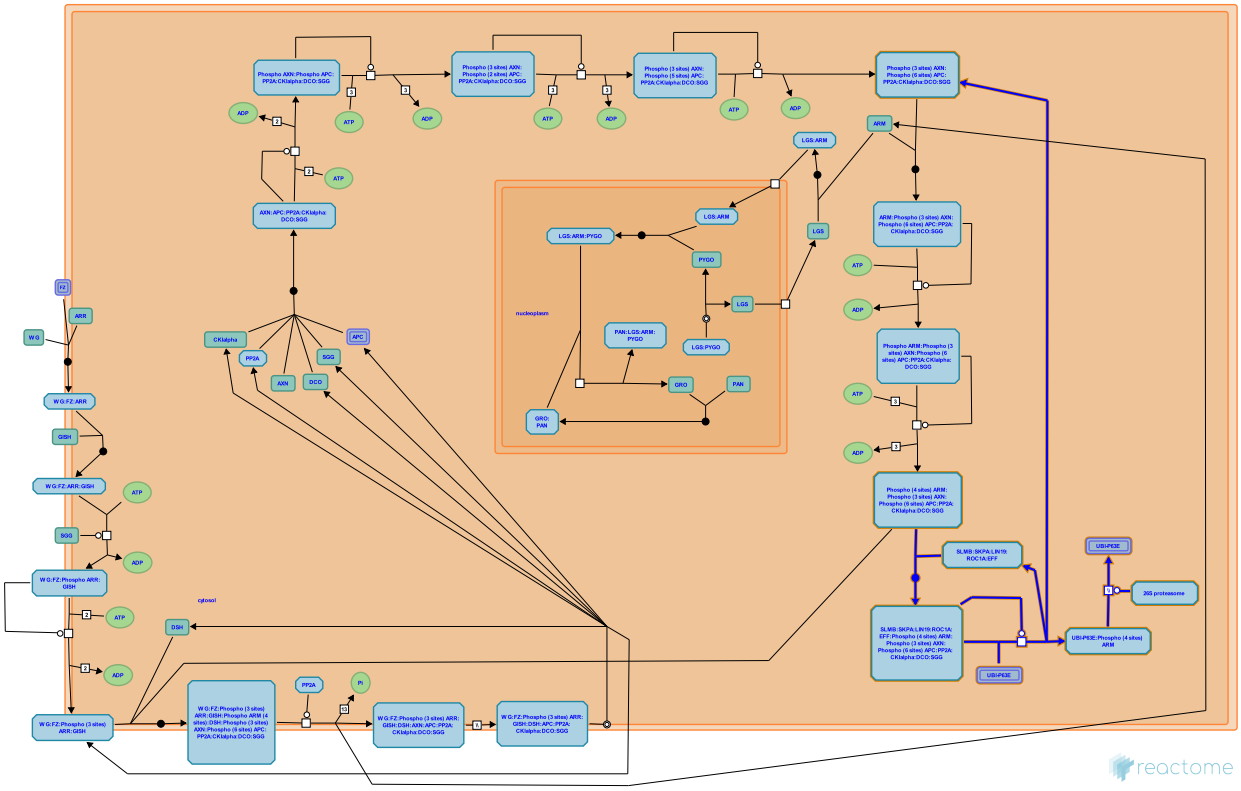
Ubiquitination and degradation of phosphorylated ARM



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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

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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.
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. ↗

