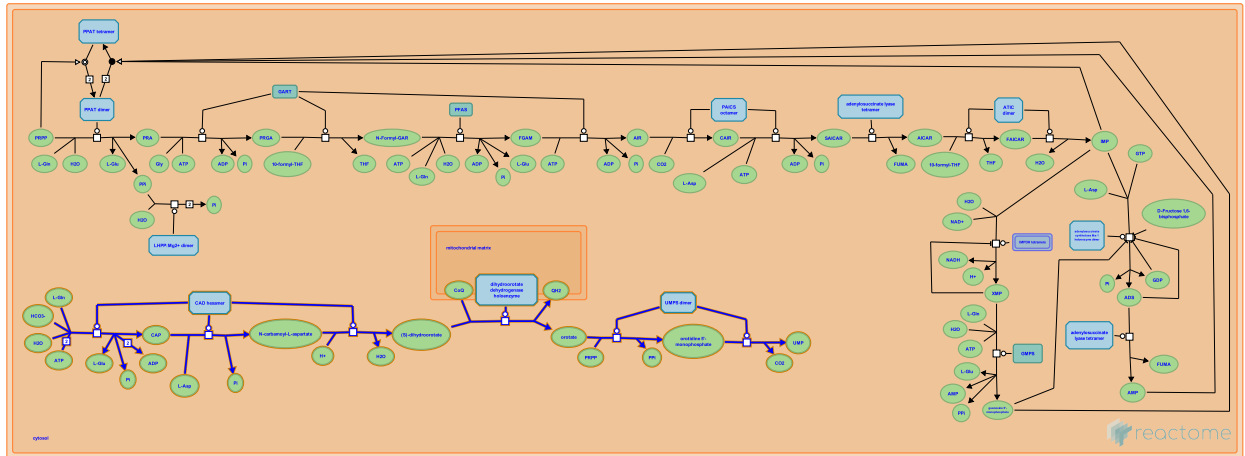


Pyrimidine biosynthesis



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

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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. [↗](#)
- 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. [↗](#)

Reactome database release: 73

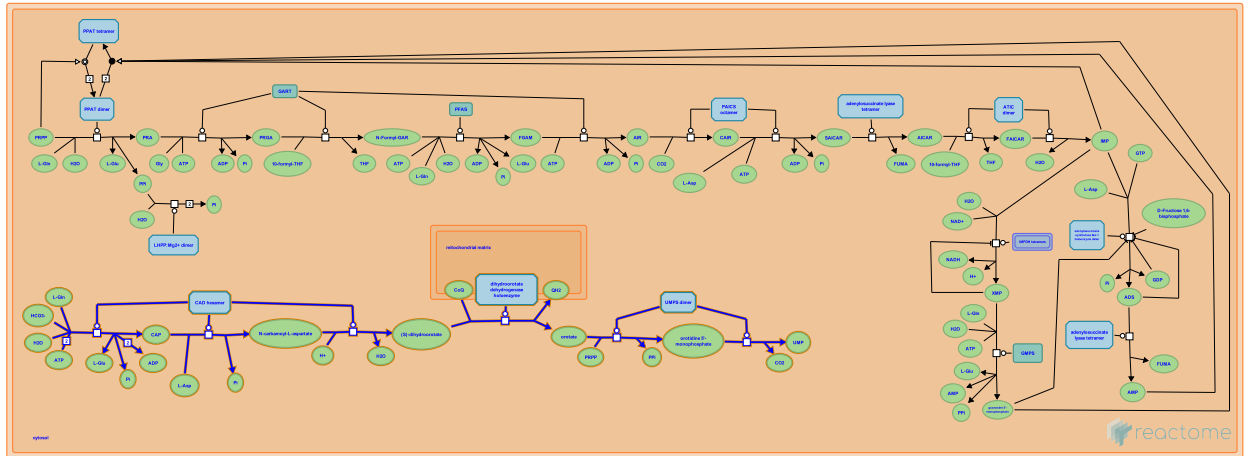
This document contains 1 pathway and 6 reactions ([see Table of Contents](#))

Pyrimidine biosynthesis ↗

Stable identifier: R-SSC-500753

Compartments: cytosol, mitochondrial inner membrane, nucleoplasm

Inferred from: [Pyrimidine biosynthesis \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

