

BLVRA:Zn²⁺, BLVRB reduce BV to BIL

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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

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- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
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Reactome database release: 74

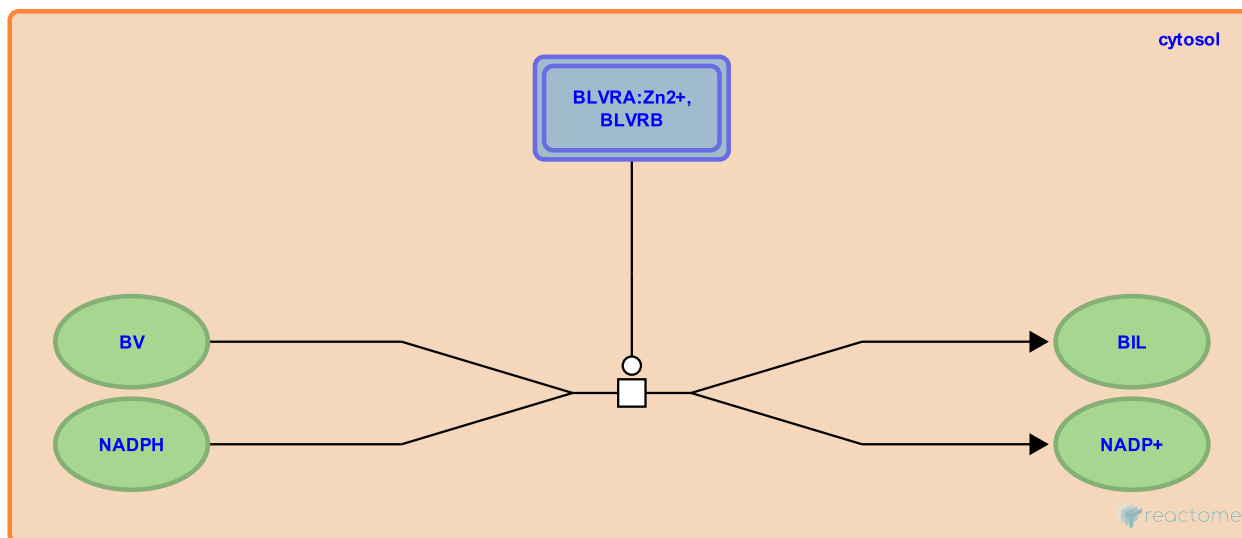
This document contains 1 reaction ([see Table of Contents](#))

BLVRA:Zn²⁺, BLVRB reduce BV to BIL [↗](#)

Stable identifier: R-HSA-189384

Type: transition

Compartments: cytosol



Bilirubin (BIL) is the breakdown product of heme, causing death if allowed to accumulate in the blood. It is highly lipophilic and requires conjugation to become more water soluble to aid excretion. BIL is formed from the reduction of biliverdin (BV) by biliverdin reductases BLVRA and BLVRB (Cunningham et al. 2000, Fu et al. 2012, O'Brien et al. 2015).

Literature references

Cunningham, O., Gore, MG., Mantle, TJ. (2000). Initial-rate kinetics of the flavin reductase reaction catalysed by human biliverdin-IXbeta reductase (BVR-B). *Biochem. J.*, 345, 393-9. [↗](#)

Fu, G., Liu, H., Doerksen, RJ. (2012). Molecular modeling to provide insight into the substrate binding and catalytic mechanism of human biliverdin-IXa reductase. *J Phys Chem B*, 116, 9580-94. [↗](#)

Editions

2007-01-24	Reviewed	Sassa, S.
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