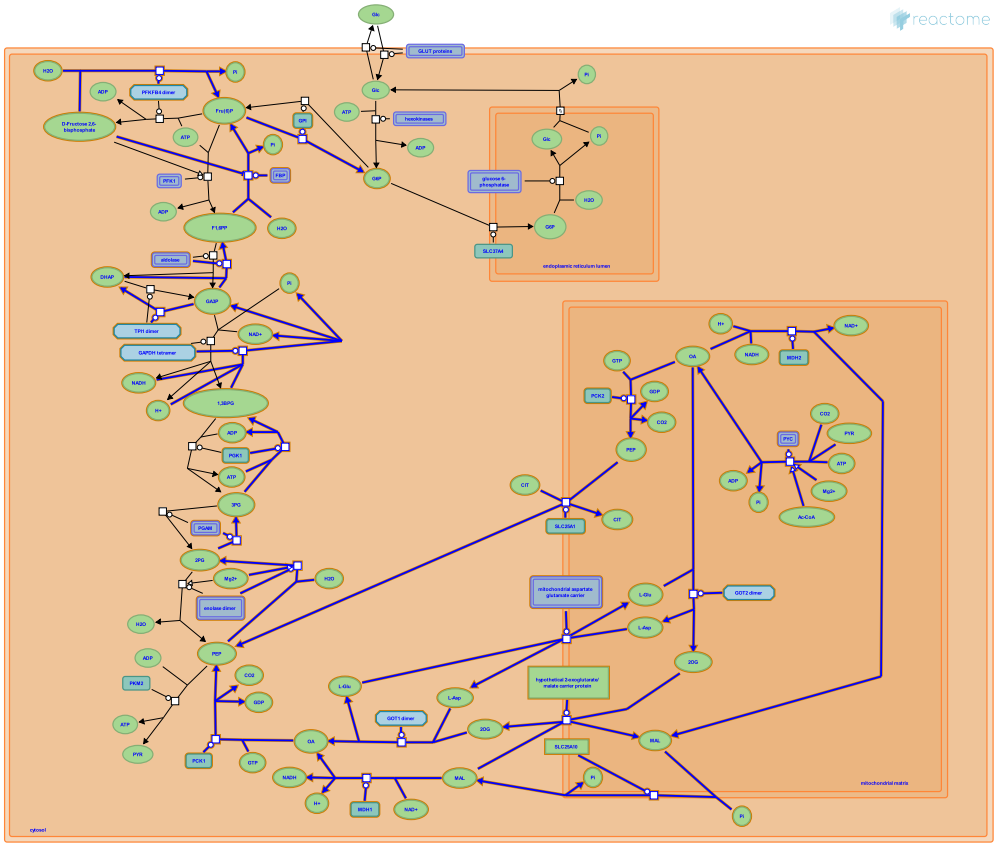
Gluconeogenesis



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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.

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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. ↗

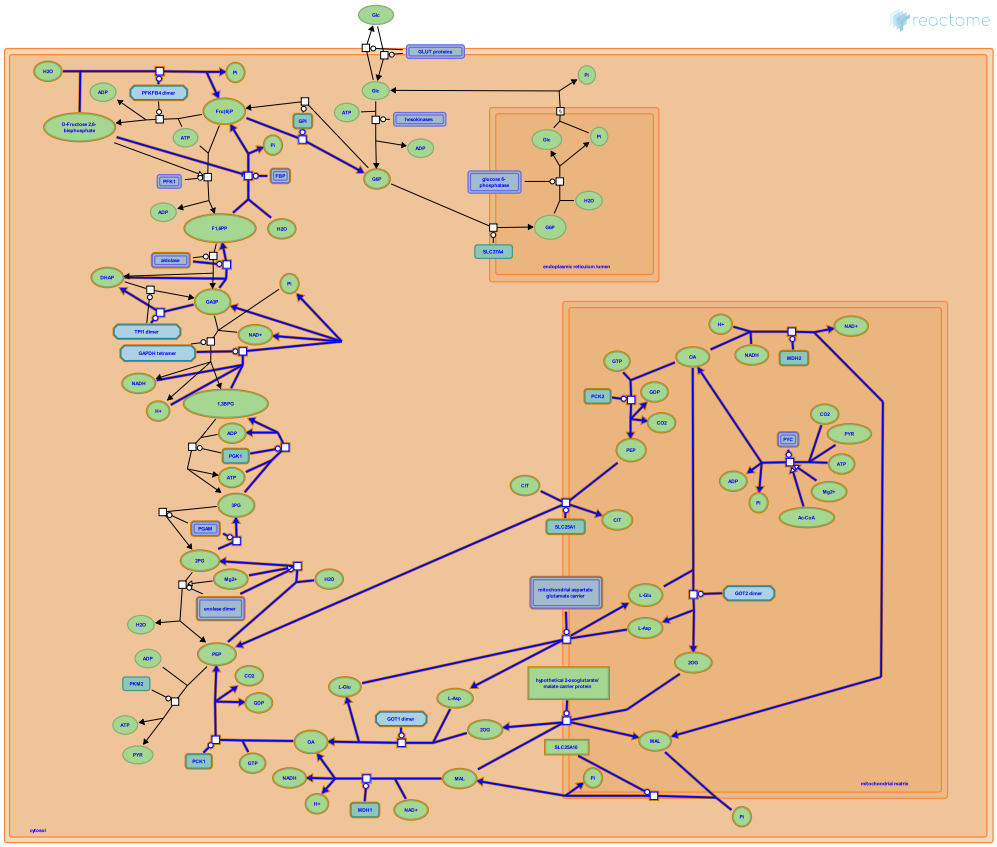
Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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. ↗

Gluconeogenesis ↗

Stable identifier: R-GGA-352875



The reactions of gluconeogenesis convert mitochondrial pyruvate to cytosolic glucose 6-phosphate which in turn can be hydrolyzed to glucose and exported from the cell. Gluconeogenesis is confined to cells of the liver and kidney and enables glucose synthesis from molecules such as lactate and alanine and other amino acids when exogenous glucose is not available. The process of gluconeogenesis as diagrammed below occurs in two parts: a network of possible reactions mediates the conversion of mitochondrial pyruvate to cytosolic phosphoenolpyruvate, which in turn is converted to glucose 6-phosphate in a single sequence of cytosolic reactions.

In the chicken, three variants of the process can be distinguished, two restricted to the kidney and one that takes place in both kidney and liver. 1) In the kidney, carbon atoms from mitochondrial oxaloacetate, via a series of transport and transamination reactions, are used to generate cytosolic oxaloacetate, which is converted to phosphoenolpyruvate by a cytosolic, hormonally regulated form of phosphoenolpyruvate carboxykinase, PCK1. This variant allows regulated glucose synthesis from lactate. 2) In the kidney, mitochondrial oxaloacetate is reduced to malate, which is exported to the cytosol and re-oxidized to oxaloacetate. This variant provides reducing equivalents to the cytosol, needed for glucose synthesis from amino acids such as alanine and glutamine. 3) In both liver and kidney, constitutively expressed mitochondrial phosphoenolpyruvate carboxykinase, PCK2, catalyzes the conversion of mitochondrial oxaloacetate to phosphoenolpyruvate which in turn is transported to the cytosol. This third variant also allows glucose synthesis from lactate (Soling et al. 1973; Wallace and Newsholme 1967; Watford et al. 1981; Weldon et al. 1990).

In all cases, the metabolism of a molecule of pyruvate requires the generation and consumption of one reducing equivalent as cytosolic NADH + H+. For pyruvate derived from lactate (variants 1 and 3), NADH + H+ is generated with the oxidation of lactate to pyruvate in the cytosol (a reaction of pyruvate metabolism not shown in the diagram). For pyruvate derived from amino acids (variant 2), mitochondrial NADH + H+ generated by glutamate dehydrogenase (a reaction of amino acid metabolism, not shown) is used to reduce oxaloacetate to malate, which is transported to the cytosol and re-oxidized, generating cytosolic NADH + H+. The metabolism of each molecule of pyruvate also requires the consumption of three high-energy phosphates, two from ATP and one from GTP.

In the second part of gluconeogenesis, cytosolic phosphoenolpyruvate, however derived, is converted to fructose 1,6-bisphosphate by reactions that are the reverse of steps of glycolysis. Hydrolysis of fructose 1,6-bisphosphate to fructose 6-phosphate is catalyzed by fructose 1,6-bisphosphatase, and fructose 6-phosphate is reversibly isomerized to glucose 6-phosphate.

