



# Human Gut Microbiota and Drug Metabolism

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## Abstract

The efficacy of drugs widely varies in individuals, and the gut microbiota plays an important role in this variability. The commensal microbiota living in the human gut encodes several enzymes that chemically modify systemic and orally administered drugs, and such modifications can lead to activation, inactivation, toxification, altered stability, poor bioavailability, and rapid excretion. Our knowledge of the role of the human gut microbiome in therapeutic outcomes continues to evolve. Recent studies suggest the existence of complex interactions between microbial functions and therapeutic drugs across the human body. Therapeutic drugs or xenobiotics can influence the composition of the gut microbiome and the microbial encoded functions. Both these deviations can alter the chemical transformations of the drugs and hence treatment outcomes. In this review, we provide an overview of (i) the genetic ecology of microbially encoded functions linked with xenobiotic degradation; (ii) the effect of drugs on the composition and function of the gut microbiome; and (iii) the importance of the gut microbiota in drug metabolism.

**Keywords** Gut microbiome · Drug metabolism · Xenobiotics · Biotransformation · Genetic ecology

## Introduction

The diverse and composite community of microorganisms residing in the human gastrointestinal (GI) tract is intensely entwined with human biology and is a key component of many processes like synthesizing vital nutrients and vitamins, digestion of complex polysaccharides, resistance against colonization of allochthonous microbiota, and immune maturation [1–3]. Although, the liver is considered as the predominant metabolic organ for biotransformation after dietary intake [4], however, recent studies indicate that the gut microbiota are the first to interact and metabolize/

modify the chemical structure of numerous orally administered xenobiotics which include a wide variety of compounds ranging from environmental pollutants, dietary components, and therapeutic drugs. The dominant human gut bacterial phyla are mainly represented by Firmicutes, Bacteroidetes, Actinobacteria, Proteobacteria, and Verrucomicrobia [5, 6]. However, the proportions of these phyla are documented to be sensitive to dietary habits, age, as well as disease conditions [7]. The gut microbiota contributes to approximately 3.3 million unique genes, which is roughly 150 times more than the human gene content [8]. This contributes to a large enzymatic repository in the gut, outnumbering that in the liver, which is capable of metabolizing numerous drugs and xenobiotics and manipulate their pharmacological effects either directly or indirectly, thus expanding the repertoire of metabolic reactions occurring within the human body [9, 10].

Although these modifications can have drastic consequences on health and treatment outcomes, our knowledge of specific gut bacterial strains and their genes and enzymes involved in xenobiotic metabolism is in infancy. An understanding of the mechanism of xenobiotic metabolism with respect to gut microbiota and hence intra-individual variations can help in planning for a better therapeutic regime as well as outcome. The microbial functions linked with

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xenobiotic metabolisms can be used as targets to modulate drug efficacy and also as diagnostic markers for clinical practices. In addition, such microbial genetic signatures can also help in developing precision medicine.

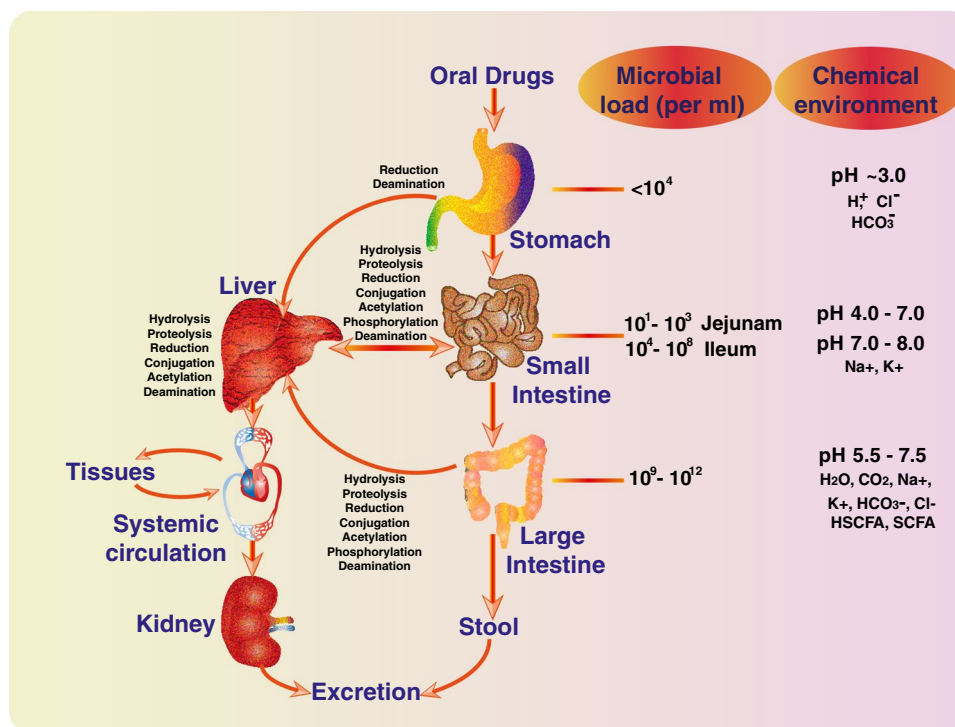
Here, we present an overview of our understanding of how the gut microbial consortia directly and indirectly modify the therapeutics and play an important role in health as well as disease. We focused on the current knowledge of the complex interactions between gut microbiota-derived functions and xenobiotics. We assessed the knowledge of overall genomic content and metabolic activities associated with the microbial community residing in the human gut. We also reviewed the current understanding of the chemical modifications of xenobiotic conjugates, drugs, and prodrugs accomplished through gut microbial consortia.

## Overview of Xenobiotics and Its Metabolism

Xenobiotics can be defined as any substance that is foreign to the human body [11, 12]. These may be classified into two types: exogenous and endogenous. Exogenous xenobiotics are synthetic compounds that gain entry within the body through diet, therapeutic drugs, or inhaled as environmental pollutants. A few examples include drugs like antibiotics, antidiabetics, antipsychotics, food additives and artificial sweeteners like saccharine, antioxidants, and anti-inflammatory compounds, pollutants like pesticides, insecticides, cosmetics, and many more. Endogenous xenobiotics are

synthesized within the body or are produced as metabolites from different biological processes. Though, they are indigenous to the body but have effects similar to exogenous xenobiotics including steroids, eicosanoids, bile acids, and certain fatty acids. The substances existing in unusually higher quantities are also termed as xenobiotics. The threat caused by these xenobiotics within human body or in environment includes carcinogenicity, toxicity, accumulation, and bioaccumulation. They can reside in fatty tissues for many years and lead to chronic problems, i.e., stunted growth, birth defects, learning disabilities, recurring diseases, brain function impairment, respiratory problems, cancer, and neurological, immunological, behavioral, and reproductive deficiencies [11, 13]. Human body has a natural detoxification mechanism to limit or diminish the acute or chronic toxicity of various xenobiotics (Fig. 1). Human gut and the liver have metabolic enzymes, which significantly reduce the concentration of any xenobiotic with certain chemical modifications before sending it to systemic circulation. This process is known as the “first pass effect.” These chemical modifications or metabolic breakdown of xenobiotics occur in two phases, i.e., phase I and phase II metabolisms. Xenobiotics are chemically modified in phase I by introducing reactive functional groups via oxidation, reduction, hydrolysis, deamination, demethylation, dehalogenation, epoxidation, and/or peroxigenation. More often, phase I metabolism also makes the parent structure more polar after the end of these chemical transformations. Importantly, it is the phase II metabolism, after phase I, which significantly enhances

