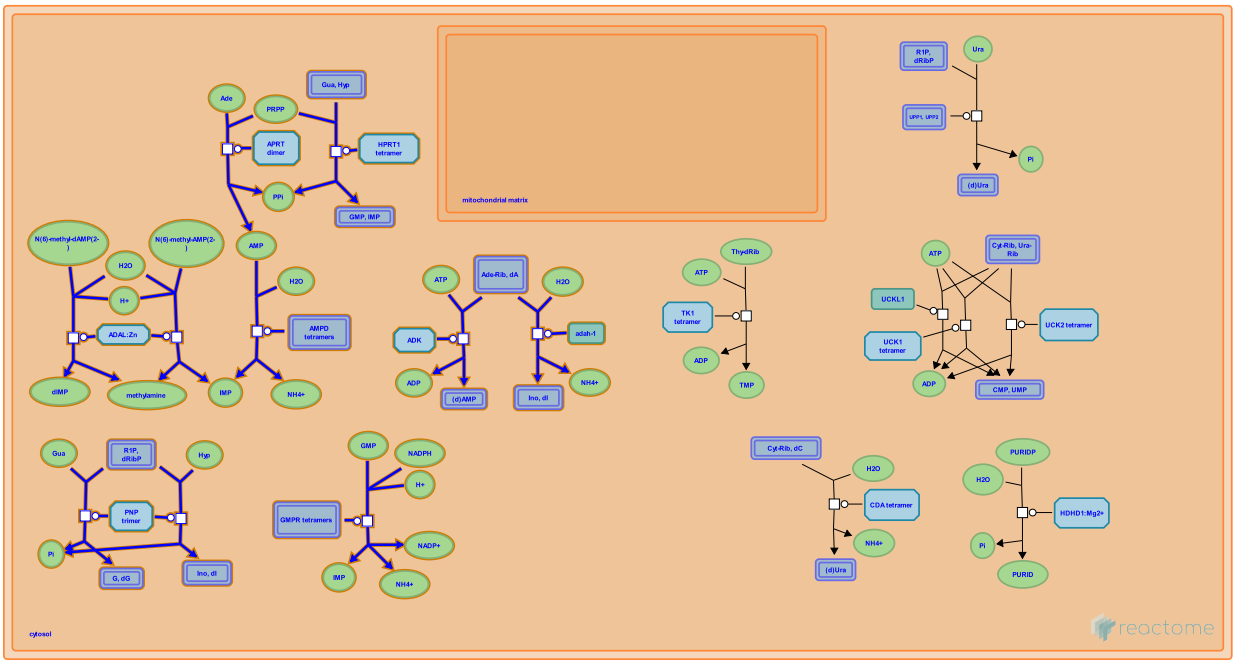
Purine salvage



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

22/07/2024

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. ↗

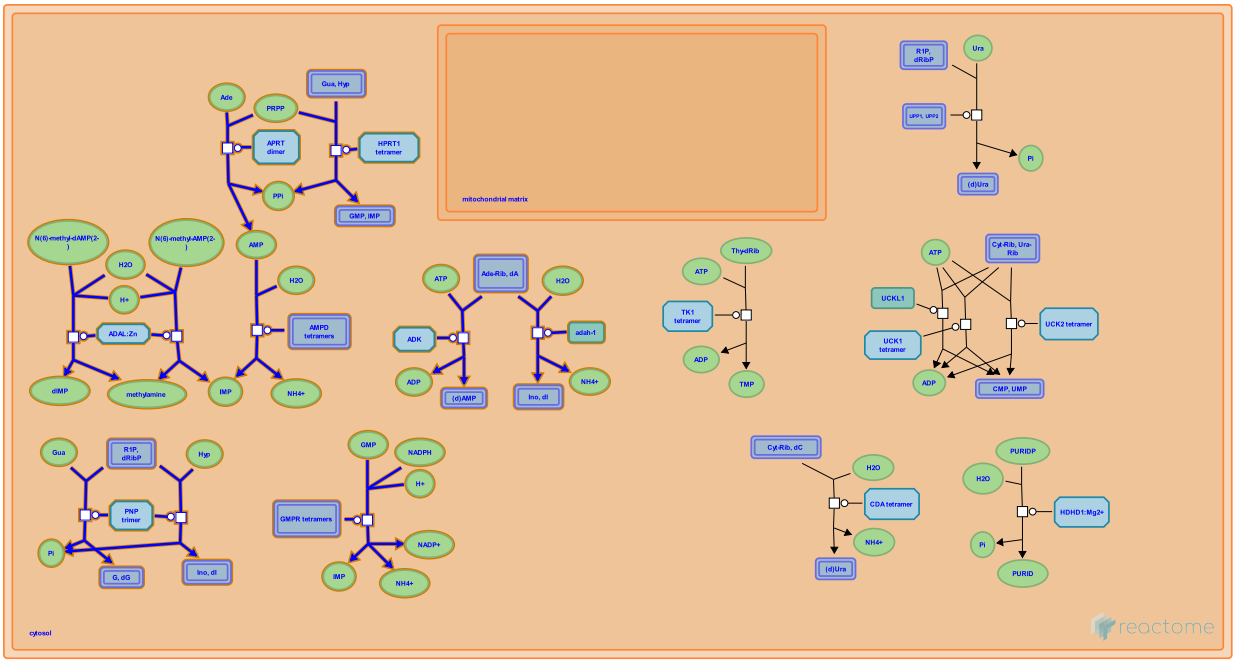
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Purine salvage ↗

Stable identifier: R-CEL-74217

