

Bacterial GUSB hydrolyses BDG to BIL

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26/02/2021

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: 75

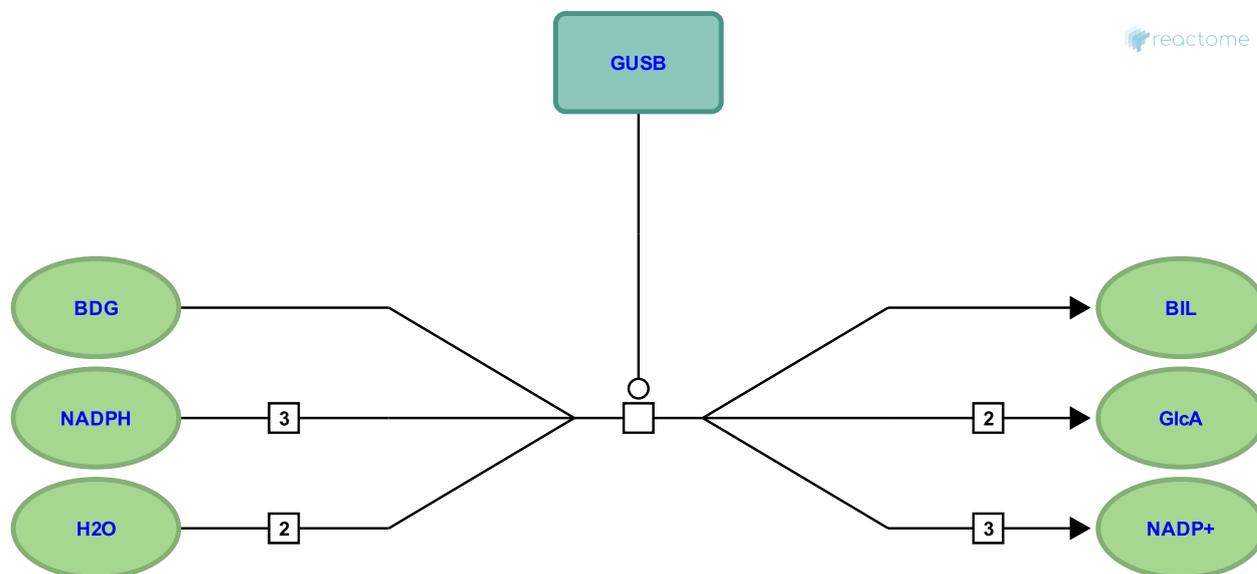
This document contains 1 reaction ([see Table of Contents](#))

Bacterial GUSB hydrolyses BDG to BIL [↗](#)

Stable identifier: R-HSA-9661820

Type: transition

Compartments: extracellular region



Bilirubin diglucuronide (BDG) is a substrate for microbial β -glucuronidase, which can cleave the glucuronosyl moieties and liberate bilirubin for reabsorption through the basolateral surfaces of the intestines where it can undergo further metabolism or pass directly back into the circulation. This process, known as enterohepatic circulation, can extend the half-life of bilirubin while adding to the total serum bilirubin load (Seyfried et al. 1976). Conjugated bilirubin is excreted in bile through the duodenum, where it can be unconjugated by enteric bacteria (Kim et al. 1995). Many bacterial β -glucuronidases can cleave the glucuronosyl moieties from conjugated bilirubins in the human gut. In vitro assays reveal the *C. perfringens* species produce beta-glucuronidase enzyme activity that is at least 30-fold higher than other bacterial species (Leung et al. 2001).

Urobilinogen (D-urobilinogen) is closely related to two other compounds: mesobilirubinogen (I-urobilinogen) and stercobilinogen (L-urobilinogen). Somewhat confusingly, all three compounds are frequently collectively referred to as "urobilinogens".

Literature references

- Seyfried, H., Klicpera, M., Leithner, C., Penner, E. (1976). [Bilirubin metabolism (author's transl)]. *Wien. Klin. Wochenschr.*, 88, 477-82. [↗](#)
- Leung, JW., Liu, YL., Leung, PS., Chan, RC., Inciardi, JF., Cheng, AF. (2001). Expression of bacterial beta-glucuronidase in human bile: an in vitro study. *Gastrointest. Endosc.*, 54, 346-50. [↗](#)
- Kim, DH., Jin, YH., Jung, EA., Han, MJ., Kobashi, K. (1995). Purification and characterization of beta-glucuronidase from *Escherichia coli* HGU-3, a human intestinal bacterium. *Biol. Pharm. Bull.*, 18, 1184-8. [↗](#)

Editions

2019-09-19	Authored, Edited	Jassal, B.
2019-10-03	Reviewed	D'Eustachio, P.