**Fig. 1** Metabolism of orally administered drugs in the human gastrointestinal tract (GI) and other body sites. Microbial loads and drug modification functions are distinct in the different parts of gastrointestinal tract. Different parts of the GI tract have different microbial load and distinct chemical environments. The parent or modified drugs may reach to the liver through portal vein or directly excrete with feces depending on the absorption attribute of the compounds. Drug excretions also take place through urinary tract



hydrophilicity by conjugation of the phase I metabolite using glucuronic acid, sulfonic acid, glutathione, certain amino acids, or some other endogenous polar molecules. [14, 15]. The extreme acidic environment of the stomach (pH 1.5) also contributes to the chemical transformation of a broad range of pH-sensitive xenobiotics by modulating hydrolysis and reduction reactions in its scaffold. Such abiotic transformations are also important in xenobiotic metabolism in addition to direct involvement of microbial or host-encoded enzymes. Polymorphisms in xenobiotic-metabolizing genes affect an individual's response to pharmaceutical and dietary interventions [16]. Recent studies suggest the role of gut microbes in metabolizing therapeutics and convert them into wide range of metabolites. For most of the orally administered drugs, the major interplay with the microbiota occurs at the gastrointestinal tract. The diverse regions of gastrointestinal tract differ in nutrient content, epithelial cell physiology, pH (duodenum 6–6.5; jejunum and ileum 7–8; colon 5.5–7), and oxygen levels (small intestine: slightly aerobic; colon: strict anaerobic), thus providing diverse habitats to microbes and affecting the types of metabolic processes [17, 18]. The range of xenobiotics subject to gut microbial metabolism is wide and expanding. Several enzymes derived from the gut microbiota actively participate in the chemical transformation of dietary compounds, including complex polysaccharides, lipids, proteins, and phytochemicals. The modified metabolites serve as nutrients and are linked to a variety of health benefits as well as disease susceptibilities. Orally ingested xenobiotics can also be modified by the action of host-derived digestive enzymes in the oral cavity and digestive tract before they are absorbed into different tissues and systemic circulation [14]. The readily absorbed xenobiotics pass through gut epithelial cells, where host enzymes may further process them before transfer to the liver through the portal vein. After processing by the metabolic enzymes of the liver, xenobiotics and their metabolites infiltrate into circulatory system, reach different tissues, and affect the distal organs. These substances in the circulatory system are further metabolized and/or excreted into the gut lumen through bile duct or through kidneys into the urine (Fig. 1). The metabolites coming back into the intestinal lumen can either move into the large intestine, where they may be excreted out through feces, or be reabsorbed in the small intestine through enterohepatic circulation. The substances that are poorly absorbed within the small intestine enter into the large intestine where they may be transformed by the gut microbiota. The host cells can reabsorb the metabolites thus produced and enter into systemic circulation or interact with the epithelial cells lining the GI tract. Eventually, these metabolites are excreted either through urine or feces. Gut microbial metabolites can have altered bioavailability, bioactivity, and toxicity, regulate the expression and function of key liver enzymes and can interfere with the

activities of human xenobiotic-metabolizing enzymes, altering the resulting metabolites from ingested substances [10]. The nutrient-rich, anaerobic intestine supports anaerobic bacterial colonization to metabolize indigestible substances like complex carbohydrates into short-chain fatty acids (SCFA) and regulate host metabolism while aiding digestion [17, 19].

## Genomics and Genetics of Xenobiotic Metabolic Functions in the Gut Microbiome

The inter-individual variability in response to a treatment therapy can impose not only health hazards but cost implications also due to poor outcomes and prolong treatment durations. This variability is largely associated with the individual's gut microbiome structure and function. The increased diversity of enzymes and the distinct selection pressures shape the differential microbial xenobiotic biotransformation capacities. Often, the microbial biotransformation capabilities are different from that of host metabolism, shifting the pharmacokinetic and pharmacodynamic properties of xenobiotics and their associated metabolites. In many cases, the bacterial genes encoding for the enzymes mediating these reactions (Table 1) remain unidentified. The microbial community genome-encoded metabolic functions are highly conserved, based on the gut environmental conditions [19]. The gut microbiome tends to be more diverse in individuals with higher social interactions [20], thereby bringing more diversity of microbial enzymes and widening the range of metabolic processes occurring within the human body. Several researches have reported distinct inter-individual variability in these biotransformations [21–24]. The enzyme classes linked with xenobiotic metabolism like hydrolases, transferases, oxidoreductases, and lyases are extensively found within sequenced gut microorganisms. In a survey by Zimmermann and coworkers, a mechanistic understanding of microbiome-mediated drug metabolism has been provided. The ability of 76 intestinal bacteria to metabolize 271 oral drugs was measured, where approximately two-thirds of these screened drugs were metabolized by at least one bacterial strain [25]. By combining high-throughput genetics with mass spectrometry, they identified and validated 30 microbiome-encoded enzymes collectively converting 20 drugs to 59 metabolite candidates. They developed a gain-of-function approach by utilizing *Bacteroides thetaiotaomicron* capable of metabolizing 46 different drugs, to discover DNA fragments that confer drug-metabolizing capability in a heterologous host. They validated the metabolic activity of identified gene, *bt4096*, for diltiazem metabolism. Diltiazem is an oral calcium channel blocker and used to treat angina pectoris, arrhythmia, and hypertension. The intestinal levels of diltiazem and its metabolites

**Table 1** Microbiota linked with chemical modification of drugs

Gut microbiota	Drug	Effect on drug	References
<i>Helicobacter pylori</i>	Levodopa	Impaired absorption and reduced efficacy	[140]
<i>Eggerthella lenta</i> possessing <i>cgr</i> operon	Digoxin	Drug inactivation	[141]
<i>E. coli</i> , <i>Enterobacter</i> , <i>Proteus</i> spp, <i>Klebsiella</i> spp, <i>Bacteroides</i> spp	Sulindac	Conversion into active compound sulindac sulfide	[142]
<i>Cunninghamella</i>	Flurbiprofen	Conversion into a variety of phase I and phase II metabolites, majorly 4'-hydroxyflurbiprofen	[143]
<i>Clostridium</i> and <i>Eubacterium</i> spp	Azo dyes and nitrated polycyclic aromatic hydrocarbons	Conversion into reduced azo and nitro compounds	[144]
<i>Clostridium leptum</i>	Nitrazepam	Nitro reduction to 7-amino-nitrazepam, a teratogenic metabolite	[145]
<i>Escherichia</i>	Metformin	Positive correlation with the hypoglycemic effect	[146]
<i>Intestinibacter</i> , <i>Clostridium</i> and <i>Romboutsia</i>	Metformin	Negative correlation with the hypoglycemic effect	[146]
<i>E. coli</i> DH5 $\alpha$	Thioguanine (TG) and mercaptopurine (MP)	Conversion into active metabolite thioguanine nucleotides (TGNs)	[147]

