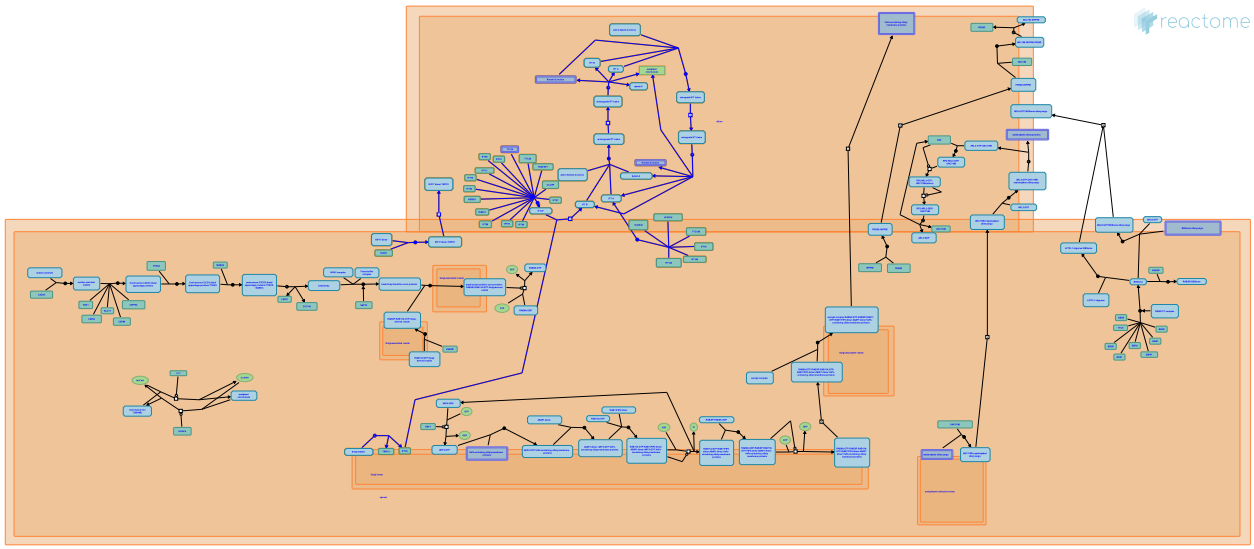
Intraflagellar transport



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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. ↗

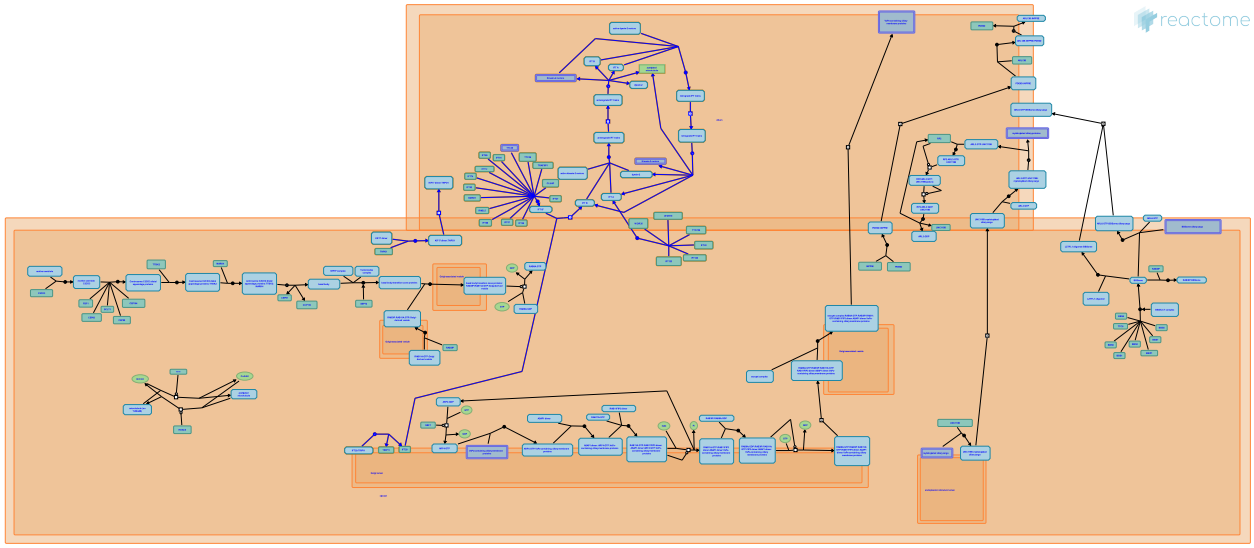
Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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. ↗

Intraflagellar transport ↗

Stable identifier: R-HSA-5620924



Intraflagellar transport (IFT) is a motor-based process that controls the anterograde and retrograde transport of large protein complexes, ciliary cargo and structural components along the ciliary axoneme (reviewed in Cole and Snell, 2009). IFT particles contain two multiprotein IFT subcomplexes, IFT A and IFT B, with ~6 and ~15 subunits, respectively. Linear arrays of IFT A and IFT B 'trains' assemble at the ciliary base along with the active plus-end directed kinesin-2 motors and the inactive dynein motors and traffic along the microtubules at a rate of ~2 micrometers per second. At the ciliary tip, the IFT trains disassemble, releasing cargo and motors, and smaller IFT trains are subsequently reassembled for retrograde traffic driven by the now active minus-end directed dynein-2 motors. Retrograde trains travel down the length of the axoneme at a rate of ~3 micrometers per second and are disassembled and recycled for further rounds of transport at the ciliary base (reviewed in Taschner et al, 2012; Bhogaraju et al, 2013; Ishikawa et al, 2011). Mutations in kinesin-2 motors or IFT B complex members tend to abrogate cilium formation, while mutations in dynein-2 motor or in IFT A complex members generally result in short, bulging cilia that abnormally accumulate IFT particles. These observations are consistent with a primary role for IFT B and IFT A complexes in anterograde and retrograde transport, respectively (see for instance, Huangfu et al, 2005; Follit et al, 2006; May et al, 2005; Tran et al, 2008; reviwed in Ishikawa et al, 2011). In addition to the IFT A and B complexes, the IFT particles may also contain the multi-protein BBSome complex, which displays typical IFT-like movement along the ciliary axoneme and which is required for cilium biogenesis and delivery and transport of some ciliary cargo (Blaque et al, 2004; Nachury et al, 2007; Ou et al, 2005; Ou et al, 2007; reviewed in Sung and Leroux, 2013; Bhorgaraju et al, 2013).