Inferred from: Purine salvage (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

APRT catalyzes the conversion of adenine to AMP ↗

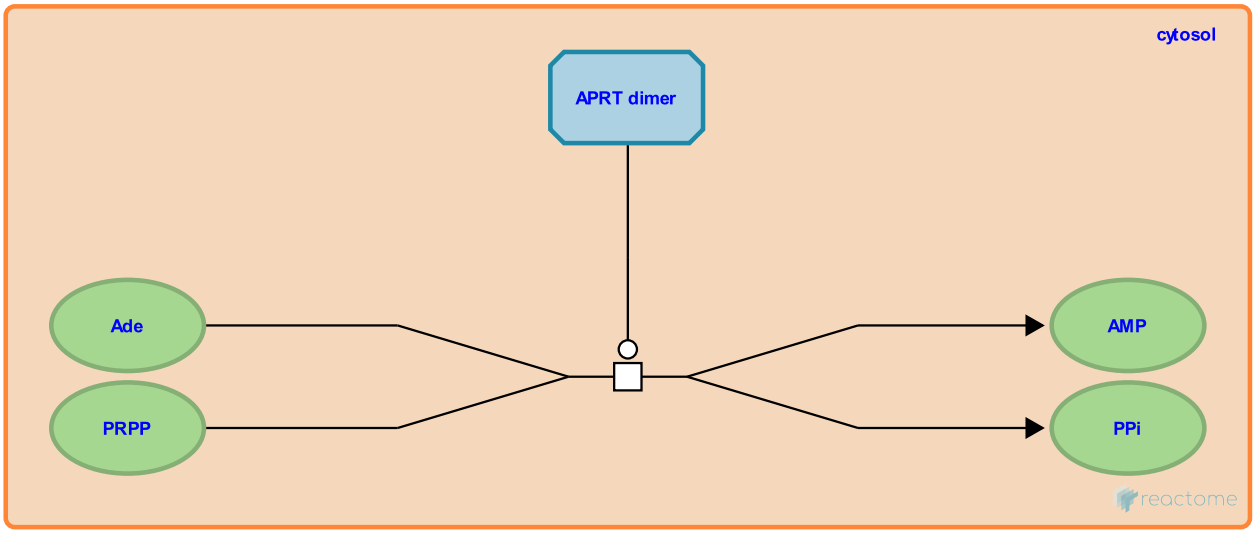
Location: Purine salvage

Stable identifier: R-CEL-74213

Type: transition

Compartments: cytosol

Inferred from: APRT catalyzes the conversion of adenine to AMP (Homo sapiens)