suggested that their deacetylation in the gut depends on *bt4096*. Using the same approach, they identified a total of 17 *B. thetaiotaomicron* gene products involved in metabolizing 18 different drugs to 41 different metabolites. These are *bt2068*, *bt2367*, *bt2961*, *bt3124*, *bt4091*, *bt1429*, *bt2366*, *bt0152*, *bt0217*, *bt0445*, *bt1192*, *bt0569*, *bt4096*, *bt4075*, *bt1006*, *bt1148*, and *bt3112*, confirming activity of each gene by targeted cloning and expression in *E. coli*. Thirteen drug-metabolizing gene products that collectively metabolize 16 drugs were identified from *Collinsella aerofaciens* and *Bacteroides dorei*. These include *ca00311*, *ca00815*, *ca01707*, *ca01846*, *ca02348*, *bd03934*, *bd03988*, *bd00571*, *bd00665*, *bd03379*, *bd03642*, *bd03937*, and *bd03091*. The genomic presence of homologs of these identified drug-metabolizing gene products was assessed by enrichment analysis for the drug-metabolizing activities across the 76 bacterial strains. Many identified gene products demonstrated significant enrichment and suggested their contribution in the observed bacterial drug metabolism. An in silico analysis by Sharma and coworkers predicted the gut bacteria and the metabolic enzymes by developing DrugBug database, an in silico tool that anticipates biotransformation of drugs through microbial enzymes mostly produced by the microbiota residing in the GI tract. This metabolic enzymes database was developed from genome of 491 human intestinal bacteria, which carried 324,697 metabolic enzymes allotted with EC numbers. From the six EC classes, the highest (65.75%) number of molecules were metabolized by enzymes belonging to EC1 and EC2 classes, i.e., oxidoreductases and transferases, respectively, whereas only 6.83% of the total molecules were metabolized by enzymes from EC5 and EC6 classes, i.e., isomerases and ligases, respectively. The group has validated the DrugBug tool by

predicting metabolic enzymes for digoxin, a cardiotonic glycoside. The molecular structure of digoxin, consisting of three sugar moieties and one aglycone digoxigenin moiety, suggested three possible sites for metabolic reactions: 3 $\beta$ -OH group, C-17 attached lactone ring, and the sugar moieties. The three potential enzyme classes to metabolize digoxin were predicted to be oxidoreductase (EC1) for the reduction of lactone ring, transferase (EC2) for the addition of sugar moieties, and hydrolases (EC3) for the removal of sugar moieties. Using DrugBug, the enzymes identified were glucosyltransferases and mannosyltransferase from the genus *Citrobacter*, *Escherichia*, *Klebsiella*, *Lactobacillus*, and *Enterococcus* and FAD-dependent oxidoreductases, disulfide reductase, and hydroxylases from the bacterial genus *Escherichia*, *Providencia*, *Klebsiella*, *Eggerthella*, and *Streptomyces*. The ten drugs used in the study are ginsenoside Rb1, quercetin-3-glucoside, loperamide oxide, methamphetamine, omeprazole, sorivudine, lactulose, zonisamide, cycasin, and cyadox [26]. Recent studies have also suggested age-related variations in gut microbial composition. In a study with 69 people, including centenarians (age 99–104) and semi-supercentenarians (age 105–109), the number of reads for genes involved in xenobiotic transformation and metabolism were higher with a concurrent decrease in genes devoted to carbohydrate metabolism with the progression of age. These functional shifts were even more prominent in the microbiome of centenarians and semi-supercentenarians. The pathways for pentose phosphate (ko00030), starch and sucrose (KEGG pathway no. ko00500), and amino sugar and nucleotide sugar (ko00520) metabolism were less expressed whereas ethylbenzene (ko00642), caprolactam (ko00930), toluene (ko00623), and chlorocyclohexane and chlorobenzene (ko00361)

degradation pathways were more pronounced. The group of young individuals had higher levels of genes for glycerophospholipid (ko00564) and sphingolipid (ko00600) metabolism, whereas, centenarians and semi-supercentenarians showed more reads for glycerolipid (ko00561) and alpha-linoleic acid (KEGG pathway no. ko00592) metabolism. As age progressed, there was a progressive increase in genes for threonine (ko00260), tyrosine (ko00350), tryptophan (ko00380), serine, and glycine amino acid metabolism. The genes for lipopolysaccharide biosynthesis (ko00540) were also more pronounced in aged people, which can be related with the existence of pathobionts and the low levels of chronic inflammation [27]. Another metagenomic study by Almeida and coworkers, retrieving 13,133 human gut metagenomic datasets suggested that the clades of the known gut colonizers still contain considerable uncultured diversity. In their study, Coriobacteriaceae (20.6%), Ruminococcaceae (9.9%), and Peptostreptococcaceae (7.4%) were the three most frequent families; *Collinsella* (17.7%), *Clostridium* (7.3%), and *Prevotella* (4.4%) were the top genera found. Screening for the presence of secondary metabolite biosynthetic gene clusters (BGCs) within both the human gut reference (HGR) and unclassified metagenomic species (UMGS) was done using antiSMASH. Over 200 BGCs coding for sactipeptides, nonribosomal peptide synthetases (NRPSs), and bacteriocins were detected. Between the UMGS and HGR genomes, KEGG pathways involved in carbohydrate metabolism had differential abundance, representing discrete metabolic resemblance between the cultured and uncultured species. UMGS had less abundant genes for antioxidant and

redox functions, which signified lower tolerance to reactive oxygen species. Also, among the UMGS genomes, genes encoding for iron–sulfur and iron binding were found enriched suggesting the UMGS may be better adapted to niches with low oxygen tension or high iron concentration, since such conditions generate high levels of ferrous ions in their environment [28].

## Effects of Drugs on the Composition and Functions of Gut Microbiome

Gut microbial perturbations due to diet, drugs, alcohol, and other environmental factors can initiate and induce the progression of metabolic disorders [29, 30]. Several health disorders are associated with lower gut microbial diversity and reduce functional potency of microbial genomes when compared to healthy subjects [31, 32]. The differential inter-individual response to therapeutic drugs depends on how the gut microbiome functions at the time and on the potency of perturbation (Table 2). The early and long-term treatment outcomes are influenced by the proliferation of either the pathogenic, beneficial, or resistant microbiota after termination of drug therapy. Recent studies suggest that prolonged drug therapy during tuberculosis treatment leads to remarkable depletion of numerous immunologically significant commensal gut bacteria, and this dysbiosis persists at least for 1.2 years [33, 34]. Similarly, another study for a short course of 4 days with a cocktail of gentamicin, vancomycin, and meropenem in

**Table 2** Different drugs linked with gut microbial dysbiosis

Drug	Type of drug	Effect on gut microbiota	References
Metformin	Anti-diabetic drug	Increased SCFA-producing gut bacteria such as <i>Butyrivibrio</i> , <i>Bifidobacterium bifidum</i> , and <i>Megasphaera</i>	[148]
Metformin	Anti-diabetic drug	Increased abundance of mucin-degrading gut bacteria <i>Akkermansia muciniphila</i>	[148]
Metformin	Anti-diabetic drug	Decreased abundance of <i>Bacteroides fragilis</i>	[149]
Metformin	Anti-diabetic drug	Increased abundance of <i>Escherichia</i> species	[148]
Metformin	Anti-diabetic drug	Significant decrease in microbial richness	[43]
Metformin	Anti-diabetic drug	Reduced abundance of <i>Faecalibacterium</i> in Indian and Danish subjects	[43]
Vildagliptin	Anti-diabetic drug	Reduced abundance of <i>Oscillibacter</i> species and increased the abundance of <i>Lactobacillus</i> species	[150]
Dapagliflozin	Anti-diabetic drug	Reduced Firmicutes: bacterioidetes ratio	[151]
Indomethacin	Non-steroidal anti-inflammatory drug (NSAID)	Increased Firmicutes: bacterioidetes ratio	[152]
Aspirin	NSAID	Shift in gut microbial composition regarding <i>Prevotella</i> , <i>Bacteroides</i> , Ruminococcaceae, and <i>Barnesiella</i>	[153]
Celecoxib and Ibuprofen	NSAID	Increased abundance of Acidaminococcaceae and Enterobacteriaceae	[153]
Ibuprofen	NSAID	Enrichment in Propionibacteriaceae, Pseudomonadaceae, Puniceicoccaceae, and Rikenellaceae species	[153]

