

# p-S67-Ensa/p-S67-Arpp19 binds PP2A-Ppp2r2d

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13/05/2024

https://reactome.org

# 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 data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

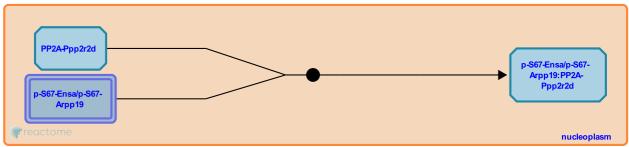
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# p-S67-Ensa/p-S67-Arpp19 binds PP2A-Ppp2r2d >

Stable identifier: R-XLA-2445086

Type: binding

Compartments: nucleoplasm



Recombinant Xenopus Ensa and Arpp19 are phosphorylated by recombinant Xenopus Mastl on serine residue S67. Once phosphorylated, Ensa and Arpp19 bind and inhibit the phosphatase activity of PP2A complexed with the regulatory subunit Ppp2r2d (B55-delta) (Mochida et al. 2010, Gharbi-Ayachi et al. 2010).

# **Literature references**

Skehel, M., Mochida, S., Hunt, T., Maslen, SL. (2010). Greatwall phosphorylates an inhibitor of protein phosphatase 2A that is essential for mitosis. *Science*, 330, 1670-3.

Lorca, T., Burgess, A., Van-Dorsselaer, A., Vigneron, S., Strub, JM., Gharbi-Ayachi, A. et al. (2010). The substrate of Greatwall kinase, Arpp19, controls mitosis by inhibiting protein phosphatase 2A. *Science*, 330, 1673-7.

# **Editions**

2012-09-04	Authored	Orlic-Milacic, M.
2012-09-14	Edited	Gillespie, ME.
2012-09-26	Reviewed	Mochida, S.
2012-09-28	Reviewed	Burgess, A.