

# ULK3:SUFU dissociates

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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.

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## 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

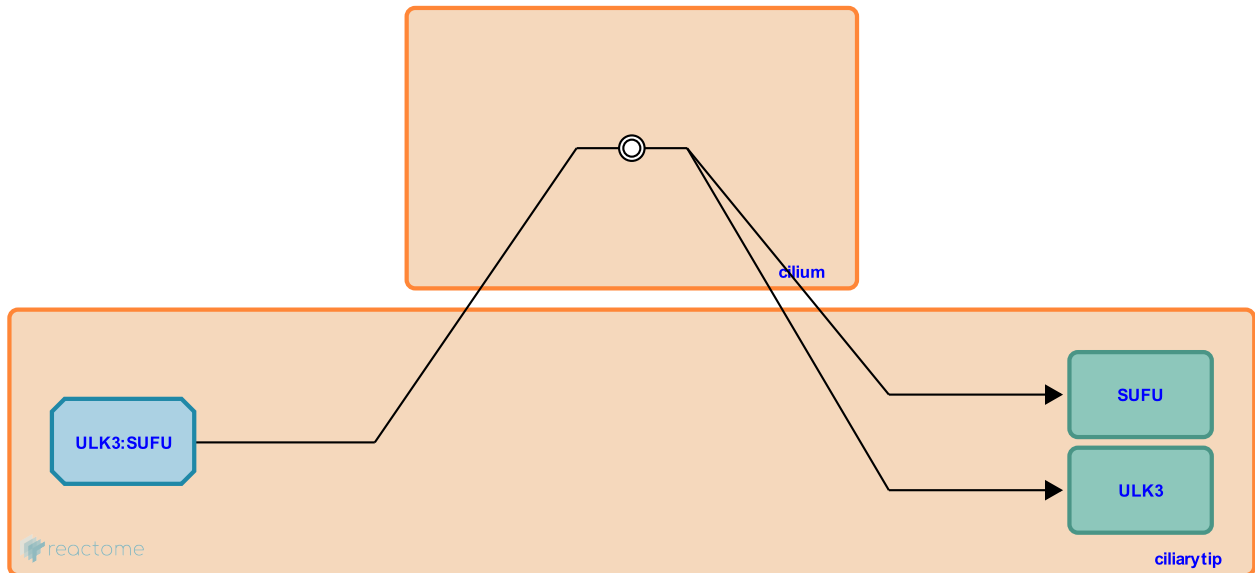
This document contains 1 reaction ([see Table of Contents](#))

## ULK3:SUFU dissociates [↗](#)

**Stable identifier:** R-HSA-5635839

**Type:** dissociation

**Compartments:** cilium



ULK3 is a serine-threonine kinase that was identified as a positive regulator of Hh signaling that regulates GLI activity by phosphorylating the full-length form (Maloverjan et al, 2010a). In the absence of Hh ligand, ULK3 forms a complex with SUFU that restricts its kinase activity (Maloverjan et al, 2010b). Upon Hh stimulation, the ULK3:SUFU complex dissociates, allowing ULK3 to phosphorylate the full-length GLI proteins and promoting their activation and nuclear localization (Maloverjan et al, 2010a; Maloverjan et al, 2010b). ULK3 is related by sequence to the vertebrate kinase STK36, homologue to *Drosophila* Fused (Fu). While Fu plays a critical role in propagating Hh signal and is part of the Hedgehog signaling complex (HSC), STK36 is not required for Hh signaling in vertebrate cells but instead contributes to the formation of motile cilia (Wilson et al, 2009; reviewed in Briscoe and Therond, 2013; Maloverjan and Piirsoo, 2012).

### Literature references

- Piirsoo, M., Maloverjan, A. (2012). Mammalian homologues of *Drosophila* fused kinase. *Vitam. Horm.*, 88, 91-113. [↗](#)
- Huang, J., Chen, JN., Chuang, PT., Gacayan, R., Yang, JH., Nguyen, CT. et al. (2009). Fused has evolved divergent roles in vertebrate Hedgehog signalling and motile ciliogenesis. *Nature*, 459, 98-102. [↗](#)
- Kogerman, P., Kasak, L., Piirsoo, M., Maloverjan, A., Østerlund, T., Peil, L. (2010). Dual function of UNC-51-like kinase 3 (Ulk3) in the Sonic hedgehog signaling pathway. *J. Biol. Chem.*, 285, 30079-90. [↗](#)
- Thérond, PP., Briscoe, J. (2013). The mechanisms of Hedgehog signalling and its roles in development and disease. *Nat. Rev. Mol. Cell Biol.*, 14, 416-29. [↗](#)
- Kogerman, P., Osterlund, T., Piirsoo, M., Maloverjan, A., Michelson, P. (2010). Identification of a novel serine/threonine kinase ULK3 as a positive regulator of Hedgehog pathway. *Exp. Cell Res.*, 316, 627-37. [↗](#)

### Editions

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