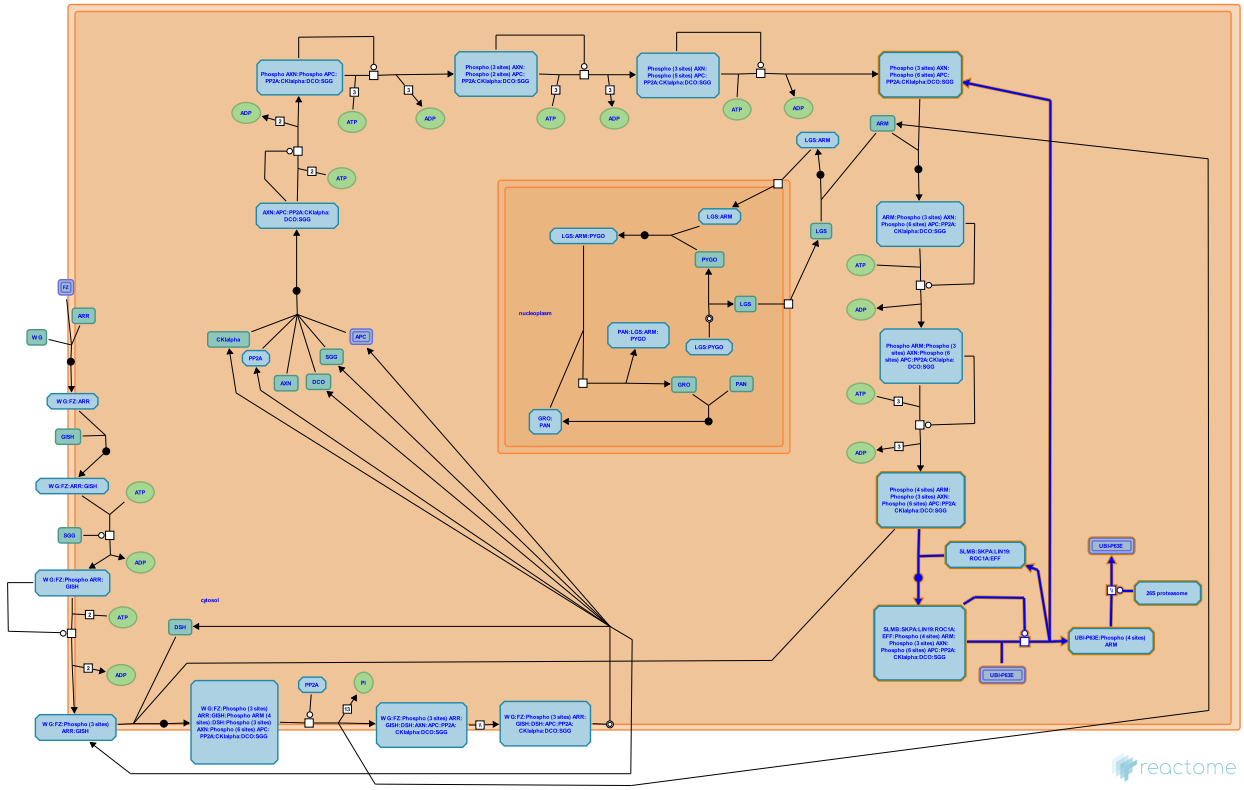
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Ubiquitination and degradation of phosphorylated ARM ↗

Stable identifier: R-DME-209461

Compartments: cytosol



Spatzle (SPZ) dimer binding leads to Toll (TL) receptor homodimerisation and activation.

Literature references

Tolwinski, NS., Wieschaus, E. (2004). Rethinking WNT signaling. *Trends Genet, 20*, 177-81. ↗

Kikuchi, A., Yamamoto, H., Kishida, S. (2006). Regulation of Wnt signaling by protein-protein interaction and post-translational modifications. *Exp Mol Med, 38*, 1-10. ↗

Logan, CY., Nusse, R. (2004). The Wnt signaling pathway in development and disease. *Annu Rev Cell Dev Biol, 20*, 781-810. ↗

Editions

2006-07-26	Authored, Edited	Williams, MG.
2008-01-19	Reviewed	Nusse, R.

