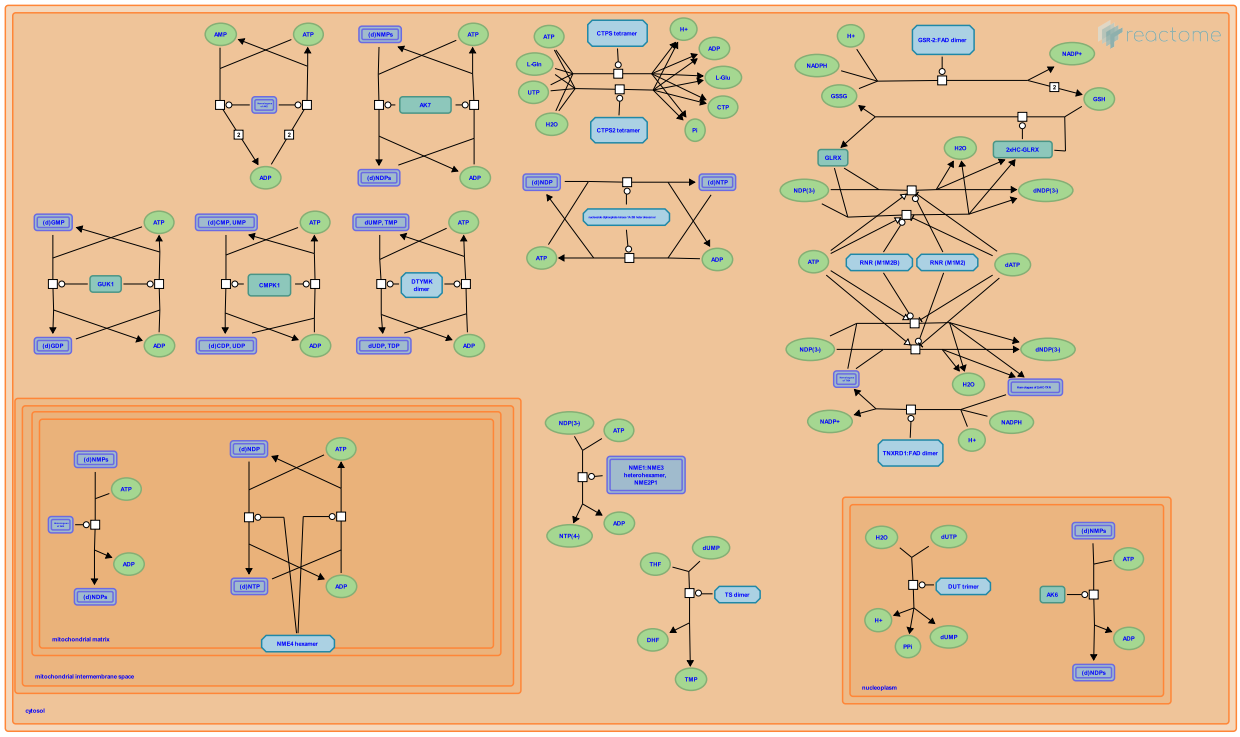
Interconversion of nucleotide di- and tri-phosphates



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

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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

16/05/2024

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. ↗

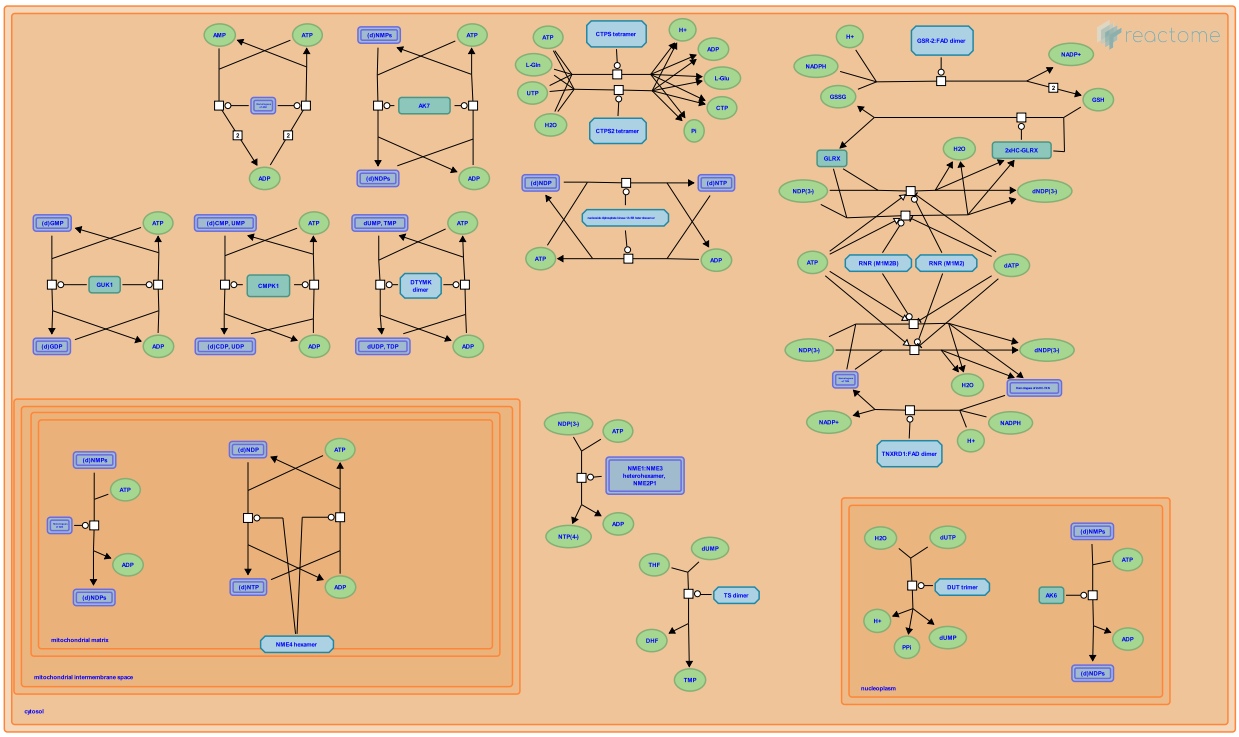
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Interconversion of nucleotide di- and triphosphates ↗

Stable identifier: R-PFA-499943

Compartments: cytosol, mitochondrial intermembrane space, nucleoplasm, mitochondrial inner membrane, mitochondrial matrix

Inferred from: Interconversion of nucleotide di- and triphosphates (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

AMP + ATP <=> ADP + ADP [AK2] ↗

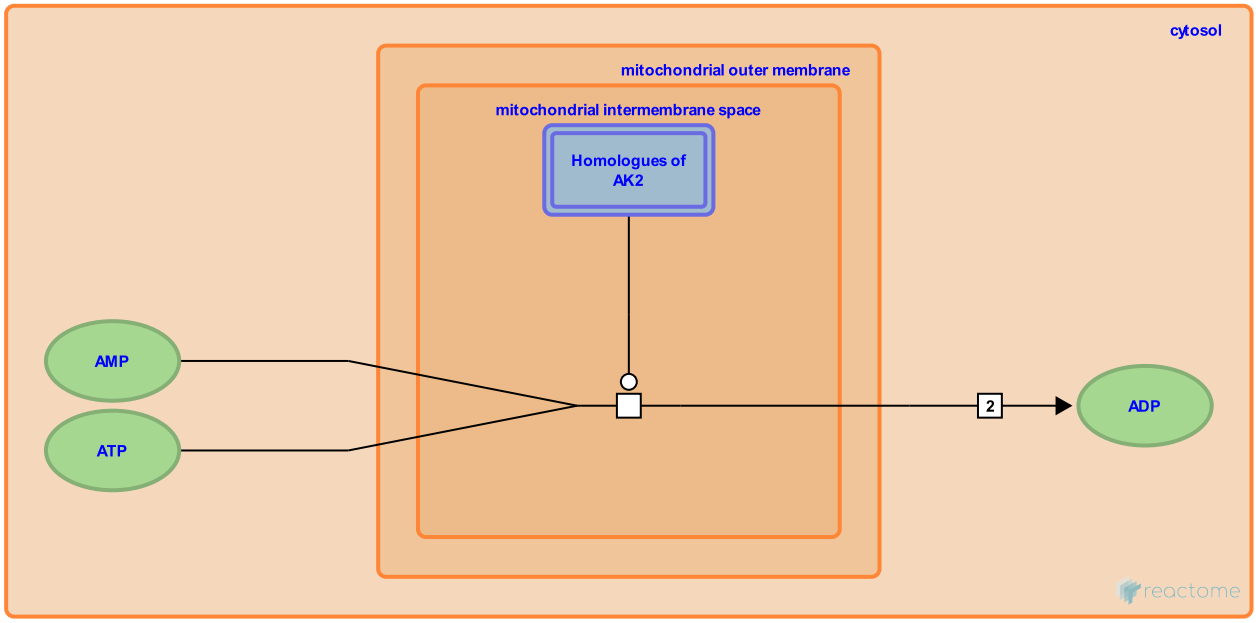
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-110145

Type: transition

Compartments: mitochondrial intermembrane space, cytosol

Inferred from: AMP + ATP <=> ADP + ADP [AK2] (Homo sapiens)



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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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ADP + ADP <=> AMP + ATP [AK2] ↗