Literature references

Tuft, RA., Pazour, GJ., Follit, JA., Fogarty, KE. (2006). The intraflagellar transport protein IFT20 is associated with the Golgi complex and is required for cilia assembly. *Mol. Biol. Cell, 17*, 3781-92. ↗

Ishikawa, H., Marshall, WF. (2011). Ciliogenesis: building the cell's antenna. *Nat. Rev. Mol. Cell Biol., 12*, 222-34. ↗

Huangfu, D., Anderson, KV. (2005). Cilia and Hedgehog responsiveness in the mouse. *Proc. Natl. Acad. Sci. U.S.A., 102*, 11325-30. ↗

Snow, JJ., Leroux, MR., Blacque, OE., Ou, G., Scholey, JM. (2005). Functional coordination of intraflagellar transport motors. *Nature, 436*, 583-7. ↗

Bhogaraju, S., Engel, BD., Lorentzen, E. (2013). Intraflagellar transport complex structure and cargo interactions. *Cilia, 2*, 10. ↗

Editions

2014-08-22	Authored	Rothfels, K.
2014-10-13	Edited	Jassal, B.
2014-11-10	Reviewed	Lorentzen, E.
2014-11-14	Reviewed	Goncalves, J.

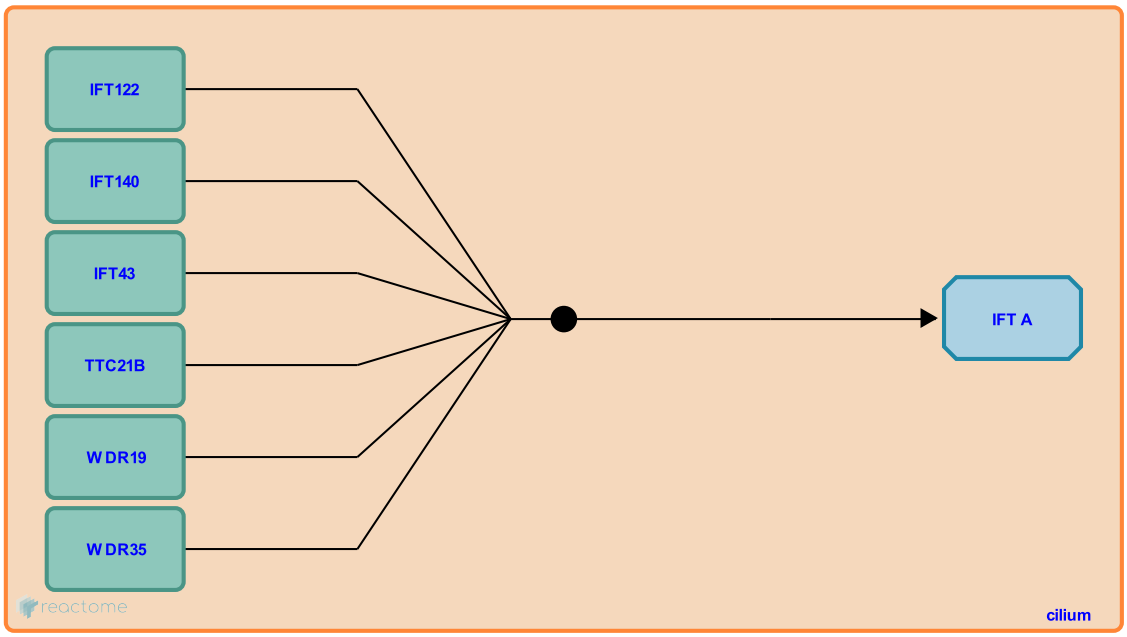
Assembly of IFT A complex ↗

Location: Intraflagellar transport

Stable identifier: R-HSA-5617829

Type: binding

Compartments: cilium



The IFT A complex is believed to be composed of six components: WDR19/IFT144, IFT140, IFT122, TTC21B/IFT139, WDR35/IFT121 and IFT43 (Piperno et al, 1998; Cole and Snell, 2009; reviewed in Taschner et al, 2012). Each of these proteins was identified as a TULP3-interacting protein in human cells, supporting the notion established in other organisms that they are all components of the IFT A complex (Mukhopadhyay et al, 2010; reviewed in Taschner et al, 2012). The IFT A proteins are large and generally have similar domain organization, consisting of N-terminal WD motifs and C-terminal TPR repeats. These protein interaction domains may help the IFT A complex scaffold recruitment of the IFT B complex, as well as recruit ciliary cargo and motor proteins. Intriguingly, the domain structure of IFT A proteins is similar to that of nucleoporins and coat proteins and it has been suggested that they evolved from a coat protein precursor, consistent with a role in vesicle trafficking (Devos et al, 2004; Jekely and Arendt, 2006).
Details of protein-protein interactions within the IFT A complex are not known, nor are the details of how and where the complex assembles in a human cell.

Literature references

Chait, BT., Alber, F., Devos, D., Dokudovskaya, S., Williams, R., Rout, MP. et al. (2004). Components of coated vesicles and nuclear pore complexes share a common molecular architecture. *PLoS Biol., 2*, e380. ↗

Snell, WJ., Cole, DG. (2009). SnapShot: Intraflagellar transport. *Cell, 137*, 784-784.e1. ↗

Piperno, G., Segil, M., Siuda, E., Vaananen, H., Henderson, S., Sassaroli, M. (1998). Distinct mutants of retrograde intraflagellar transport (IFT) share similar morphological and molecular defects. *J. Cell Biol., 143*, 1591-601. ↗

Lane, WS., Scales, SJ., Wen, X., Chih, B., Jackson, PK., Nelson, CD. et al. (2010). TULP3 bridges the IFT-A complex and membrane phosphoinositides to promote trafficking of G protein-coupled receptors into primary cilia. *Genes Dev., 24*, 2180-93. ↗

Arendt, D., Jékely, G. (2006). Evolution of intraflagellar transport from coated vesicles and autogenous origin of the eukaryotic cilium. *Bioessays, 28*, 191-8. ↗

Editions

2014-08-07	Authored	Rothfels, K.
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Assembly of IFT B complex ↗

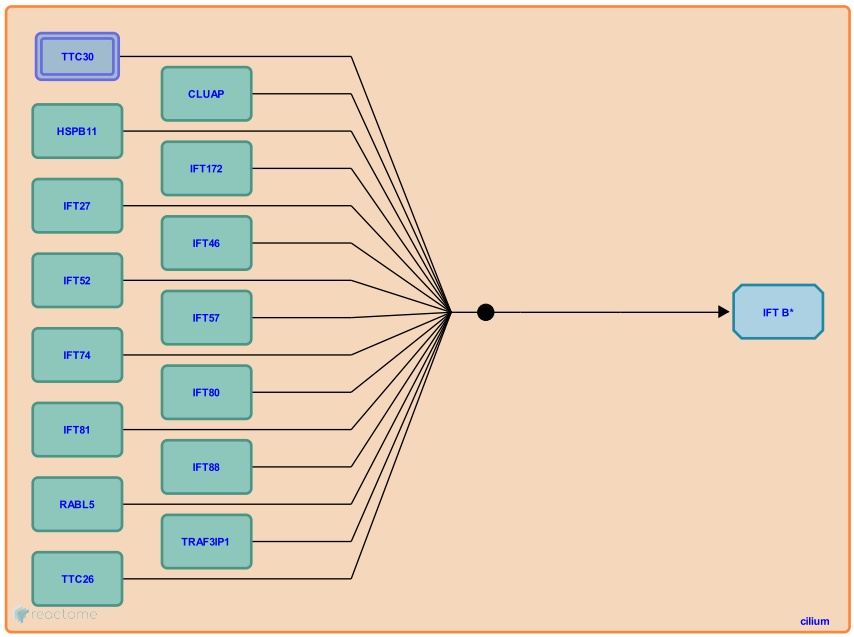
Location: Intraflagellar transport

Stable identifier: R-HSA-5617820

Type: binding

Compartments: cilium

Inferred from: assembly of IftB complex (Mus musculus)



