Recruitment of transition zone proteins

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04/05/2024

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

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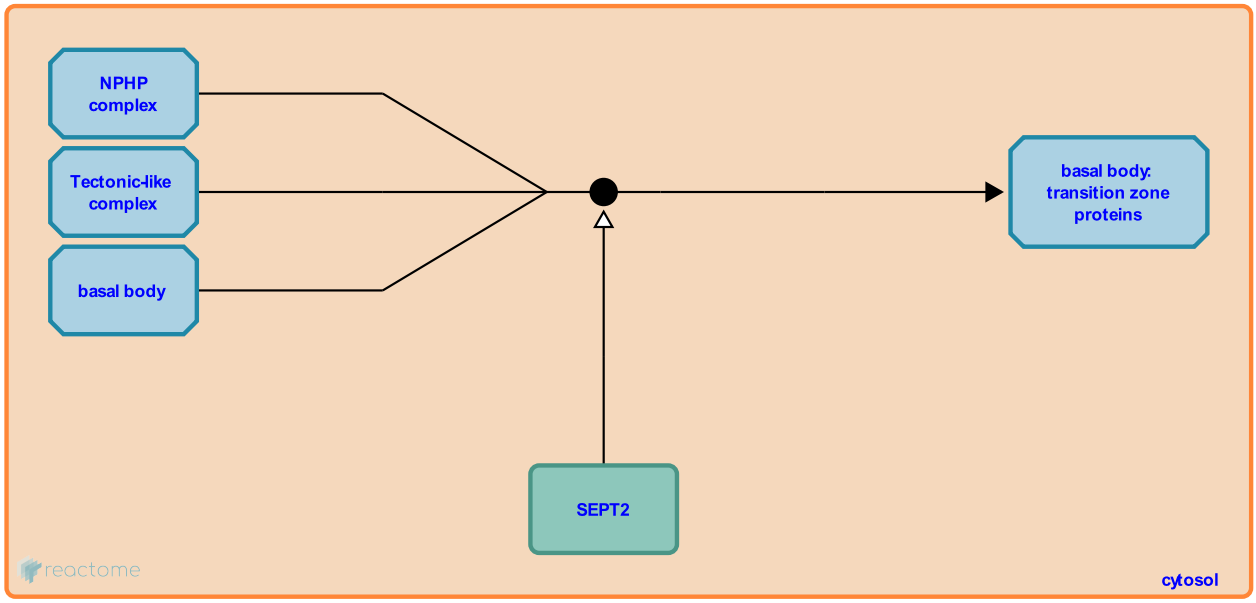
Stable identifier: R-HSA-5626681

Type: binding

Compartments: cytosol



The transition zone is a protein-rich zone at the base of the cilium that forms after maturation of the mother centriole and prior to or concurrent with the initiation of intraflagellar transport (IFT) (reviewed in Benzing and Schermer, 2011; Reiter et al, 2012). The transition zone consists of a growing number of proteins and protein complexes, many of whose genes are associated with ciliopathies such as nephronophthisis, Meckel-Gruber syndrome and Joubert's syndrome (Reiter et al, 2006; Hu et al, 2010; Sang et al, 2011; Williams et al, 2011; Garcia-Gonzalo et al, 2011; Chih et al, 2012; reviewed in Reiter et al, 2012). In conjunction with SEPT2, which was recently shown to form a septin ring diffusion barrier at the base of the cilium, the transition zone and its resident proteins contribute to protein sorting and ciliary membrane composition and act as a ciliary gate (Hu et al, 2010; Williams et al, 2011; Garcia-Gonzalo et al, 2011; Chih et al, 2012; reviewed in Reiter et al, 2012).

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Editions

2014-10-09	Authored	Rothfels, K.
2014-10-13	Edited	Jassal, B.
2014-11-10	Reviewed	Lorentzen, E.
2014-11-14	Reviewed	Goncalves, J.