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Followed by: AMP + H2O => IMP + NH4+ (AMPD)

AMP + H2O => IMP + NH4+ (AMPD) ↗

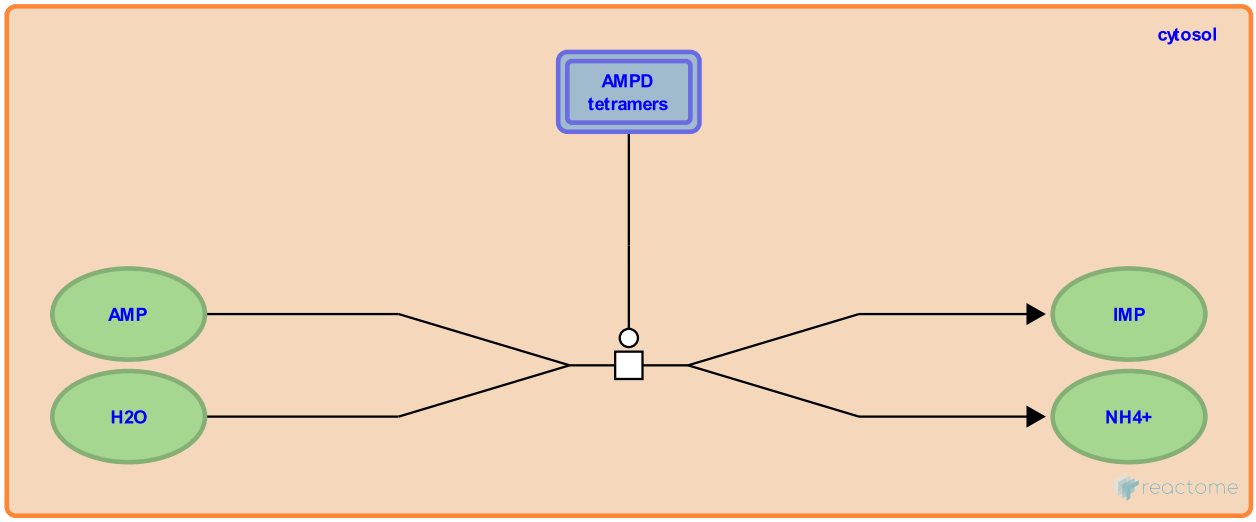
Location: Purine salvage

Stable identifier: R-CEL-76590

Type: transition

Compartments: cytosol

Inferred from: AMP + H2O => IMP + NH4+ (AMPD) (Homo sapiens)



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Preceded by: APRT catalyzes the conversion of adenine to AMP