Literature references

Wallace, JC., Newsholme, EA. (1967). A comparison of the properties of fructose 1,6-diphosphatase, and the activities of other key enzymes of carbohydrate metabolism, in the livers of embryonic and adult rat, sheep and domestic fowl. *Biochem J, 104*, 378-84. ↗

Janson, G., Kleineke, J., Söling, HD., Willms, B., Kuhn, A. (1973). Relationship between intracellular distribution of phosphoenolpyruvate carboxykinase, regulation of gluconeogenesis, and energy cost of glucose formation. *Eur J Biochem, 37*, 233-43. ↗

Hanson, RW., Utter, MF., Hod, Y., Chiao, YB., Watford, M. (1981). The unique role of the kidney in gluconeogenesis in the chicken. The significance of a cytosolic form of phosphoenolpyruvate carboxykinase. *J Biol Chem, 256*, 10023-7. ↗

Hanson, RW., Savon, S., Cook, JS., Kalonick, PA., Hod, Y., Weldon, SL. et al. (1990). Mitochondrial phosphoenolpyruvate carboxykinase from the chicken. Comparison of the cDNA and protein sequences with the cytosolic isozyme. *J Biol Chem, 265*, 7308-17. ↗

Editions

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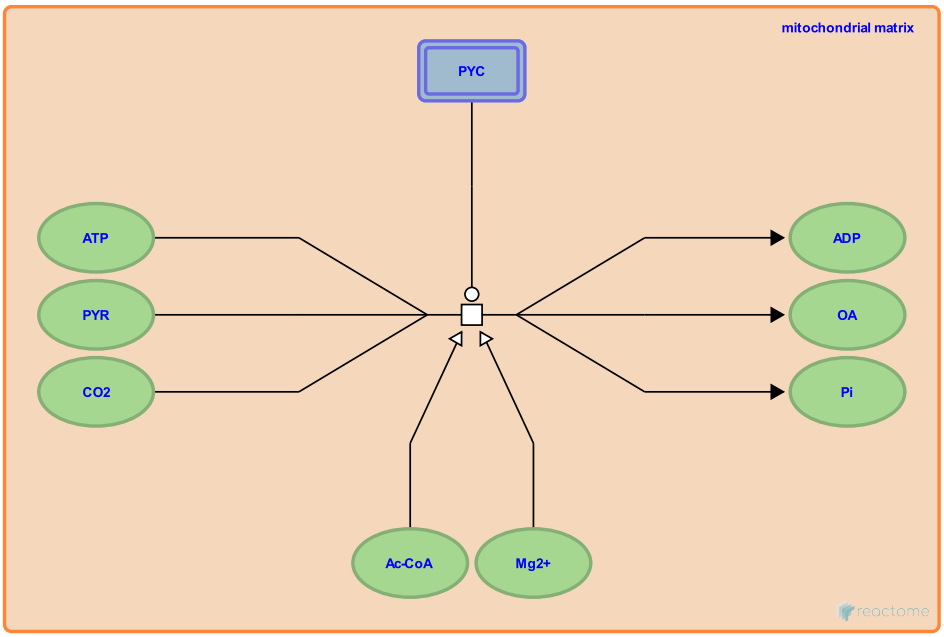
pyruvate + CO2 + ATP => oxaloacetate + ADP + orthophosphate ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-353154

Type: transition

Compartments: mitochondrial matrix



Pyruvate carboxylase catalyzes the reaction of pyruvate, ATP, and bicarbonate to form oxaloacetate, ADP, and orthophosphate. The active form of the enzyme is a tetramer, with one molecule each of biotin and Mn++ associated with each protein monomer. The reaction requires Mg++. Acetyl CoA is an allosteric activator of pyruvate carboxylase; the reaction does not proceed to a significant extent in its absence (Keech and Utter 1963; Scrutton and Utter 1967; Jitrapakdee et al. 2002).

Followed by: oxaloacetate + GTP => phosphoenolpyruvate + GDP + CO2 [mitochondrial matrix], oxaloacetate + glutamate <=> aspartate + alpha-ketoglutarate (2-oxoglutarate), oxaloacetate + NADH + H+ <=> malate + NAD+

Literature references

Jitrapakdee, S., Khew-Goodall, Y., Cassady, AI., Wallace, JC., Nezic, MG. (2002). Molecular cloning and domain structure of chicken pyruvate carboxylase. *Biochem Biophys Res Commun, 295*, 387-93. ↗

Utter, MF., Scrutton, MC. (1967). Pyruvate carboxylase. IX. Some properties of the activation by certain acyl derivatives of coenzyme A. *J Biol Chem, 242*, 1723-35. ↗

Utter, MF., Keech, DB. (1963). Pyruvate carboxylase. II. Properties. *J Biol Chem, 238*, 2609-14. ↗

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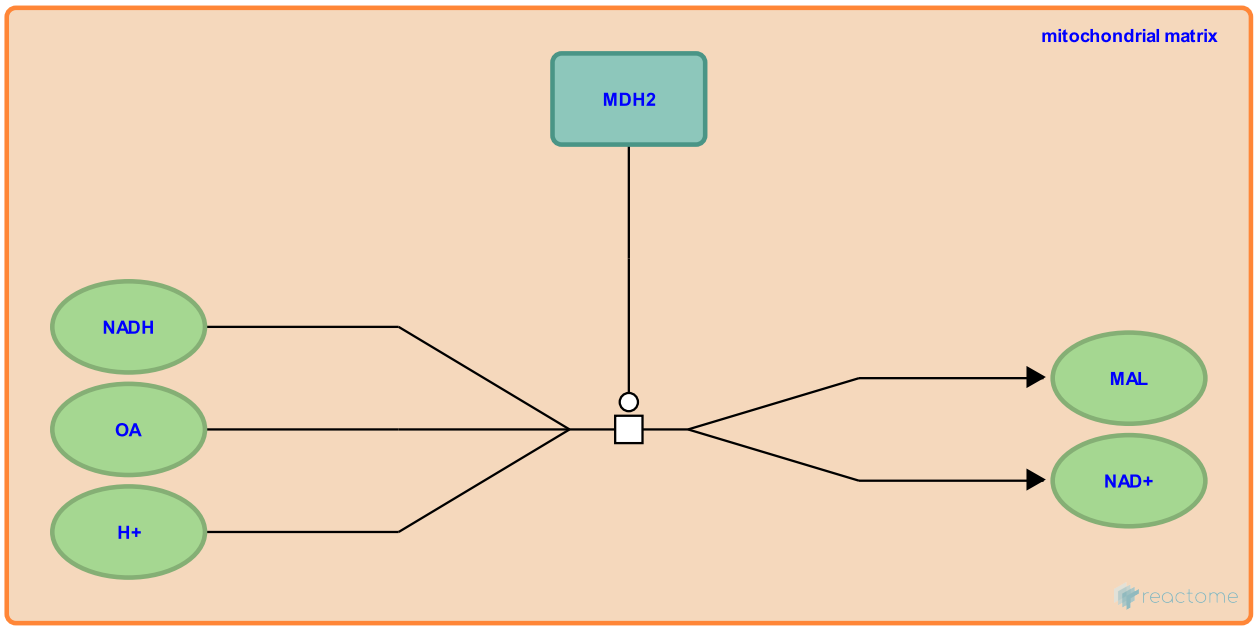
oxaloacetate + NADH + H+ <=> malate + NAD+ ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-372422

Type: transition

Compartments: mitochondrial matrix



Oxaloacetate is reversibly reduced by NADH + H+ to form malate and NAD+. No chicken enzyme capable of catalyzing this reaction has been identified, although an open reading frame capable of encoding a protein closely similar to authentic human mitochondrial malate dehydrogenase (MDH2) has been identified computationally in the ENSEMBL chicken gene set. This reaction is inferred from the known properties of mammalian MDH2 (Wolfe & Neilands 1956).

Preceded by: pyruvate + CO2 + ATP => oxaloacetate + ADP + orthophosphate

Followed by: malate [mitochondrial matrix] + orthophosphate [cytosol] <=> malate [cytosol] + orthophosphate [mitochondrial matrix]

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malate [mitochondrial matrix] + orthophosphate [cytosol] <=> malate [cytosol] + orthophosphate [mitochondrial matrix] ↗

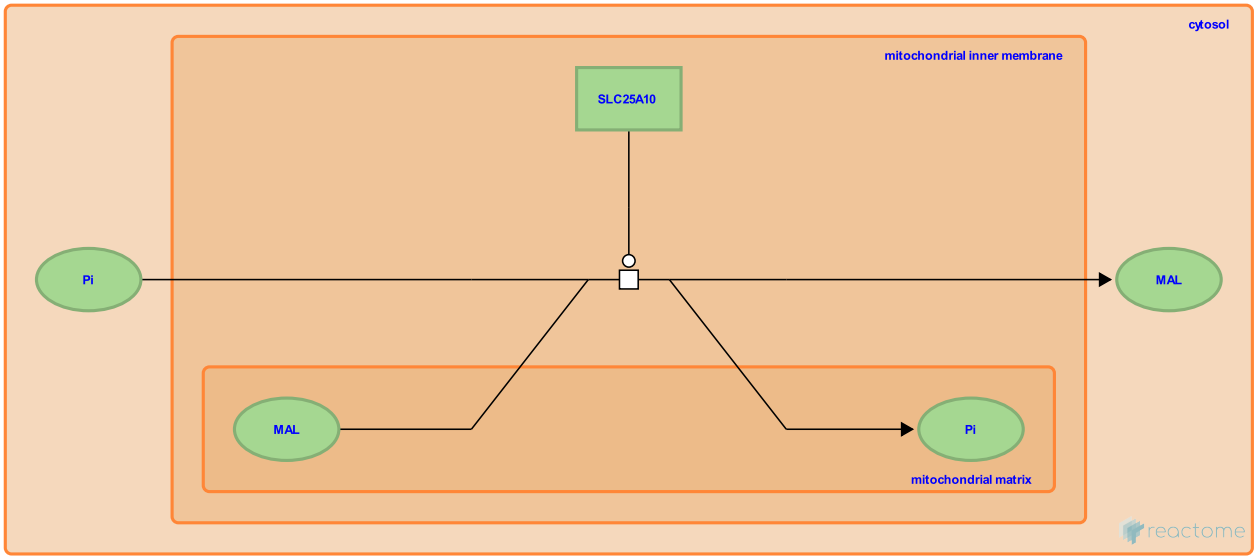
Location: Gluconeogenesis

Stable identifier: R-GGA-372852

Type: transition

Compartments: mitochondrial inner membrane, mitochondrial matrix, cytosol

Inferred from: SLC25A10 mediates exchange of malate and phosphate (Homo sapiens)



SLC25A10, the mitochondrial dicarboxylate carrier protein in the inner mitochondrial membrane, mediates the reversible exchange of mitochondrial malate for cytosolic phosphate. No chicken transport protein capable of mediating this reaction has been identified, although an open reading frame capable of encoding a protein closely similar to authentic human SLC25A10 has been identified computationally in the ENSEMBL chicken gene set. This reaction is inferred from its human counterpart.