L-glutamine + 2 ATP + HCO₃⁻ + H₂O => carbamoyl phosphate + L-glutamate + 2 ADP + orthophosphate ↗

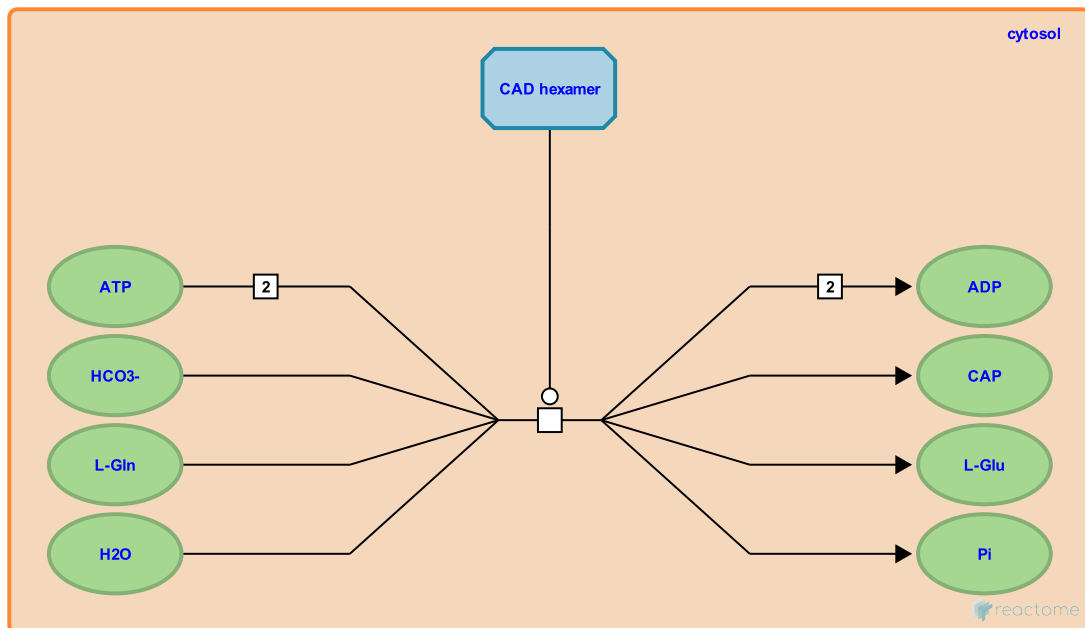
Location: [Pyrimidine biosynthesis](#)

Stable identifier: R-SSC-73577

Type: transition

Compartments: cytosol

Inferred from: [L-glutamine + 2 ATP + HCO₃⁻ + H₂O => carbamoyl phosphate + L-glutamate + 2 ADP + orthophosphate \(Homo sapiens\)](#)



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.

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Followed by: [carbamoyl phosphate + L-aspartate <=> N-carbamoyl L-aspartate + orthophosphate](#)

carbamoyl phosphate + L-aspartate \rightleftharpoons N-carbamoyl L-aspartate + orthophosphate



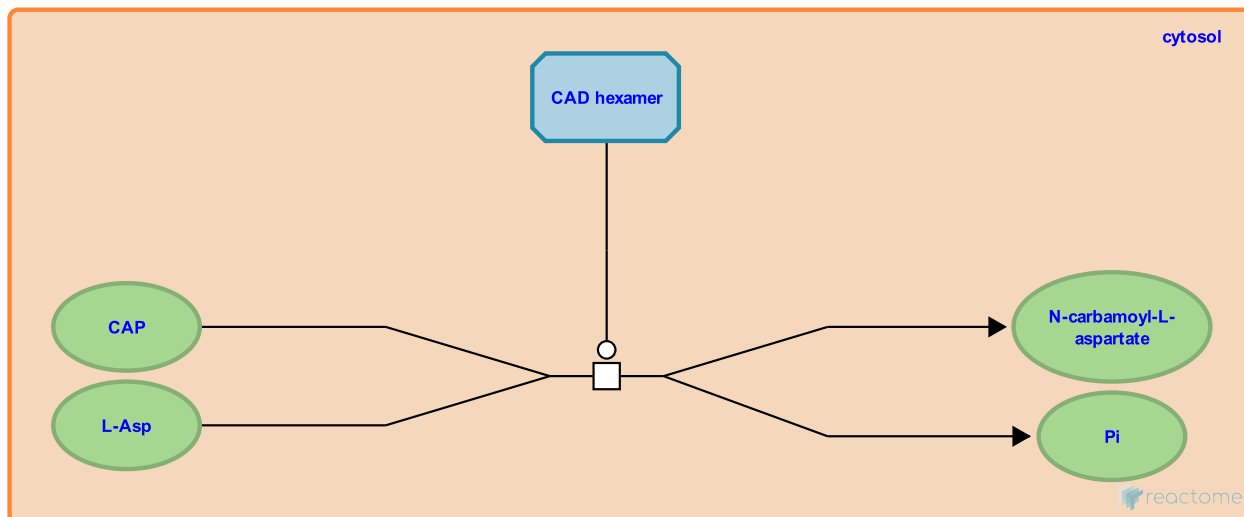
Location: [Pyrimidine biosynthesis](#)

