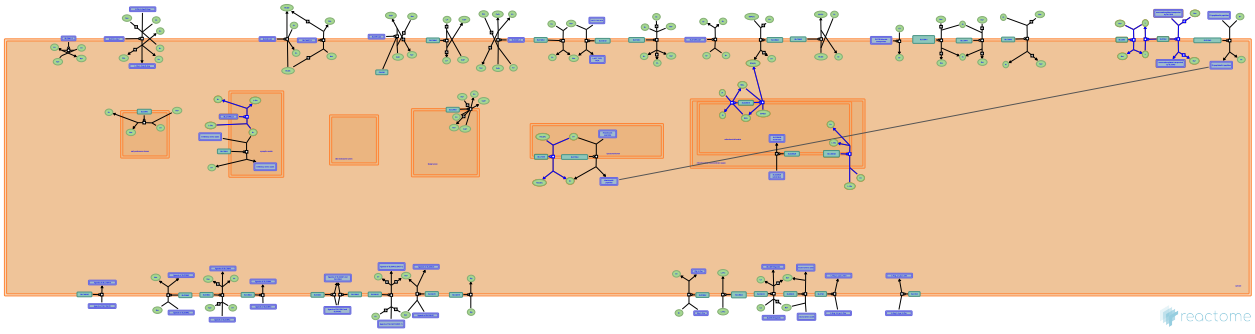
Organic anion transporters



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

01/12/2020

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. ↗

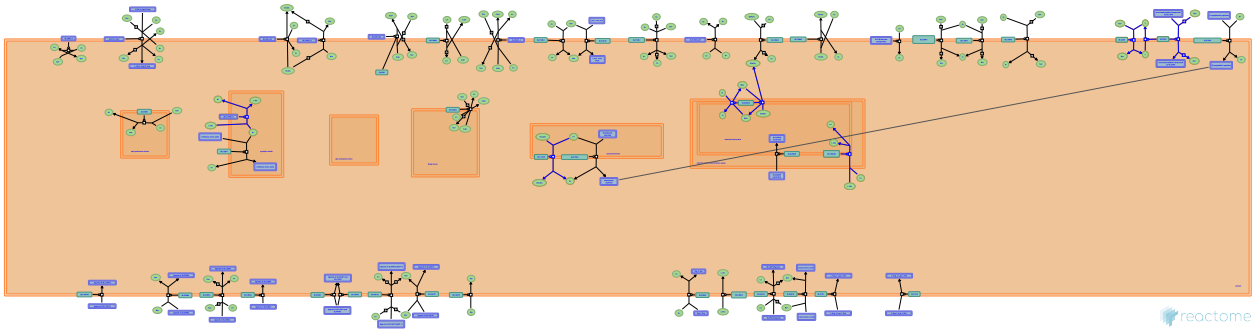
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Organic anion transporters ↗

Stable identifier: R-BTA-428643

Inferred from: Organic anion transporters (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