HPRT1 catalyzes the conversion of guanine or hypoxanthine to GMP or IMP ↗

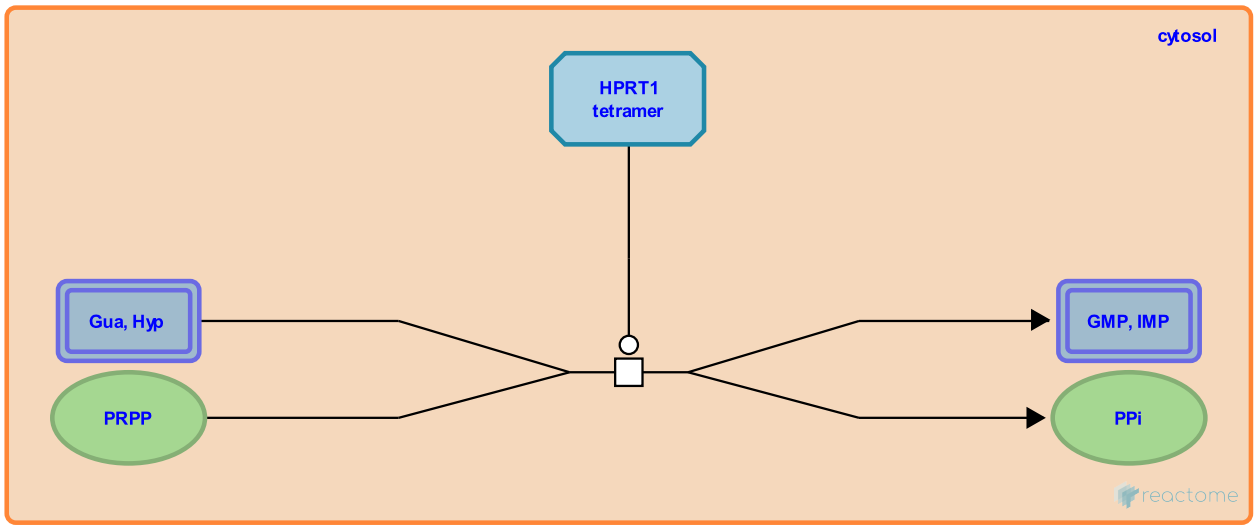
Location: Purine salvage

Stable identifier: R-CEL-74215

Type: transition

Compartments: cytosol

Inferred from: HPRT1 catalyzes the conversion of guanine or hypoxanthine to GMP or IMP (Homo sapiens)



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Followed by: GMP + NADPH + H+ => IMP + NADP+ + NH4+ (GMPR,GMPR2)

ADAL1 hydrolyzes N6-methyl-AMP to IMP and methylamine ↗

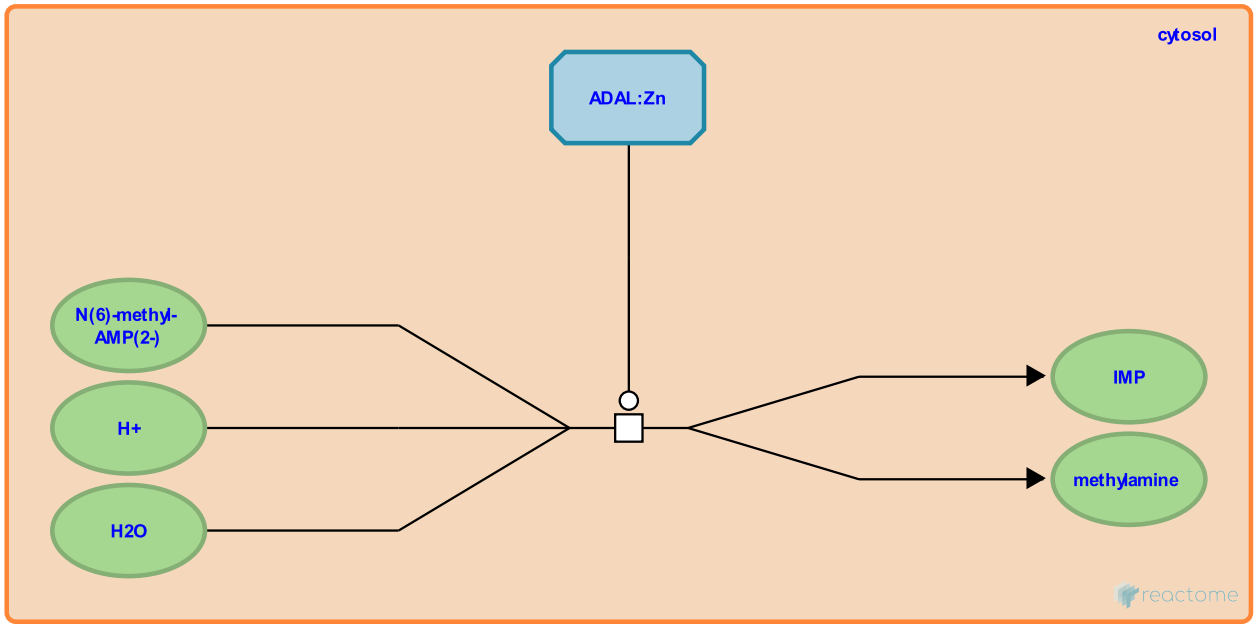
Location: Purine salvage

Stable identifier: R-CEL-2161187

Type: transition

Compartments: cytosol

Inferred from: ADAL1 hydrolyzes N6-methyl-AMP to IMP and methylamine (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