Preceded by: oxaloacetate + NADH + H+ <=> malate + NAD+

Followed by: malate + NAD+ <=> oxaloacetate + NADH + H+

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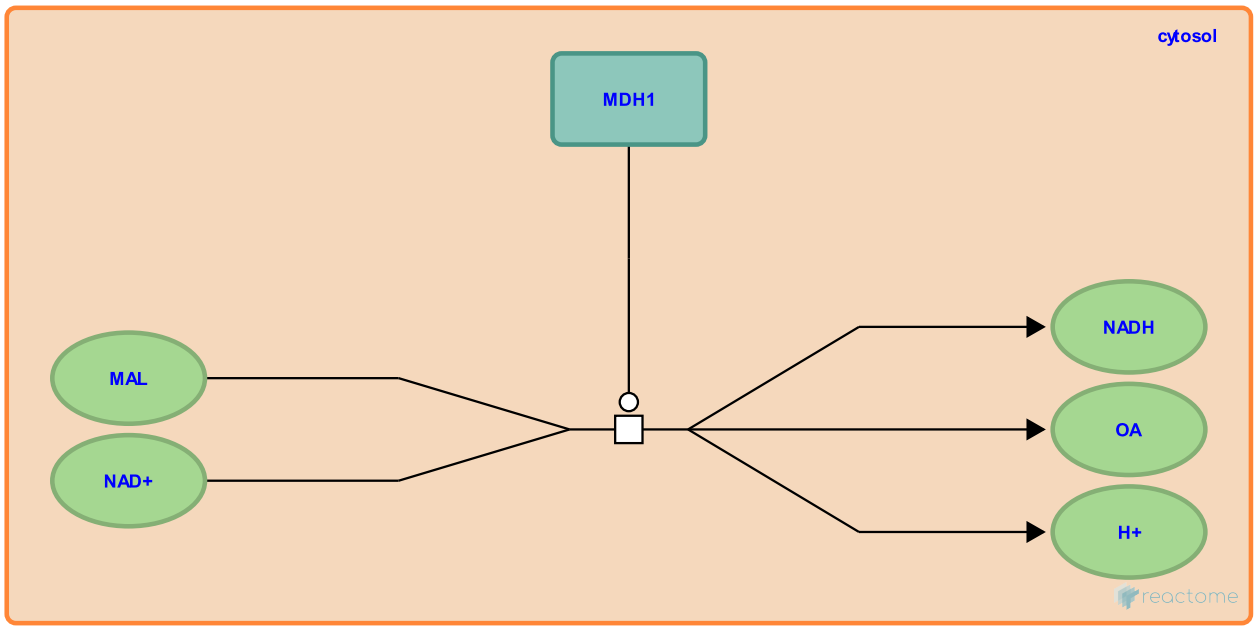
malate + NAD+ <=> oxaloacetate + NADH + H+ ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-372855

Type: transition

Compartments: cytosol



Cytosolic malate dehydrogenase catalyzes the reaction of malate and NAD+ to form oxaloacetate and NADH + H+. While a cDNA capable of encoding a protein similar to mammalian cytosolic malate dehydrogenase has been identified, its protein product has not been functionally characterized and this reaction is inferred from the enzymatic properties of its human counterpart (Friedrichet al. 1987).

Preceded by: malate [mitochondrial matrix] + orthophosphate [cytosol] <=> malate [cytosol] + orthophosphate [mitochondrial matrix]

Followed by: oxaloacetate + GTP => phosphoenolpyruvate + GDP + CO2 [cytosol]

Editions

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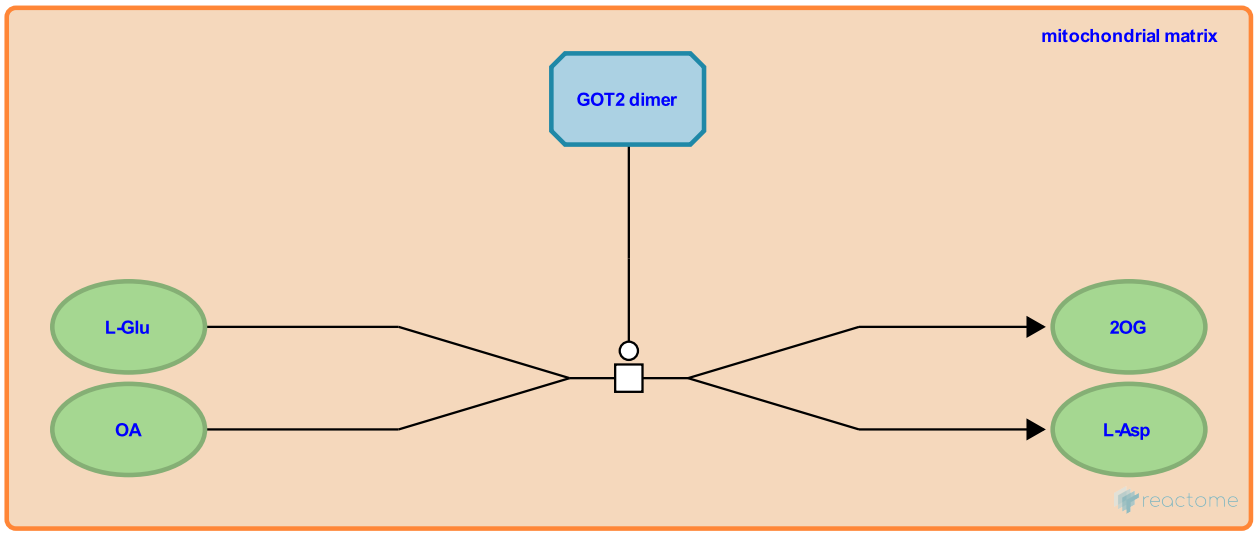
oxaloacetate + glutamate <=> aspartate + alpha-ketoglutarate (2-oxoglutarate) ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-372564

Type: transition

Compartments: mitochondrial matrix



Mitochondrial GOT2 catalyzes the reversible transamination of oxaloacetate and glutamate to form aspartate and alpha-ketoglutarate (2-oxoglutarate). The active form of the enzyme is a homodimer, with one molecule of pyridoxal phosphate bound to each enzyme monomer (Graf-Hausner et al. 1983; McPhalen et al. 1992).

Preceded by: pyruvate + CO2 + ATP => oxaloacetate + ADP + orthophosphate

Followed by: 2-oxoglutarate [mitochondrial matrix] + malate [cytosol] <=> 2-oxoglutarate [cytosol] + malate [mitochondrial matrix], aspartate [mitochondrial matrix] + glutamate [cytosol] <=> aspartate [cytosol] + glutamate [mitochondrial matrix]

Literature references

Wilson, KJ., Christen, P., Graf-Hausner, U. (1983). The covalent structure of mitochondrial aspartate aminotransferase from chicken. Identification of segments of the polypeptide chain invariant specifically in the mitochondrial isoenzyme. *J Biol Chem, 258*, 8813-26. ↗

Vincent, MG., Jansonius, JN., McPhalen, CA. (1992). X-ray structure refinement and comparison of three forms of mitochondrial aspartate aminotransferase. *J Mol Biol, 225*, 495-517. ↗

Editions

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2-oxoglutarate [mitochondrial matrix] + malate [cytosol] <=> 2-oxoglutarate [cytosol] + malate [mitochondrial matrix] ↗

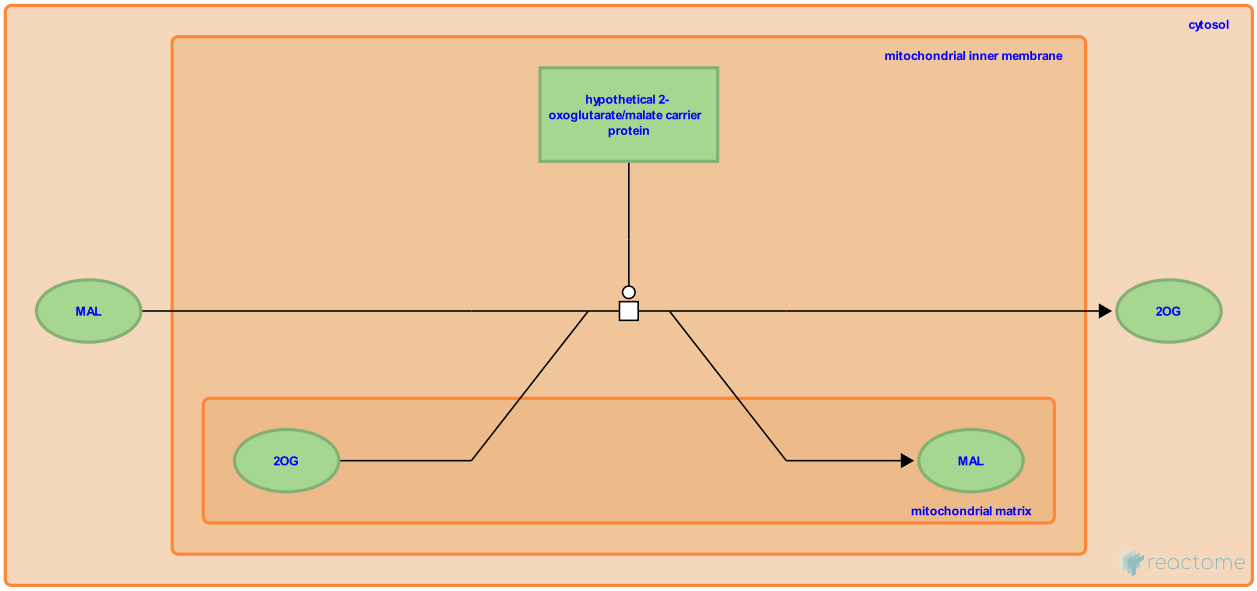
Location: Gluconeogenesis

Stable identifier: R-GGA-376887

Type: transition

Compartments: mitochondrial inner membrane, cytosol, mitochondrial matrix

Inferred from: SLC25A11 exchanges malate and alpha-ketoglutarate (2-oxoglutarate) across the inner mitochondrial membrane (Homo sapiens)



The exchange of cytosolic malate for mitochondrial 2-oxoglutarate (alpha-ketoglutarate) mediated by the transport protein SLC25A11 is well-studied in humans, and this exchange reaction, a key part of glucose, lipid, and amino acid metabolism seems likely to occur in chickens. OrthoMCL analysis of genomic sequences indicates that SLC25A11 is well-conserved over diverse species, but no chicken ortholog of the gene has yet been detected. This reaction is thus inferred on the hypothesis that the lack of a chicken SLC25A11 ortholog represents a gap in the chicken genomic sequence.