healthy subjects, suggested that the gut microbiota was restored to near-baseline composition within 1.5 months. This treatment resulted in the depletion of *Bifidobacterium* species, *Methanobrevibacter smithii*, and butyrate producers while enterobacteria and other pathobionts, such as *Fusobacterium nucleatum* and *Enterococcus faecalis*, were thriving. However, nine species common in all the study subjects before treatment initiation were not recovered in most of the subjects even after 6 months [35]. Both categories of therapeutic drugs, i.e., antibiotics and non-antibiotic drugs, can induce the acquisition of antimicrobial resistance (AMR) [36] and aid in intra/inter-species transmission of AMR genes within the gut microbiota, causing the emergence of potential drug-resistant pathogens. Paracetamol and opioids have a positive association with Streptococcaceae. Selective serotonin reuptake inhibitors (SSRIs) are negatively associated with Turicibacteraceae abundance but positively associated with *Eubacterium ramulus* and *Bifidobacterium dentium*, which are abundant in PPI users. The abundance of *Streptococcus salivarius* increases with the intake of oral steroids, PPIs, platelet aggregation inhibitors, vitamin D supplements, and SSRI antidepressants. Laxatives increase the abundance of *Bacteroides* and *Alistipes* and *Clostridium leptum* [37]. IBD patients' guts have lower abundances of beneficial microorganisms, including butyrate-producing *Faecalibacterium prausnitzii* and *Prevotella copri* [38]. The use of oral steroids like levothyroxine increases the abundance of *Methanobrevibacter smithii* and Actinomycetes [39]. A study suggested that the gut microbiota composition of drug-sensitive epilepsy was similar to healthy control. However, the gut microbiota of drug-resistant epilepsy was altered to an increased abundance of microbes primarily from the phylum Firmicutes, with a reduction in commensal gut bacteria (Table 2). Also, there was a significant increase in the phylum Verrucomicrobia in these patients [40]. Studies also suggest that drug usage also modifies the functional component of the gut microbiota. A widely used antidepressant, duloxetine, induces higher diversity in synthetic bacterial communities and affects the purine metabolism of *B. uniformis* and *C. saccharolyticum* [41]. A recent study by Vila and coworkers has shown a correlation between 411 microbial pathways and the usage of 11 drugs. Proton-pump inhibitors (PPI), metformin, and laxatives were found to have a strong association with the abundance of microbial taxonomies and pathways. The largest associations were found for PPIs with approximately 40 altered taxa and 166 altered microbial pathways. Altered functions included the increase of fermentation; NAD metabolism; fatty acid and lipid biosynthesis; purine deoxyribonucleoside degradation; and biosynthesis of L-arginine. Metformin caused changes in the gut microbiome's metabolic potential, including

increased quinone biosynthesis, butanoate production, polymyxin resistance, and sugar derivative degradation pathways [42, 43]. Another study suggested that 27% of non-antibiotic human-targeted drugs repressed the growth of at least one gut bacterial species [36]. Around 47 drugs, which were anti-infectives against viruses or eukaryotes, exhibited anti-commensal activity [36]. Artificial sweeteners can also affect the gut microbiome positively or negatively, leading to altered metabolic changes impacting SCFA production, insulin sensitivity, inflammation, or lipid metabolism [44]. In a recent in vitro study, the effects of eight oral antiviral drugs, which include lopinavir, chloroquine, ritonavir, darunavir, arbidol, ribavirin, oseltamivir, and favipiravir, were studied on the metabolism of four glycosides (i.e., geniposide, polydatin, glycyrrhizin, quercitrin) and on the activities of three major glycosidases ( $\beta$ -glucosidase,  $\beta$ -glucuronidase,  $\alpha$ -rhamnosidase) from gut microbiota (Table 1) and determined by LC-MS/MS [45]. One or more anti-coronavirus drugs at 100  $\mu$ M concentration extensively inhibited the metabolism of all four glycosides. Chloroquine and darunavir had no inhibition effect on  $\alpha$ -rhamnosidase, while they had a weak effect on  $\beta$ -glucosidase and  $\beta$ -glucuronidase, respectively [45].

## Microbial Functions and Drug Metabolism

Many recent studies suggest that the gut microbiota manipulates xenobiotic metabolism through direct and indirect mechanisms and alters the effectiveness, quality, and toxicity of xenobiotics and drugs [46]. The two broad mechanisms by which gut microbiota mediates drug metabolism: direct biotransformation mechanism where metabolism of drugs is performed by microbial enzymes, while indirect biotransformation mechanism suggests the impact of microbial metabolites on host receptors and signaling pathways. The gut microbiota can directly influence a person's response to a specific drug through directly interacting or by producing enzymes and inducing major or minor biochemical transformations in the drug to make it either more or less active/inactive or produce toxic metabolites [47–50] (Table 1). Besides this, microbiota indirectly interact with administered drugs by inducing reactivation of secreted inactive drug metabolites [51], producing metabolites to compete with drugs for the same host-metabolizing enzymes [52], modulating immune cell dynamics during immunomodulatory interventions like conditioning [53], and altering the levels of metabolizing enzymes in the intestine and liver [54–56]. As the gut microenvironment is anaerobic or rarely oxygenated, the drug metabolism by gut microbiota majorly involves hydrolytic and reductive biotransformations [57, 58].

## Direct Biotransformation of Drugs by Microbial Enzymes

Direct microbial biotransformation of ingested xenobiotics takes place when the compounds reach the intestinal lumen where a collection of bacterial enzymes capable of performing various chemical reactions acts upon them. The abundant glucuronides in the human intestine are processed by bacterial-glucuronidase enzymes to produce glucuronic acids from conjugated compounds [59]. According to one study, there are 3013 microbiome-encoded-glucuronidases with distinct functional capabilities for different glucuronide substrates [60]. Besides the hydrolytic biotransformations of the glucuronide conjugates, there are other abundant intestinal bacterial enzymes (Table 1) like polysaccharide lyases, transferases, reductases (nitroreductases and azoreductases), lipases, mono and dioxygenases, sulfatases, endoglycosidases, and glycol radical enzymes [10, 61]. The administration of probiotics has been shown to alter the structural and functional (enzyme activity) components of the intestinal microbiota. A study by Kim and coworkers suggested that the coadministration of probiotic strains with drugs resulted in altered pharmacokinetics of the drugs. The introduction of *Lactobacillus reuteri* K8 resulted in an increased abundance of Bifidobacteria, Enterococci, Clostridia, and Cyanobacteria. It enhanced the degradation of acetaminophen by itself and by the gut microbiota and arylsulfate sulfotransferase activities without changing the intestinal metabolic activities. While *Lactobacillus rhamnosus* K9 administration increased Deferribacteres and decreased Bifidobacteria, it had no effect on acetaminophen degradation [62, 63]. According to one study, NSAID-associated GI-toxicity is induced by glucuronidase enzyme (encoded by the *gus* gene)-mediated aglycone release, which then initiates a cascade of events resulting in cell injury when it comes into contact with enterocytes [64]. However, inhibition of bacterial-glucuronidase by Inh-1 [1-((6,8-dimethyl-2-oxo-1,2-dihydroquinolin-3-yl)-3-(4-ethoxyphenyl)-1-(2-hydroxyethyl)thiourea] protected mice from NSAID-induced enteropathy caused by indomethacin, ketoprofen, and diclofenac [65]. For the cisplatin-associated hepatotoxicity, the gut microbial role remained unclear. However, when antibiotics were co-administered with cisplatin, it resulted in reduced toxicity, thereby confirming the gut microbiota regulated cisplatin-induced hepatotoxicity [66].