Based on studies done in C. reinhardtii, C. elegans and mouse, the human IFT B complex likely consists of, minimally, IFT20, RABL5/IFT22, HSPB11/IFT25, IFT27, IFT46, IFT52, TRAF3IP1/IFT54, IFT74, IFT80, IFT81, IFT88, CLUAP/QILIN, IFT70/TTC30, and TTC26/IFT56, with IFT172 being an additional candidate (Follit et al, 2009; Piperno and Mead, 1997; Cole et al, 1998; Cole, 2003; Ou, 2007; Hallbritter et al, 2013; reviewed in Taschner et al, 2012). Work in C. reinhardtii and mouse suggests that IFT B consists of a salt stable core complex of IFT88, IFT81, IFT74, IFT70, IFT52, IFT46 IFT 27, IFT25 and IFT22 with peripheral, weakly associated subunits IFT 172, IFT80, IFT57, CLUAP, TTC26 and IFT20 (Lucker et al, 2005; Lucker et al, 2010; Follit et al, 2009; Bhogaraju et al, 2011). In Chlamydomonas, core components IFT81 and IFT74 have been shown to interact directly and a stable sub-complex of IFT81/74/27/25 has been demonstrated (Lucker et al, 2005; Taschner et al, 2011). Human IFT81 and IFT74 have likewise been shown to directly interact and to form a tubulin-binding complex (Bhogaraju et al, 2013). A recent study has elucidated more detail of the protein-protein interactions that direct the assembly of the IFTB complex (Taschner et al, 2014).
This reaction shows putative human IFT B proteins assembling in a single step; details of how and when this assembly occurs are not shown, nor are the specific protein-protein interactions within the complex or details of how IFT B is regulated. Moreover, this reaction shows the formation of a presumptive IFT B* complex, lacking IFT20, to allow the recruitment of IFT20 from the Golgi compartment to be depicted.

Followed by: TRAF3IB1 recruits IFT20 to the IFT B complex from the Golgi

Literature references

Leo, PJ., Gee, HY., Tory, K., Moorani, KN., Leroux, MR., Schmidts, M. et al. (2013). Defects in the IFT-B component IFT172 cause Jeune and Mainzer-Saldino syndromes in humans. *Am. J. Hum. Genet., 93*, 915-25. ↗

Xu, F., Pazour, GJ., Follit, JA., Keady, BT. (2009). Characterization of mouse IFT complex B. *Cell Motil. Cytoskeleton, 66* , 457-68. ↗

Braeuer, P., Kotsis, F., Taschner, M., Lorentzen, E., Kuehn, EW. (2014). Crystal structures of IFT70/52 and IFT52/46 provide insight into intraflagellar transport B core complex assembly. *J. Cell Biol., 207*, 269-82. ↗

Weber, K., Mizuno, N., Fort, C., Bhogaraju, S., Blisnick, T., Nigg, EA. et al. (2013). Molecular basis of tubulin transport within the cilium by IFT74 and IFT81. *Science, 341*, 1009-12. ↗

Miller, MS., Dziedzic, SA., Lucker, BF., Blackmarr, PT., Cole, DG. (2010). Direct interactions of intraflagellar transport complex B proteins IFT88, IFT52, and IFT46. *J. Biol. Chem., 285*, 21508-18. ↗

Editions

2014-08-07	Authored	Rothfels, K.
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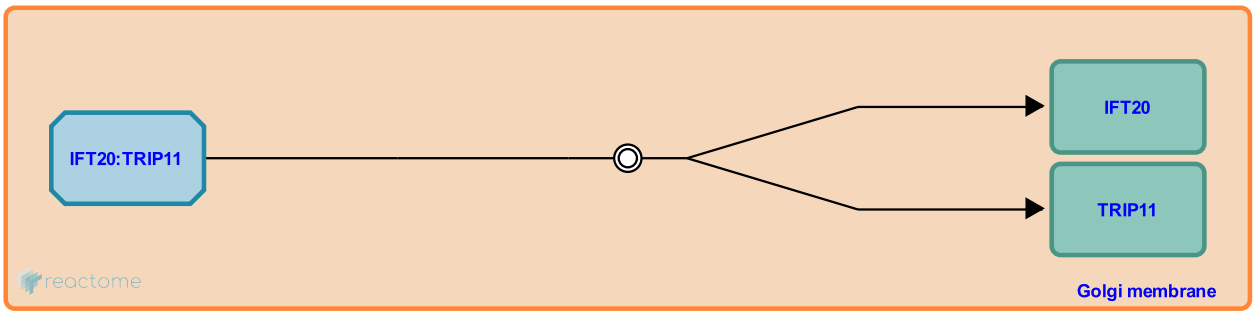
TRIP11:IFT20 dissociates ↗

Location: Intraflagellar transport

Stable identifier: R-HSA-5617828

Type: dissociation

Compartments: Golgi membrane



IFT20 is a member of the IFT B anterograde complex that is required for cilia formation and that, uniquely among IFT proteins, is found at the Golgi in addition to the centrosome and the cilium. Fluorescently-labelled IFT20 shuttles between the Golgi complex and the cilium and the ciliary microtubules (Follit et al, 2006; Follit et al, 2009). Golgi-association of IFT20 depends on interaction with the peripheral membrane protein TRIP11 and this interaction occurs independently of the IFT B complex (Follit et al, 2008). Golgi-localization of IFT20 is abolished in cells lacking TRIP11, and cilia in these cells are short and have a depleted complement of polycystin-2, a ciliary-localized membrane protein (Follit et al, 2008). RNAi-depletion of IFT20 in mammalian cells similarly compromises the traffic of polycystin-2 to the cilium (Follit et al, 2006). These data suggest that IFT20 may have a role at the Golgi complex in sorting and transporting membrane proteins that are destined for the cilium (Follit et al, 2006; Follit et al, 2008; Follit et al, 2009). IFT54, another IFT B component that is localized at the cilia, interacts with IFT20 but not with TRIP11, and overexpression of IFT54 displaces IFT20 from the Golgi. This supports a model where, after dissociation of the TRIP11:IFT20 complex, IFT54 docks IFT20 at the cilium, possibly on the surface of Golgi-derived vesicles, thus completing assembly of the IFT B complex and delivering ciliary membrane and membrane proteins to the site of cilium assembly (Follit et al, 2009; Omori et al, 2008; Li et al, 2008).