Preceded by: oxaloacetate + glutamate <=> aspartate + alpha-ketoglutarate (2-oxoglutarate)

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aspartate [mitochondrial matrix] + glutamate [cytosol] <=> aspartate [cytosol] + glutamate [mitochondrial matrix] ↗

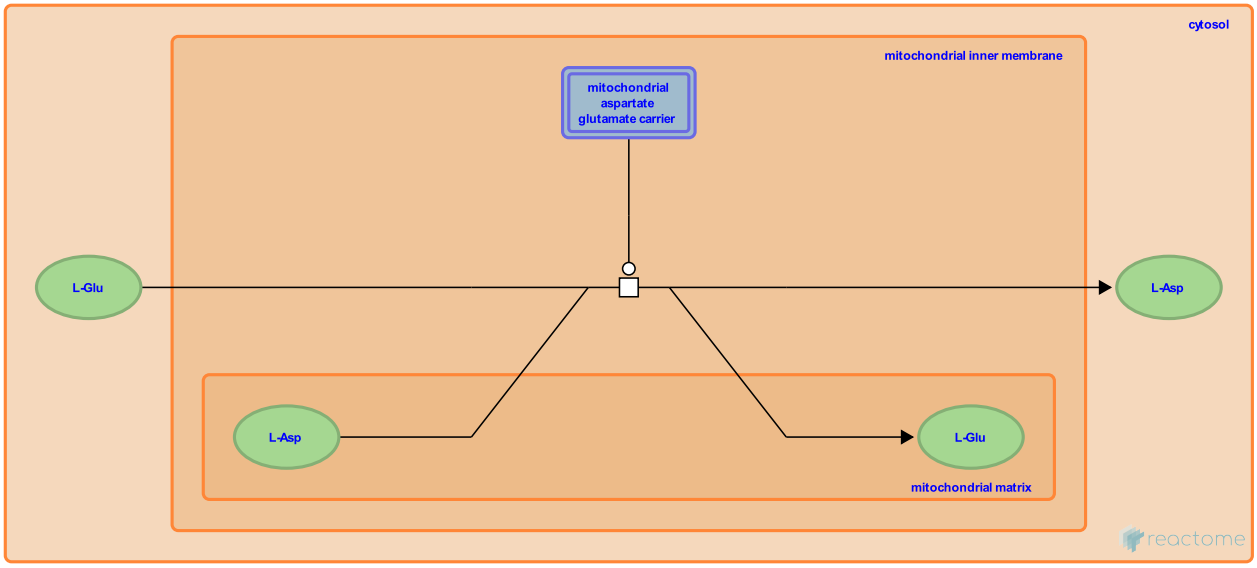
Location: Gluconeogenesis

Stable identifier: R-GGA-372726

Type: transition

Compartments: mitochondrial inner membrane, mitochondrial matrix, cytosol

Inferred from: SLC25A12,13 exchange L-Glu and L-Asp (Homo sapiens)



SLC25A12 and SLC25A13 each mediate the exchange of cytosolic aspartate and mitochondrial glutamate. Both transport proteins are localized in the inner mitochondrial membrane. No chicken transport proteins capable of mediating this reaction has been identified, although open reading frames capable of encoding a protein closely similar to authentic human SLC25A12 and SLC25A13 have been identified computationally in the ENSEMBL chicken gene set. This reaction is inferred from its human counterpart.

Preceded by: oxaloacetate + glutamate <=> aspartate + alpha-ketoglutarate (2-oxoglutarate)

Followed by: aspartate + alpha-ketoglutarate (2-oxoglutarate) <=> oxaloacetate + glutamate

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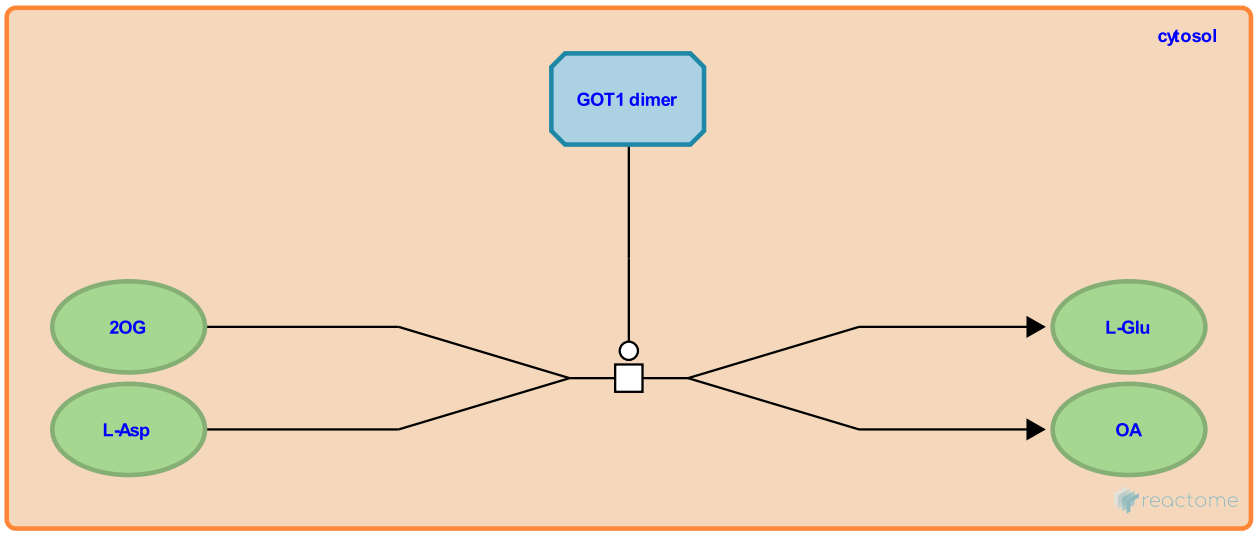
aspartate + alpha-ketoglutarate (2-oxoglutarate) <=> oxaloacetate + glutamate ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-372719

Type: transition

Compartments: cytosol



Cytosolic GOT1 catalyzes the reversible transamination of aspartate and alpha-ketoglutarate (2-oxoglutarate) to form oxaloacetate and glutamate. The active form of the enzyme is a homodimer, with one molecule of pyridoxal phosphate bound to each enzyme monomer (Shlyapnikov et al. 1979).

Preceded by: aspartate [mitochondrial matrix] + glutamate [cytosol] <=> aspartate [cytosol] + glutamate [mitochondrial matrix]

Followed by: oxaloacetate + GTP => phosphoenolpyruvate + GDP + CO2 [cytosol]

Literature references

Myasnikov, AN., Myagkova, MA., Shlyapnikov, SV., Severin, ES., Braunstein, AE., Torchinsky, YM. (1979). Primary structure of cytoplasmic aspartate aminotransferase from chicken heart and its homology with pig heart isoenzymes. *FEBS Lett, 106*, 385-8. ↗

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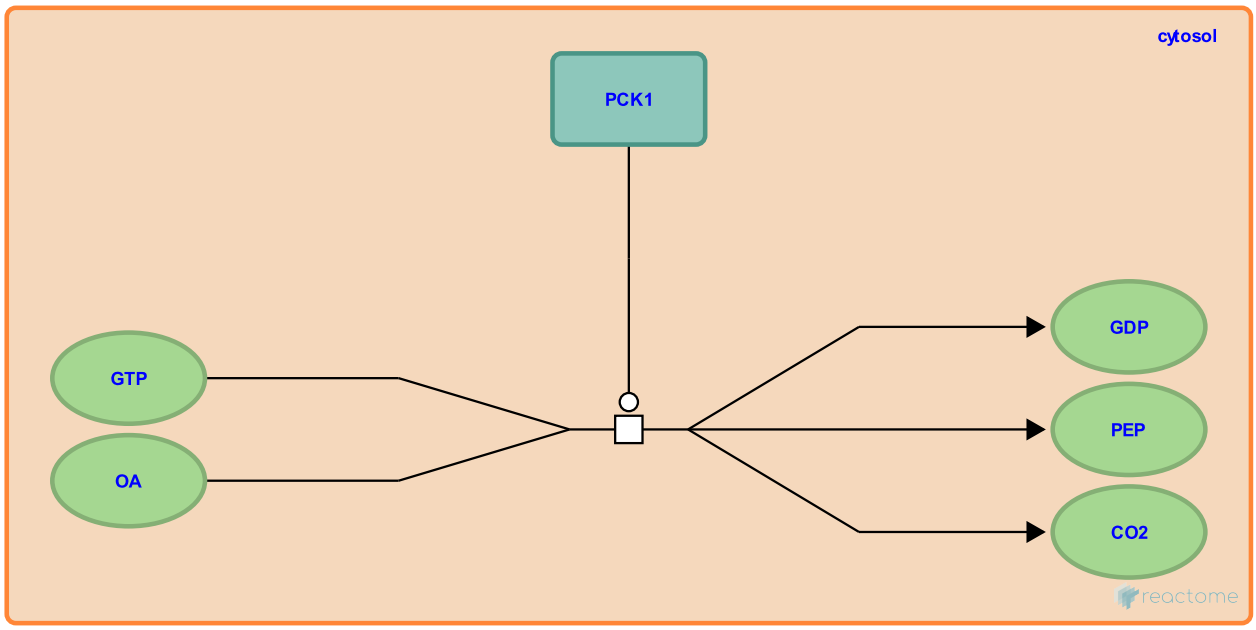
oxaloacetate + GTP => phosphoenolpyruvate + GDP + CO2 [cytosol] ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-372741

Type: transition

Compartments: cytosol



PCK1, the cytosolic form of phosphoenolpyruvate carboxykinase, catalyzes the reaction of oxaloacetate and GTP to form phosphoenolpyruvate, GDP, and CO2. In the chicken, expression of PCK1 is confined to the kidney and is hormonally regulated (Hod et al. 1982; Cook et al. 1986).

