PADIs:Ca2+ deiminate L-Arg to L-Cit in proteins

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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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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. ↗

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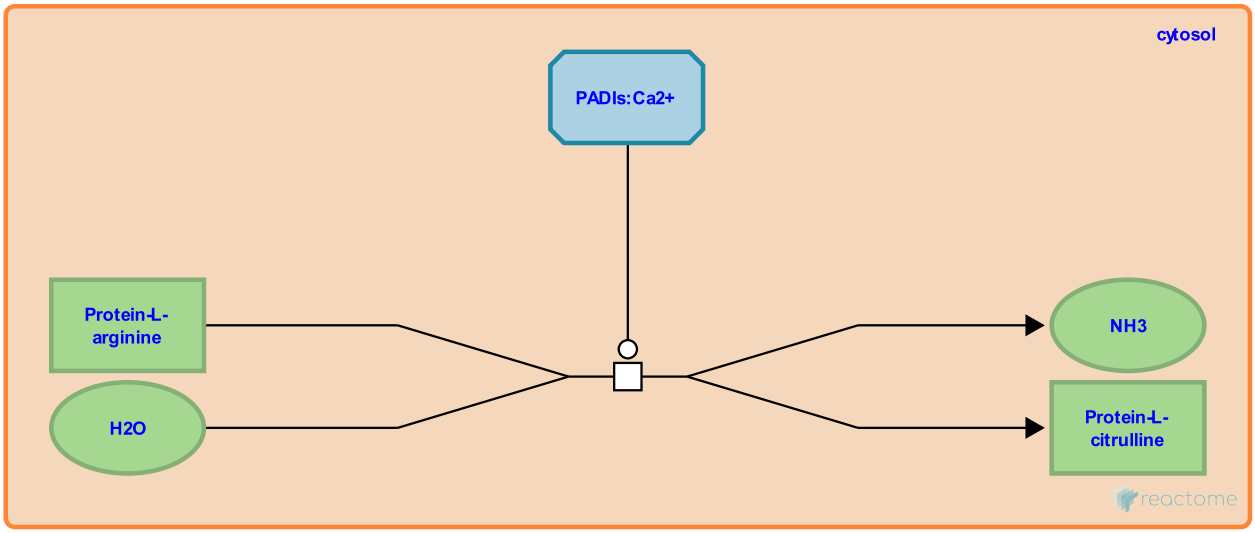
Stable identifier: R-HSA-1183128

Type: transition

Compartments: cytosol



Methylation of histones by protein arginine methyltransferases (PRMTs), in general, is required for mammalian development and plays an important and dynamic role in gene regulation. Protein-arginine deiminases (PADIs) catalyse the deimination of L-arginine residues (L-Arg) in proteins to L-citrulline (L-Cit), thus playing a role in the regulation of development (Guerrin et al. 2003, Ishigami et al. 2002, Kanno et al. 2000, Wang et al. 2004, Nakayama-Hamada et al. 2005, Chavanas et al. 2004).

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Editions

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