SLC17A6,7,8 exchange cytosolic L-Glu for synaptic vesicle H+ ↗

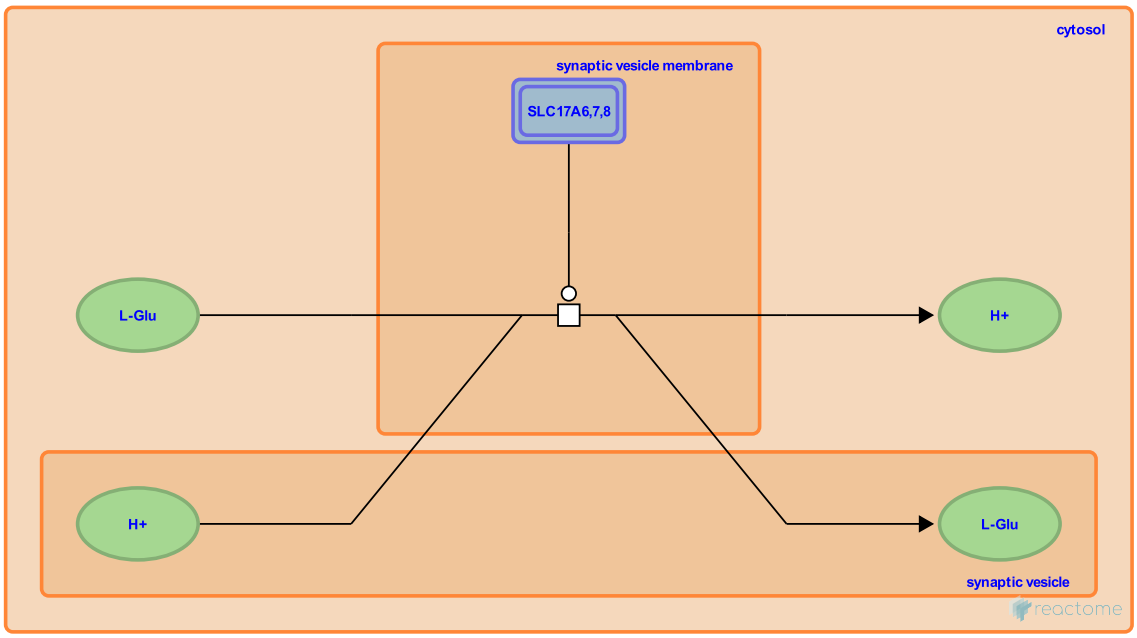
Location: Organic anion transporters

Stable identifier: R-BTA-428052

Type: transition

Compartments: synaptic vesicle membrane, cytosol, synaptic vesicle

Inferred from: SLC17A6,7,8 exchange cytosolic L-Glu for synaptic vesicle H+ (Homo sapiens)



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SLC17A5 cotransports Neu5Ac, H+ from lysosomal lumen to cytosol ↗