Preceded by: aspartate + alpha-ketoglutarate (2-oxoglutarate) <=> oxaloacetate + glutamate, malate + NAD+ <=> oxaloacetate + NADH + H+

Followed by: phosphoenolpyruvate + H2O <=> 2-phosphoglycerate

Literature references

Hanson, RW., Utter, MF., Hod, Y. (1982). The mitochondrial and cytosolic forms of avian phosphoenolpyruvate carboxykinase (GTP) are encoded by different messenger RNAs. *J Biol Chem, 257*, 13787-94. ↗

Hanson, RW., Cook, JS., Hod, Y., Weldon, SL., Garcia-Ruiz, JP. (1986). Nucleotide sequence of the mRNA encoding the cytosolic form of phosphoenolpyruvate carboxykinase (GTP) from the chicken. *Proc Natl Acad Sci U S A, 83*, 7583-7. ↗

Editions

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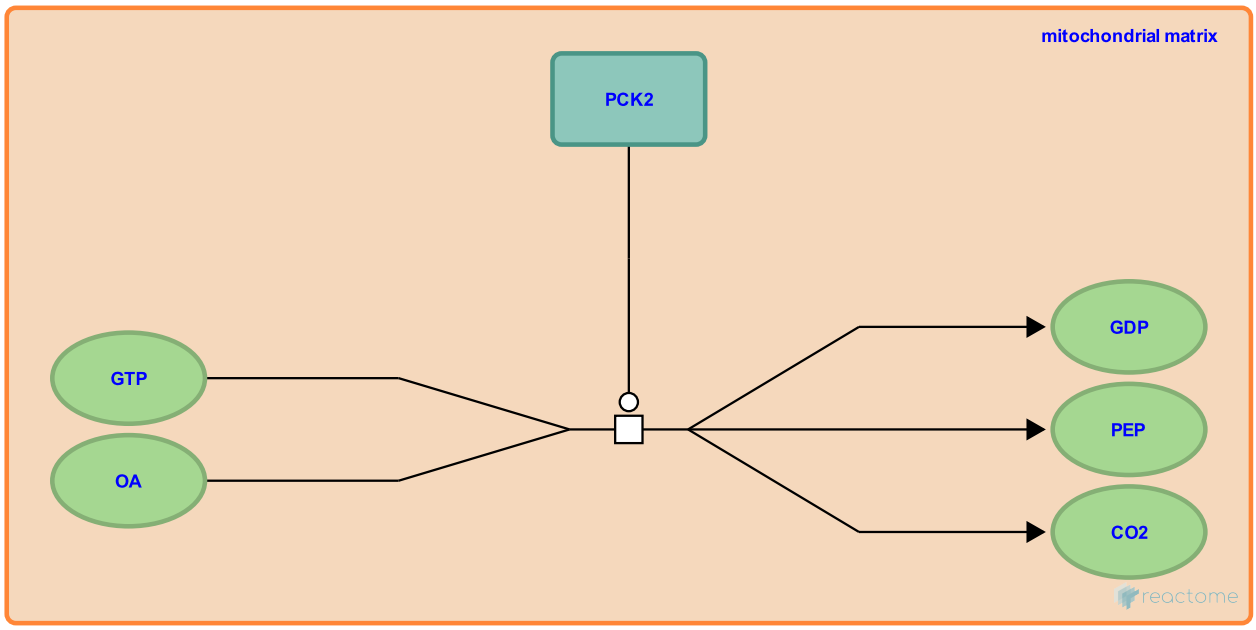
oxaloacetate + GTP => phosphoenolpyruvate + GDP + CO2 [mitochondrial matrix] ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-372724

Type: transition

Compartments: mitochondrial matrix



PCK2, the mitochondrial matrix form of phosphoenopyruvate carboxykinase, catalyzes the reaction of oxaloacetate and GTP to form phosphoenolpyruvate, GDP, and CO2. In the chicken, PCK2 is constitutively expressed in liver, where it is the only form of the enzyme, and kidney, where cytosolic PCK1 is also expressed (Kurahashi et al. 1957; Hod et al. 1982; Weldon et al. 1990).

Preceded by: pyruvate + CO2 + ATP => oxaloacetate + ADP + orthophosphate

Followed by: phosphoenolpyruvate [mitochondrial matrix] + citrate [cytosol] <=> phosphoenolpyruvate [cytosol] + citrate [mitochondrial matrix]

Literature references

Hanson, RW., Utter, MF., Hod, Y. (1982). The mitochondrial and cytosolic forms of avian phosphoenolpyruvate carboxykinase (GTP) are encoded by different messenger RNAs. *J Biol Chem, 257*, 13787-94. ↗

Utter, MF., Pennington, RJ., Kurahashi, K. (1957). Nucleotide specificity of oxalacetic carboxylase. *J Biol Chem, 226*, 1059-75. ↗

Hanson, RW., Savon, S., Cook, JS., Kalonick, PA., Hod, Y., Weldon, SL. et al. (1990). Mitochondrial phosphoenolpyruvate carboxykinase from the chicken. Comparison of the cDNA and protein sequences with the cytosolic isozyme. *J Biol Chem, 265*, 7308-17. ↗

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2008-09-10	Reviewed	Harris, RA.

phosphoenolpyruvate [mitochondrial matrix] + citrate [cytosol] <=> phosphoenolpyruvate [cytosol] + citrate [mitochondrial matrix] ↗

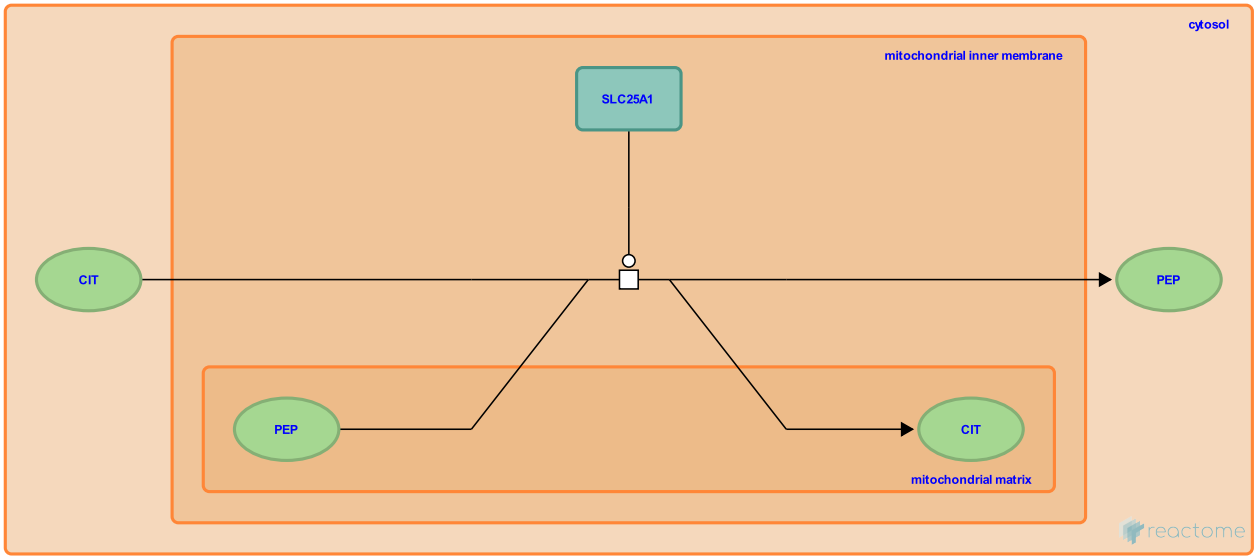
Location: Gluconeogenesis

Stable identifier: R-GGA-372723

Type: transition

Compartments: mitochondrial inner membrane, mitochondrial matrix, cytosol

Inferred from: SLC25A1 may exchange mitochondrial PEP for cytosolic anion (Homo sapiens)



SLC25A1, in the inner mitochondrial membrane, mediates the exchange of cytosolic citrate for mitochondrial phosphoenolpyruvate. No chicken transport protein capable of mediating this reaction has been identified, although an open reading frame capable of encoding a protein closely similar to authentic human SLC25A1 has been identified computationally in the ENSEMBL chicken gene set. This reaction is inferred from its human counterpart.

