 gene disrupt nephrin targeting to lipid raft microdomains. *Hum Mol Genet, 12*, 3397-405. ↗

Faul, C., Saleem, MA., Kriz, W., Shaw, AS., Simons, M., Schwarz, K. et al. (2001). Podocin, a raft-associated component of the glomerular slit diaphragm, interacts with CD2AP and nephrin. *J Clin Invest, 108*, 1621-9. ↗

Editions

2008-02-26	Authored	de Bono, B., Garapati, P V.
2010-03-01	Edited	Garapati, P V.
2010-05-20	Reviewed	Huber, TB., Grahammer, Florian.

Nephrin binds CD2AP ↗

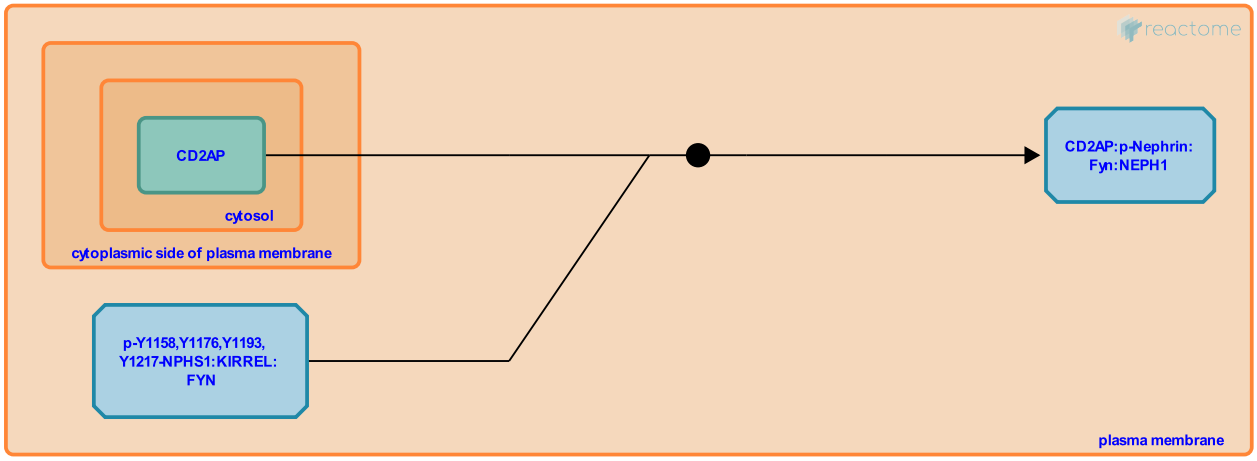
Location: Nephrin family interactions

Stable identifier: R-HSA-373727

Type: binding

Compartments: plasma membrane

Inferred from: Nephrin binds CD2AP (Mus musculus)



CD2-associated protein (CD2AP) is an adapter molecule of the immunoglobulin superfamily that was first identified as an SH3-containing protein that binds to the cytoplasmic domain of CD2. In the glomerulus, CD2AP is located in the cytoplasm beneath the slit-diaphragm, where it binds to the cytoplasmic domain of nephrin. CD2AP acts as a linker protein and may be involved in connecting nephrin to the actin cytoskeleton in podocytes, although direct evidence of this is still lacking. Interaction with CD2AP might be important in the steady-state situation. In addition CD2AP can facilitate nephrin-induced PI3K-AKT signaling, a pathway that has been shown to be important for nephrin-mediated actin reorganization in podocytes and protection of podocytes from apoptosis.

Preceded by: Phosphorylation of nephrin by FYN

Followed by: p85 associates with both p-Nephrin and CD2AP

Editions

2008-02-26	Authored	de Bono, B., Garapati, P V.
2010-03-01	Edited	Garapati, P V.
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p85 associates with both p-Nephrin and CD2AP ↗