ADAL1 hydrolyzes N6-methyl-dAMP to dIMP and methylamine ↗

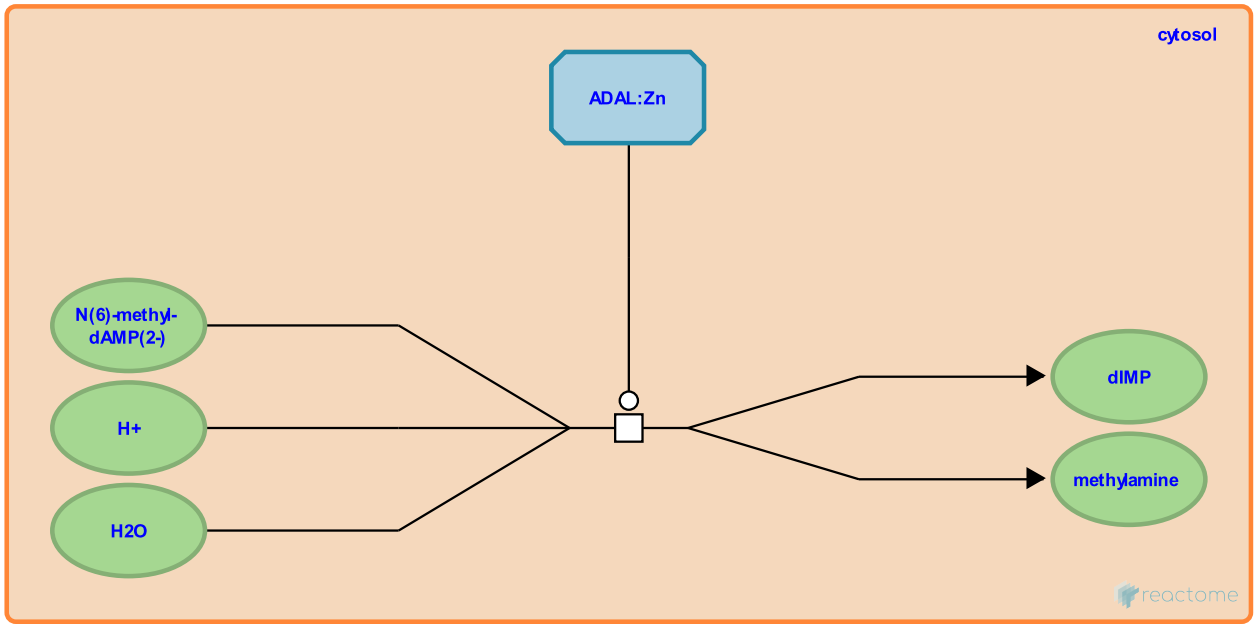
Location: Purine salvage

Stable identifier: R-CEL-9731661

Type: transition

Compartments: cytosol

Inferred from: ADAL1 hydrolyzes N6-methyl-dAMP to dIMP and methylamine (Homo sapiens)



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(2'-deoxy)adenosine + ATP => (d)AMP + ADP (ADK) ↗