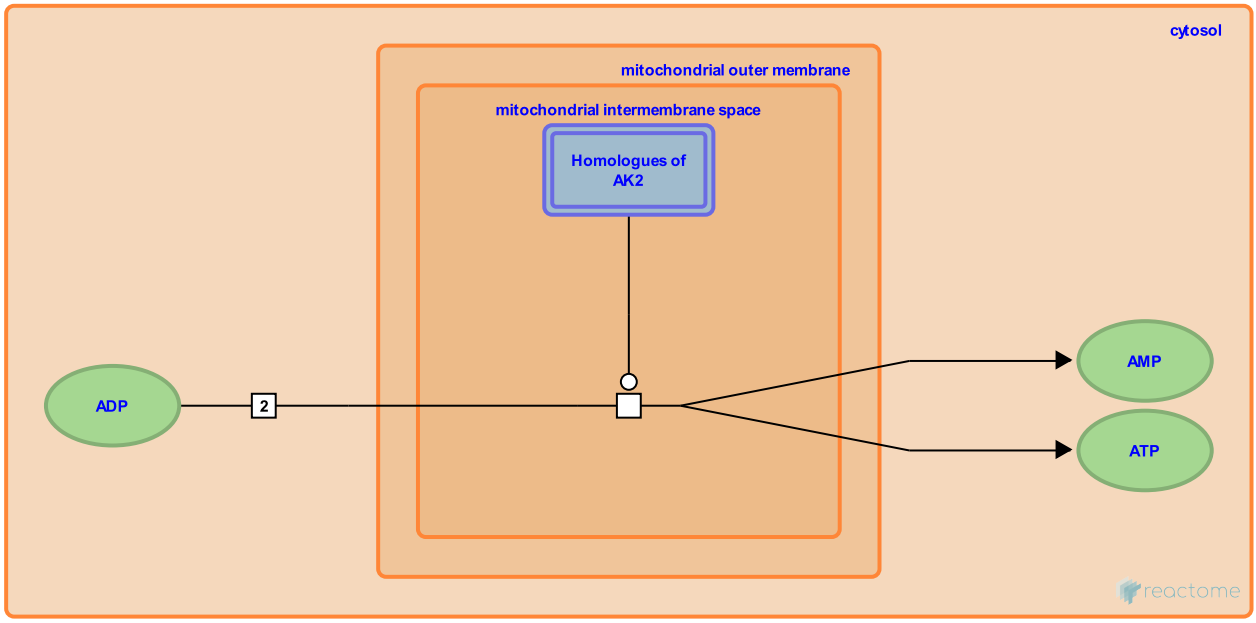
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-110144

Type: transition

Compartments: mitochondrial intermembrane space, cytosol

Inferred from: ADP + ADP <=> AMP + ATP [AK2] (Homo sapiens)



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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

AK5,7,8,9 phosphorylates (d)NMPs to (d)NDPs ↗

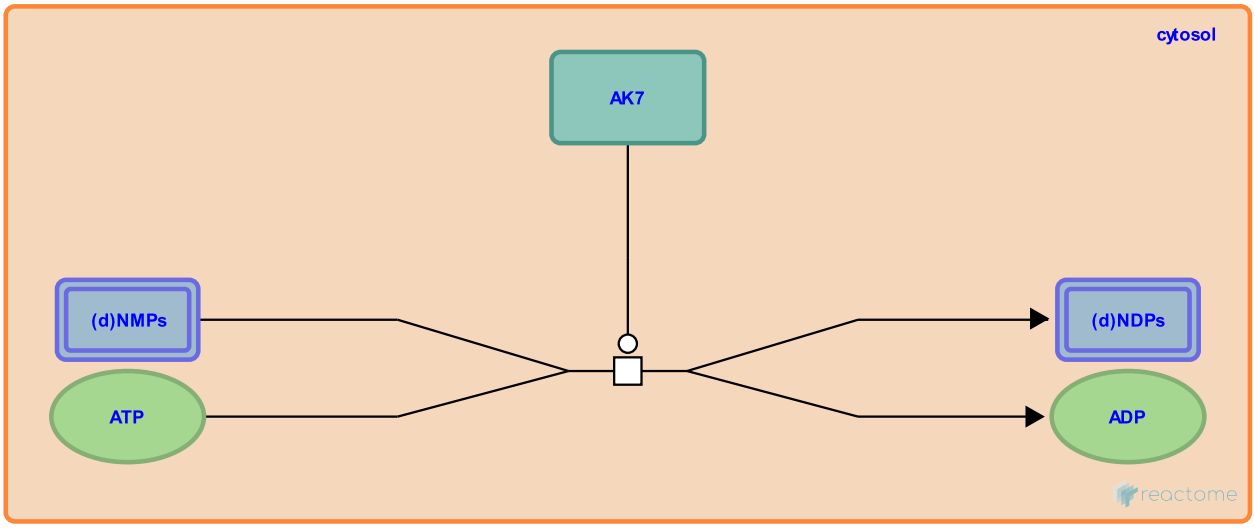
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-110138

Type: transition

Compartments: cytosol

Inferred from: AK5,7,8,9 phosphorylates (d)NMPs to (d)NDPs (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

(d)ADP or (d)CDP + ADP <=> (d)AMP or (d)CMP + ATP ↗

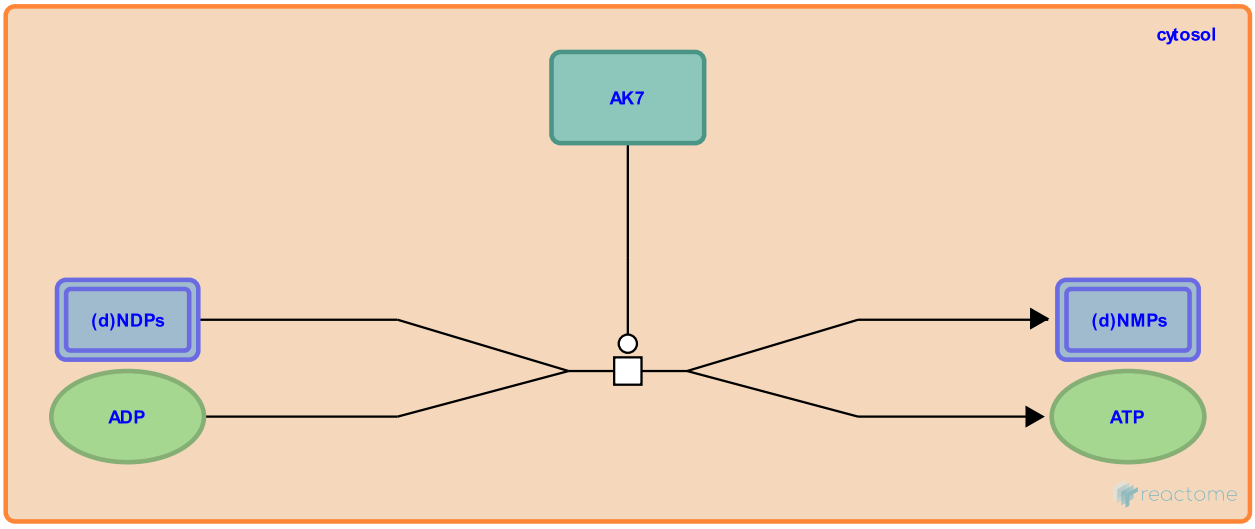
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-110137

Type: transition

Compartments: cytosol

Inferred from: (d)ADP or (d)CDP + ADP <=> (d)AMP or (d)CMP + ATP (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

AK4 phosphorylates (d)NMPs to (d)NDPs ↗

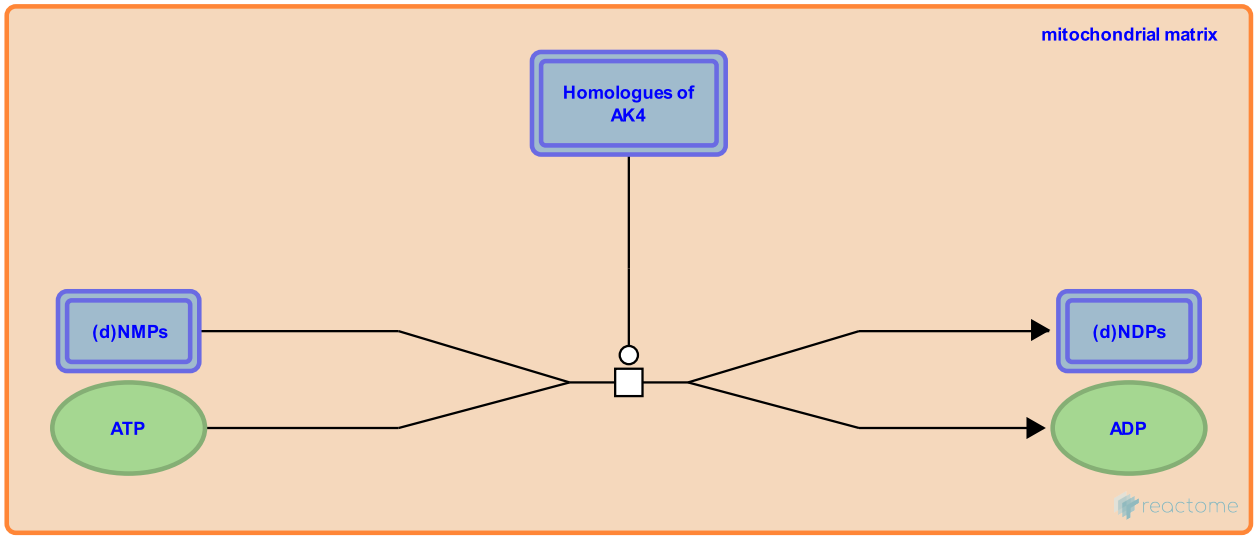
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-6788798

Type: transition

Compartments: mitochondrial matrix

Inferred from: AK4 phosphorylates (d)NMPs to (d)NDPs (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