## Microbial Regulation of Hepatic Enzyme Functions and Drug Metabolism

Research with germ-free animals revealed that gut bacteria play a significant role in regulating functions of host-encoded metabolic enzymes. Cytochrome P450s, enzymes encompassing heme as cofactor and a major subset is phase-I oxidation enzymes, have an important role in drug metabolism and biosynthesis of endogenous biomolecules. P450s have hepatic as well as extrahepatic expression. The human CYP3A4 is involved in metabolizing more than 60% of all drugs [67]. The mRNA and protein expression of its mouse homolog CYP3a11 were significantly lower in the livers of adult germ-free mice [67]. However, the same study also suggested enhanced gene expression of Cyp1a2 (metabolic deactivation of certain anticancer drugs and activation of procarcinogens) and Cyp4a14 (metabolism of eicosanoids and fatty acids) in germ-free mice. The host-associated xenobiotic metabolizing enzymes (XMEs) involved in phase II metabolism were also differentially expressed in germ-free rats compared to conventional rats [54].

## Hydrolysis of Drugs, Prodrugs, and Xenobiotic Conjugates

Hydrolases are the enzymes produced by both the host and gut microbiota to break down orally ingested substances into smaller molecules that may be further metabolized. These enzymes add a water molecule to a substrate, which is followed by the bond cleavage. The hydrolases frequently found in the gastrointestinal tract are proteases, sulfatases, glycosidases, and esterases. The proteases act on the peptide bonds, chopping off the amino acid linkages in the polypeptide chain. They are classified into four classes on the basis of their catalytic sites: cysteine proteases, serine proteases, aspartic proteases, and metalloproteases. Different regions of the human intestine are equipped with different types of proteases. The human colon is dominated by many microbial cysteine and metalloproteases, whereas the pancreatic serine proteases are majorly present in small intestine. These enzymes differ in substrate specificities leading to potentially different therapeutic outcomes [68, 69]. The study of ~10 million genes from human gut metagenomic catalog resulted in recognizing 285 putative serine protease sequences from human intestinal microbiota. Fifty-six genera from five different phyla, namely Firmicutes, Bacteroidetes, Actinobacteria, Proteobacteria, and Fusobacteria contributed to these sequences [70]. Single amino acid prodrugs or

peptide prodrugs form the simplest group of drug-conjugates containing a short linker adhered to the drug [71]. They have negligible activity in the conjugated state until the drug is released by the target protease to gain high potency. Legumain, a cysteine protease, recognizes asparagine (Asn) to a much higher extent to aspartate (Asp) at the P1 position of very high specificity [72]. Thus, many legumains target prodrugs contain Asn conjugated with cytotoxic drug [73]. The hydrolysis of carbohydrate/glycosyl conjugates is carried by glycosidases. These enzymes hydrolyze glycosidic bonds using a dyad of carboxylic acid residues and a water molecule, releasing free sugars [74]. The three major glycosidases are  $\alpha$ -rhamnosidase,  $\beta$ -glucosidase, and  $\beta$ -glucuronidase. These are largely disseminated across gut microbiota [75, 76]. The most important enzyme for xenobiotic metabolism is  $\beta$ -glucuronidase, which hydrolyzes glucuronides which enter the gut through biliary secretion. A good example of this mechanism is provided by the chemotherapeutic drug irinotecan, which is metabolically inactivated via glucuronidation in the liver. However, upon entering the intestine, it is metabolically reactivated by the activity of bacterially expressed  $\beta$ -glucuronidase [77]. This reactivation causes severe, dose-limiting GI toxicity [78–81]. Sulfatases, the hydrolytic metalloenzymes, hydrolyze sulfate esters generated by phase II metabolism using the unusual amino acid residue formyl glycine on their active site [82–84]. The hydrate form of this residue is thought to undergo transesterification with a sulfate ester substrate to generate a tetrahedral intermediate that breaks down to release sulfate and reform the aldehyde [85]. The microbial sulfatases reactivate sulfated metabolite conjugates, which enter the GI tract for excretion [86–88]. This reactivation enables these molecules to either undergo enterohepatic recirculation or exert local effects on gut epithelium. Eighty percent of gut microbial sulfatases arise from Bacteroidetes and are Ser-type enzymes, whereas the remaining 20% are Cys-type sulfatases arising from Firmicutes, Proteobacteria, Fusobacteria, Verrucomicrobia, and Spirochaetes [89]. Using protein structure-guided methods, Ervin and coworkers have identified 728 discrete microbiome-encoded sulfatase proteins from 4.8 million unique proteins in the HMP stool sample database. A total of 1766 gut microbial sulfatases were identified from the 9.9 million sequences present in the integrated gene catalogue database [90]. Hydrolytic reactions alter both the physical properties and activities of xenobiotics and their metabolites. For example, removal of a glucuronide in the gut lumen is generally accompanied by a decrease in polarity that can allow reabsorption by host cells and thereby extend the lifetime of a molecule within the body, as seen with glucuronide conjugates of nonsteroidal anti-inflammatory drugs and the cancer therapy irinotecan [51, 65]. Esterases belong to

hydrolases class of enzymes, which catalyze the conversion of an ester group to a carboxylic acid and an alcohol by a hydrolysis reaction. These include carboxylesterases, acetylerases, and arylesterases. *Rhodobacterium sphaeroides*, *Bacillus subtilis*, *Geobacillus stercorophilus*, *Pseudomonas fluorescens*, *Arthrobacter globiformis*, *Archaeoglobus fulgidus*, *Alicyclobacillus acidocaldarius*, *Lactobacillus casei*, *Klebsiella* sp., *Sulfolobus solfataricus*, *Serratia* sp. SES-01, and *Sulfolobus tokodaii* exhibited carboxylic ester hydrolase activities to hydrolyze phenylacetate, 4-nitrophenylacetate, naphthylbutyrate, and some drugs such as ketoprofen, aspirin, and naproxen [91]. Enzymes like arylsulfatases and  $\beta$ -glucuronidases produced by gut bacterial flora can cleave the conjugates formed by the sulfo- and glucuronosyltransferases, leading back to the parent compound, thereby enhancing the half-life of the drug [92]. Often, hydrolysis is a prerequisite before further processing, for instance, the fermentation of sugars released from indigestible polysaccharides [93]. The end products of these reactions frequently support growth of gut commensals and their survival within gut [10].