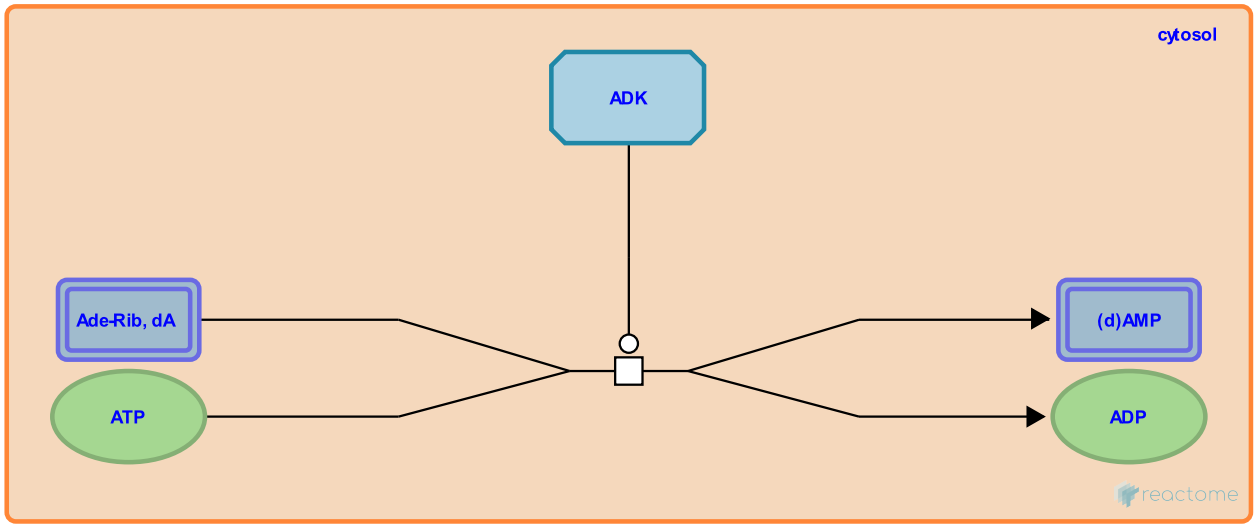
Location: Purine salvage

Stable identifier: R-CEL-109624

Type: transition

Compartments: cytosol

Inferred from: (2'-deoxy)adenosine + ATP => (d)AMP + ADP (ADK) (Homo sapiens)



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ADA catalyzes the deamination of (deoxy)adenosine ↗

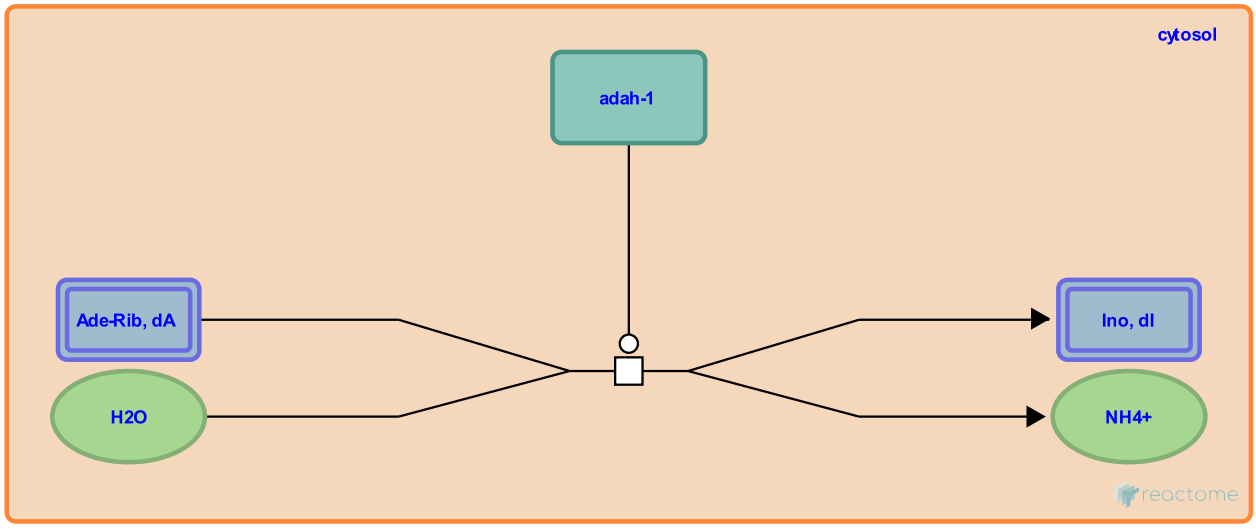
Location: Purine salvage

Stable identifier: R-CEL-74241

Type: transition

Compartments: cytosol

Inferred from: ADA catalyzes the deamination of (deoxy)adenosine (Homo sapiens)