AK6 phosphorylates (d)NMPs to (d)NDPs ↗

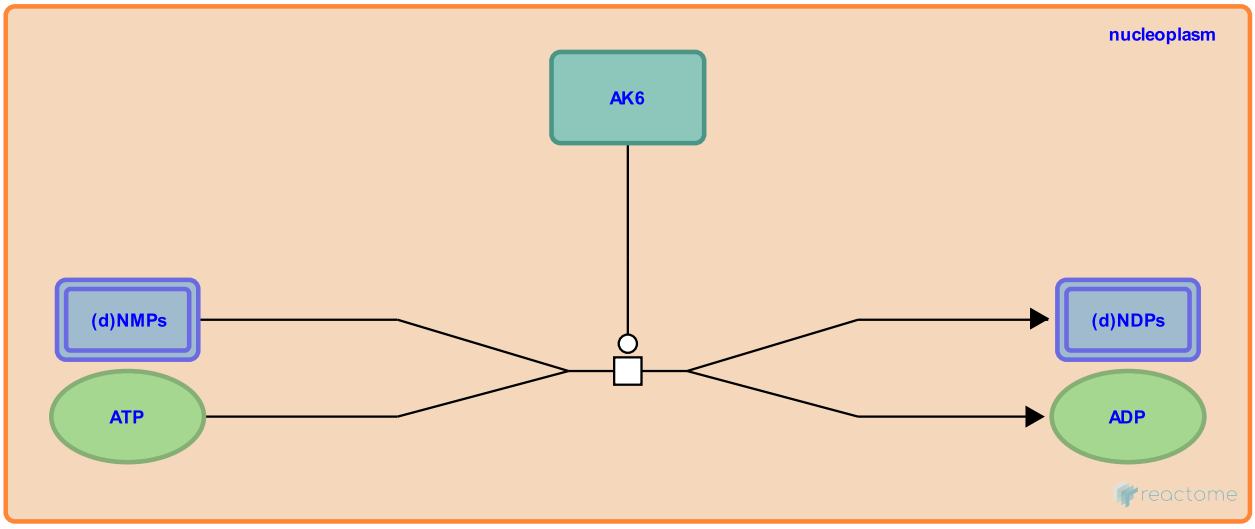
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-6788810

Type: transition

Compartments: nucleoplasm

Inferred from: AK6 phosphorylates (d)NMPs to (d)NDPs (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

(d)GMP + ATP <=> (d)GDP + ADP (GUK1) ↗

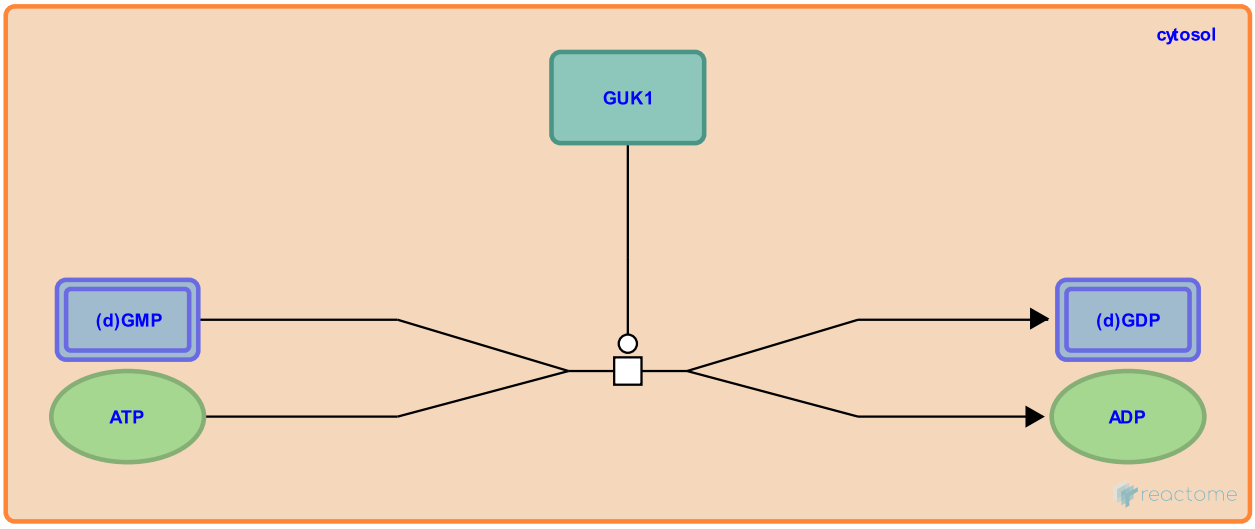
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-73788

Type: transition

Compartments: cytosol

Inferred from: (d)GMP + ATP <=> (d)GDP + ADP (GUK1) (Homo sapiens)



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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

Followed by: (d)NDP + ATP <=> (d)NTP + ADP (NME1,2,3)

(d)GDP + ADP <=> (d)GMP + ATP (GUK1) ↗

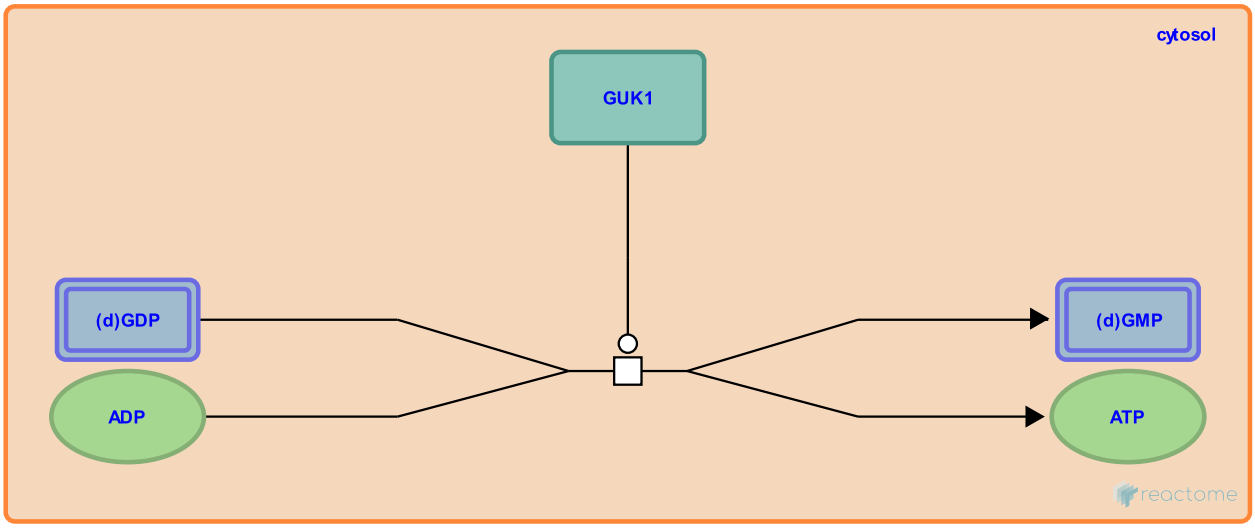
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-110133

Type: transition

Compartments: cytosol

Inferred from: (d)GDP + ADP <=> (d)GMP + ATP (GUK1) (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

(d)CMP or UMP + ATP <=> (d)CDP or UDP + ADP (CMPK1) ↗

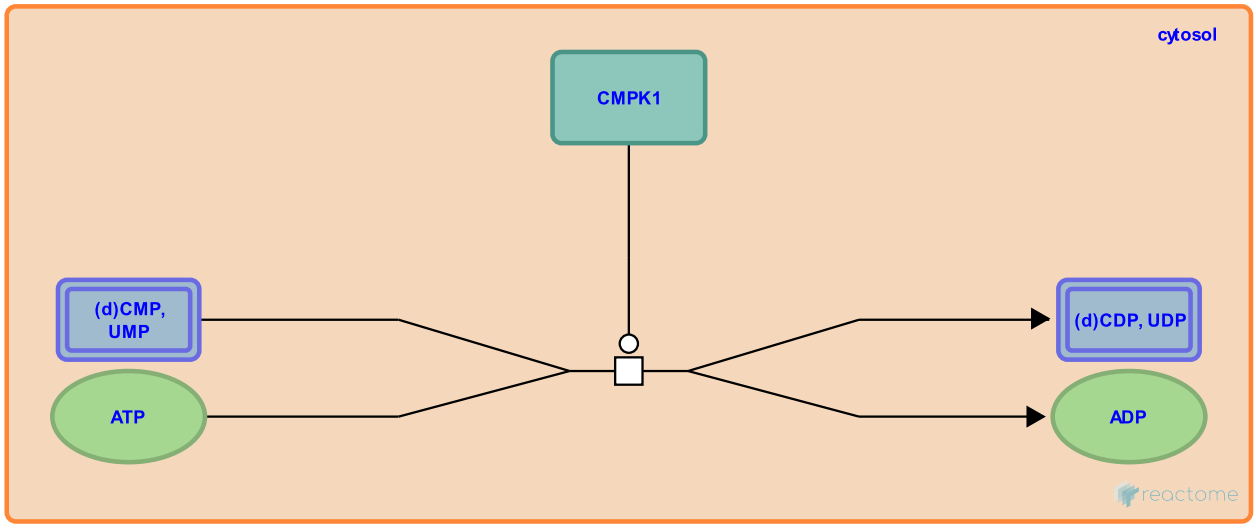
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-73548

Type: transition

Compartments: cytosol

Inferred from: (d)CMP or UMP + ATP <=> (d)CDP or UDP + ADP (CMPK1) (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

Followed by: (d)NDP + ATP <=> (d)NTP + ADP (NME1,2,3)

