

Digestion of linear starch (amylose) by extracellular amylase

D'Eustachio, P., Nichols, BL.

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 <u>Creative Commons Attribution 4.0 International (CC BY 4.0)</u> <u>License</u>. For more information see our <u>license</u>.

02/11/2024

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. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- 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. *オ*

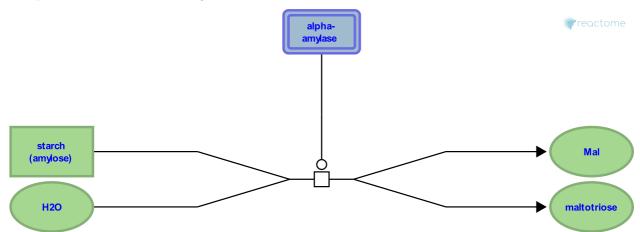
This document contains 1 reaction (see Table of Contents)

Digestion of linear starch (amylose) by extracellular amylase 7

Stable identifier: R-HSA-188979

Type: transition

Compartments: extracellular region



Extracellular amylose starch, linear polymers of glucose joined by alpha-1,4 linkages, is digested by the endoglucosidase activity of alpha-amylases, yielding maltose, maltotriose, and longer maltosides. The human genome contains five functional alpha-amylase genes, encoding structurally closely related isoenzymes (Gumucio et al. 1988). Three of these genes encode proteins synthesized in the parotid glands and released into the saliva (amylase 1A, B, and C), and the other two encode proteins synthesized in the exocrine pancreas and released into the small intestine (amylase 2A and B). In the human body, starch digestion thus commences in the mouth, mediated by salivary amylases, and is continued in the small intestine, mediated by the pancreatic ones.

X-ray crystallographic studies of amylase 1A and 2A proteins show them to be monomers, complexed with single calcium and chloride ions (Ramasubbu et al. 1996; Brayer et al. 2000). Biochemical characterization of amylase 2A indicates that the enzyme efficiently cleaves poly-glucose chains so as to release maltose - a glucose disaccharide - from the reducing end of the chain (Braun et al. 1993; Brayer et al. 2000).

Literature references

- Caldwell, RM., Meisler, MH., Samuelson, LC., Wiebauer, K., Gumucio, DL. (1988). Concerted evolution of human amylase genes. *Mol Cell Biol*, *8*, 1197-205.
- Ramasubbu, N., Luo, Y., Paloth, V., Levine, MJ., Brayer, GD. (1996). Structure of human salivary alpha-amylase at 1.6 A resolution: implications for its role in the oral cavity. *Acta Crystallogr D Biol Crystallogr, 52*, 435-46.
- Braun, C., Wang, Y., Nguyen, NT., Brayer, GD., Overall, CM., Sidhu, G. et al. (2000). Subsite mapping of the human pancreatic alpha-amylase active site through structural, kinetic, and mutagenesis techniques. *Biochemistry*, 39, 4778-91. *¬*

Editions

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