BIL binds GSTA1, FABP1

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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.

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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. ↗

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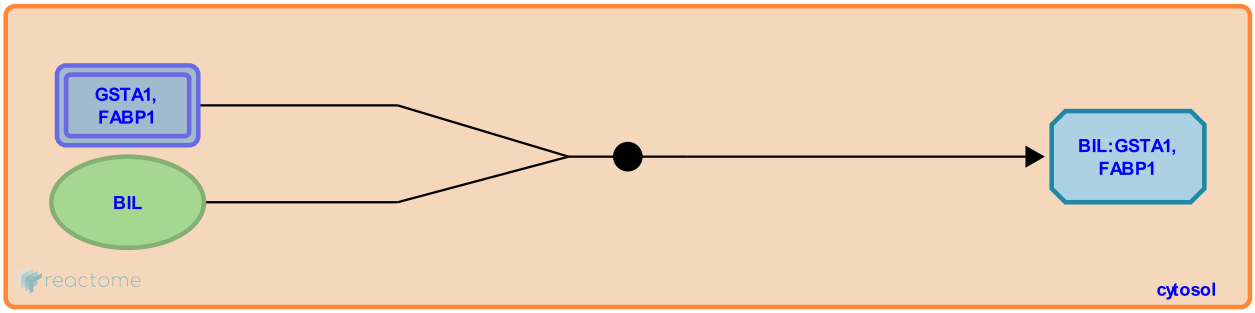
Stable identifier: R-HSA-9663511

Type: binding

Compartments: cytosol



Upon entry into the hepatocyte, bilirubin (BIL) can bind to one of two cytosolic binding proteins; glutathione S-transferase A1 (GSTA1 aka ligandin, Y-protein), a major cytosolic protein that has both transport and detoxification functions or fatty acid-binding protein (FABP1 aka Z-protein) (Levi et al. 1969, Simons & Jagt 1980, Arias 2012). It is assumed GSTA1 transports BIL to the ER where it is detoxified by conjugation with a glucuronosyl moiety.

Literature references

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Simons, PC., Jagt, DL. (1980). Bilirubin binding to human liver ligandin (glutathione S-transferase). *J. Biol. Chem., 255* , 4740-4. ↗

Editions

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