Stable identifier: R-SSC-73573

Type: transition

Compartments: cytosol

Inferred from: [carbamoyl phosphate + L-aspartate \$\rightleftharpoons\$ N-carbamoyl L-aspartate + orthophosphate](#)
([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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [L-glutamine + 2 ATP + HCO₃⁻ + H₂O \$\Rightarrow\$ carbamoyl phosphate + L-glutamate + 2 ADP + orthophosphate](#)

Followed by: [N-carbamoyl L-aspartate + H⁺ \$\rightleftharpoons\$ \(S\)-dihydroorotate + H₂O](#)

N-carbamoyl L-aspartate + H+ <=> (S)-dihydroorotate + H2O ↗

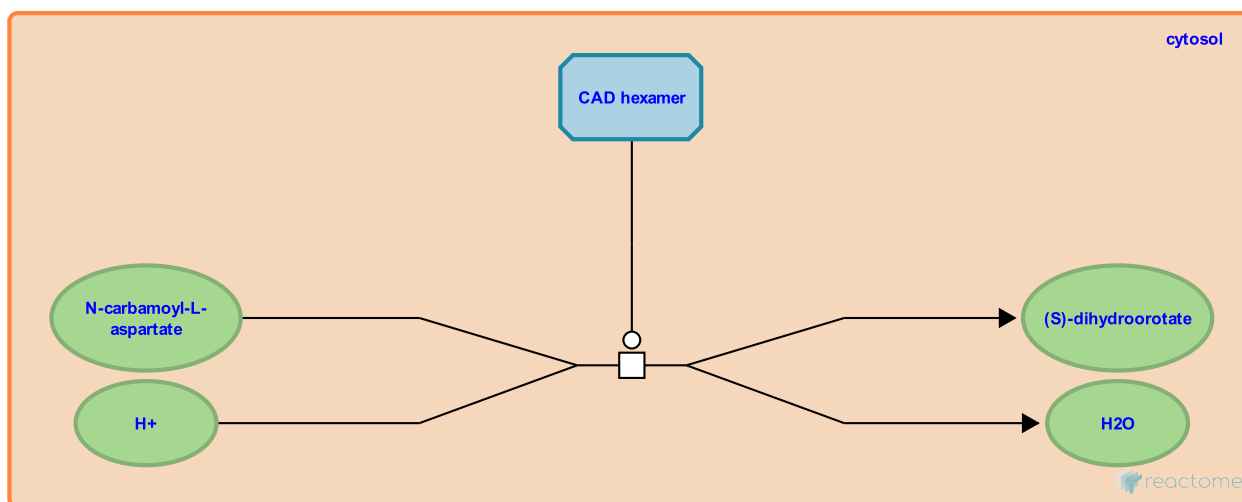
Location: [Pyrimidine biosynthesis](#)

Stable identifier: R-SSC-73571

Type: transition

Compartments: cytosol

Inferred from: [N-carbamoyl L-aspartate + H+ <=> \(S\)-dihydroorotate + H2O \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [carbamoyl phosphate + L-aspartate <=> N-carbamoyl L-aspartate + orthophosphate](#)

Followed by: [\(S\)-dihydroorotate + ubiquinone => orotate + ubiquinol](#)

