I4P is dephosphorylated to Ins by IMPA1/2 in the cytosol

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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. ↗

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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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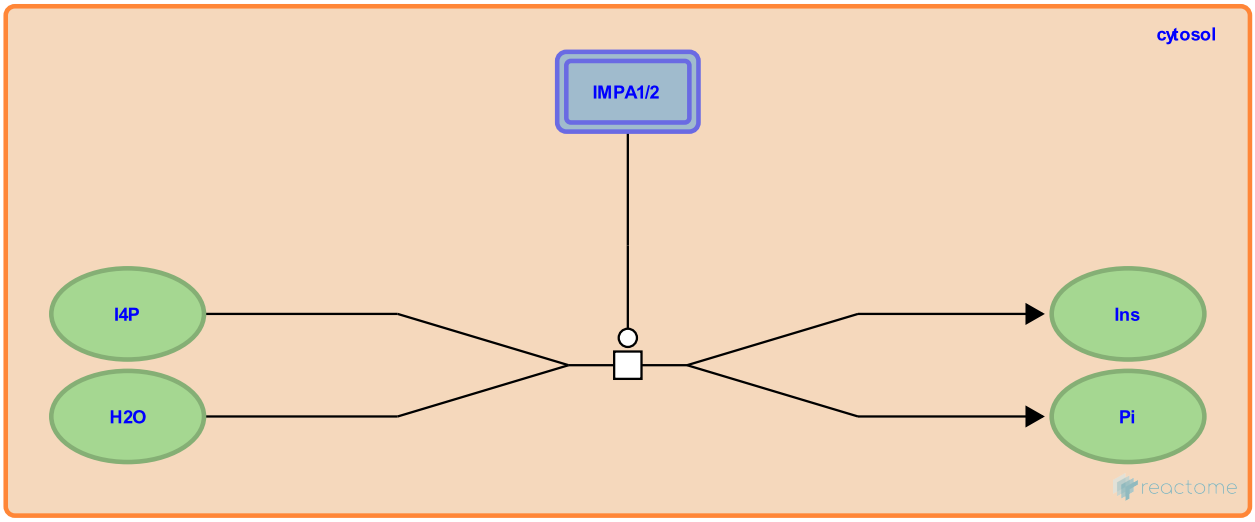
Stable identifier: R-HSA-1855211

Type: transition

Compartments: cytosol



Inositol monophosphatase 1 (IMPA1) and 2 (IMPA2) homodimers dephosphorylate inositol 4-phosphate (I4P) to inositol (Ins). In vitro, IMPA1 and 2 differ in their pH optima and IMPA1 has a significantly greater activity on IP4 than does IMPA2 (Ohnishi et al. 2007).

Literature references

Seo, KC., Sato, Y., Ohba, H., Ohnishi, T., Chung, SK., Furuichi, T. et al. (2007). Spatial expression patterns and biochemical properties distinguish a second myo-inositol monophosphatase IMPA2 from IMPA1. *J Biol Chem, 282*, 637-46. ↗

Editions

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