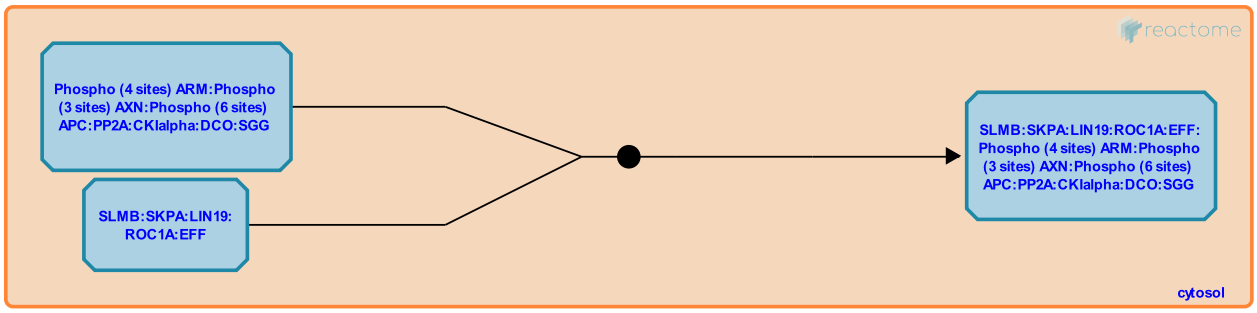
SLMB binds to phosphorylated ARM to form the 'destruction complex' ↗

Location: Ubiquitination and degradation of phosphorylated ARM

Stable identifier: R-DME-209102

Type: binding

Compartments: cytosol



The phosphorylated Armadillo (ARM) is now recognised and bound by the F-box protein Slimb (SLMB), in the E3 ubiquitin ligase assembled complex additionally containing the S-phase kinase-associated protein SKPA, the Cullin orthologue, LIN19, the Ring-box protein containg ROC1A, and the ubiquitin-conjugating enzyme orthologue EFF.

Preceded by: Dissociation of free ubiquitinated and phosphorylated ARM from SLMB and the 'destruction complex'

Followed by: Dissociation of free ubiquitinated and phosphorylated ARM from SLMB and the 'destruction complex'

Editions

2006-07-26	Authored	Williams, MG.
2008-01-19	Reviewed	Nusse, R.
2014-05-20	Edited	Williams, MG.

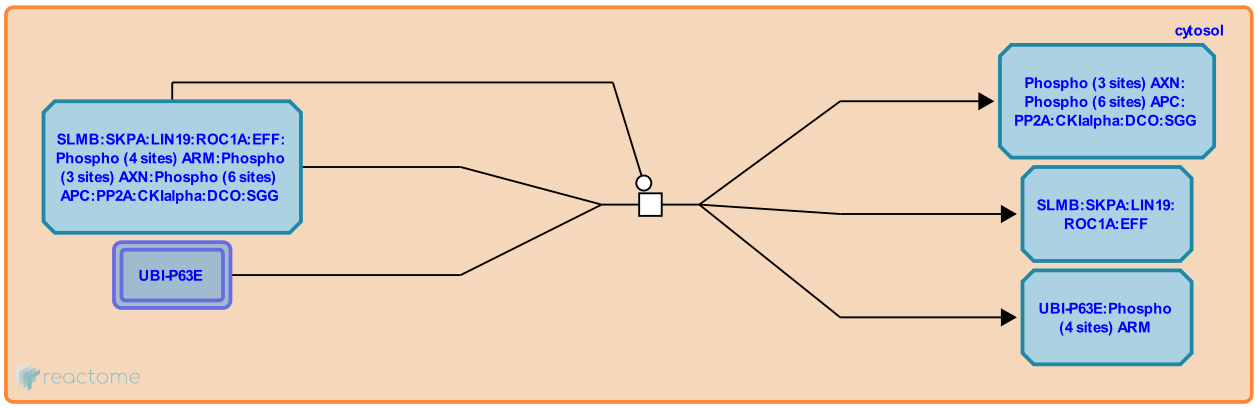
Dissociation of free ubiquitinated and phosphorylated ARM from SLMB and the 'destruction complex' ↗