(S)-dihydroorotate + ubiquinone => orotate + ubiquinol ↗

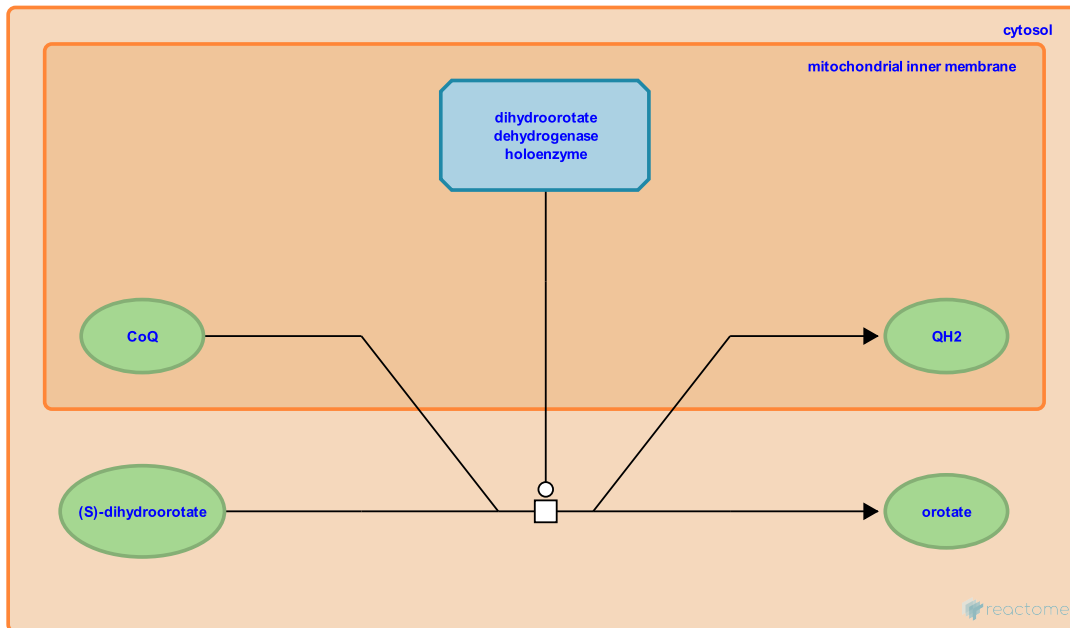
Location: [Pyrimidine biosynthesis](#)

Stable identifier: R-SSC-73569

Type: transition

Compartments: cytosol, mitochondrial inner membrane

Inferred from: [\(S\)-dihydroorotate + ubiquinone => orotate + ubiquinol \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [N-carbamoyl L-aspartate + H+ <=> \(S\)-dihydroorotate + H2O](#)

Followed by: [orotate + 5-phospho-alpha-D-ribose 1-diphosphate \(PRPP\) <=> orotidine 5'-monophosphate \(OMP\) + pyrophosphate](#)

orotate + 5-phospho-alpha-D-ribose 1-diphosphate (PRPP) \rightleftharpoons orotidine 5'-monophosphate (OMP) + pyrophosphate \nearrow