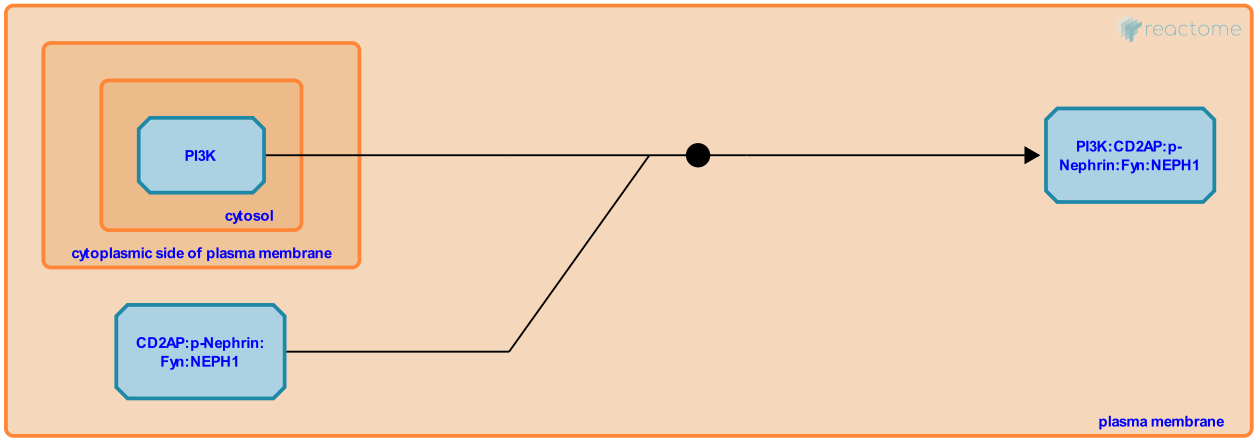
Location: Nephrin family interactions

Stable identifier: R-HSA-451758

Type: binding

Compartments: plasma membrane

Inferred from: p85 associates with both p-Nephrin and CD2AP (Rattus norvegicus)



The regulatory p85 subunit of PI3K recognizes and binds to both phosphorylated nephrin and its binding partner, CD2AP. By mutation analysis, nephrin Y1158 was shown to be necessary for the interaction. This interaction allows the catalytic subunit p110 to act on phospholipids of the inner leaflet of the cell membrane. This leads to downstream phosphorylation and inactivation of the apoptotic factor Bad via the serine-threonine kinase AKT.

Preceded by: Nephrin binds CD2AP

Editions

2008-02-26	Authored	de Bono, B., Garapati, P V.
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2010-05-20	Reviewed	Huber, TB., Grahammer, Florian.

Nephrin binds CASK ↗

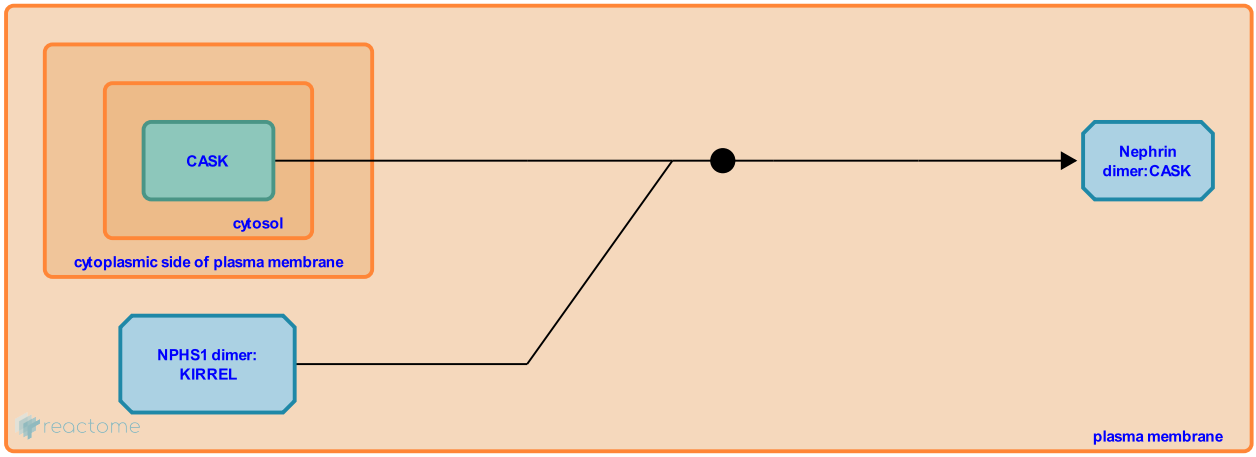
Location: Nephrin family interactions

Stable identifier: R-HSA-373722

Type: binding

Compartments: plasma membrane

Inferred from: Nephrin binds Cask (Rattus norvegicus)



CASK is a scaffolding protein that participates in maintenance of polarized epithelial cell architecture by linking membrane proteins and signaling molecules to the actin cytoskeleton. CASK is identified as one of the binding partners of nephrin and this interaction likely plays an important role in establishing the structural integrity and functional properties of the glomerular slit diaphragm.

Preceded by: Cis-Heterodimerization of nephrin and KIRREL

Editions

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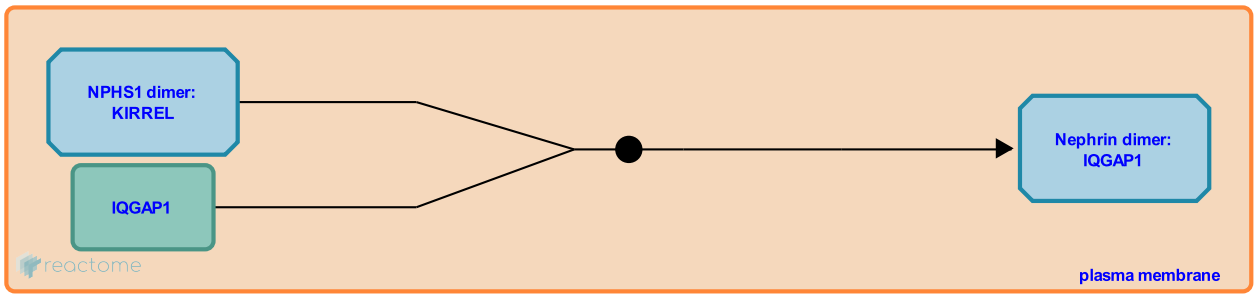
Interaction of IQGAP1 with nephrin ↗