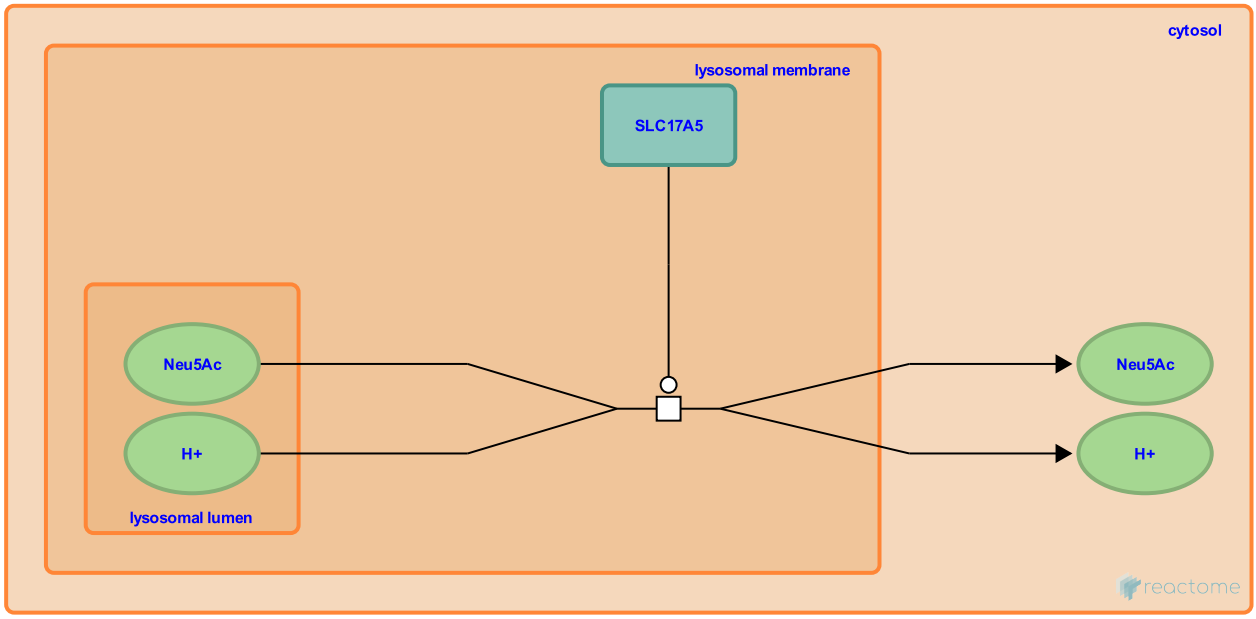
Location: Organic anion transporters

Stable identifier: R-BTA-428585

Type: transition

Compartments: lysosomal membrane, cytosol, lysosomal lumen

Inferred from: SLC17A5 cotransports Neu5Ac, H+ from lysosomal lumen to cytosol (Homo sapiens)



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SLC5A5 cotransports Na+ with I- from extracellular region to cytosol ↗

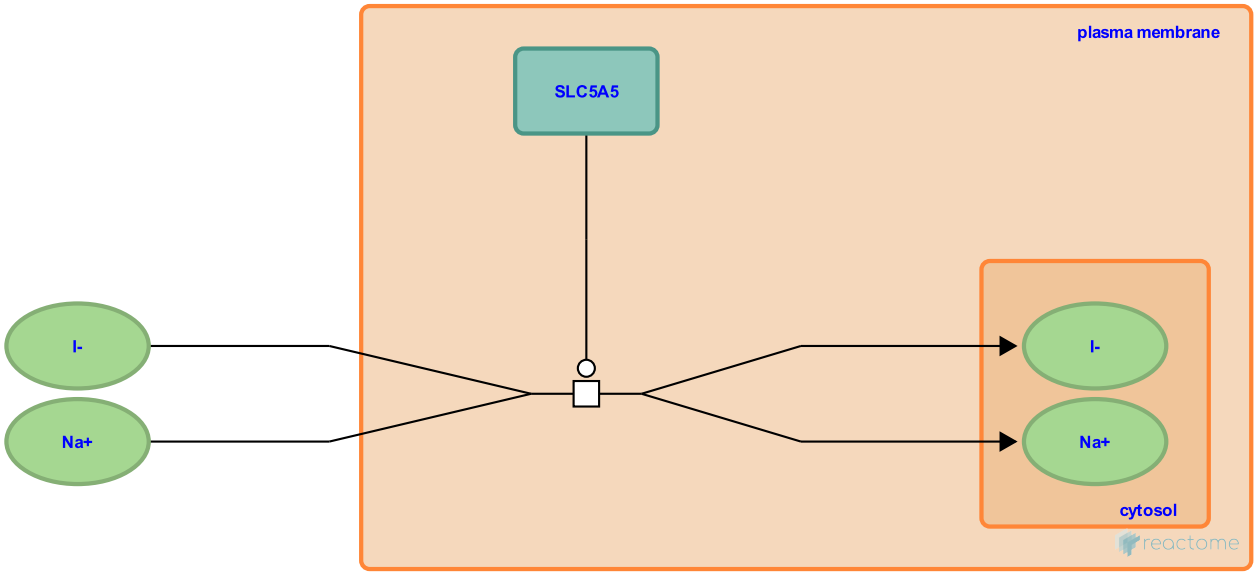
Location: Organic anion transporters

Stable identifier: R-BTA-429591

Type: transition

Compartments: plasma membrane, cytosol, extracellular region

Inferred from: SLC5A5 cotransports Na+ with I- from extracellular region to cytosol (Homo sapiens)



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Followed by: Passive I- efflux mediated by SMCT1