Location: Ubiquitination and degradation of phosphorylated ARM

Stable identifier: R-DME-209094

Type: transition

Compartments: cytosol



The bound and phosphorylated Armadillo (ARM) is ubiquitated by the ubiquitin ligase assembled complex, whether this occurs when ARM is bound to the 'destruction complex' or after it has dissociated from it is unclear. The interaction between Slimb (SLMB) and ARM has weakened the latter's binding to the scaffolding molecules in the 'destruction complex'. ARM and the bound ubiquitin ligase assembled complex dissociate from Axin (AXN), APC (APC/APC2) and also from each other to leave free ubiquitinated and phosphorylated ARM which is now marked for degradation by the 26S proteasome.

Preceded by: SLMB binds to phosphorylated ARM to form the 'destruction complex'

Followed by: Ubiquitinated and phosphorylated ARM binds to and is degraded by the proteasome complex, SLMB binds to phosphorylated ARM to form the 'destruction complex'

Editions

2006-07-26	Authored	Williams, MG.
2008-01-19	Reviewed	Nusse, R.
2014-05-20	Edited	Williams, MG.

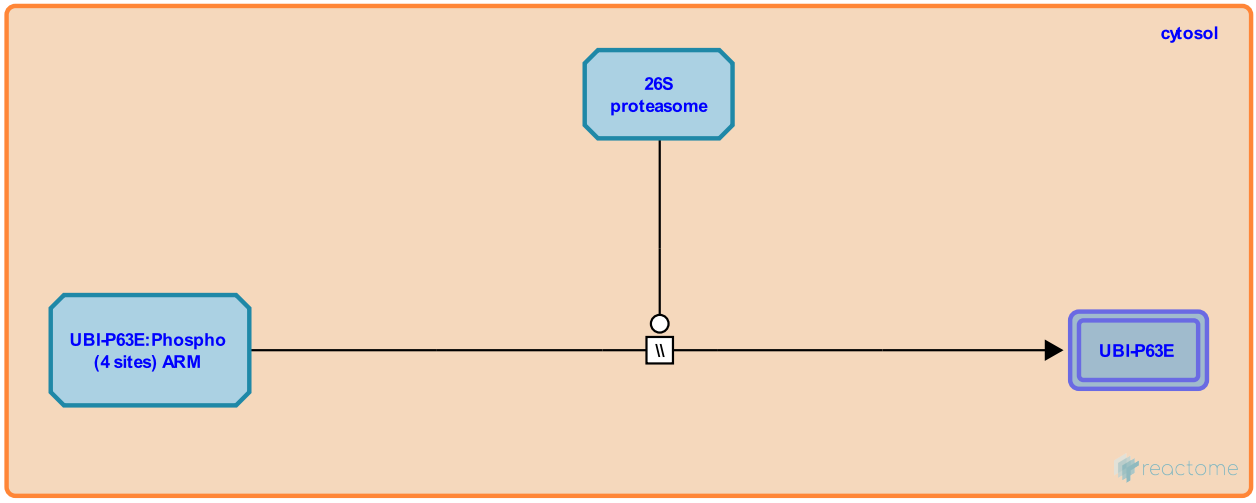
Ubiquitinated and phosphorylated ARM binds to and is degraded by the proteasome complex ↗

Location: Ubiquitination and degradation of phosphorylated ARM

Stable identifier: R-DME-209129

Type: omitted

Compartments: cytosol



The free ubiquitinated and phosphorylated Armadillo (ARM) is now targeted by the 26S proteasome which binds and then degrades it. The cytoplasmic concentration of Armadillo is now reduced.

Preceded by: Dissociation of free ubiquitinated and phosphorylated ARM from SLMB and the 'destruction complex'

Editions

2006-07-26	Authored	Williams, MG.
2008-01-19	Reviewed	Nusse, R.
2014-05-20	Edited	Williams, MG.

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