

# Assembly of IFT A complex

Goncalves, J., Jassal, B., Lorentzen, E., Rothfels, K.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

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

- 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: 88

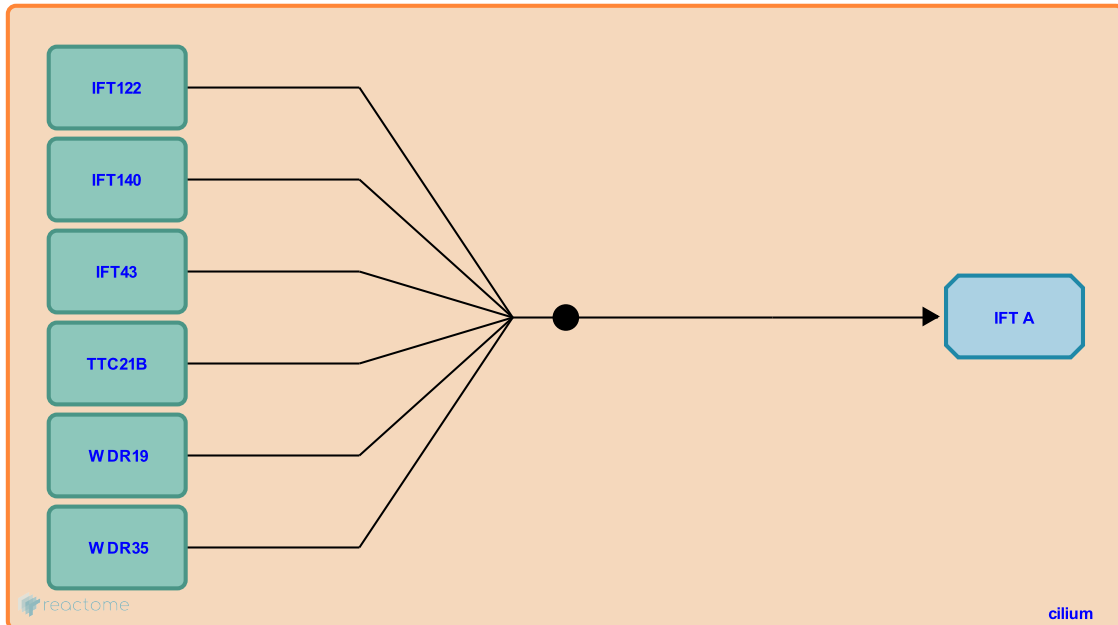
This document contains 1 reaction ([see Table of Contents](#))

## Assembly of IFT A complex ↗

**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; Jékely 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.
2014-10-13	Edited	Jassal, B.
2014-11-10	Reviewed	Lorentzen, E.
2014-11-14	Reviewed	Goncalves, J.