(d)CDP or UDP + ADP <=> (d)CMP or UMP + ATP (CMPK1) ↗

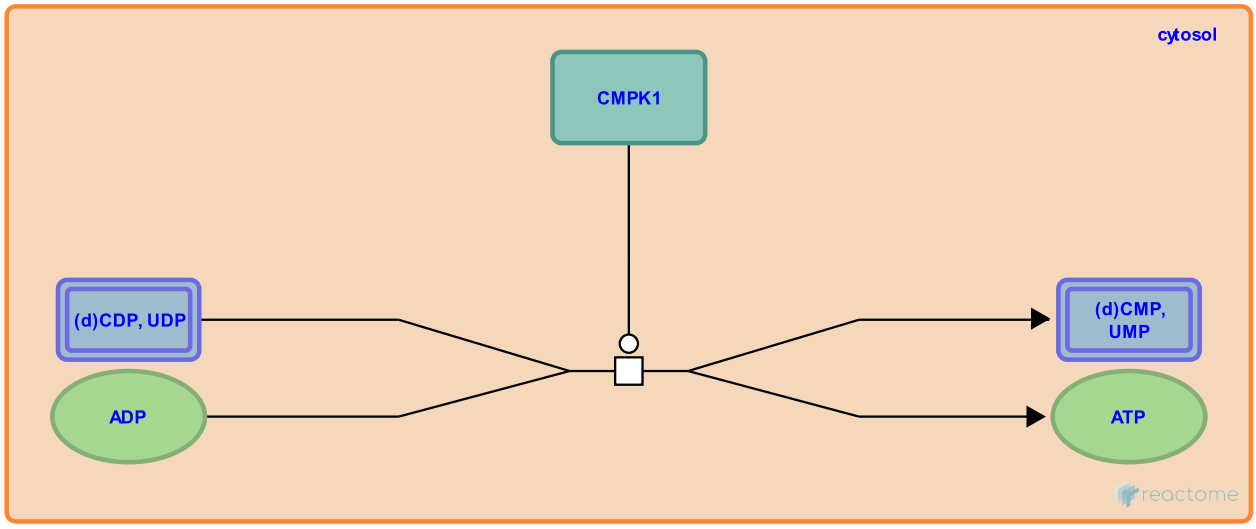
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-75125

Type: transition

Compartments: cytosol

Inferred from: (d)CDP or UDP + ADP <=> (d)CMP or UMP + ATP (CMPK1) (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

dUMP or TMP + ATP <=> dUDP or TDP + ADP [DTYMK] ↗

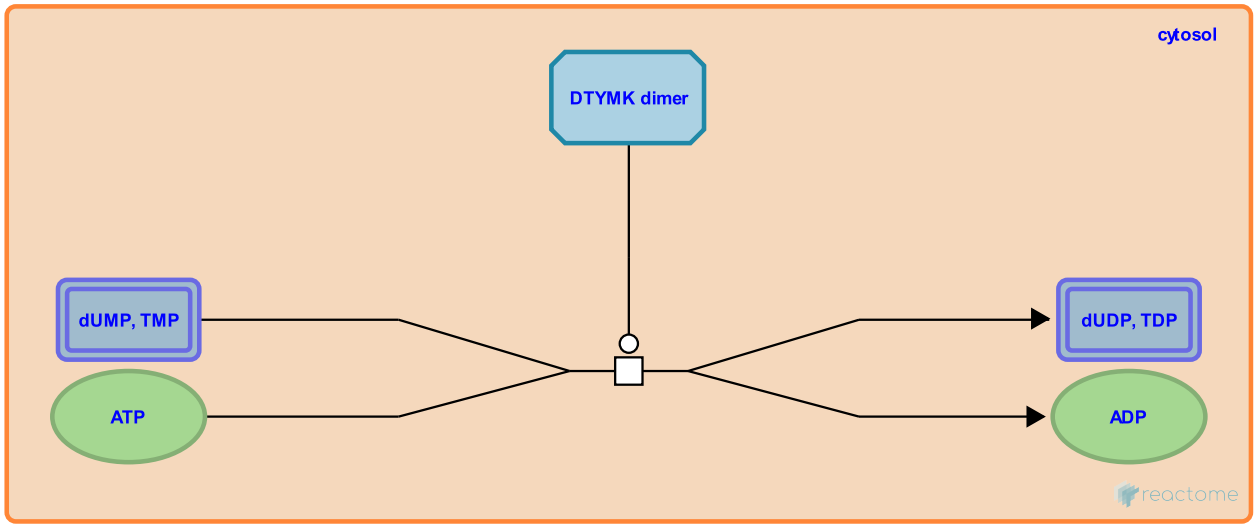
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-73635

Type: transition

Compartments: cytosol

Inferred from: dUMP or TMP + ATP <=> dUDP or TDP + ADP [DTYMK] (Homo sapiens)



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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

Preceded by: dUMP + N5,N10-methylene tetrahydrofolate => TMP + dihydrofolate

Followed by: (d)NDP + ATP <=> (d)NTP + ADP (NME1,2,3)

dUDP or TDP + ADP <=> dUMP or TMP + ATP [DTYMK] ↗

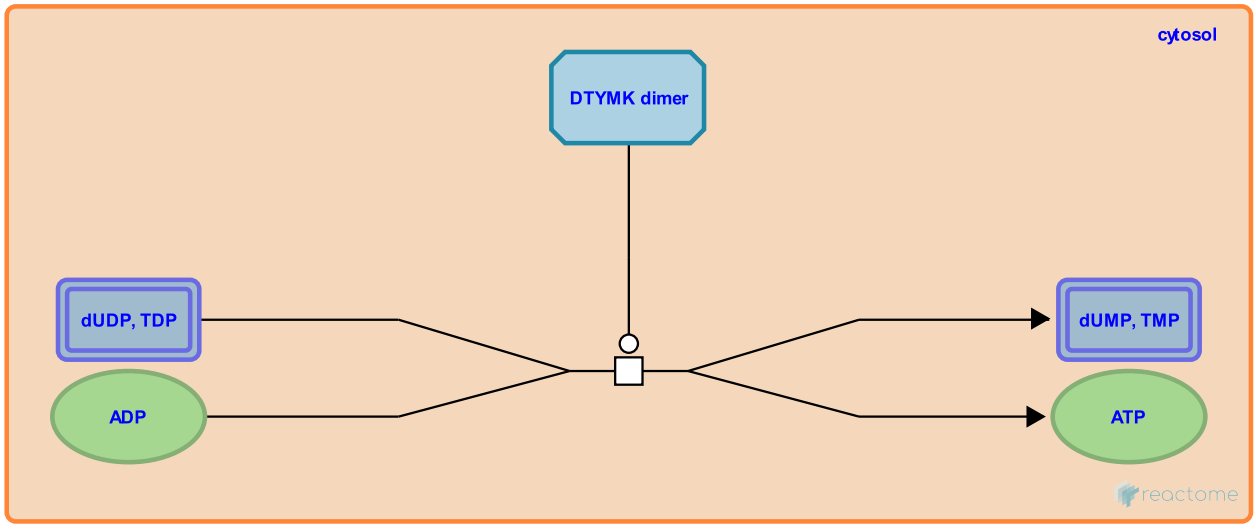
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-75126

Type: transition

Compartments: cytosol

Inferred from: dUDP or TDP + ADP <=> dUMP or TMP + ATP [DTYMK] (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

UTP + glutamine + ATP + H2O => CTP + glutamate + ADP + orthophosphate [CTPS] ↗

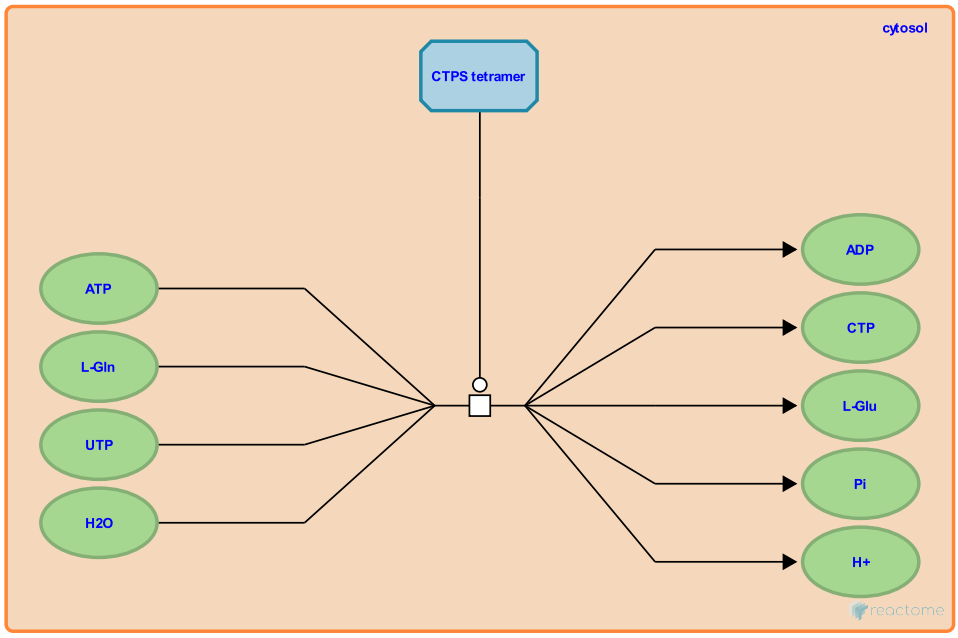
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-73647

Type: transition

Compartments: cytosol

Inferred from: UTP + glutamine + ATP + H2O => CTP + glutamate + ADP + orthophosphate [CTPS] (Homo sapiens)



