PRKACA phosphorylates PLN

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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. ↗

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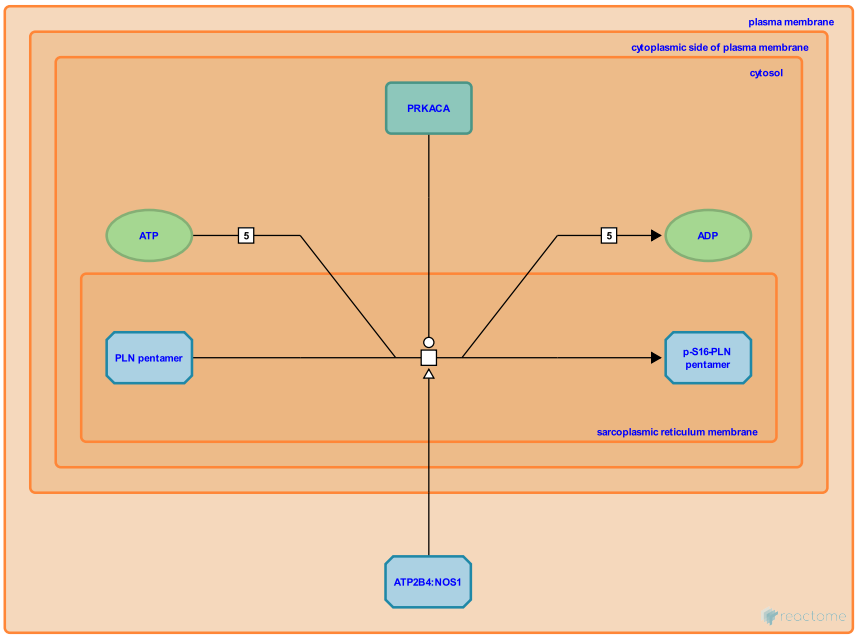
Stable identifier: R-HSA-5617182

Type: transition

Compartments: sarcoplasmic reticulum membrane, cytosol



Cardiac muscle phospholamban (PLN aka PLB) modulates cardiac contractility by inhibiting the sarcoplasmic reticulum calcium pump (ATP2A2 aka SERCA). This process is dynamically regulated by beta-adrenergic stimulation and phosphorylation of PLN. Protein kinase A (PRKACA) is able to phosphorylate PLN at serine 16, relieving its inhibition of ATP2A2 and modulating cardiac contractility (Glaves et al. 2011, Ceholski et al. 2012). The ATP2B4:NOS1 complex, via cAMP, increases PRKACA activity, thereby regulating the response of the heart to beta-adrenergic agonists.

Literature references

Young, HS., Stokes, DL., Trieber, CA., Ceholski, DK., Glaves, JP. (2011). Phosphorylation and mutation of phospholamban alter physical interactions with the sarcoplasmic reticulum calcium pump. *J. Mol. Biol., 405*, 707-23. ↗

Young, HS., Trieber, CA., Holmes, CF., Ceholski, DK. (2012). Lethal, hereditary mutants of phospholamban elude phosphorylation by protein kinase A. *J. Biol. Chem., 287*, 26596-605. ↗

Editions

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