## Modifications of Drug Scaffold by Reduction

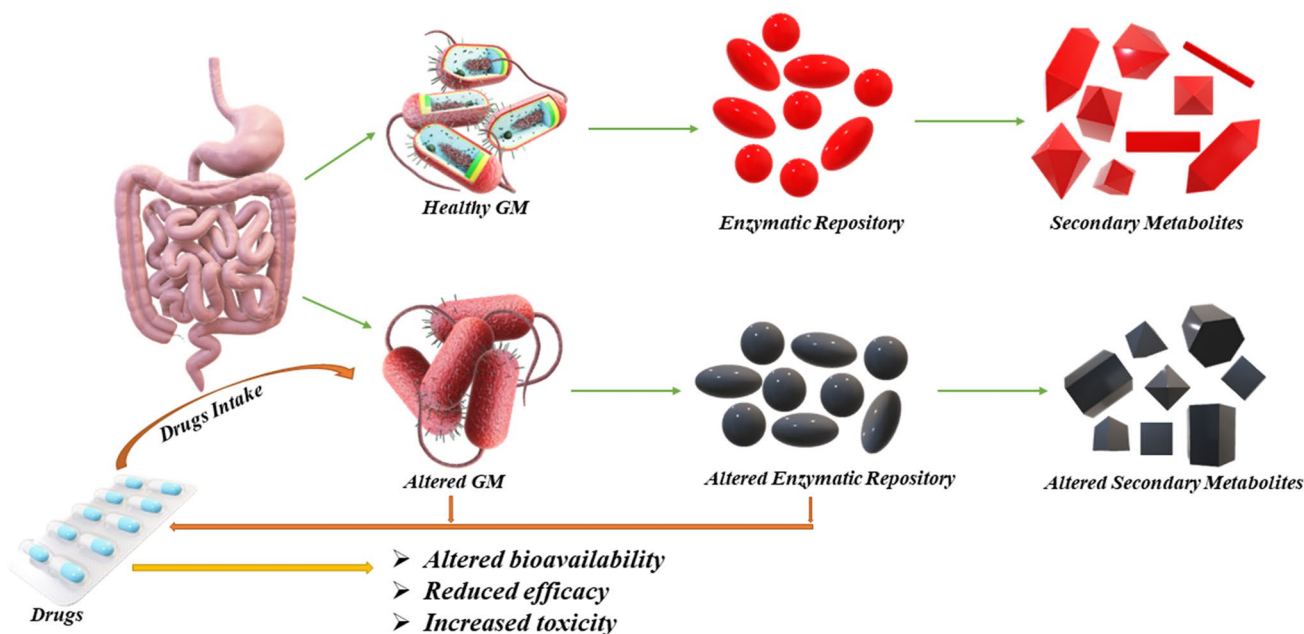
Reductive transformations are performed by enzymes and reductases, by making use of a variety of cofactors like flavin, NAD(P)H, i.e., NADH or NADPH, molybdenum cofactor, Fe–S clusters, (sio) heme, and other metallocofactors. With these enzymes, gut microbes can reduce various functional groups by transferring hydride equivalents or electrons ( $H^+$ ,  $2e^-$ ) to substrates [94–96]. The reductive transformation usually leads to decrease in polarity of metabolites by modifying the charge, electrophilicity, or hybridization. This usually influences the activity and life span of these metabolites in the body [97–99]. The six major reductive transformations include nitro ( $NO_2$ ), azo ( $-N=N-$ ), ketone ( $-C=O$ ), alkene ( $-C=C-$ ), sulfoxide ( $-S=O$ ), and N-oxide ( $-N-O$ ) [100]. The bacterial genera *Clostridium* sp., *Eubacterium* sp., *Clostridium leptum*, *C. paraputrificum*, *C. perfringens*, and *C. clostridiiforme* exhibited nitroreductase and azoreductase activities in the human GI tract [101–104]. Misal and Gawai have classified azoreductase superfamily into five different groups, depending upon their preference for nicotinamide and flavin: (1) flavin-containing NADPH-dependent azoreductase [105, 106], (2) flavin-containing NAD(P)H-dependent azoreductase [107–110], (3) flavin-containing NADH-dependent azoreductase [111, 112], (4) flavin-containing NAD(P)H-dependent quinine oxidoreductases [113, 114], and (5) flavin-free NAD(P)H-dependent azoreductase [115–118]. Azo drugs like olsalazine, asacol, pentasa, balsalazide, azulfid



dine, and salazopyrin for the treatment of ulcerative colitis and inflammatory bowel disease (IBD) [119, 120] are prodrugs, having 5-aminosalicylate (5-ASA), a non-steroidal anti-inflammatory molecule, and an inert carrier are linked with an azo bond, in order to avoid their rapid adsorption [121, 122]. The activities of these drugs rely upon azo bond cleavage by azoreductases secreted by gut microbiota, to release 5-ASA [100]. The enzymes nitroreductases catalyze the reduction of nitro-containing molecules. The bacterial nitroreductases can either be oxygen-insensitive (type I) or oxygen-sensitive (type II) or both [123, 124]. On the basis of electron donor preference, the well-studied oxygen-insensitive nitroreductases are broadly classified into major protein group for employing nicotinamide adenine dinucleotide phosphate (NADPH) and minor protein group employing both, nicotinamide adenine dinucleotide (NAPH) and NADPH as electron donors [125]. Chloramphenicol, a natural nitroaromatic compound, is reduced to the amine metabolite through nitroreductases exhibited by *Bacteroides fragilis*. The amine metabolite displays very weak antibacterial activity [126, 127].

## Modifications of Drug by Adding and Removing Functional Groups

The gut microbiota also performs a wide range of biotransformation reactions involving transfer of functional groups (Fig. 2). These reactions include deamination, demethylation, deacylation, decarboxylation, dehydroxylation, and oxidation. Transferase enzymes that move the functional groups amid two substrates through nucleophilic substitution reactions execute this activity. The action of gut microbiota-encoded deaminases in the conversion of 5-fluorocytosine to 5-fluorouracil is responsible, at least in part, for toxicity associated with 5-fluorocytosine chemotherapy [58, 128]. Using an anaerobic in vitro study, the biotransformation of 12 structurally diverse polymethoxyflavones (PMFs) was reported by gut bacteria *Blautia* sp. MRG-PMF1 to identify the metabolic intermediates. 5,7-dimethoxyflavone, 5-hydroxy-7-methoxyflavone, 3,5,7-trimethoxyflavone, 5-hydroxy-3,7-dimethoxyflavone, 5,7,4'-trimethoxyflavone, 5-hydroxy-7,4'-dimethoxyflavone, 3,5,7,4'-tetramethoxyflavone, 5-hydroxy-3,7,4'-trimethoxyflavone, 5,7,3',4'-tetramethoxyflavone, 3,5,7,3',4'-pentamethoxyflavone, 5-hydroxy-3,7,3',4'-tetramethoxyflavone, and 5,3'-dihydroxy-3,7,4'-trimethoxyflavone were converted to chrysin, apigenin, galanga, kaempferol, luteolin, and quercetin after complete demethylation [129]. Additional reactions usually require chemically activated cosubstrates like acetyl



**Fig. 2** Representation of bidirectional effect of gut microbiota and drugs. In a healthy individual, the gut microbiota (GM)-encoded enzymes synthesize and modify metabolites, which help in maintaining good health. However, during therapeutic interventions, there

is an alteration of compositions and/or functions of GM, which act on drugs differentially, thereby resulting into altered bioavailability, reduced efficacy, and increased toxicity of drugs

coenzyme A (CoA), S-adenosylmethionine (SAM), or adenosine triphosphate (ATP). The enzymatic removal of acyl groups usually depends on hydrolysis. Demethylases utilize cofactors like tetrahydrofolate and cob(I)alamin proficient in nucleophilic catalysis [130, 131].

## Other Microbial Enzymes Involved in Biotransformations Within the Gut

### Lyases

Lyases are the enzymes which catalyze the C–C or C–X (X may be N, O, P, S, or halides) bond breakage. These enzymes catalyze the reactions without requiring oxidation or addition of water. Polysaccharide lyases (PLs), along with glycoside hydrolases, encoded by the genome of intestinal microbiota, help in utilizing dietary or mucin glycans [18, 132]. The host-mediated xenobiotic metabolism is usually performed by cytochrome (CYP) P450 in the liver. During detoxification process, the liver produces glutathione conjugates, which are then carried with the bile to intestine where the gut bacteria-encoded C-S lyases act upon them. Alginate (sodium alginate ref. no. 00148), used as stabilizing and gelling agents in food and pharmaceuticals [133], is a linear polysaccharide, consisting of 1,4-linked  $\beta$ -D-mannuronic acid (M) and  $\alpha$ -L-guluronic acid (G), was thought to be non-digestible by humans. However intestinal bacteria like *Bacteroides thetaiotaomicron*, *B. xylanisolvens*, and *B. ovatus*, isolated from human stools can utilize alginate in vitro to form healthy short-chain fatty acids [134, 135]. Bacteria like *Bacteroidetes*, *Lactobacilli*, and *Bifidobacteria* have positive association with alginate presence in the gut of rats [136]. In a recent study, a polysaccharide lyase family 6 alginate lyase (*BcelPL6*) was identified in the genome of gut bacteria *Bacteroides cellulosilyticus* [137]. Another study reported a gene (BT\_3328) encoding a novel polysaccharide lyase, BtCDH from *B. thetaiotaomicron*, capable of degrading the dermatan sulfate, chondroitin sulfate, and hyaluronic acid of glycosaminoglycans, an important player in host–microbial interactions [138].