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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

Followed by: (d)NTP + ADP <=> (d)NDP + ATP (NME1,2,3)

UTP + glutamine + ATP + H2O => CTP + glutamate + ADP + orthophosphate [CTPS2] ↗

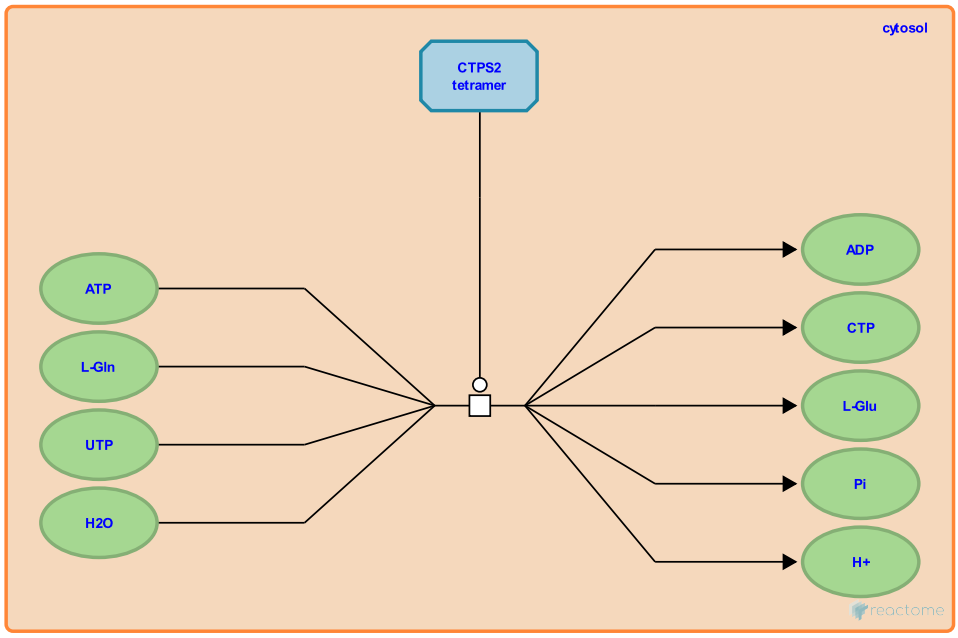
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-504054

Type: transition

Compartments: cytosol

Inferred from: UTP + glutamine + ATP + H2O => CTP + glutamate + ADP + orthophosphate [CTPS2] (Homo sapiens)



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RNR (M1M2) reduces nucleotide diphosphates to deoxynucleotide diphosphates (glutaredoxin) ↗

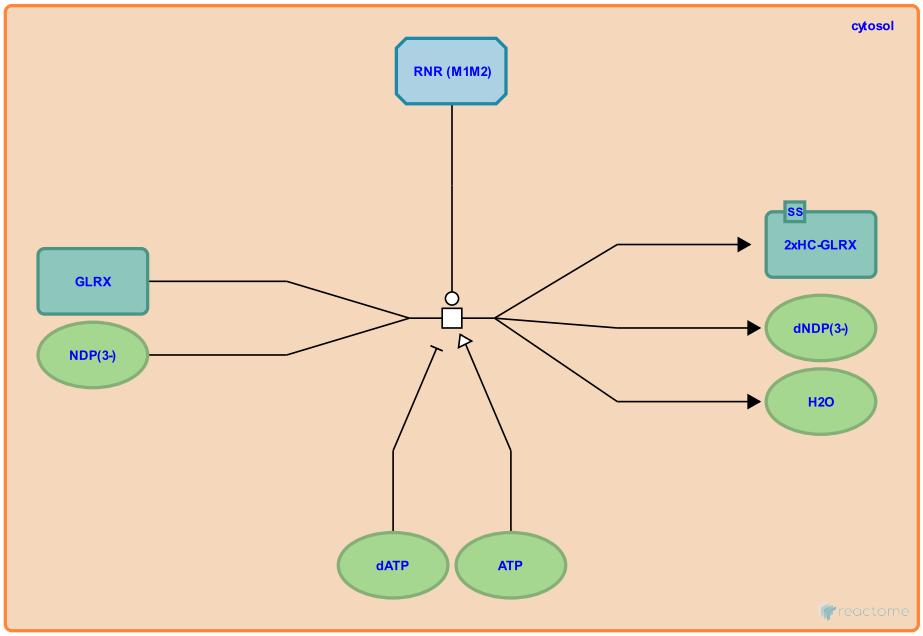
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-111742

Type: transition

Compartments: cytosol

Inferred from: RNR (M1M2) reduces nucleotide diphosphates to deoxynucleotide diphosphates (glutaredoxin) (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: glutaredoxin (oxidized) + glutathione (reduced) => glutaredoxin (reduced) + glutathione (oxidized)

RNR (M1M2) reduces nucleotide diphosphates to deoxynucleotide diphosphates (thioredoxin) ↗

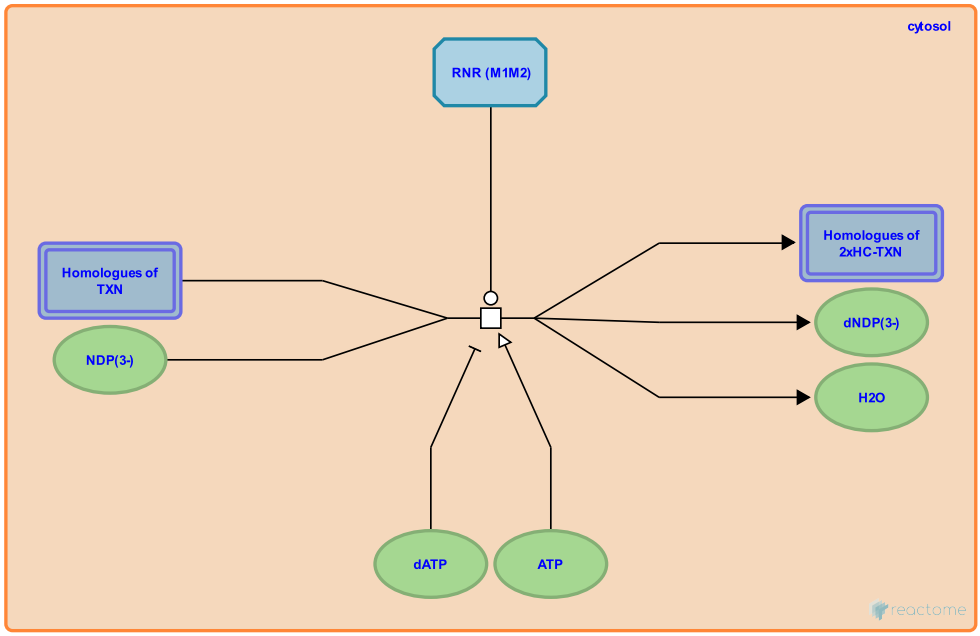
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-111751

Type: transition

Compartments: cytosol

Inferred from: RNR (M1M2) reduces nucleotide diphosphates to deoxynucleotide diphosphates (thioredoxin) (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

Preceded by: thioredoxin, oxidized + NADPH + H+ => thioredoxin, reduced + NADP+

RNR (M1M2B) reduces nucleotide diphosphates to deoxynucleotide diphosphates (glutaredoxin) ↗

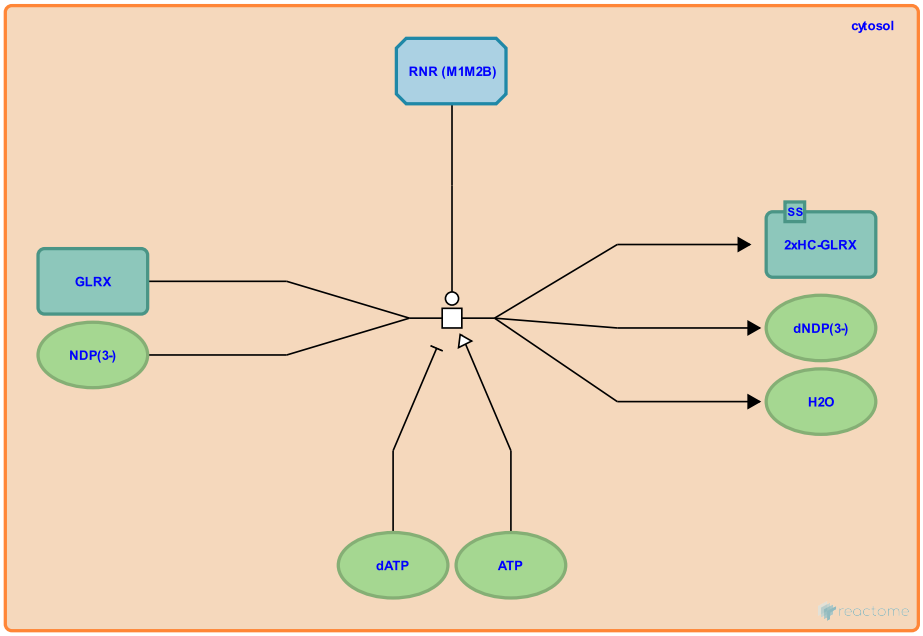
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-8866405

Type: transition

Compartments: cytosol

Inferred from: RNR (M1M2B) reduces nucleotide diphosphates to deoxynucleotide diphosphates (glutaredoxin) (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

Preceded by: glutaredoxin (oxidized) + glutathione (reduced) => glutaredoxin (reduced) + glutathione (oxidized)

RNR (M1M2B) reduces nucleotide diphosphates to deoxynucleotide diphosphates (thioredoxin) ↗

