

SCF-FBXL7 ubiquitinates AURKA

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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

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- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
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Reactome database release: 88

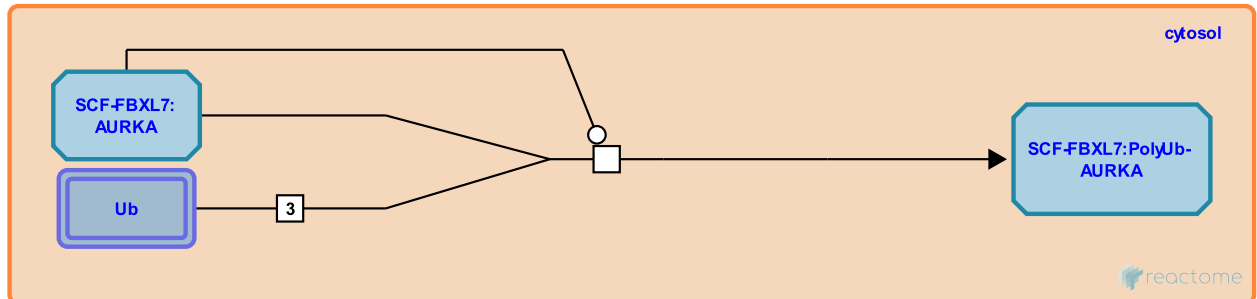
This document contains 1 reaction ([see Table of Contents](#))

SCF-FBXL7 ubiquitinates AURKA [↗](#)

Stable identifier: R-HSA-8854041

Type: transition

Compartments: cytosol



The SCF-FBXL7 E3 ubiquitin ligase complex, composed of SKP1, CUL1, RBX1 and FBXL7, ubiquitinates aurora kinase A (AURKA), targeting it for degradation (Coon et al. 2012).

Literature references

Glasser, JR., Chen, BB., Coon, TA., Mallampalli, RK. (2012). Novel E3 ligase component FBXL7 ubiquitinates and degrades Aurora A, causing mitotic arrest. *Cell Cycle*, 11, 721-9. [↗](#)

Editions

2016-01-27	Authored, Edited	Orlic-Milacic, M.
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