Location: Nephrin family interactions

Stable identifier: R-HSA-451377

Type: binding

Compartments: plasma membrane



IQGAP1, an effector protein of the small GTPases Rac1 and Cdc42 and a putative regulator of cell-cell adherens junctions, is expressed in podocytes at significant levels, and located in the immediate vicinity of the slit diaphragm. IQGAP1 is identified as one of the interacting partners of nephrin. This interaction takes place strictly and specifically between the C-terminal half of the nephrin intracellular domain and IQGAP1. IQGAP1 knock-out mouse does not have any obvious nephrotic phenotype, hence IQGAP1 function can either be substituted by other proteins or its role in vivo is much less important than that attributed to it from cell culture experiments.

Preceded by: Cis-Heterodimerization of nephrin and KIRREL

Literature references

Pikkarainen, T., Sun, Y., Wartiovaara, J., Liu, XL., Jonsson, AP., Morgunova, E. et al. (2005). Characterization of the interactions of the nephrin intracellular domain. *FEBS J, 272*, 228-43. ↗

Holthofer, H., Kudlicka, K., Lehtonen, S., Farquhar, MG., Lehtonen, E. (2004). Nephrin forms a complex with adherens junction proteins and CASK in podocytes and in Madin-Darby canine kidney cells expressing nephrin. *Am J Pathol, 165*, 923-36. ↗

Wang, Q., Li, S., Bernards, A., Bronson, RT., Chakladar, A. (2000). Gastric hyperplasia in mice lacking the putative Cdc42 effector IQGAP1. *Mol Cell Biol, 20*, 697-701. ↗

Kudlicka, K., Zhou, H., Lehtonen, S., Farquhar, MG., Iino, N., Ryan, JJ. (2005). Cell junction-associated proteins IQGAP1, MAGI-2, CASK, spectrins, and alpha-actinin are components of the nephrin multiprotein complex. *Proc Natl Acad Sci U S A, 102*, 9814-9. ↗

Editions

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Interaction of nephrin with adherens junction-associated proteins ↗

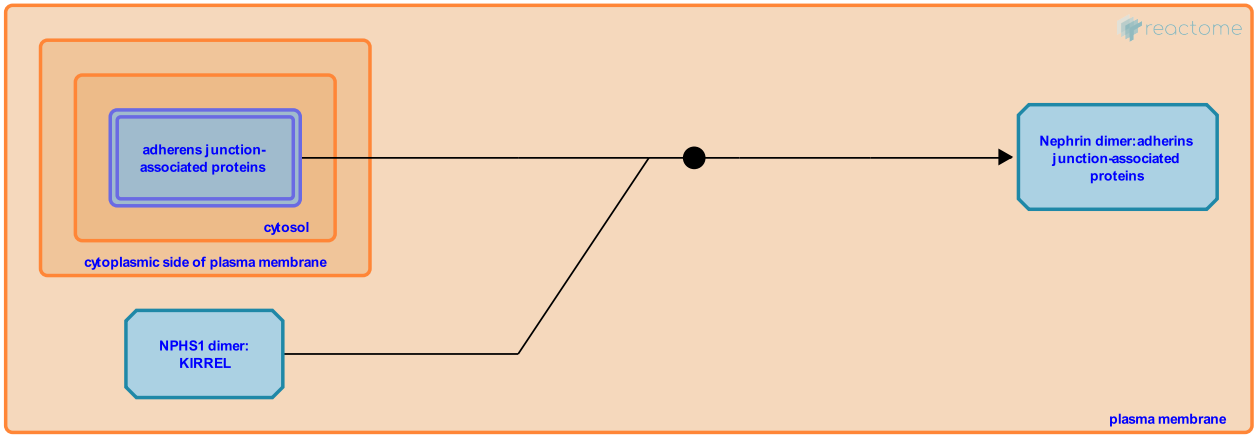
Location: Nephrin family interactions

Stable identifier: R-HSA-451403

Type: binding

Compartments: plasma membrane

Inferred from: Interaction of nephrin with adherens junction-associated proteins (Rattus norvegicus)



The nephrin-slit diaphragm protein complex contains a group of scaffolding proteins that function to connect junctional membrane proteins to the actin cytoskeleton and signaling cascades. By mass spectrometry four of the proteins identified, alphaII spectrin, betaII spectrin, alpha-actinin, and IQGAP1, represent adherens junction-associated proteins, and two, MAGI-2/S-SCAM and CASK, represent MAGUK family scaffolding proteins that associate with Ig superfamily proteins. The presence of these proteins in slit diaphragms and their association with nephrin suggests that they may form a scaffolding protein complex in the podocyte slit diaphragm and thus contribute to the regulation of ultrafiltration by binding slit membrane proteins and establishing their cytosolic connections.

Preceded by: Cis-Heterodimerization of nephrin and KIRREL

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