Preceded by: oxaloacetate + GTP => phosphoenolpyruvate + GDP + CO2 [mitochondrial matrix]

Followed by: phosphoenolpyruvate + H2O <=> 2-phosphoglycerate

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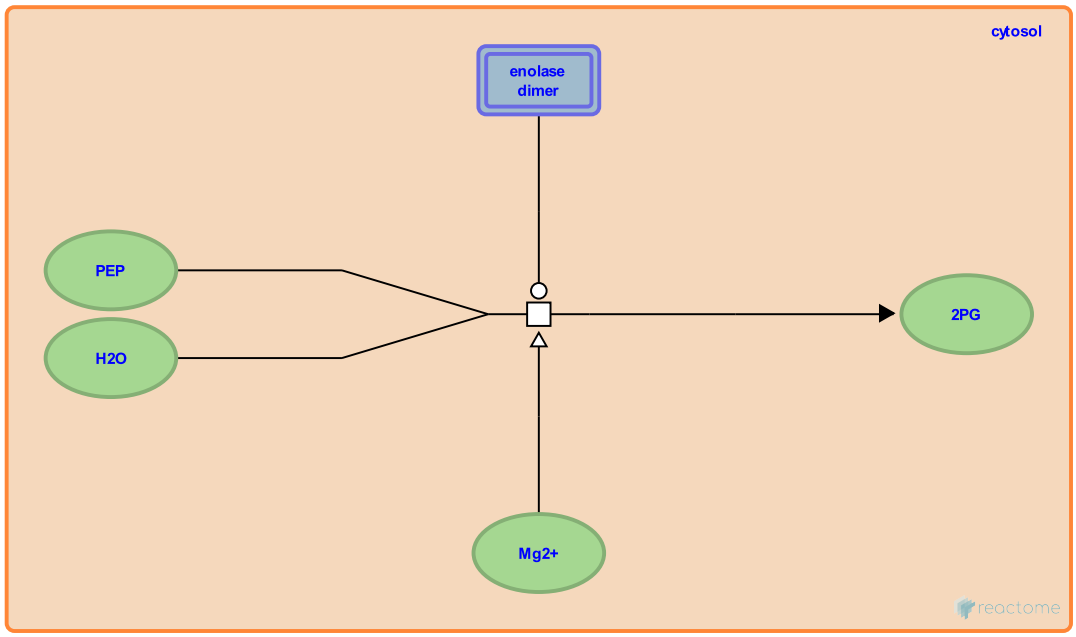
phosphoenolpyruvate + H2O <=> 2-phosphoglycerate ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-352981

Type: transition

Compartments: cytosol



Cytosolic enolase catalyzes the reversible magnesium-dependent hydration of phosphoenolpyruvate to form 2-phosphoglycerate. The active form of the enzyme is a dimer. Three enolase isoforms have been isolated and biochemically characterized, 1 (alpha), 2 (gamma), and 3 (beta), as have 1:1, 1:2, 2:2, and 3:3 enolase dimers (Russell et al. 1986; Tanaka et al. 1985, 1995, 1998).

Preceded by: phosphoenolpyruvate [mitochondrial matrix] + citrate [cytosol] <=> phosphoenolpyruvate [cytosol] + citrate [mitochondrial matrix], oxaloacetate + GTP => phosphoenolpyruvate + GDP + CO2 [cytosol]

Followed by: 2-phosphoglycerate <=> 3-phosphoglycerate

Literature references

Taniguchi, T., Nakashima, K., Tanaka, M., Ohkubo, T. (1998). cDNA cloning and characterization of neuron-specific enolase from chicken. *Biochim Biophys Acta, 1395*, 28-33. ↗

Nakashima, K., Maeda, K., Tanaka, M. (1995). Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-phosphorylation site: cDNA cloning and nucleotide sequence analysis. *J Biochem, 117*, 554-9. ↗

Dunbar, B., Fothergill-Gilmore, LA., Russell, GA. (1986). The complete amino acid sequence of chicken skeletal-muscle enolase. *Biochem J, 236*, 115-26. ↗

Nakashima, K., Sugisaki, K., Tanaka, M. (1985). Purification, characterization, and distribution of enolase isozymes in chicken. *J Biochem, 98*, 1527-34. ↗

Editions

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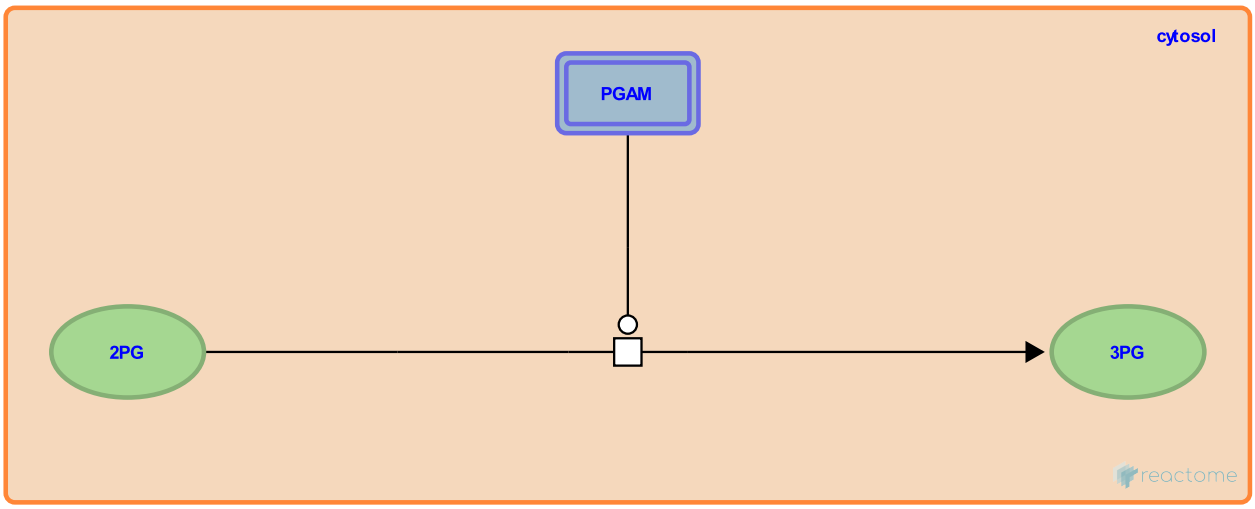
2-phosphoglycerate <=> 3-phosphoglycerate ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-353014

Type: transition

Compartments: cytosol



Cytosolic PGAM (phosphoglycerate mutase) catalyzes the reversible conversion of 2-phosphoglycerate to 3-phosphoglycerate. A protein with an amino acid sequence homologous to that of human PGAM has been identified in a high-thoughput analysis of chicken embryonic proteins (Agudo et al. 2005). Six additional proteins, PGAM1-like1, 2, and 3, PGAM2-like1 and 2, and PGAM5 are predicted to have phosphoglycerate mutase activity based on OrthoMCL analysis of the ENSEMBL chicken gene set.

Preceded by: phosphoenolpyruvate + H2O <=> 2-phosphoglycerate

Followed by: 3-phosphoglycerate + ATP <=> 1,3-bisphosphoglycerate + ADP

Literature references

Diaz-Gil, G., Schneider, J., Linares, R., Delcan, J., Gomez-Esquer, F., Agudo, D. et al. (2005). Proteomic analysis of the Gallus gallus embryo at stage-29 of development. *Proteomics, 5*, 4946-57. ↗

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2008-09-10	Reviewed	Harris, RA.

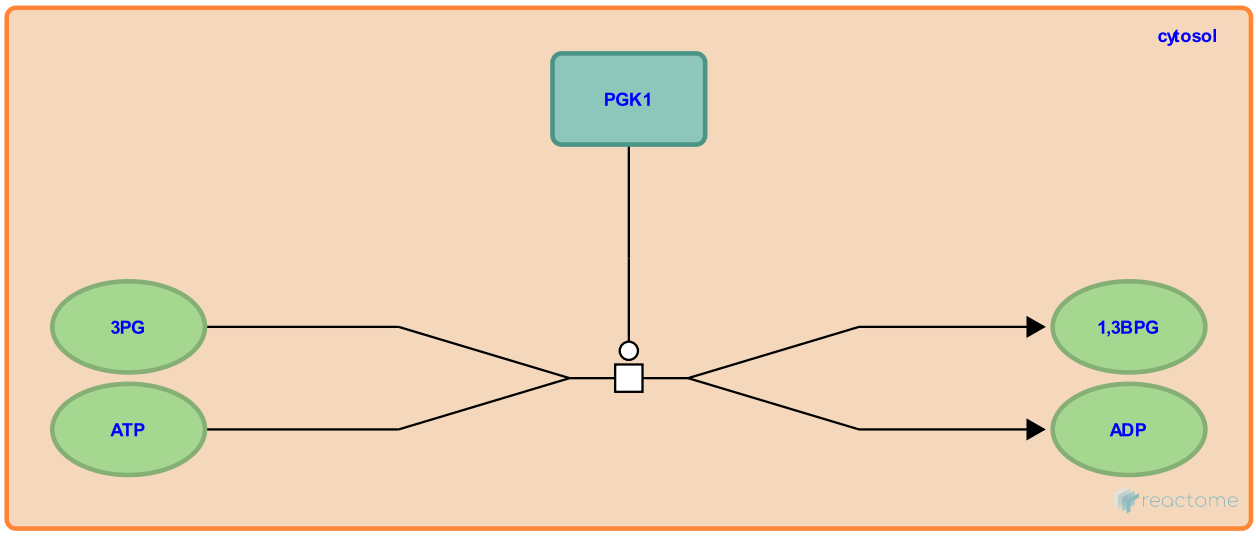
3-phosphoglycerate + ATP <=> 1,3-bisphosphoglycerate + ADP ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-353023

Type: transition

Compartments: cytosol



Cytosolic PGK (phosphoglycerate kinase) catalyzes the reversible reaction of 3-phosphoglycerate and ATP to form 1,3-bisphosphoglycerate and ADP. Catalytically active PGK activity has been purified from chicken muscle (Fifis and Scopes 1978) and a gene similar in sequence to known PGK genes from other species has been cloned (Rauen et al. 1994).