Literature references

Tuft, RA., Pazour, GJ., Follit, JA., Fogarty, KE. (2006). The intraflagellar transport protein IFT20 is associated with the Golgi complex and is required for cilia assembly. *Mol. Biol. Cell, 17*, 3781-92. ↗

Zhen, M., Bialas, NJ., Healey, MP., Swoboda, P., Leroux, MR., Inglis, PN. et al. (2008). An essential role for DYF-11/MIP-T3 in assembling functional intraflagellar transport complexes. *PLoS Genet., 4*, e1000044. ↗

Xu, F., Pazour, GJ., Follit, JA., Keady, BT. (2009). Characterization of mouse IFT complex B. *Cell Motil. Cytoskeleton, 66* , 457-68. ↗

Sengupta, P., Malicki, J., Kim, W., Veraksa, A., Mukhopadhyay, S., Zhao, C. et al. (2008). Elipsa is an early determinant of ciliogenesis that links the IFT particle to membrane-associated small GTPase Rab8. *Nat. Cell Biol., 10*, 437-44. ↗

Xu, F., Pazour, GJ., San Agustin, JT., Follit, JA., Jonassen, JA., Lo, CW. et al. (2008). The Golgin GMAP210/TRIP11 anchors IFT20 to the Golgi complex. *PLoS Genet., 4*, e1000315. ↗

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TRAF3IB1 recruits IFT20 to the IFT B complex from the Golgi ↗

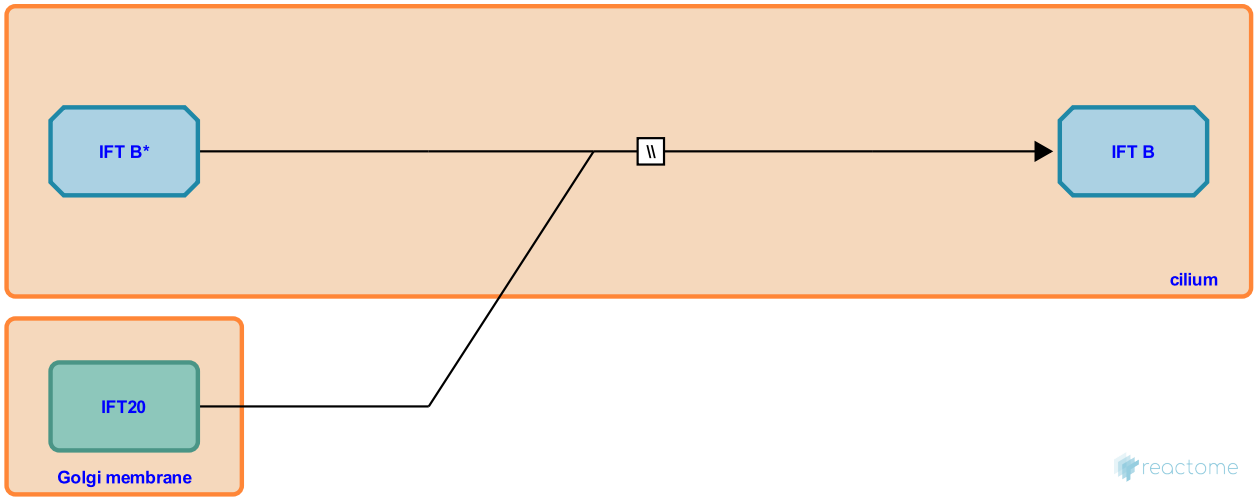
Location: Intraflagellar transport

Stable identifier: R-HSA-5617825

Type: omitted

Compartments: cilium

Inferred from: Traf3ip1 binds Ift20 (Mus musculus)



IFT20 is unique among IFT B components in that, in addition to being localized at the cilium and the centrosome, a pool of IFT20 exists at the Golgi in complex with the golgin protein TRIP11 (Follit et al, 2006; Follit et al, 2008; Follit et al, 2009). Independent of its interaction with TRIP11, IFT20 has been shown to interact with the IFT B complex member TRAF3IP1 at the cilium, and overexpression of TRAF3IP1 displaces IFT20 from the Golgi (Follit et al, 2009). Partial depletion of IFT20 disrupts the traffic of membrane proteins to the cilium (Follit et al, 2006; Follit et al, 2009). Taken together, these data suggest a model where TRAF3IP1 mediates recruitment of IFT20-carrying vesicles from the Golgi to the site of cilium assembly, thus completing assembly of the IFT B complex and delivering both lipid and protein cargo for cilium biogenesis (Follit et al, 2008; Follit et al, 2009; reviewed in Ishikawa et al, 2011).

Preceded by: Assembly of IFT B complex

Literature references

Ishikawa, H., Marshall, WF. (2011). Ciliogenesis: building the cell's antenna. *Nat. Rev. Mol. Cell Biol., 12*, 222-34. ↗

Tuft, RA., Pazour, GJ., Follit, JA., Fogarty, KE. (2006). The intraflagellar transport protein IFT20 is associated with the Golgi complex and is required for cilia assembly. *Mol. Biol. Cell, 17*, 3781-92. ↗

Xu, F., Pazour, GJ., Follit, JA., Keady, BT. (2009). Characterization of mouse IFT complex B. *Cell Motil. Cytoskeleton, 66* , 457-68. ↗

Xu, F., Pazour, GJ., San Agustin, JT., Follit, JA., Jonassen, JA., Lo, CW. et al. (2008). The Golgin GMAP210/TRIP11 anchors IFT20 to the Golgi complex. *PLoS Genet., 4*, e1000315. ↗

Editions

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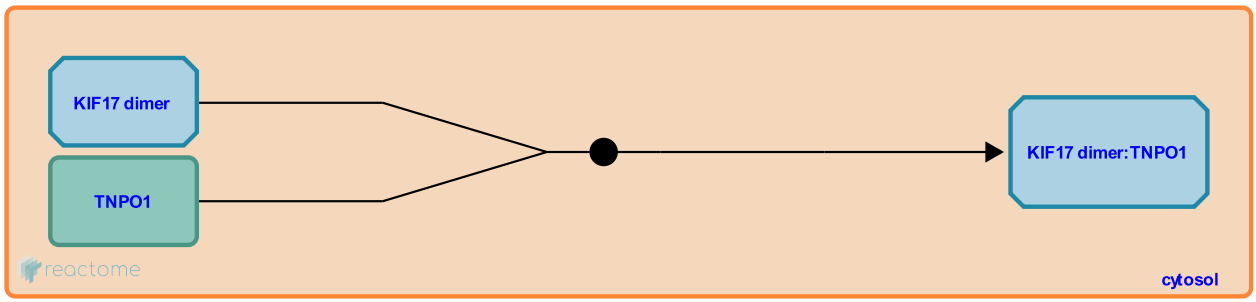
TNPO1 binds KIF17 dimer ↗

Location: Intraflagellar transport

Stable identifier: R-HSA-5624951

Type: binding

Compartments: cytosol



KIF17 is an alternate kinesin-2 motor that is required in some cell types for anterograde IFT and for the ciliary localization of CNG (Ou et al, 2005; Jenkins et al, 2006; Insinna et al, 2008; Insinna et al, 2009; Li et al, 2010; reviewed in Scholey, 2008; Verhey et al, 2011). KIF17 contains a C-terminal ciliary localization signal that mediates its interaction with nuclear import factor TNPO1 (importin beta-2). This interaction is required for the ciliary targeting of KIF17 and is regulated by RAN GTP levels such that the interaction is promoted in the cytosol where RAN:GTP levels are low, and is destabilized in the cilium where RAN:GTP levels are high (Dishinger et al, 2010). The roles of TNPO1 and the RAN:GTP gradient in promoting ciliary localization of KIF17 are analogous to their roles in nuclear import and provide evidence for the first time of conserved mechanisms governing nuclear and ciliary localization (Dishinger et al, 2010; Devos et al, 2004; Gruss, 2010).