Passive I- efflux mediated by SMCT1 ↗

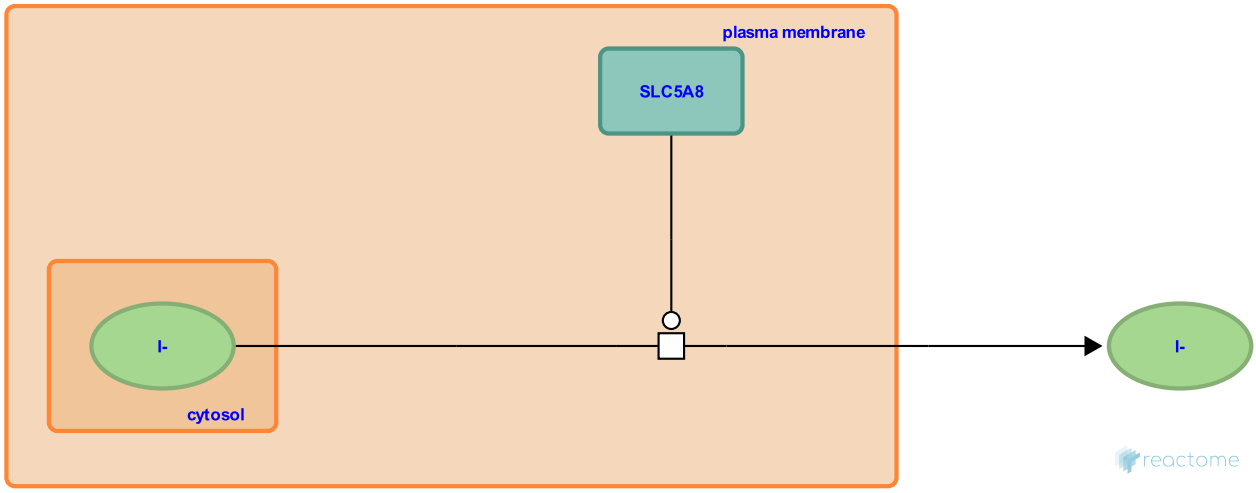
Location: Organic anion transporters

Stable identifier: R-BTA-429767

Type: transition

Compartments: plasma membrane, cytosol, extracellular region

Inferred from: Passive I- efflux mediated by SMCT1 (Homo sapiens)



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Preceded by: SLC5A5 cotransports Na+ with I- from extracellular region to cytosol

SLC5A8 transports monocarboxylates from extracellular region to cytosol ↗

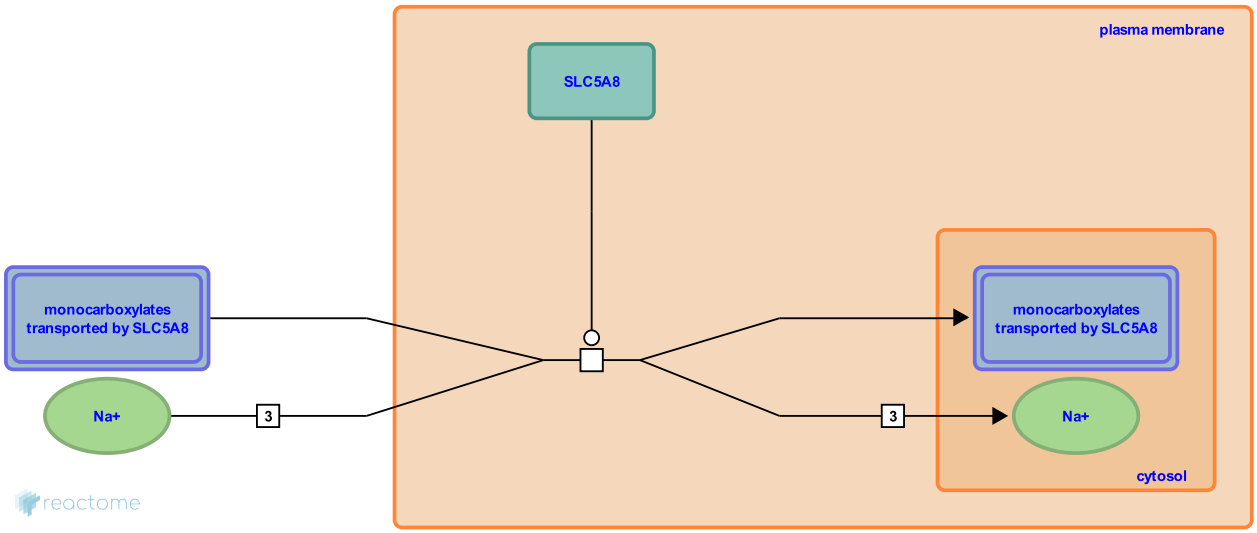
Location: Organic anion transporters

Stable identifier: R-BTA-429749

Type: transition

Compartments: plasma membrane, cytosol, extracellular region

Inferred from: SLC5A8 transports monocarboxylates from extracellular region to cytosol (Homo sapiens)