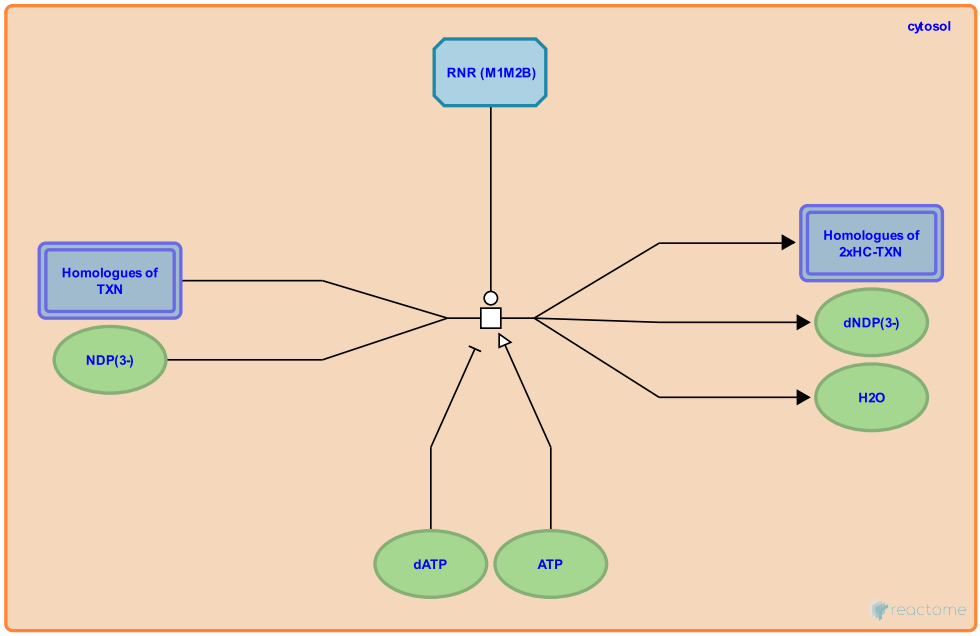
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-111804

Type: transition

Compartments: cytosol

Inferred from: RNR (M1M2B) reduces nucleotide diphosphates to deoxynucleotide diphosphates (thioredoxin) (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

Preceded by: thioredoxin, oxidized + NADPH + H+ => thioredoxin, reduced + NADP+

glutaredoxin (oxidized) + glutathione (reduced) => glutaredoxin (reduced) + glutathione (oxidized) ↗

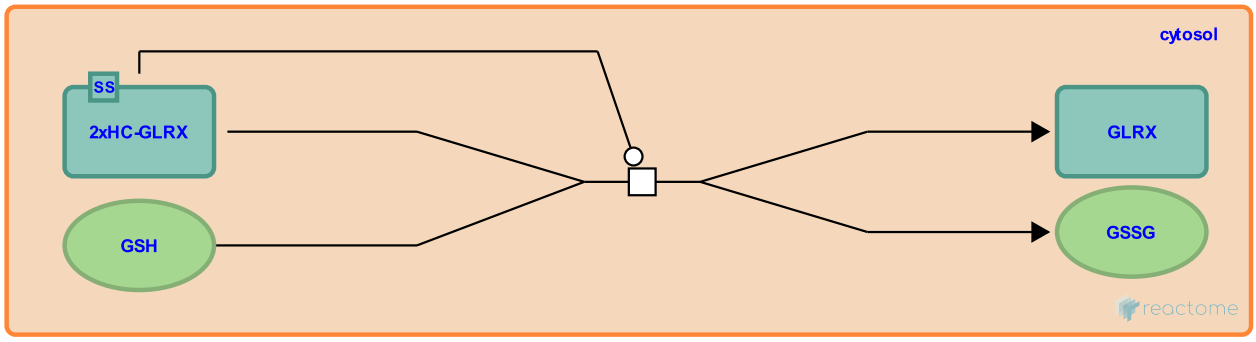
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-111746

Type: transition

Compartments: cytosol

Inferred from: glutaredoxin (oxidized) + glutathione (reduced) => glutaredoxin (reduced) + glutathione (oxidized) (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

Followed by: RNR (M1M2) reduces nucleotide diphosphates to deoxynucleotide diphosphates (glutaredoxin), RNR (M1M2B) reduces nucleotide diphosphates to deoxynucleotide diphosphates (glutaredoxin), glutathione (oxidized) + NADPH + H+ => 2 glutathione (reduced) + NADP+

glutathione (oxidized) + NADPH + H+ => 2 glutathione (reduced) + NADP+ ↗

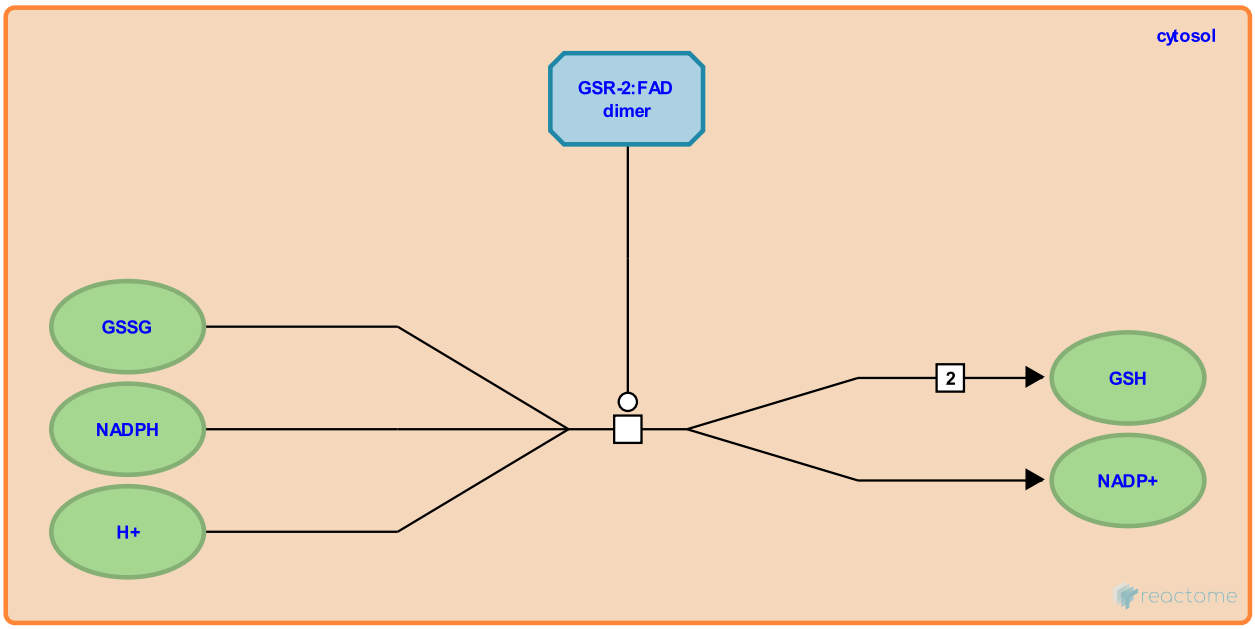
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-71682

Type: transition

Compartments: cytosol

Inferred from: glutathione (oxidized) + NADPH + H+ => 2 glutathione (reduced) + NADP+ (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

Preceded by: glutaredoxin (oxidized) + glutathione (reduced) => glutaredoxin (reduced) + glutathione (oxidized)

thioredoxin, oxidized + NADPH + H+ => thioredoxin, reduced + NADP+ ↗

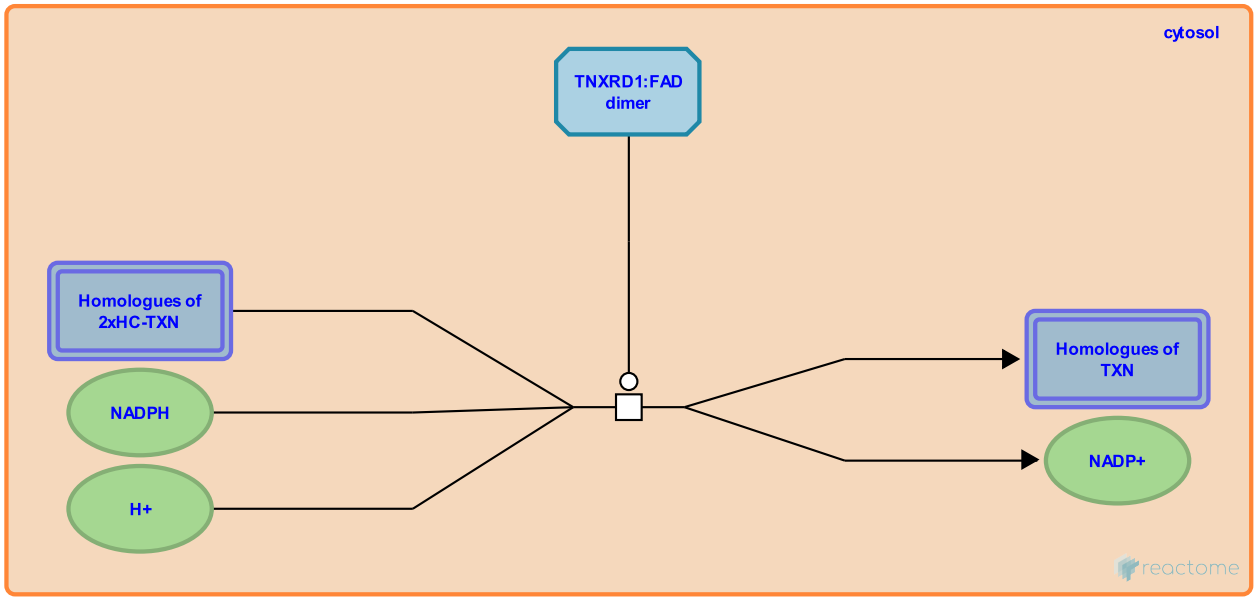
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-73646