Followed by: KIF17 enters the cilium

Literature references

Chait, BT., Alber, F., Devos, D., Dokudovskaya, S., Williams, R., Rout, MP. et al. (2004). Components of coated vesicles and nuclear pore complexes share a common molecular architecture. *PLoS Biol., 2*, e380. ↗

Kee, HL., Verhey, KJ., Dishinger, J. (2011). Kinesin motors and primary cilia. *Biochem. Soc. Trans., 39*, 1120-5. ↗

Sedmak, T., Humby, M., Insinna, C., Wolfrum, U., Besharse, JC. (2009). Different roles for KIF17 and kinesin II in photoreceptor development and maintenance. *Dev. Dyn., 238*, 2211-22. ↗

Snow, JJ., Leroux, MR., Blacque, OE., Ou, G., Scholey, JM. (2005). Functional coordination of intraflagellar transport motors. *Nature, 436*, 583-7. ↗

Gruss, OJ. (2010). Nuclear transport receptor goes moonlighting. *Nat. Cell Biol., 12*, 640-1. ↗

Editions

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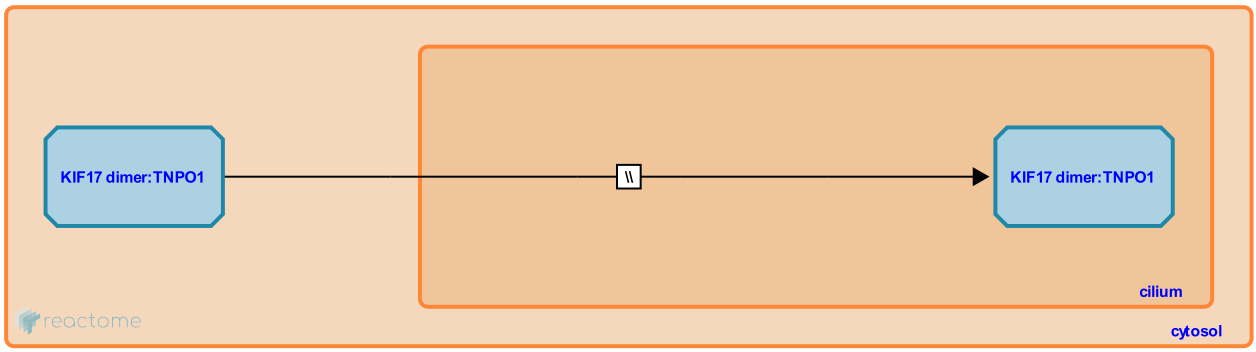
KIF17 enters the cilium ↗

Location: Intraflagellar transport

Stable identifier: R-HSA-5624948

Type: omitted

Compartments: cilium



Ciliary localization of the alternative kinesin-2 motor KIF17 depends on TNPO1 and the RAN:GDP/RAN:GTP gradient. Once in the cilium, the TNPO1:KIF17 complex is likely dissociated by RAN:GTP binding and subsequent GTP hydrolysis, freeing KIF17 to play its role in anterograde IFT transport (Dishinger et al, 2010).

Preceded by: TNPO1 binds KIF17 dimer

Literature references

Hurd, TW., Kee, HL., Martens, JR., Truong, YN., Hammond, JW., Jenkins, PM. et al. (2010). Ciliary entry of the kinesin-2 motor KIF17 is regulated by importin-beta2 and RanGTP. *Nat. Cell Biol., 12*, 703-10. ↗

Editions

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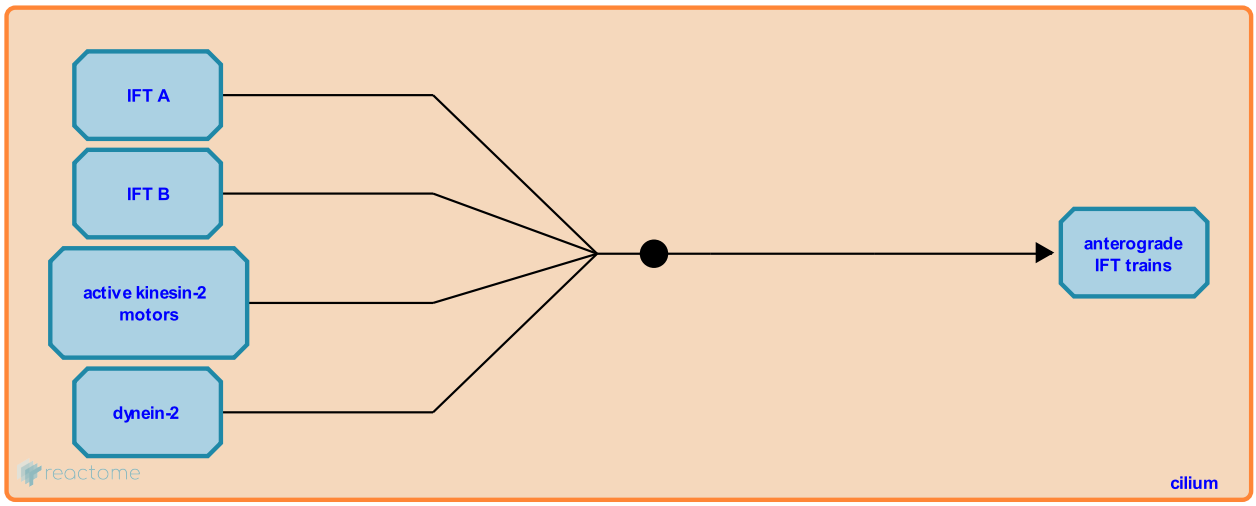
Assembly of the anterograde IFT train ↗