Preceded by: 2-phosphoglycerate <=> 3-phosphoglycerate

Followed by: 1,3-bisphosphoglycerate + NADH + H+ <=> glyceraldehyde 3-phosphate + NAD+ + phosphate

Literature references

Abbott, UK., Le Ciel, CD., Hutchison, NJ., Rauen, KA. (1994). Localization of the chicken PgK gene to chromosome 4p by fluorescence in situ hybridization. *J Hered, 85*, 147-50. ↗

Fifis, T., Scopes, RK. (1978). Purification of 3-phosphoglycerate kinase from diverse sources by affinity elution chromatography. *Biochem J, 175*, 311-9. ↗

Editions

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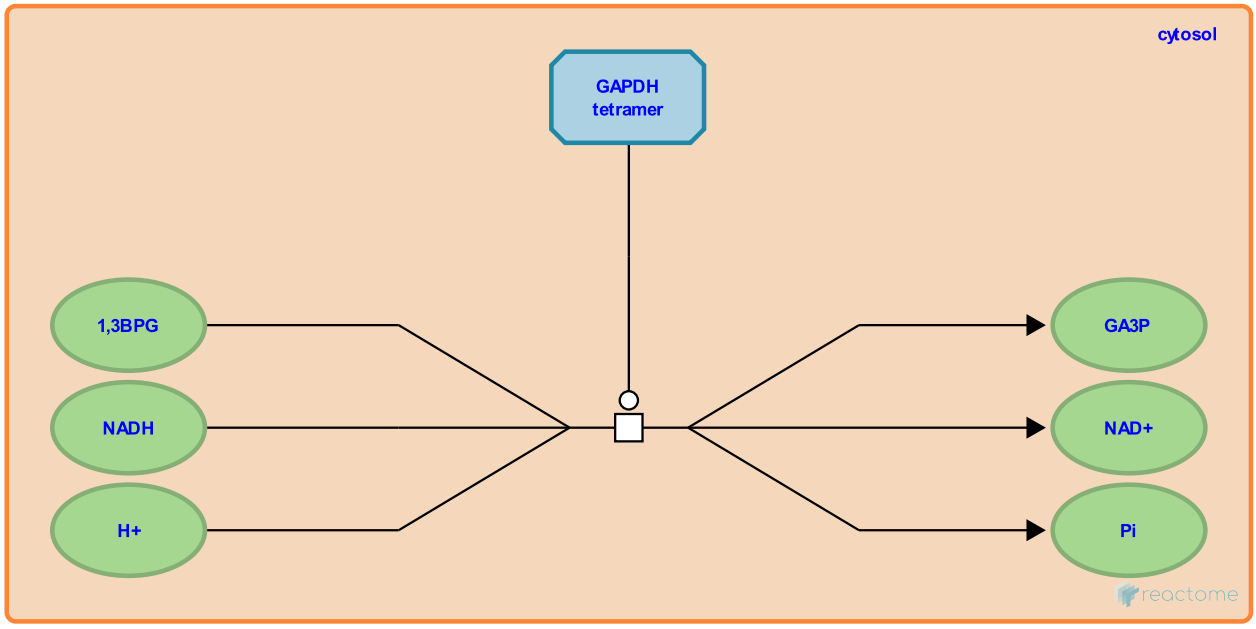
1,3-bisphosphoglycerate + NADH + H+ <=> glyceraldehyde 3-phosphate + NAD+ + phosphate ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-352921

Type: transition

Compartments: cytosol



Cytosolic GAPDH catalyzes the reversible reaction of 1,3-bisphosphoglycerate and NADH + H+ to form glyceraldehyde 3-phosphate, NAD+, and phosphate. The active form of the enzyme is a homotetramer (Allison and Kaplan 1964; Dugaiczyk et al. 1983).

Preceded by: 3-phosphoglycerate + ATP <=> 1,3-bisphosphoglycerate + ADP

Followed by: dihydroxyacetone phosphate + glyceraldehyde 3-phosphate <=> fructose 1,6-bisphosphate, glyceraldehyde 3-phosphate <=> dihydroxyacetone phosphate

Literature references

Dugaiczyk, A., Rothblum, KN., Dennison, OE., Schwartz, RJ., Stone, EM., Haron, JA. (1983). Cloning and sequencing of a deoxyribonucleic acid copy of glyceraldehyde-3-phosphate dehydrogenase messenger ribonucleic acid isolated from chicken muscle. *Biochemistry, 22*, 1605-13. ↗

Kaplan, NO., Allison, WS. (1964). The comparative enzymology of triophosphate dehydrogenase. *J Biol Chem, 239*, 2140-52. ↗

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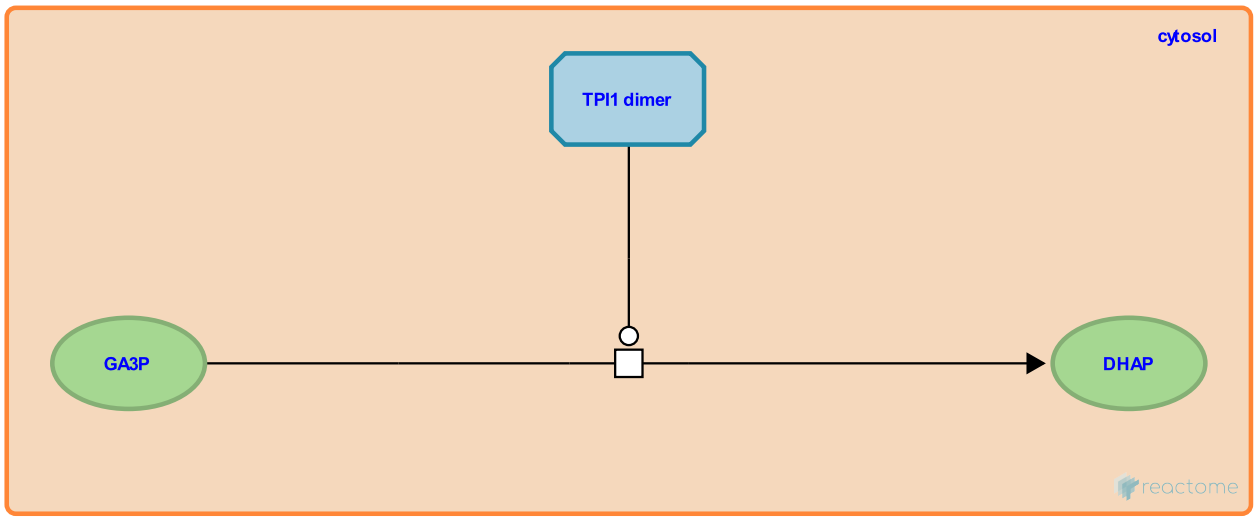
glyceraldehyde 3-phosphate <=> dihydroxyacetone phosphate ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-352914

Type: transition

Compartments: cytosol



Cytosolic TPI1 (triosephosphate isomerase 1) catalyzes the reversible isomerization of glyceraldehyde 3-phosphate to form dihydroxyacetone phosphate (Furth et al. 1974; Straus and Gilbert 1985).

Preceded by: 1,3-bisphosphoglycerate + NADH + H+ <=> glyceraldehyde 3-phosphate + NAD+ + phosphate

Followed by: dihydroxyacetone phosphate + glyceraldehyde 3-phosphate <=> fructose 1,6-bisphosphate

Literature references

Gilbert, W., Straus, D. (1985). Chicken triosephosphate isomerase complements an Escherichia coli deficiency. *Proc Natl Acad Sci U S A, 82*, 2014-8. ↗

Furth, AJ., Offord, RE., Milman, JD., Priddle, JD. (1974). Studies on the subunit structure and amino acid sequence of triose phosphate isomerase from chicken breast muscle. *Biochem J, 139*, 11-22. ↗

Editions

2008-09-10	Authored, Edited	D'Eustachio, P.
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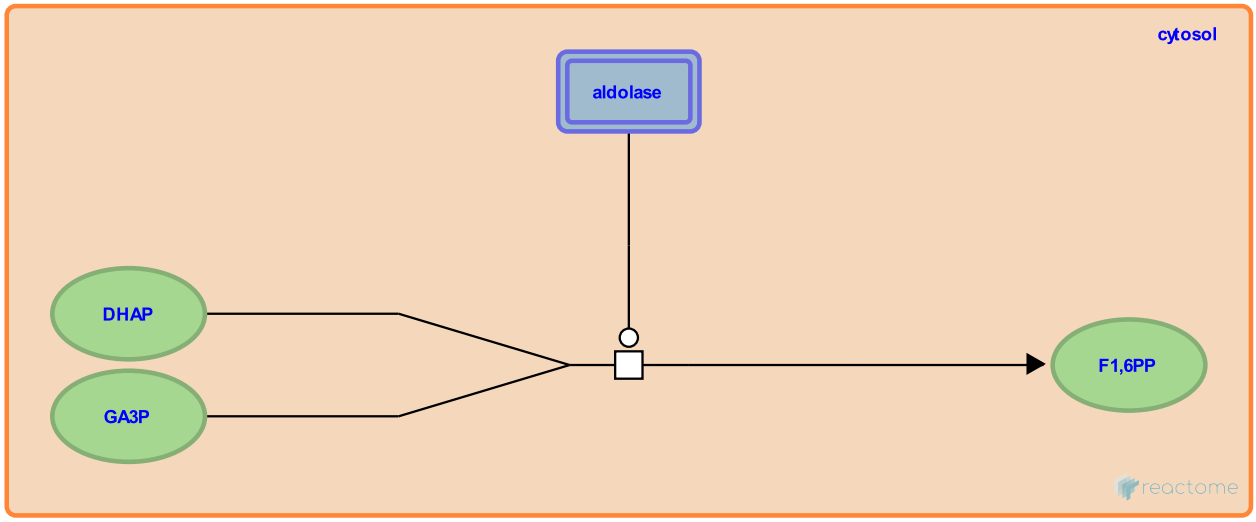
dihydroxyacetone phosphate + glyceraldehyde 3-phosphate <=> fructose 1,6-bisphosphate ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-352961

Type: transition

Compartments: cytosol



Cytosolic aldolase catalyzes the reversible reaction of dihydroxyacetone phosphate and glyceraldehyde 3-phosphate to form fructose 1,6-bisphosphate. In mammals, tissue-specific aldolase isozymes have been characterized. Chicken orthologs of two of these have been found through DNA cloning experiments; the biochemical properties of the proteins they encode have not been determined (Burgess and Penhoet 1985; Meighan-Mantha and Tolan 1995).