### Radical Chemistry

Radical biotransformations are useful in catalyzing those reactions, which may be difficult to catalyze by polar or other modes of biotransformation. The major gut bacterial enzymes involved in radical mediated biotransformations are glyceryl radical enzymes (GREs), cobalamin (B12)-dependent enzymes, and S-Adenosylmethionine (SAM) enzymes [10]. These enzymes produce high-energy intermediates having an unpaired electron, and these reactions are usually sensitive towards oxygen and require

significant amount of energy. These enzymes are highly abundant in the intestinal microbiota and often execute primary metabolism in anaerobic bacteria, thereby influencing the fate of xenobiotics directly or indirectly within the human body. The SAM enzymes are involved in drug resistance are Cfr and its homolog RlmN, which methylate adenine base A2503 located in the peptidyl transferase center of 23S rRNA (*E. coli* numbering), at C8 and C2 positions, respectively. This modification develops resistance towards ribosomal antibiotics like pleuromutilins, oxazolidinones, lincosamides, streptogramins A, and phenicols, acting on the peptidyl transferase center [139].

## Conclusion

In addition to their primary contribution to the metabolic process of the host, the gut microbiome is also crucial for modulating the efficacy of oral and systemic drugs routinely used in the health sector. Recent advances in multi-omics platforms, germ-free animal models, and in vitro mechanistic experiments are assisting in the identification of microbial functions and the exploration of the molecular mechanisms underlying the microbiome–drug metabolism axis. This knowledge can greatly help translational research of microbiota-targeted interventions, increase drug efficacy, avoid drug toxicity, and improve metabolic health.

### Box 1: Questions of scientific and clinical interests

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- (i) Do gut microbial load, richness, diversity, dynamics, and genomic content be used to predict the efficacy of a drug and therapeutic duration of an acute or chronic disease?
  - (ii) How to select a correct sample and specific site of gastrointestinal tract to identify microbial taxa which has maximum impact on the drug metabolism and drug efficacy?
  - (iii) Is there any simple and robust method to detect and differentiate drug metabolites in the systemic circulation derived from host or microbes-mediated modifications?
  - (iv) How to select a suitable animal model and analysis method to screen microbiome–drug interactions and predict drug toxicity?
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## Declarations

**Competing Interests** The authors declare no competing interests.

## References

- Morowitz MJ, Carlisle E, Alverdy JC (2011) Contributions of intestinal bacteria to nutrition and metabolism in the critically ill. *Surg Clin North Am* 91(4):771–785. <https://doi.org/10.1016/j.suc.2011.05.001>
- Carding S, Verbeke K, Vipond DT, Corfe BM, Owen LJ (2015) Dysbiosis of the gut microbiota in disease. *Microb Ecol Health Dis* 26:26191. <https://doi.org/10.3402/mehd.v26.26191>
- Pickard JM, Zeng MY, Caruso R, Núñez G (2017) Gut microbiota: role in pathogen colonization, immune responses and inflammatory disease. *Immunol Rev* 279(1):70–89. <https://doi.org/10.1111/imr.12567>
- Michalopoulos GK (2007) Liver regeneration. *J Cell Physiol* 213(2):286–300. <https://doi.org/10.1002/jcp.21172>
- Arumugam M, Raes J, Pelletier E, Le Paslier D, Yamada T, Mende DR, Fernandes GR, Tap J, Bruls T, Batto JM, Bertalan M, Borruel N, Casellas F, Fernandez L, Gautier L, Hansen T, Hattori M, Hayashi T, Kleerebezem M, Kurokawa K, Leclerc M, Levenez F, Manichanh C, Nielsen HB, Nielsen T, Pons N, Poulain J, Qin J, Sicheritz-Ponten T, Tims S, Torrents D, Ugarte E, Zoetendal EG, Wang J, Guarner F, Pedersen O, de Vos WM, Brunak S, Doré J, MetaHIT Consortium (additional members), Weissenbach J, Ehrlich SD, Bork P (2011) Enterotypes of the human gut microbiome. *Nature* 473:174–180.
- Magne F, Gotteland M, Gauthier L, Zazueta A, Pesoa S, Navarrete P, Balamurugan R (2020) The Firmicutes/Bacteroidetes ratio: a relevant marker of gut dysbiosis in obese patients? *Nutrients* 12:1474. <https://doi.org/10.3390/nu12051474>
- Rinninella E, Raoul P, Cintoni M, Franceschi F, Miggiano GAD, Gasbarrini A, Mele MC (2019) What is the healthy gut microbiota composition? A changing ecosystem across age, environment, diet, and diseases. *Microorganisms* 7:14. <https://doi.org/10.3390/microorganisms7010014>
- Qin J, Li R, Raes J, Arumugam M, Burgdorf KS, Manichanh C, Nielsen T, Pons N, Levenez F, Yamada T, Mende DR, Li J, Xu J, Li S, Li D, Cao J, Wang B, Liang H, Zheng H, Xie Y, Tap J, Lepage P, Bertalan M, Batto JM, Hansen T, Paslier DL, Linneberg A, Nielsen HB, Pelletier E, Renault P, Sicheritz-Ponten T, Turner K, Zhu H, Yu C, Li S, Jian M, Zhou Y, Li Y, Zhang X, Li S, Qin N, Yang H, Wang J, Brunak S, Doré J, Guarner F, Kristiansen K, Pedersen O, Parkhill J, Weissenbach J, MetaHIT Consortium, Bork P, Ehrlich DS, Wang J (2010) A human gut microbial gene catalogue established by metagenomic sequencing. *Nature* 464:59e65
- Li J, Jia H, Cai X, Zhong H, Feng Q, Sunagawa S, Arumugam M, Kultima JR, Prifti E, Nielsen T, Juncker AS, Manichanh C, Chen B, Zhang W, Levenez F, Wang J, Xu X, Xiao L, Liang S, Zhang D, Zhang Z, Chen W, Zhao H, Al-Aama JY, Edris S, Yang H, Wang J, Hansen T, Nielsen HB, Brunak S, Kristiansen K, Guarner F, Pedersen O, Doré J, Ehrlich SD, MetaHIT Consortium, Bork P, Wang J (2014) An integrated catalog of reference genes in the human gut microbiome. *Nature Biotechnology* 32:834–841. <https://doi.org/10.1038/nbt.2942>; pmid: 24997786
- Koppel N, Rekdal VM, Balskus EP (2017) Chemical transformation of xenobiotics by the human gut microbiota. *Science* 356:1246
- Qadir A, Hashmi MZ, Mahmood A (2017) Xenobiotics, types, and mode of action. In: M.Z. Hashmi, V Kumar, A Varma (eds.), *Xenobiotics in the soil environment: monitoring, toxicity and management*, Soil biology 49:1–7 Switzerland: Springer International Publishing AG. [https://doi.org/10.1007/978-3-319-47744-2\\_1](https://doi.org/10.1007/978-3-319-47744-2_1)
- Collins SL, Patterson AD (2020) The gut microbiome an orchestrator of xenobiotic metabolism *Acta Pharmaceutica Sinica B* 10;(1) 19e32
- Harrison PTC, Humfrey CDN, Litcheld M, Peakall D, Shuker LK (1995) *Environmental oestrogens: consequences to human health and wildlife*. IEH-Medical Research Council, Leicester.
- Wang B, Hu L, Siahaan T (2016) *Drug delivery: principles and applications* (Wiley, ed. 2, 2016).
- Jancova P, Anzenbacher P, Anzenbacherova E (2010) Phase II drug metabolizing enzymes. *Biomed Pap Med Fac Univ Palacky Olomouc Czech Repub* 154:103–116
- Johnson CH, Patterson AD, Idle JR, Gonzalez FJ (2012) Xenobiotic metabolomics: major impact on the metabolome. *Annu Rev Pharmacol Toxicol* 52:37–56. <https://doi.org/10.1146/annurev-pharmtox-010611-134748>
- Blaut M (2011) Ecology and physiology of the intestinal tract. *Curr Top Microbiol Immunol* 358:247–272. [https://doi.org/10.1007/82\\_2011\\_192](https://doi.org/10.1007/82_2011_192)
- Thursby E, Juge N (2017) Introduction to the human gut microbiota. *Biochem J* 474:1823–1836. <https://doi.org/10.1042/BCJ20160510>
- Zhu B, Wang X, Li L (2010) Human gut microbiome: the second genome of human body. *Protein Cell* 1(8):718–725. <https://doi.org/10.1007/s13238-010-0093-z>
- Brito IL, Gurry T, Zhao S, Huang K, Young SK, Shea TP, Naisilisili W, Jenkins AP, Jupiter SD, Gevers D, Alm EJ (2019) Transmission of human-associated microbiota along family and social networks. *Nat Microbiol* 4:964–971
- Zanger UM, Schwab M (2013) Cytochrome P450 enzymes in drug metabolism: regulation of gene expression, enzyme activities, and impact of genetic variation. *Pharmacol Ther* 138:103–141
- Ahmed S, Zhou Z, Zhou J, Chen SQ (2016) Pharmacogenomics of drug metabolizing enzymes and transporters: relevance to precision medicine. *Genom Proteom Bioinform* 14:298–313
- Javdan B, Lopez JG, Chankhamjon P, Lee YCJ, Hull R, Wu Q, Wang X, Chatterjee S, Donia MS (2020) Personalized mapping of drug metabolism by the human gut microbiome. *Cell* 181:1661–1679. <https://doi.org/10.1016/j.cell.2020.05.001>
- Kerimi A, Kraut NU, da Encarnacao JA, Williamson G (2020) The gut microbiome drives inter- and intra-individual differences in metabolism of bioactive small molecules. *Sci Rep* 10:19590
- Zimmermann M, Kogadeeva MZ, Wegmann R, Goodman AL (2019) Mapping human microbiome drug metabolism by gut bacteria and their genes. *Nature* 570:462–467
- Sharma AK, Jaiswal SK, Chaudhary N, Sharma VK (2017) A novel approach for the prediction of species-specific biotransformation of xenobiotic/drug molecules by the human gut microbiota. *Sci Rep* 7:9751
- Rampelli S, Soverini M, D'Amico F, Barone M, Tavella T, Monti D, Capri M, Astolfi A, Brigidi P, Biagi E, Franceschi C, Turrioni S, Candela M (2020) Shotgun metagenomics of gut microbiota in humans with up to extreme longevity and the increasing role of xenobiotic degradation. *mSystems* 5:e00124–20. <https://doi.org/10.1128/mSystems.00124-20>
- Almeida A, Mitchell AL, Boland M, Forster SC, Gloor GB, Tarkowska A, Lawley TD, Finn RD (2019) A new genomic blueprint of the human gut microbiota. *Nature* 568:499–504
- Hur KY, Lee MS (2015) Gut microbiota and metabolic disorders. *Diabetes Metab J* 39(3):198–203