Location: Intraflagellar transport

Stable identifier: R-HSA-5624949

Type: binding

Compartments: cilium



IFT particles were first characterized in Chlamydomonas reinhardtii, where they were observed by differential interference contrast microscopy as electron-dense granules that move along doublet microtubules of the ciliary axoneme (Kozminski et al, 1993; Kozminski et al, 1995; reviewed in Pedersen et al, 2008). More recent ultrastructural analysis of Chlamydomonas flagella confirms the presence of two distinct types of IFT trains, a longer, less electron-opaque anterograde train and shorter, more opaque retrograde trains. Both the anterograde and retrograde trains are associated with the outer microtubule doublets and with the inner surface of the flagellar membrane (Pigino et al, 2009). Isolation and characterization of IFT particles revealed that they consist of 2 biochemically distinct subcomplexes, IFT A and IFT B that are widely conserved in ciliated organisms (Piperno et al, 1997; Cole et al, 1998; reviewed in Sung and Leroux, 2013). Anterograde traffic is driven by kinesin-2 type motors in an ATP-dependent manner. Evidence from C. elegans suggests distinct and sequential roles for the canonical heterotrimeric kinesin-2 motor and the alternate homodimeric kinesin-2, OSM-3 (homologue of human KIF17) in mediating anterograde transport, but this has not been demonstrated in human cells where the canonical kinesin-2 motor predominates (Evans et al, 2006; Snow et al, 2004; Ou et al, 2005). Human KIF17 appears to be required in some cell types for cilia formation, and plays a role in the import of some ciliary cargo (Jenkins et al, 2006; Insinna et al, 2008; Insinna et al, 2009; Dishinger et al, 2010; reviewed in Verhey et al, 2011). Assembly of the anterograde IFT trains at the base of the cilium may be facilitated by the BBSome complex, which has also been shown to display IFT-like movement along the axoneme; however, the BBSome is highly sub-stoichiometric with respect to the IFT complex, so this notion requires more substantiation (Ou et al, 2005; Wei et al, 2012; Blacque et al, 2004; Nachury et al, 2007; Lechtreck et al, 2009; reviewed in Sung and Leroux, 2013). Studies in C. elegans also suggest a role for ARL13B and ARL3 in regulating the stability of the anterograde IFT train (Li et al, 2010).

Followed by: Anterograde IFT

Literature references

Sedmak, T., Humby, M., Insinna, C., Wolfrum, U., Besharse, JC. (2009). Different roles for KIF17 and kinesin II in photoreceptor development and maintenance. *Dev. Dyn., 238*, 2211-22. ↗

Snow, JJ., Gunnarson, AL., McDonald, KL., Stahlberg, H., Ou, G., Evans, JE. et al. (2006). Functional modulation of IFT kinesins extends the sensory repertoire of ciliated neurons in Caenorhabditis elegans. *J. Cell Biol., 172*, 663-9. ↗

Snow, JJ., Leroux, MR., Blacque, OE., Ou, G., Scholey, JM. (2005). Functional coordination of intraflagellar transport motors. *Nature, 436*, 583-7. ↗

Ling, K., Wei, Q., Hu, J., Zhang, Q., Li, Y., Zhang, Y. (2012). The BBSome controls IFT assembly and turnaround in cilia. *Nat. Cell Biol., 14*, 950-7. ↗

Zhang, L., Hurd, TW., Martens, JR., Brown, RL., Jenkins, PM., Verhey, KJ. et al. (2006). Ciliary targeting of olfactory CNG channels requires the CNGB1b subunit and the kinesin-2 motor protein, KIF17. *Curr. Biol., 16*, 1211-6. ↗

Editions

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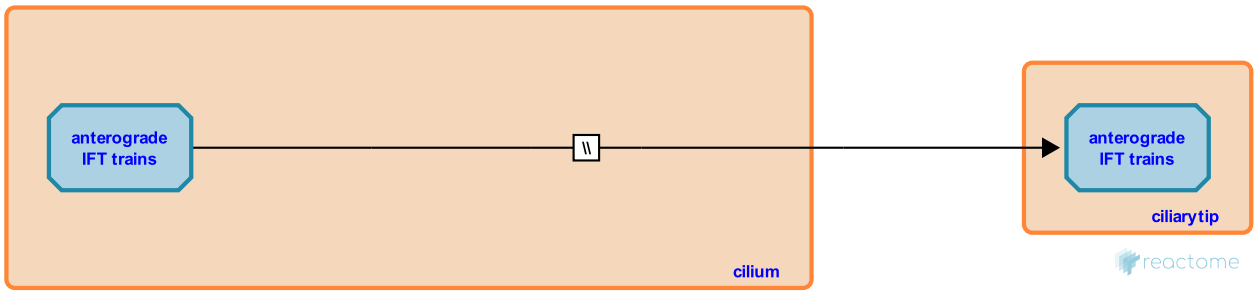
Anterograde IFT ↗

Location: Intraflagellar transport

Stable identifier: R-HSA-5625416

Type: omitted

Compartments: cilium



Anterograde trains travel along the axoneme of the cilium at an estimated rate of 2 micrometers per second in an ATP- and kinesin-2-dependent fashion (reviewed in Cole and Snell, 2009). Although the particulars of IFT train-cargo interactions have not been fully elaborated, recent studies in C. reinhardtii and human cells have shown that the IFT B components IFT74 and IFT81 have tubulin-binding sites, while IFT46 is required for the ciliary transport of the outer dynein arm, and more recently, TTC26 has been shown to be required for the transport of motility-related proteins into the flagella (Bhogaraju et al, 2013; Ahmed et al, 2008; Hou et al, 2007; Ishikawa et al, 2014; reviewed in Bhogarju et al, 2014).

Preceded by: Assembly of the anterograde IFT train

Followed by: The anterograde IFT train dissociates

Literature references

Witman, GB., Hou, Y., Pazour, GJ., Follit, JA., Qin, H., Rosenbaum, JL. (2007). Functional analysis of an individual IFT protein: IFT46 is required for transport of outer dynein arms into flagella. *J. Cell Biol., 176*, 653-65. ↗

Snell, WJ., Cole, DG. (2009). SnapShot: Intraflagellar transport. *Cell, 137*, 784-784.e1. ↗

Weber, K., Mizuno, N., Fort, C., Bhogaraju, S., Blisnick, T., Nigg, EA. et al. (2013). Molecular basis of tubulin transport within the cilium by IFT74 and IFT81. *Science, 341*, 1009-12. ↗

Mitchell, DR., Lucker, BF., Gao, C., Ahmed, NT., Cole, DG. (2008). ODA16 aids axonemal outer row dynein assembly through an interaction with the intraflagellar transport machinery. *J. Cell Biol., 183*, 313-22. ↗

Stainier, DY., Ide, T., Jiang, X., Ishikawa, H., Marshall, WF., Qin, H. et al. (2014). TTC26/DYF13 is an intraflagellar transport protein required for transport of motility-related proteins into flagella. *Elife, 3*, e01566. ↗

Editions

2014-10-04	Authored	Rothfels, K.
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2014-11-14	Reviewed	Goncalves, J.

