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

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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. ↗

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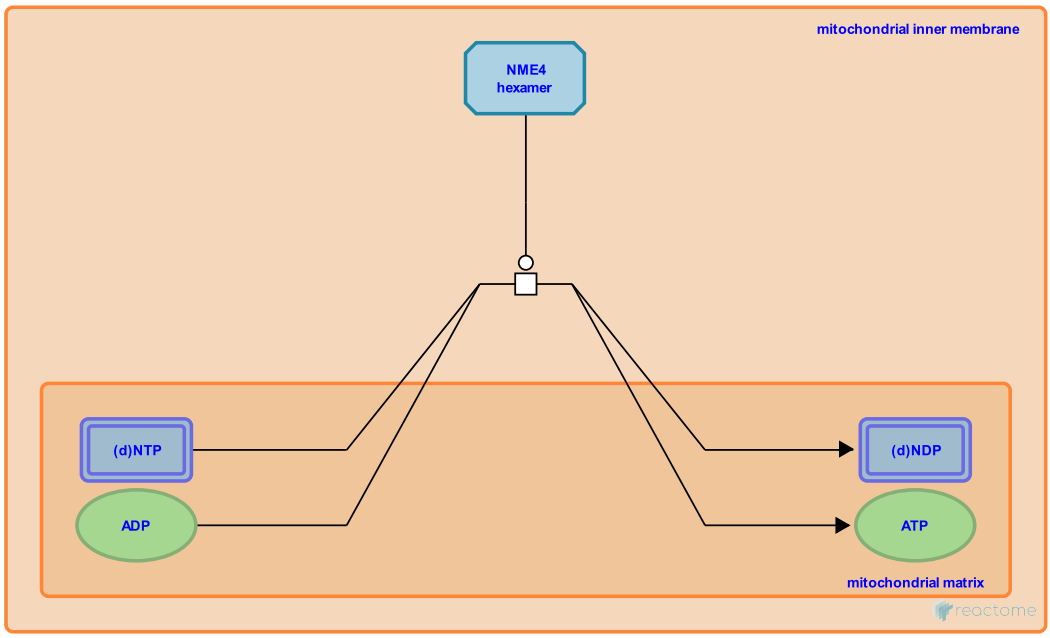
Stable identifier: R-HSA-482812

Type: transition

Compartments: mitochondrial matrix, mitochondrial inner membrane



Nucleoside diphosphate kinase NME4 associated with the inner mitochondrial membrane (Tokarska-Schlattner et al. 2008) catalyzes the reversible reaction of ribonucleoside and deoxyribonucleoside 5'-diphosphates with ADP to form the corresponding nucleoside 5'-diphosphates and ATP. The active form of the enzyme is a hexamer of NME4 polypeptides whose amino-terminal 33 residues, a mitochondrial translocation signal, have been removed (Milon et al. 2000). The substrate specificity of NME4 has not been examined in detail, but is inferred to be broad like that of the homologous NME1, 2, and 3 kinases (Schaertl et al. 1998).

Literature references

Munier, A., Mailleau, C., Lacombe, ML., Speer, O., Borot, C., Boissan, M. et al. (2008). The nucleoside diphosphate kinase D (NM23-H4) binds the inner mitochondrial membrane with high affinity to cardiolipin and couples nucleotide transfer with respiration. *J Biol Chem, 283*, 26198-207.

Konrad, M., Geeves, MA., Schaertl, S. (1998). Substrate specificity of human nucleoside-diphosphate kinase revealed by transient kinetic analysis. *J Biol Chem, 273*, 5662-5669.

Janin, J., Capeau, J., Milon, L., Munier, A., Lacombe, ML., Karlsson, A. et al. (2000). The human nm23-H4 gene product is a mitochondrial nucleoside diphosphate kinase. *J Biol Chem, 275*, 14264-14272.

Editions

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