Digestion of 1-6 linkages of limit dextrins to yield maltose, maltotriose, longer maltosides, and glucose

D'Eustachio, P., Nichols, BL.

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

13/05/2024

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. ↗

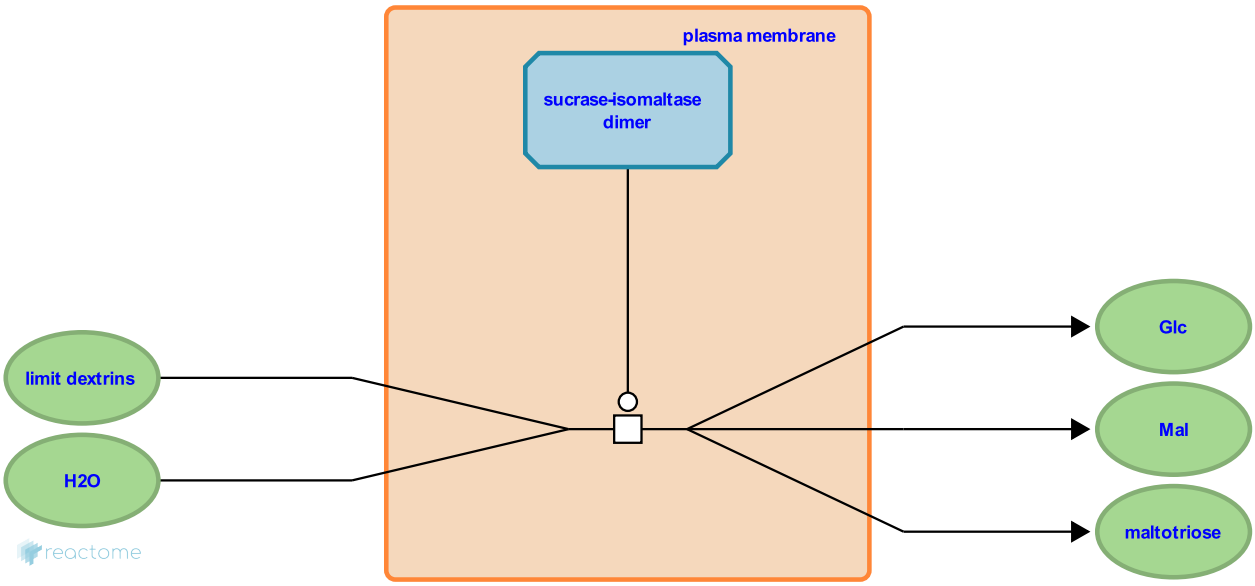
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Digestion of 1-6 linkages of limit dextrins to yield maltose, maltotriose, longer maltosides, and glucose

Stable identifier: R-HSA-189053

Type: transition

Compartments: extracellular region, plasma membrane



The 1-6 linkages in extracellular limit dextrins are hydrolyzed by sucrase-isomaltase to yield maltose, maltotriose, longer maltosides, and glucose (Conklin et al. 1975; Nichols et al. 1998). In the body, this enzyme is found on the external face of enterocytes in microvilli of the small intestine (Hauri et al. 1985), and acts on limit dextrins generated by the hydrolysis of amylopectin starch.

Literature references

Hauri, HP., Fransen, JA., Bienz, D., Marxer, A., Sterchi, EE. (1985). Expression and intracellular transport of microvillus membrane hydrolases in human intestinal epithelial cells. *J Cell Biol, 101*, 838-51.

Quaroni, A., Eldering, J., Hahn, D., Nichols, BL., Avery, S. (1998). Human small intestinal maltase-glucoamylase cDNA cloning. Homology to sucrase-isomaltase. *J Biol Chem, 273*, 3076-81.

Gray, GM., Conklin, KA., Yamashiro, KM. (1975). Human intestinal sucrase-isomaltase. Identification of free sucrase and isomaltase and cleavage of the hybrid into active distinct subunits. *J Biol Chem, 250*, 5735-41.

Editions

2006-11-03	Authored, Edited	D'Eustachio, P.
2007-01-16	Reviewed	Nichols, BL.
2007-01-18	Revised	D'Eustachio, P.