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Sulfate is exported to the cytosol in exchange for dicarboxylate ↗

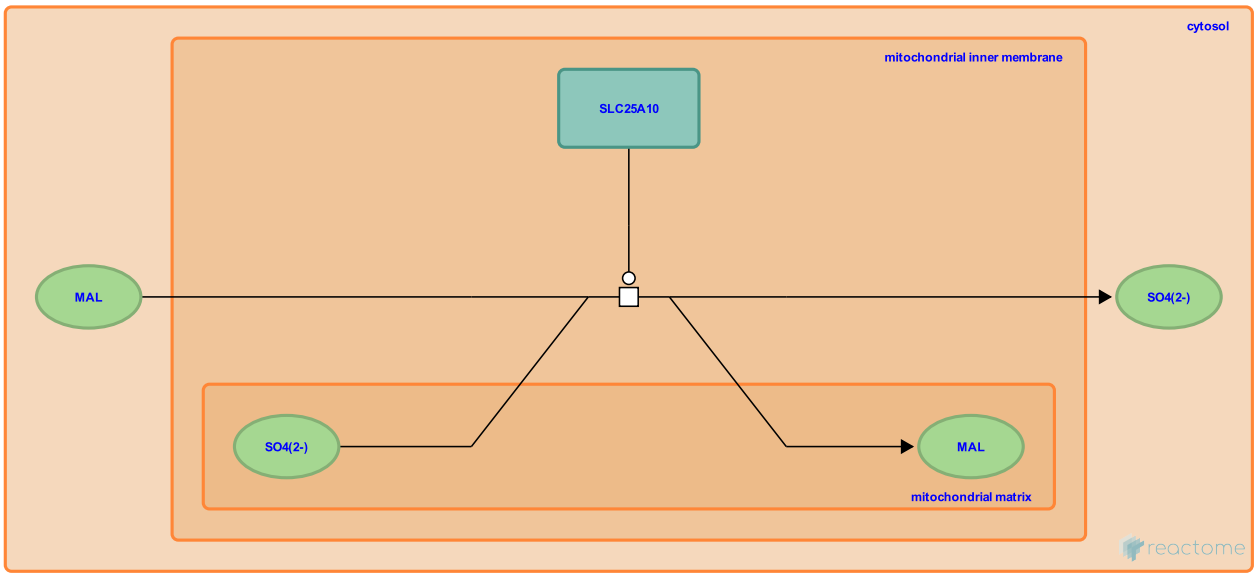
Location: Organic anion transporters

Stable identifier: R-BTA-1614546

Type: transition

Compartments: mitochondrial inner membrane, cytosol, mitochondrial matrix

Inferred from: Sulfate is exported to the cytosol in exchange for dicarboxylate (Homo sapiens)