Type: transition

Compartments: cytosol

Inferred from: thioredoxin, oxidized + NADPH + H+ => thioredoxin, reduced + NADP+ (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

Followed by: RNR (M1M2B) reduces nucleotide diphosphates to deoxynucleotide diphosphates (thioredoxin), RNR (M1M2) reduces nucleotide diphosphates to deoxynucleotide diphosphates (thioredoxin)

(d)NDP + ATP <=> (d)NTP + ADP (NME1,2,3) ↗

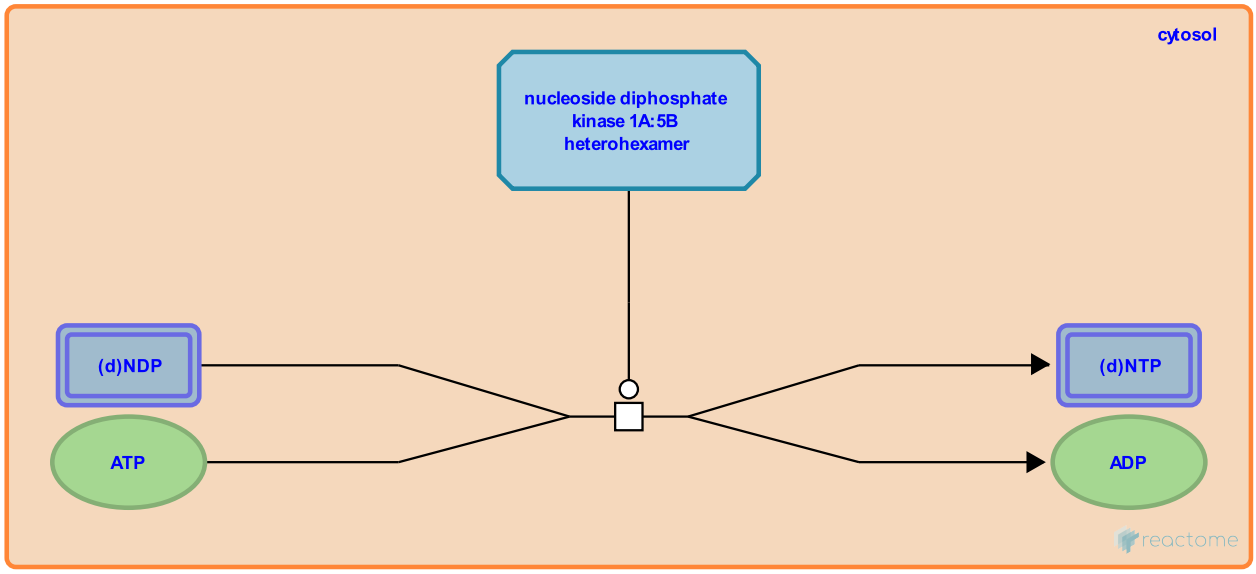
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-482619

Type: transition

Compartments: cytosol

Inferred from: (d)NDP + ATP <=> (d)NTP + ADP (NME1,2,3) (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

Preceded by: (d)CMP or UMP + ATP <=> (d)CDP or UDP + ADP (CMPK1), dUMP or TMP + ATP <=> dUDP or TDP + ADP [DTYMK], (d)GMP + ATP <=> (d)GDP + ADP (GUK1)

(d)NTP + ADP <=> (d)NDP + ATP (NME1,2,3) ↗

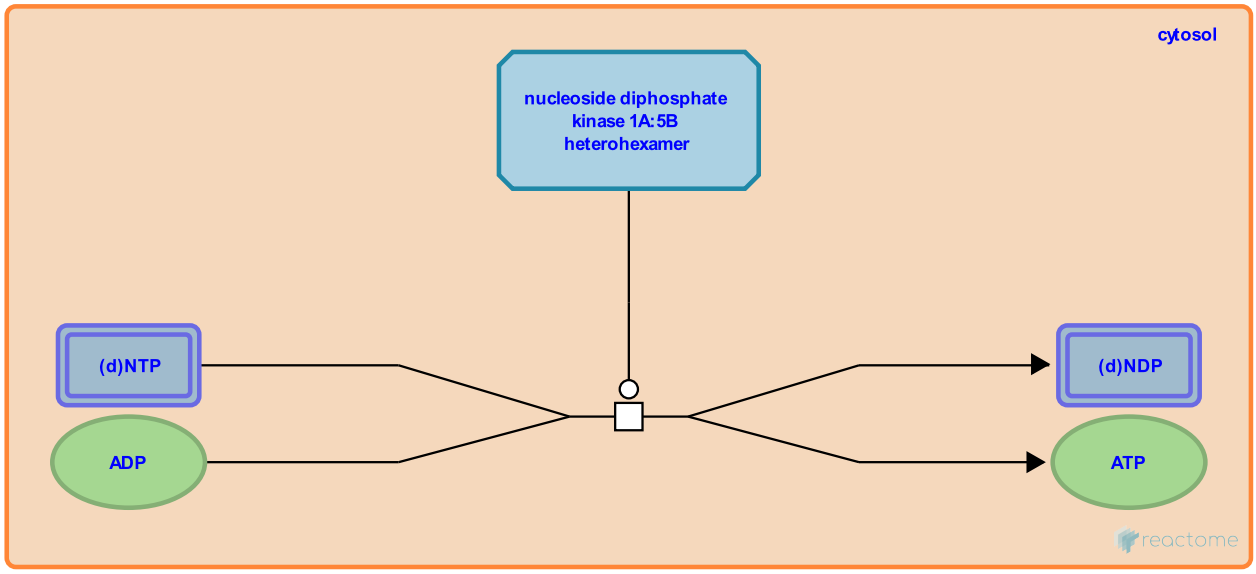
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-482621

Type: transition

Compartments: cytosol

Inferred from: (d)NTP + ADP <=> (d)NDP + ATP (NME1,2,3) (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

Preceded by: UTP + glutamine + ATP + H2O => CTP + glutamate + ADP + orthophosphate [CTPS]

(d)NDP + ATP <=> (d)NTP + ADP (NME4) ↗

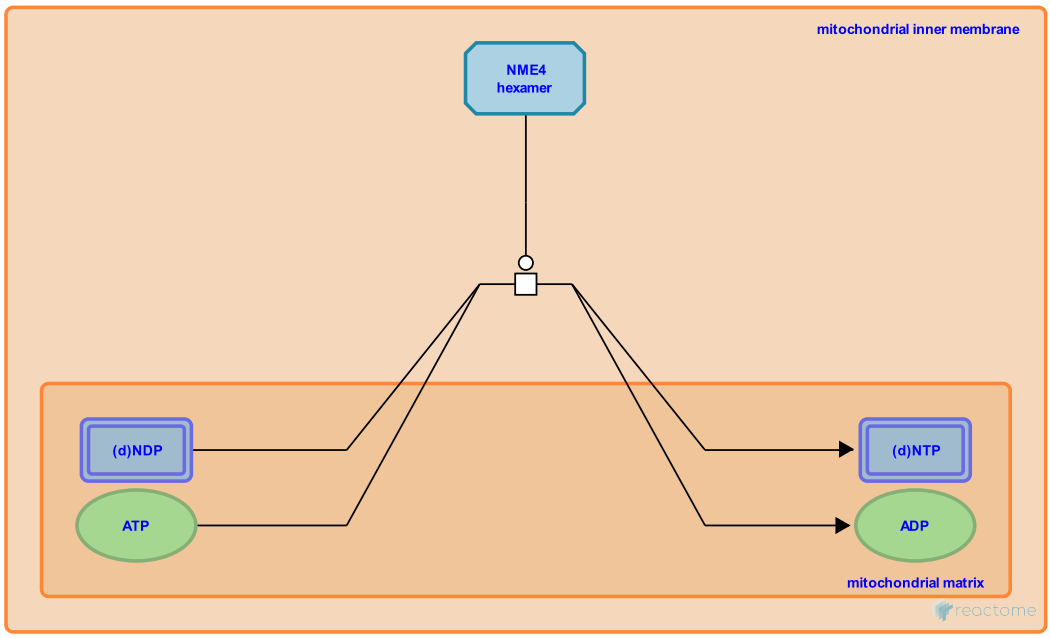
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-482804

Type: transition

Compartments: mitochondrial inner membrane, mitochondrial matrix

Inferred from: (d)NDP + ATP <=> (d)NTP + ADP (NME4) (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

