PLPP1,2,3 dephosphorylate cytosolic sphingosine-1-phosphate

D'Eustachio, P., Hannun, YA., Jassal, B., Luberto, C.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of Creative Commons Attribution 4.0 International (CC BY 4.0) License. For more information see our license.

28/04/2024

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. ↗

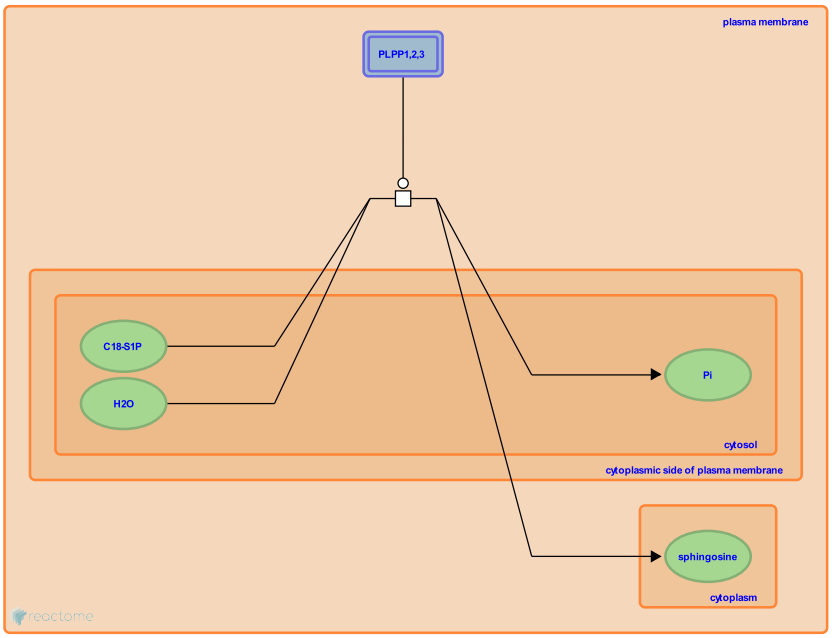
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

PLPP1,2,3 dephosphorylate cytosolic sphingosine-1-phosphate ↗

Stable identifier: R-HSA-428696

Type: transition

Compartments: cytosol, plasma membrane



Phospholipid phosphatases 1 (PLPP1, PPAP2A, LPP1), 2 (PLPP2, LPP2, PPAP2C), and 3 (PLPP3, LPP3, PPAP2B) associated with the plasma membrane catalyze the hydrolysis of cytosolic sphingosine 1-phosphate to form sphingosine and orthophosphate (Roberts et al. 1998). PLPPs have roles in angiogenesis and cancer (reviewed by Tang et al., 2015; Tang & Brindley, 2020).

Literature references

Tang, X., Brindley, DN. (2020). Lipid Phosphate Phosphatases and Cancer. *Biomolecules, 10*. ↗

Morris, AJ., Roberts, R., Sciorra, VA. (1998). Human type 2 phosphatidic acid phosphohydrolases. Substrate specificity of the type 2a, 2b, and 2c enzymes and cell surface activity of the 2a isoform. *J Biol Chem, 273*, 22059-67. ↗

Tang, X., Benesch, MG., Brindley, DN. (2015). Lipid phosphate phosphatases and their roles in mammalian physiology and pathology. *J Lipid Res, 56*, 2048-60. ↗

Editions

2009-08-21	Authored, Edited	D'Eustachio, P.
2009-08-21	Reviewed	Jassal, B.
2009-11-19	Reviewed	Hannun, YA., Luberto, C.
2023-10-24	Reviewed	D'Eustachio, P.