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

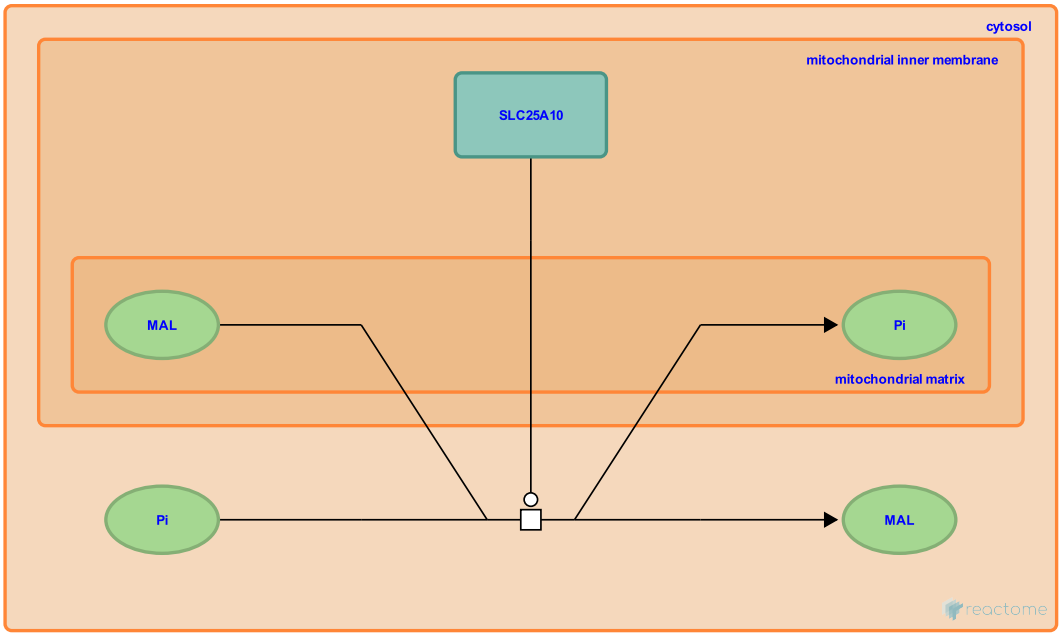
Location: Organic anion transporters

Stable identifier: R-BTA-372843

Type: transition

Compartments: cytosol, mitochondrial inner membrane, mitochondrial matrix

Inferred from: malate [mitochondrial matrix] + orthophosphate [cytosol] <=> malate [cytosol] + orthophosphate [mitochondrial matrix] (Homo sapiens)



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SLC25A18,A22 cotransport Glu, H+ from cytosol to mitochondrial matrix ↗

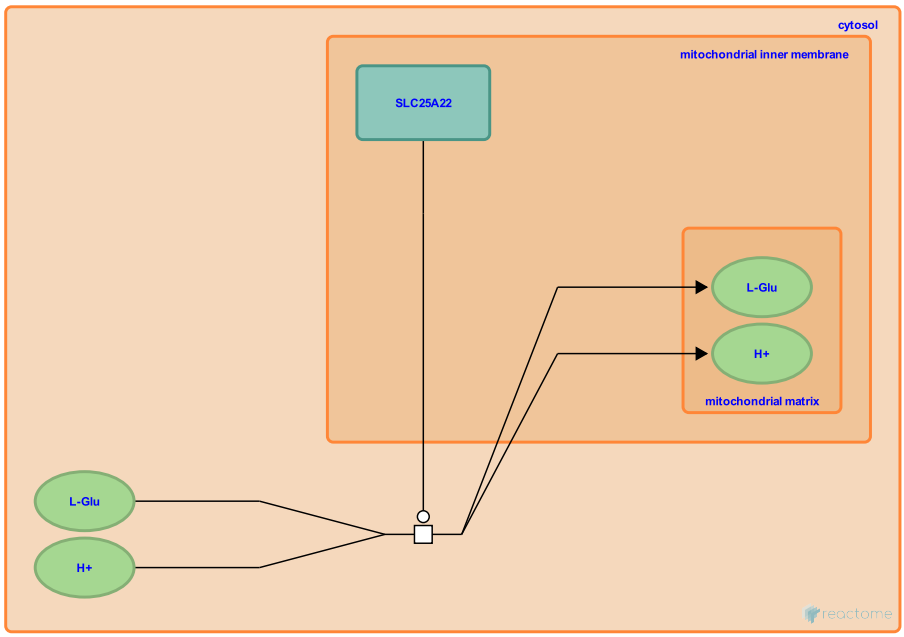
Location: Organic anion transporters

Stable identifier: R-BTA-8875623

Type: transition

Compartments: cytosol, mitochondrial inner membrane, mitochondrial matrix

Inferred from: SLC25A18,A22 cotransport Glu, H+ from cytosol to mitochondrial matrix (Homo sapiens)



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