(d)NTP + ADP <=> (d)NDP + ATP (NME4) ↗

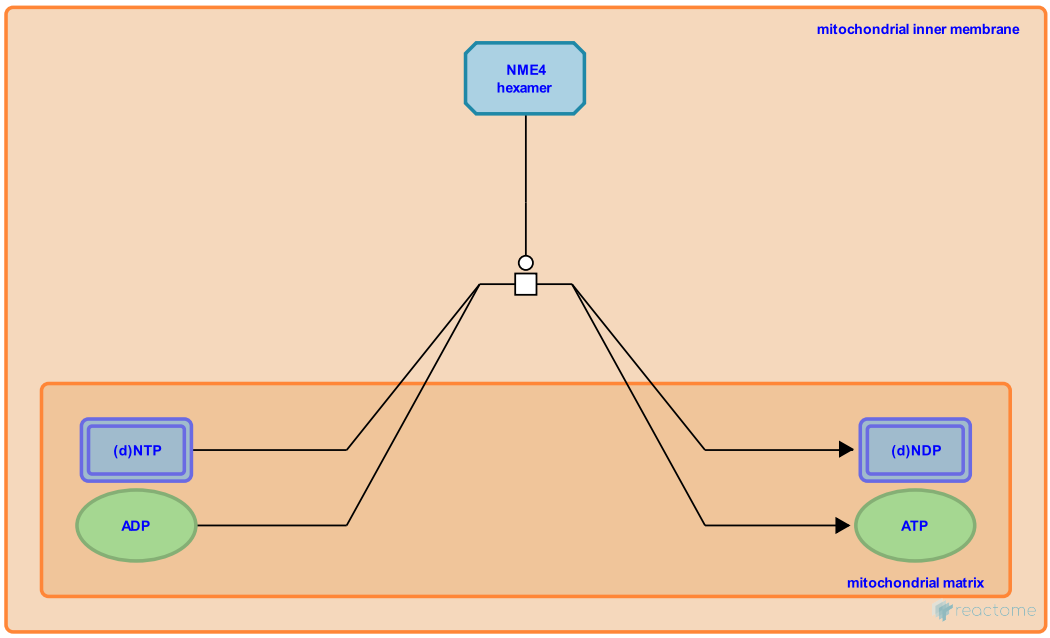
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-482812

Type: transition

Compartments: mitochondrial inner membrane, mitochondrial matrix

Inferred from: (d)NTP + ADP <=> (d)NDP + ATP (NME4) (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

NME1:NME3 heterohexamer, NME2P1 phosphorylate NDPs to NTPs ↗

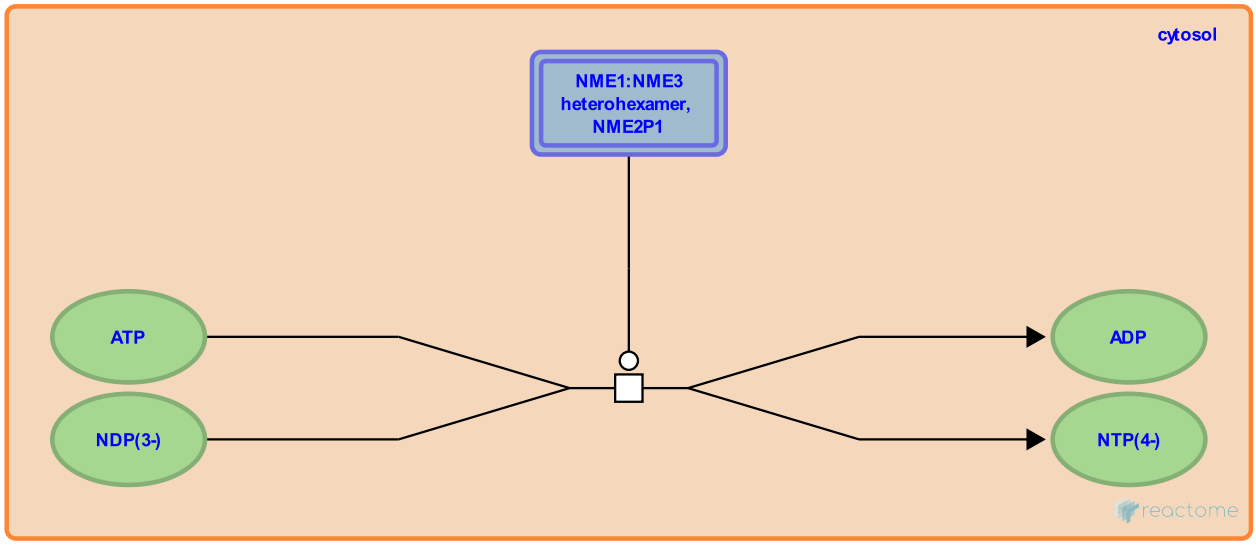
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-6806877

Type: transition

Compartments: cytosol

Inferred from: NME1:NME3 heterohexamer, NME2P1 phosphorylate NDPs to NTPs (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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dUTP + H2O => dUMP + pyrophosphate ↗

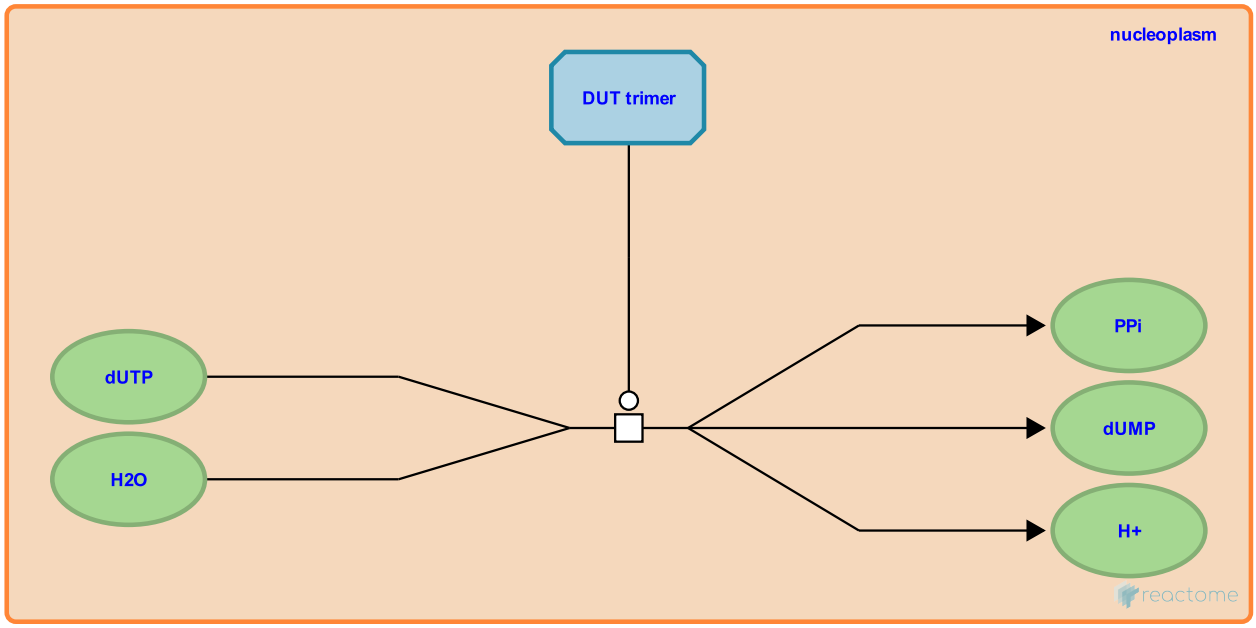
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-73666

Type: transition

Compartments: nucleoplasm

Inferred from: dUTP + H2O => dUMP + 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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: dUMP + N5,N10-methylene tetrahydrofolate => TMP + dihydrofolate

dUMP + N5,N10-methylene tetrahydrofolate => TMP + dihydrofolate ↗

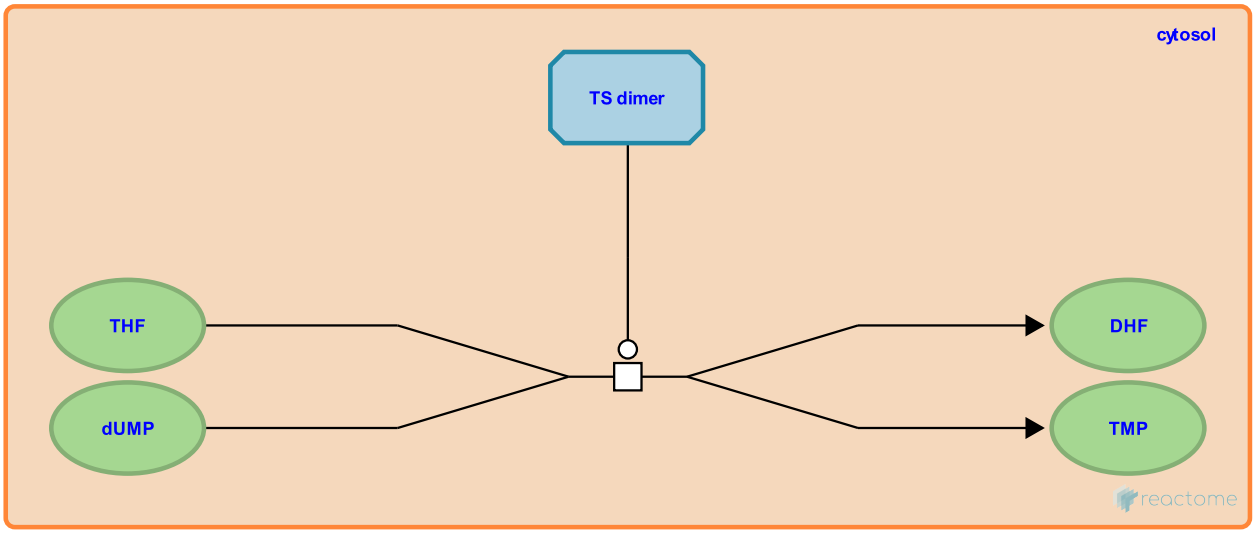
Location: Interconversion of nucleotide di- and triphosphates

Stable identifier: R-PFA-73605

Type: transition

Compartments: cytosol

Inferred from: dUMP + N5,N10-methylene tetrahydrofolate => TMP + dihydrofolate (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

Preceded by: dUTP + H2O => dUMP + pyrophosphate

Followed by: dUMP or TMP + ATP <=> dUDP or TDP + ADP [DTYMK]

Table of Contents