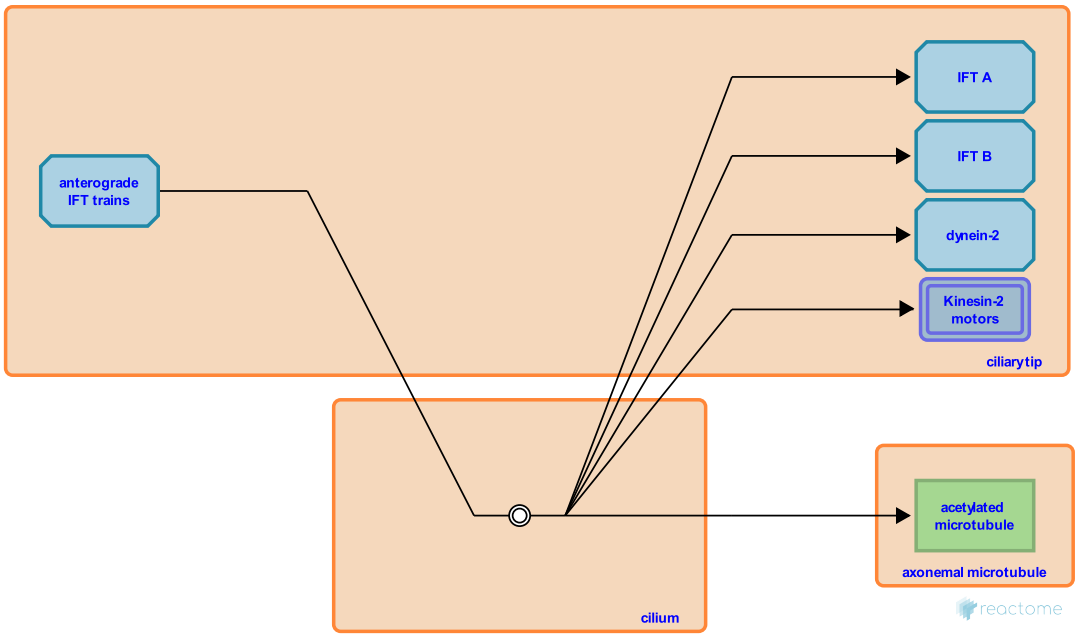
The anterograde IFT train dissociates ↗

Location: Intraflagellar transport

Stable identifier: R-HSA-5625421

Type: dissociation

Compartments: cilium



Based on work done in C. reinhardtii and Trypanosoma brucei, anterograde IFT trains are believed to disassemble at the ciliary tip, releasing cargo and the IFT motors. Smaller retrograde trains are subsequently reassembled for transport back to the ciliary base (Iomini et al, 2001; Buisson et al, 2013; Pigino et al, 2009; reviewed in Ishikawa et al, 2011; Bhogaraju et al, 2013). A direct interaction between IFT27 and the nucleotide-free form of ARL6 may contribute to ARL6 activation and in this way contribute to ciliary exit of some cargo (Liew et al, 2014).

Preceded by: Anterograde IFT

Followed by: Assembly of the retrograde IFT train

Literature references

Ishikawa, H., Marshall, WF. (2011). Ciliogenesis: building the cell's antenna. *Nat. Rev. Mol. Cell Biol., 12*, 222-34. ↗

Pigino, G., Lanzavecchia, S., Lupetti, P., Geimer, S., Diener, DR., Paccagnini, E. et al. (2009). Electron-tomographic analysis of intraflagellar transport particle trains in situ. *J. Cell Biol., 187*, 135-48. ↗

Babaev-Khaimov, V., Piperno, G., Iomini, C., Sassaroli, M. (2001). Protein particles in Chlamydomonas flagella undergo a transport cycle consisting of four phases. *J. Cell Biol., 153*, 13-24. ↗

Ye, F., Aguiar, M., Nager, A R., Gygi, S., Murphy, J P., Liew, G M. et al. (2014). The intraflagellar transport protein IFT27 promotes BBSome exit from cilia through the GTPase ARL6/BBS3. *DevCell, 31*, 265-278. ↗

Bhogaraju, S., Engel, BD., Lorentzen, E. (2013). Intraflagellar transport complex structure and cargo interactions. *Cilia, 2*, 10. ↗

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2014-09-30	Authored	Rothfels, K.
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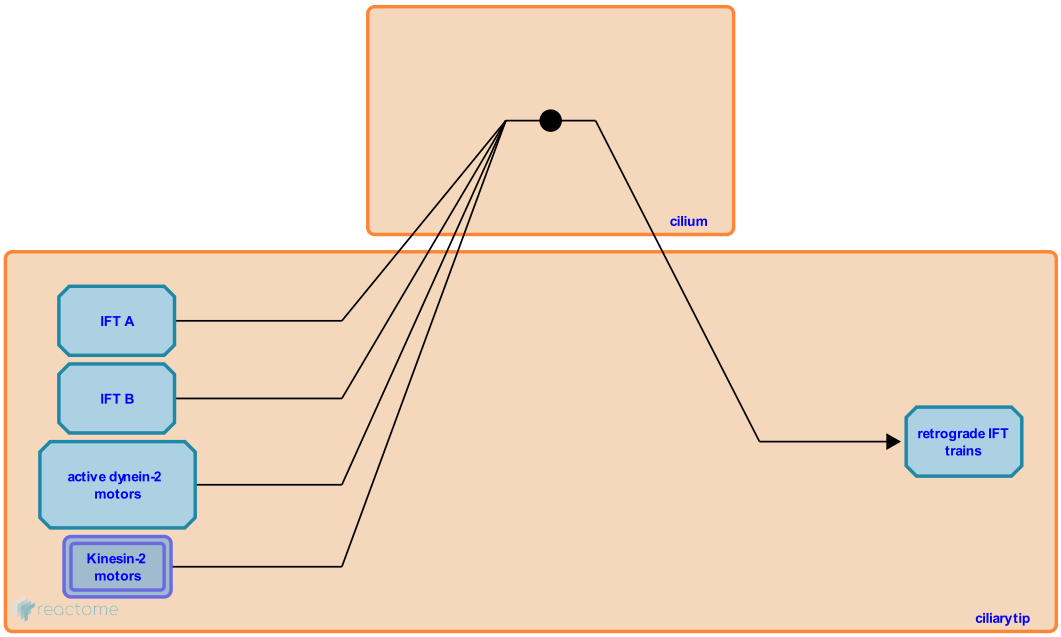
Assembly of the retrograde IFT train ↗

Location: Intraflagellar transport

Stable identifier: R-HSA-5624952

Type: binding

Compartments: cilium



Remodelling of IFT trains is thought to occur at the ciliary tip (Iomini et al, 2001; Buisson et al, 2013; reviewed in Snell and Cole, 2009). Retrograde transport is driven by the multi-subunit dynein-2 motor in an ATP-dependent fashion (Hou et al, 2004; Pazour et al, 1999; Porter et al, 1999; reviewed in Cole and Snell, 2009; Ishikawa et al, 2011). Mutations in genes encoding members of the IFT A complex or the dynein-2 motor generally result in short, swollen cilia that abnormally acccumulate IFT components (Iomini et al, 2009; Piperno et al, 1998; Pazour et al, 1999). The subunit composition of the human dynein-2 complex has recently been analyzed and preliminary characterization of the IFT A complex has begun, but detailed understanding of the molecular architecture of the retrograde IFT trains is still lacking (Assante et al, 2014; Piperno et al, 1998; Mukhopadhyay et al, 2010; reviewed in Taschner et al, 2012).