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PNP catalyzes the conversion of guanine and (deoxy)ribose to (deoxy)guanosine ↗

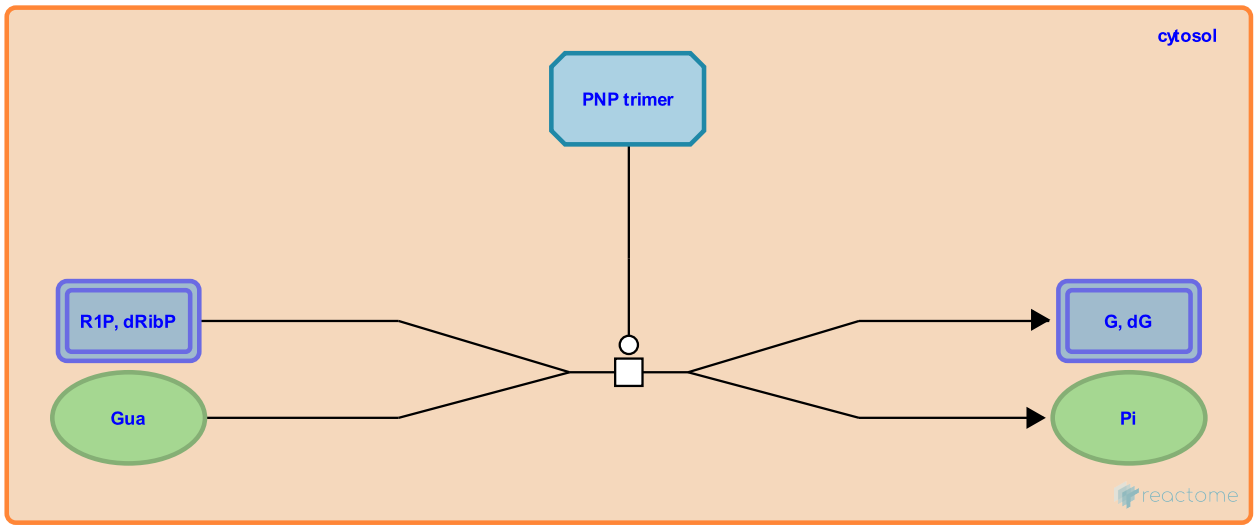
Location: Purine salvage

Stable identifier: R-CEL-112034

Type: transition

Compartments: cytosol

Inferred from: PNP catalyzes the conversion of guanine and (deoxy)ribose to (deoxy)guanosine (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

PNP catalyzes the conversion of hypoxanthine and (deoxy)ribose to (deoxy)inosine ↗

