

## Bile Acid Metabolism and Gut Microbiota

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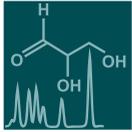
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### Message from the Guest Editors

Bile acids, which have a primary function in nutrient absorption, are also heavily involved in gut–microbiota host signalling. Primary bile acids are synthesized in the liver by the host and then conjugated before release into the intestinal tract. Here, they can be reabsorbed and transported with the portal blood to the liver, forming the enterohepatic circulation. In the gut, conjugated primary bile acids can be deconjugated, followed by conversion to secondary bile acids by specific bacteria. The bile acids present in the gut influence the composition of the gut microbiota because of their differing bactericidal properties. In addition, secondary bile acids are reabsorbed in the colon and are known to act as signalling molecules in several host processes including glucose homeostasis, immune system regulation and lipogenesis. Thus, bile acid and gut microbiota research is a compelling field with imperative health implications.

This Special Issue of *Metabolites*, “Bile Acids and Gut Microbiota”, will be dedicated to dealing with interactions between bile acids and the gut microbiota as well as the resulting host effects. This Issue is not only intended for results from basic research (cell or animal models) but is also open to results from epidemiological studies. In addition, new measurement methods, bioinformatical tools and data analysis concepts are welcome.





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## Editor-in-Chief

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## Message from the Editor-in-Chief

The metabolome is the result of the combined effects of genetic and environmental influences on metabolic processes. Metabolomic studies can provide a global view of metabolism and thereby improve our understanding of the underlying biology. Advances in metabolomic technologies have shown utility for elucidating mechanisms which underlie fundamental biological processes including disease pathology. *Metabolites* is proud to be part of the development of metabolomics and we look forward to working with many of you to publish high quality metabolomic studies.

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