

LKB1 forms a trimeric complex with STRAD and MO25

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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

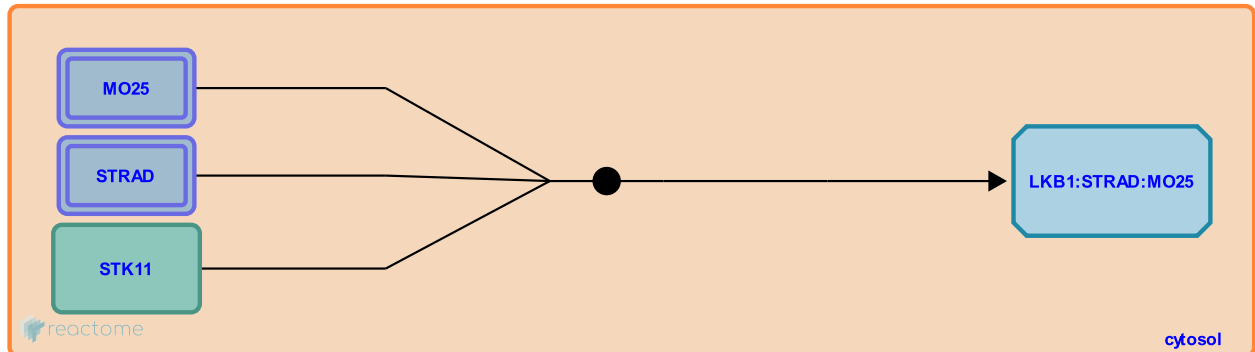
This document contains 1 reaction ([see Table of Contents](#))

LKB1 forms a trimeric complex with STRAD and MO25 [↗](#)

Stable identifier: R-HSA-380942

Type: binding

Compartments: cytosol



Upon complex formation with STRAD and MO25, LKB1 (also known as serine/threonine kinase 11, STK11) is mostly cytosolic. LKB1 attains 20x activity towards the substrates belonging to the subfamily of AMPK-like kinases (5'AMP-activated protein kinases).

Literature references

Clevers, HC., Medema, R., Smit, L., Alessi, DR., Baas, AF., Morrice, NA. et al. (2003). Activation of the tumour suppressor kinase LKB1 by the STE20-like pseudokinase STRAD. *EMBO J*, 22, 3062-72. [↗](#)

Prescott, AR., Clevers, HC., Schutkowski, M., Kieloch, A., Alessi, DR., Deak, M. et al. (2003). MO25alpha/beta interact with STRADalpha/beta enhancing their ability to bind, activate and localize LKB1 in the cytoplasm. *EMBO J*, 22, 5102-14. [↗](#)

Editions

2008-11-19	Edited	Jassal, B.
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