

ROK phosphorylates SQH

Axelrod, JD., Williams, MG.

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

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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

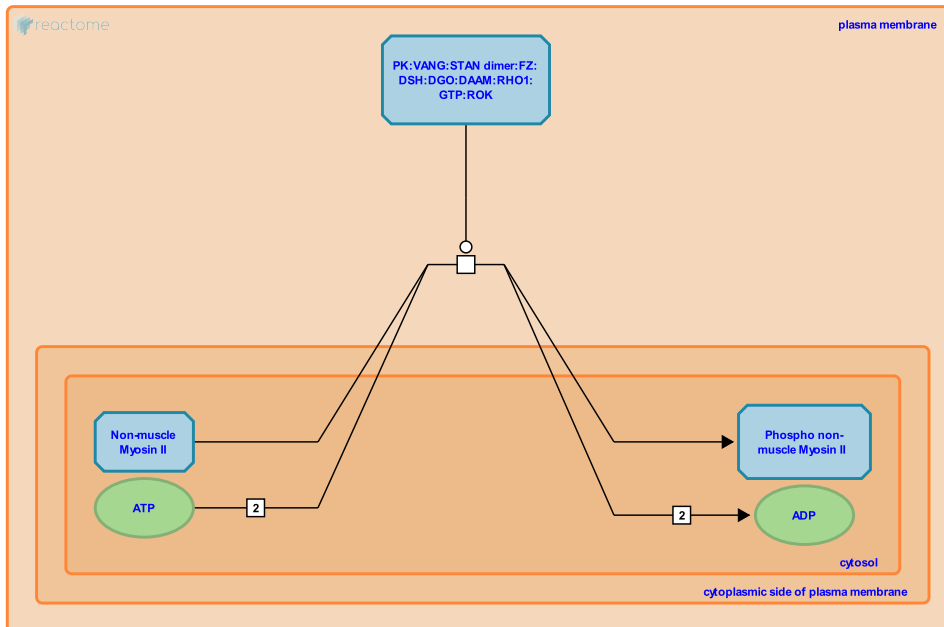
This document contains 1 reaction ([see Table of Contents](#))

ROK phosphorylates SQH [↗](#)

Stable identifier: R-DME-350444

Type: transition

Compartments: cytosol, plasma membrane



Myosin regulatory light chain (MRLC) orthologue Spaghetti Squash (SQH) is phosphorylated at Thr20 and Ser21 by Rho-kinase (ROK). Zipper (ZIP) the myosin heavy chain orthologue would be expected to have its conformation modified and catalytic activity elevated upon SQH phosphorylation. This leads to cytoskeletal organisation and correct pre-hair orientation.

Literature references

White-Cooper, H., Kirchner, J., Bennett, D., Vereshchagina, N., Alphey, L., Vissi, E. et al. (2004). The essential role of PP1beta in *Drosophila* is to regulate nonmuscle myosin. *Mol Biol Cell*, 15, 4395-405. [↗](#)

Winter, CG., Axelrod, JD., Ballew, A., Royou, A., Wang, B., Karess, R. et al. (2001). *Drosophila* Rho-associated kinase (Drok) links Frizzled-mediated planar cell polarity signaling to the actin cytoskeleton. *Cell*, 105, 81-91. [↗](#)

Editions

| | | |
|------------|----------|---------------|
| 2008-05-20 | Authored | Williams, MG. |
| 2009-11-19 | Reviewed | Axelrod, JD. |
| 2014-05-20 | Edited | Williams, MG. |