Preceded by: The anterograde IFT train dissociates

Followed by: Retrograde IFT

Literature references

Ishikawa, H., Marshall, WF. (2011). Ciliogenesis: building the cell's antenna. *Nat. Rev. Mol. Cell Biol., 12*, 222-34. ↗

Witman, GB., Hou, Y., Pazour, GJ. (2004). A dynein light intermediate chain, D1bLIC, is required for retrograde intraflagellar transport. *Mol. Biol. Cell, 15*, 4382-94. ↗

Snell, WJ., Cole, DG. (2009). SnapShot: Intraflagellar transport. *Cell, 137*, 784-784.e1. ↗

Witman, GB., Pazour, GJ., Wilkerson, CG. (1998). A dynein light chain is essential for the retrograde particle movement of intraflagellar transport (IFT). *J. Cell Biol., 141*, 979-92. ↗

Babaev-Khaimov, V., Piperno, G., Iomini, C., Sassaroli, M. (2001). Protein particles in Chlamydomonas flagella undergo a transport cycle consisting of four phases. *J. Cell Biol., 153*, 13-24. ↗

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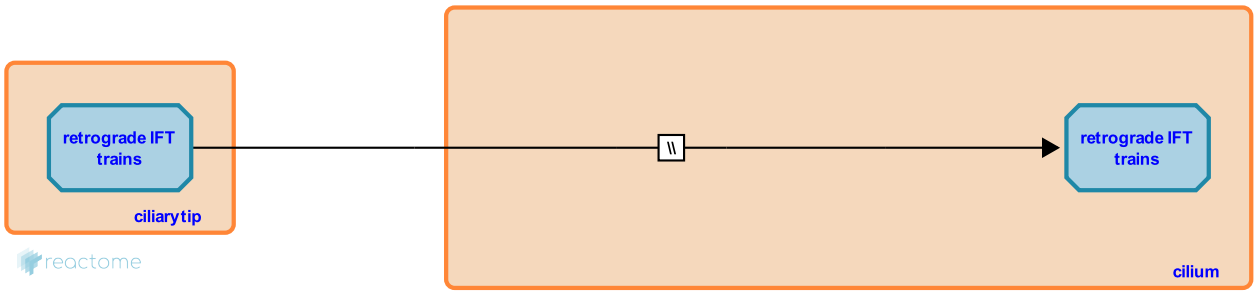
Retrograde IFT ↗

Location: Intraflagellar transport

Stable identifier: R-HSA-5625426

Type: omitted

Compartments: cilium



Retrograde trains are shorter than anterograde particles and travel along the cilliary axoneme at an estimated rate of 3 micrometers per second (reviewed in Cole and Snell, 2009).

Preceded by: Assembly of the retrograde IFT train

Followed by: The retrograde IFT train dissociates

Literature references

Snell, WJ., Cole, DG. (2009). SnapShot: Intraflagellar transport. *Cell, 137*, 784-784.e1. ↗

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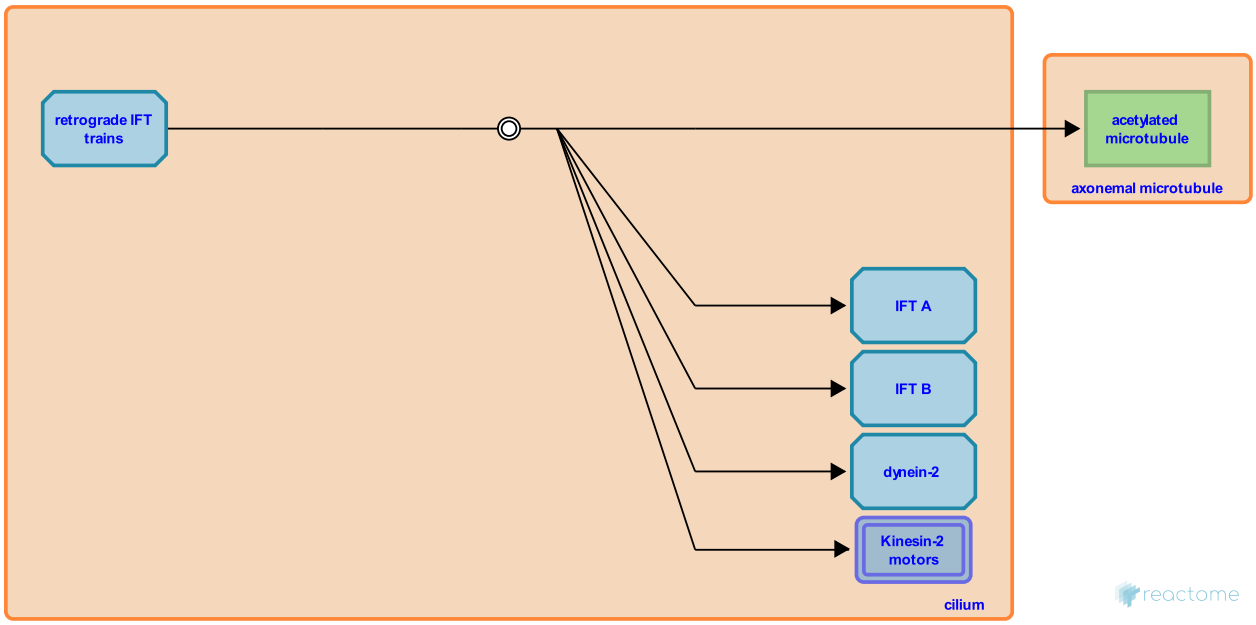
The retrograde IFT train dissociates ↗

Location: Intraflagellar transport

Stable identifier: R-HSA-5625424

Type: dissociation

Compartments: cilium



At the base of the cilium, retrograde trains are believed to disassemble and recycle for a subsequent round of IFT transport (Iomini et al, 2001; Buisson et al, 2013; reviewed in Ishikawa et al, 2011; Cole and Snell, 2009).

Preceded by: Retrograde IFT

Literature references

Ishikawa, H., Marshall, WF. (2011). Ciliogenesis: building the cell's antenna. *Nat. Rev. Mol. Cell Biol., 12*, 222-34. ↗

Snell, WJ., Cole, DG. (2009). SnapShot: Intraflagellar transport. *Cell, 137*, 784-784.e1. ↗

Babaev-Khaimov, V., Piperno, G., Iomini, C., Sassaroli, M. (2001). Protein particles in Chlamydomonas flagella undergo a transport cycle consisting of four phases. *J. Cell Biol., 153*, 13-24. ↗

Blisnick, T., Buisson, J., Bastin, P., Olivo-Marin, JC., Lagache, T., Chenouard, N. (2013). Intraflagellar transport proteins cycle between the flagellum and its base. *J. Cell. Sci., 126*, 327-38. ↗

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