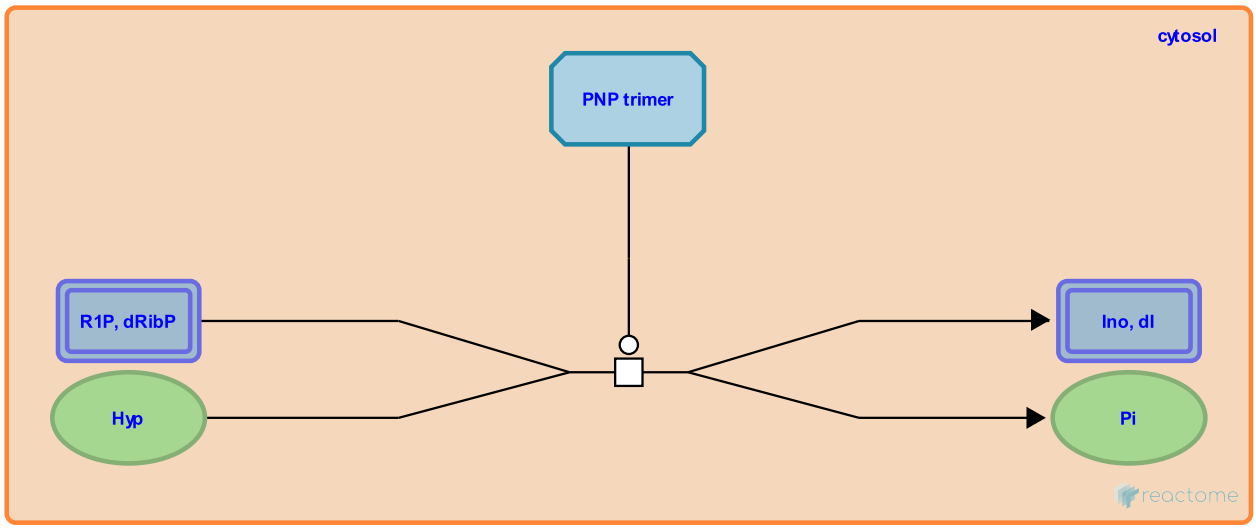
Location: Purine salvage

Stable identifier: R-CEL-112033

Type: transition

Compartments: cytosol

Inferred from: PNP catalyzes the conversion of hypoxanthine and (deoxy)ribose to (deoxy)inosine (Homo sapiens)



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GMP + NADPH + H+ => IMP + NADP+ + NH4+ (GMPR,GMPR2) ↗

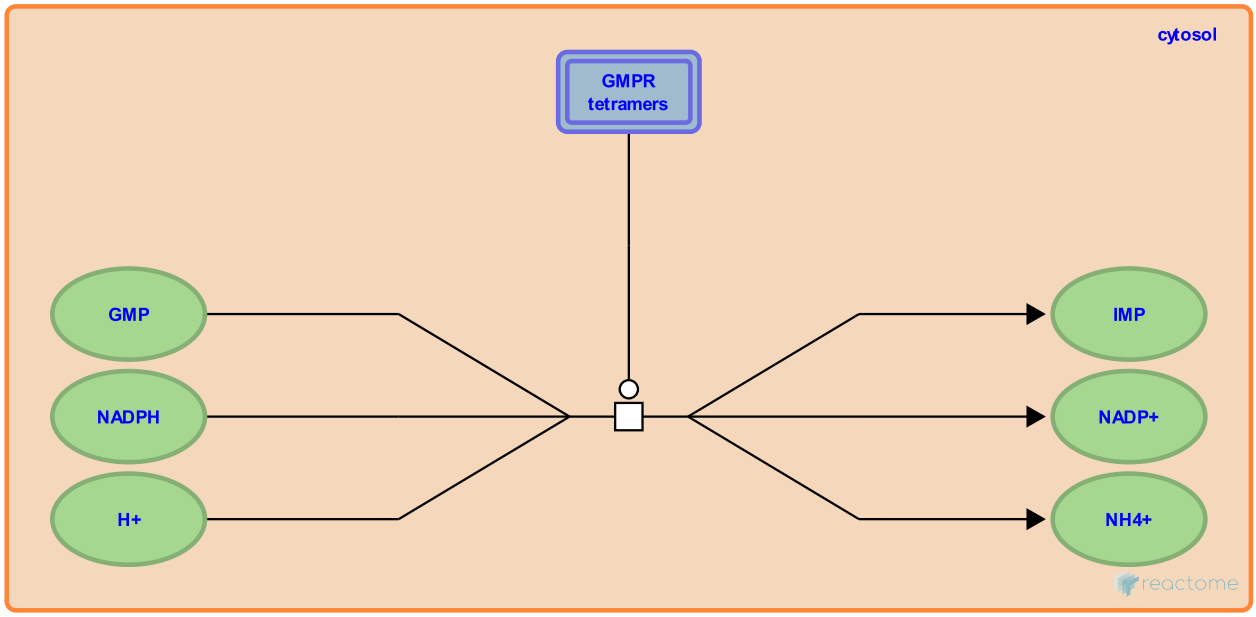
Location: Purine salvage

Stable identifier: R-CEL-514604

Type: transition

Compartments: cytosol

Inferred from: GMP + NADPH + H+ => IMP + NADP+ + NH4+ (GMPR,GMPR2) (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: HPRT1 catalyzes the conversion of guanine or hypoxanthine to GMP or IMP

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