Preceded by: 1,3-bisphosphoglycerate + NADH + H+ <=> glyceraldehyde 3-phosphate + NAD+ + phosphate, glyceraldehyde 3-phosphate <=> dihydroxyacetone phosphate

Followed by: fructose 1,6-bisphosphate + H2O => fructose 6-phosphate + orthophosphate

Literature references

Burgess, DG., Penhoet, EE. (1985). Characterization of the chicken aldolase B gene. *J Biol Chem, 260*, 4604-14. ↗

Meighan-Mantha, RL., Tolan, DR. (1995). Noncoordinate changes in the steady-state mRNA expressed from aldolase A and aldolase C genes during differentiation of chicken myoblasts. *J Cell Biochem, 57*, 423-31. ↗

Editions

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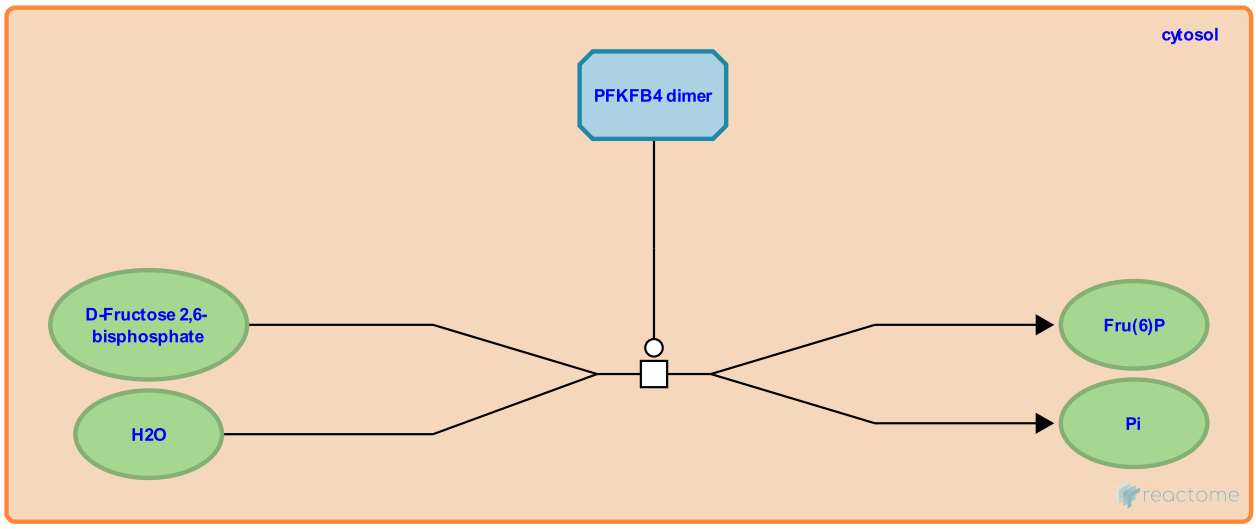
fructose 2,6-bisphosphate + H2O => fructose 6-phosphate + orthophosphate ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-372425

Type: transition

Compartments: cytosol



The phosphatase activity of cytosolic phosphofructokinase 2 / fructose 2,6-bisphosphatase catalyzes the hydrolysis of fructose 2,6-bisphosphate to form fructose 6-phosphate and orthophosphate (Van Schaftingen and Hers 1986; Chaekal et al. 1983).

Literature references

Chaekal, OK., Harris, RA., Boaz, JC., Sugano, T. (1983). Role of fructose 2,6-bisphosphate in the regulation of glycolysis and gluconeogenesis in chicken liver. *Arch Biochem Biophys, 225*, 771-8. ↗

Hers, HG., Van Schaftingen, E. (1986). Purification and properties of phosphofructokinase 2/fructose 2,6-bisphosphatase from chicken liver and from pigeon muscle. *Eur J Biochem, 159*, 359-65. ↗

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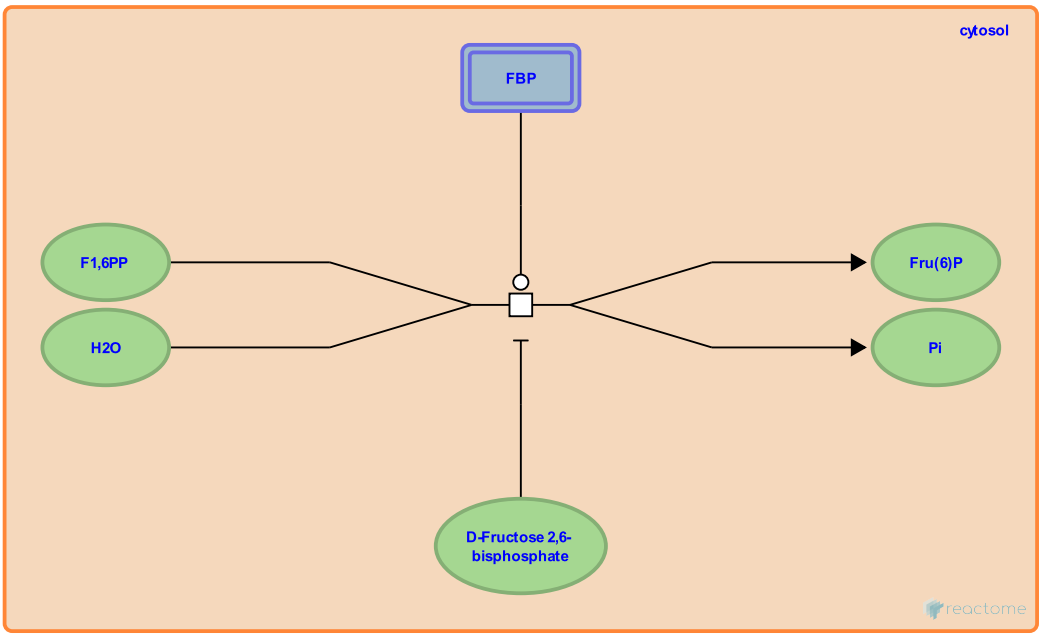
fructose 1,6-bisphosphate + H2O => fructose 6-phosphate + orthophosphate ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-372388

Type: transition

Compartments: cytosol



The phosphatase activity of cytosolic fructose 1,6-bisphosphatase catalyzes the hydrolysis of fructose 1,6-bisphosphate to form fructose 6-phosphate and orthophosphate. This reaction is negatively regulated by fructose 2,6-bisphosphate (Chaekal et al. 1983).

Preceded by: dihydroxyacetone phosphate + glyceraldehyde 3-phosphate <=> fructose 1,6-bisphosphate

Followed by: fructose 6-phosphate <=> glucose 6-phosphate

Literature references

Chaekal, OK., Harris, RA., Boaz, JC., Sugano, T. (1983). Role of fructose 2,6-bisphosphate in the regulation of glycolysis and gluconeogenesis in chicken liver. *Arch Biochem Biophys, 225*, 771-8. ↗

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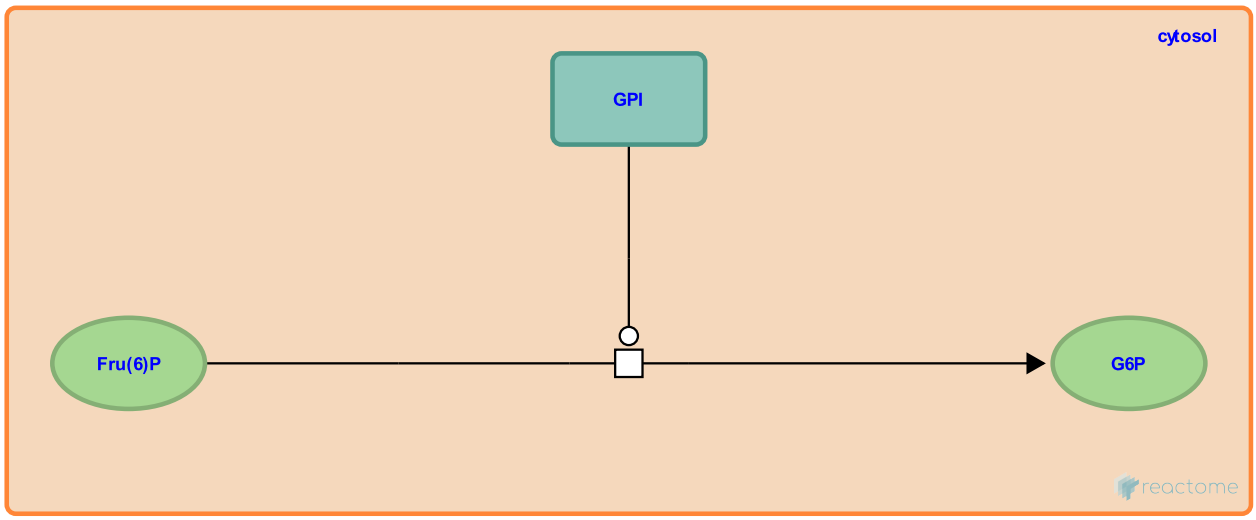
fructose 6-phosphate <=> glucose 6-phosphate ↗

Location: Gluconeogenesis

Stable identifier: R-GGA-352872

Type: transition

Compartments: cytosol



Glucose phosphate isomerase catalyzes the reversible conversion of fructose 6-phosphate and glucose 6-phosphate. A cDNA corresponding to chicken GPI has been cloned and used to demonstrate that the gene is widely expressed in embryonic and adult tissues (Halbook et al. 1989). At the level of resolution provided by starch gel electrophoresis, two entities with glucose phosphate isomerase activity can be detected in chicken muscle (Scopes 1968).

Preceded by: fructose 1,6-bisphosphate + H2O => fructose 6-phosphate + orthophosphate

Literature references

Ebendal, T., Barbany, G., Persson, H., Hallbook, F. (1989). Development and regional expression of chicken neuroleukin (glucose-6-phosphate isomerase) messenger RNA. *J Neurosci Res, 23*, 142-51. ↗

Scopes, RK. (1968). Methods for starch-gel electrophoresis of sarcoplasmic proteins. An investigation of the relative mobilities of the glycolytic enzymes from the muscles of a variety of species. *Biochem J, 107*, 139-50. ↗

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