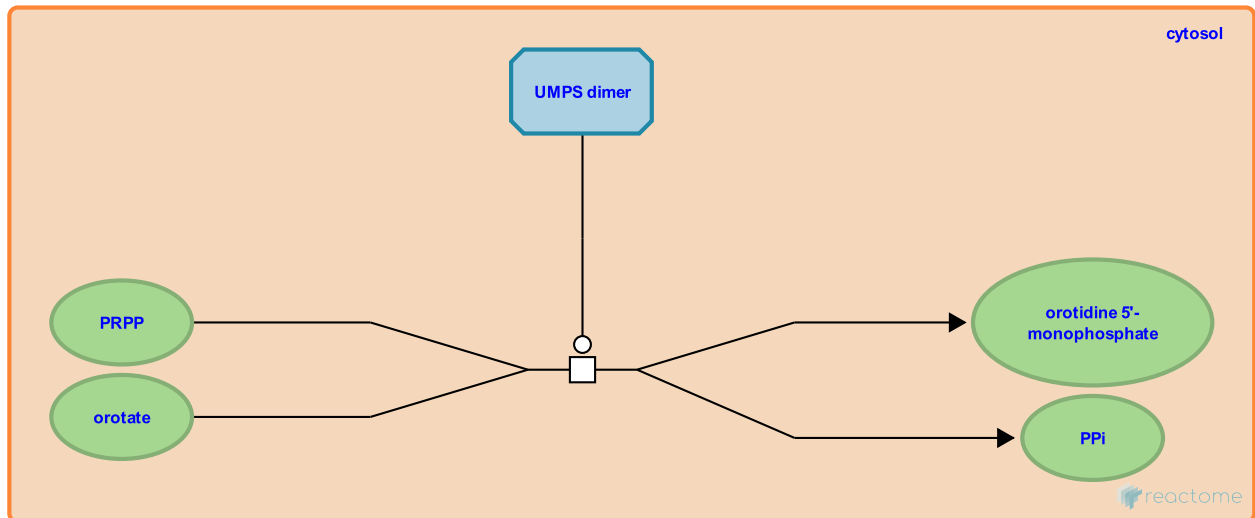
Location: [Pyrimidine biosynthesis](#)

Stable identifier: R-SSC-73567

Type: transition

Compartments: cytosol

Inferred from: [orotate + 5-phospho-alpha-D-ribose 1-diphosphate \(PRPP\) \$\rightleftharpoons\$ orotidine 5'-monophosphate \(OMP\) + pyrophosphate \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [\(S\)-dihydroorotate + ubiquinone \$\Rightarrow\$ orotate + ubiquinol](#)

Followed by: [orotidine 5'-monophosphate \$\Rightarrow\$ uridine 5'-monophosphate + CO2](#)

orotidine 5'-monophosphate => uridine 5'-monophosphate + CO2 ↗

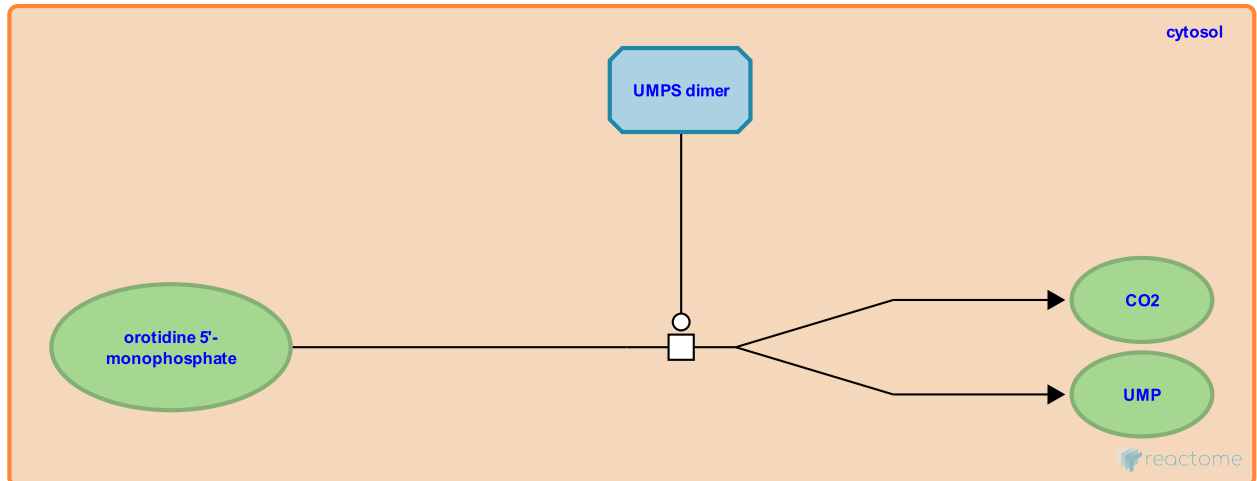
Location: [Pyrimidine biosynthesis](#)

Stable identifier: R-SSC-73564

Type: transition

Compartments: cytosol

Inferred from: [orotidine 5'-monophosphate => uridine 5'-monophosphate + CO2 \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [orotate + 5-phospho-alpha-D-ribose 1-diphosphate \(PRPP\) <=> orotidine 5'-monophosphate \(OMP\) + pyrophosphate](#)

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