

isomaltose + H2O => 2 D-glucose (sucraseisomaltase)

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of CC BY 4.0)
<u>License.</u> For more information see our License.

30/04/2024

https://reactome.org

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.

Reactome database release: 88

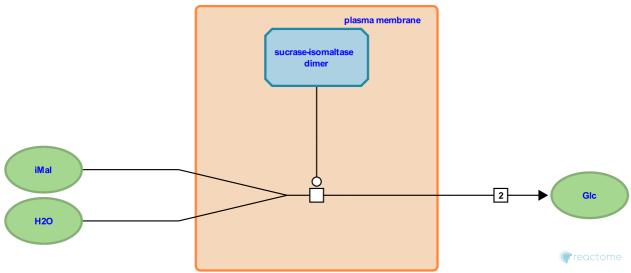
This document contains 1 reaction (see Table of Contents)

https://reactome.org Page 2

Stable identifier: R-HSA-5659861

Type: transition

Compartments: extracellular region, plasma membrane



The alpha-1,6 linkages of extracellular isomaltose are hydrolyzed to yield glucose in a reaction catalyzed by sucrase-maltase (Sim et al. 2010). In the body, this enzyme is found as a dimer on the external face of enterocytes in microvilli of the small intestine (Hauri et al. 1985). The predominant form of mature SI in the membrane is a dimer, as established from a variety of studies of the processing of the porcine enzyme (Cowell et al. 1986; Danielsen 1994) and crystallographic studies of the human one (Sim et al. 2010).

Literature references

Rose, DR., Sim, L., Pinto, BM., Willemsma, C., Mohan, S., Naim, HY. (2010). Structural basis for substrate selectivity in human maltase-glucoamylase and sucrase-isomaltase N-terminal domains. *J. Biol. Chem.*, 285, 17763-70.

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.

Danielsen, EM. (1994). Dimeric assembly of enterocyte brush border enzymes. *Biochemistry*, 33, 1599-605.

Tranum-Jensen, J., Cowell, GM., Sjöström, H., Norén, O. (1986). Topology and quaternary structure of prosucrase/isomaltase and final-form sucrase/isomaltase. *Biochem J.*, 237, 455-61.