30. Boulangé CL, Neves AL, Chilloux J, Nicholson JK, Dumas ME (2016) Impact of the gut microbiota on inflammation, obesity, and metabolic disease. *Genome Med* 8:42
31. Wang B, Yao M, Lv L, Ling Z, Li L (2017) The human microbiota in health and disease. *Engineering* 3:71–82
32. Álvarez-Mercado AI, Navarro-Oliveros M, Robles-Sánchez C, Plaza-Díaz J, Sáez-Lara MJ, Muñoz-Quezada S, Fontana L, Abadía-Molina F (2019) Microbial population changes and their relationship with human health and disease. *Microorganisms* 7(3):68. <https://doi.org/10.3390/microorganisms7030068>
33. Wipperfurth MF, Fitzgerald DW, Juste MAJ, Taur Y, Namavivayam S, Sher A, Bean JM, Buccì V, Glickman MS (2017) Antibiotic treatment for tuberculosis induces a profound dysbiosis of the microbiome that persists long after therapy is completed. *Sci Rep* 7(1):10767
34. Eribo OA, du Plessis N, Ozturk M, Guler R, Walzl G, Chegou N, N, (2020) The gut microbiome in tuberculosis susceptibility and treatment response: guilty or not guilty? *Cell Mol Life Sci* 77(8):1497–1509
35. Palleja A, Mikkelsen KH, Forslund SK, Kashani A, Allin KH, Nielsen T, Hansen TH, Liang S, Feng Q, Zhang C, Pyl PT, Coelho LP, Yang H, Wang J, Typas A, Nielsen MF, Nielsen HB, Bork P, Wang J, Vilsbøll T, Hansen T, Knop FK, Arumugam M, Pedersen O (2018) Recovery of gut microbiota of healthy adults following antibiotic exposure. *Nat Microbiol* 3:1255–1265
36. Maier L, Pruteanu M, Kuhn M, Zeller G, Telzerow A, Anderson EE, Brochado AR, Fernandez KC, Dose H, Mori H, Patil KR, Bork P, Typas A (2018) Extensive impact of non-antibiotic drugs on human gut bacteria. *Nature* 555:623–628
37. Jackson MA, Verdi S, Maxan ME, Shin CM, Zierer J, Bowyer RCE, Martin T, Williams FMK, Menni C, Bell JT, Spector TD, Steves CJ (2018) Gut microbiota associations with common diseases and prescription medications in a population-based cohort. *Nat Commun* 9:2655
38. Kedia S, Ghosh ST, Jain S, Desigamani A, Kumar A, Gupta V, Bopanna S, Yadav DP, Goyal S, Makharia G, Travis SPL, Das B, Ahuja V (2021) Gut microbiome diversity in acute severe colitis is distinct from mild to moderate ulcerative colitis. *J Gastroenterol Hepatol* 36(3):731–739
39. Halfvarson J, Brislawn CJ, Lamendella R, Vázquez-Baeza Y, Walters WA, Bramer LM, D'Amato M, Bonfiglio F, McDonald D, Gonzalez A, McClure EE, Dunklebarger MF, Knight R, Jansson JK (2017) Dynamics of the human gut microbiome in inflammatory bowel disease. *Nat Microbiol* 2:17004
40. Peng A, Qiu X, Lai W, Li W, Zhang L, Zhu X, He S, Duan J, Chen L (2018) Altered composition of the gut microbiome in patients with drug-resistant epilepsy. *Epilepsy Res* 147:102–107
41. Klünemann M, Andrejev S, Blasche S, Mateus A, Phapale P, Devendran S, Vappiani J, Simon B, Scott TA, Kafkia E, Konstantinidis D, Zirngibl K, Mastroianni E, Banzhaf M, Mackmull MT, Hövelmann F, Nesme L, Brochado AR, Maier L, Bock T, Periwäl V, Kumar M, Kim Y, Tramontano M, Schultz C, Beck M, Hennig J, Zimmermann M, Sévin DC, Cabreiro F, Savitski MM, Bork P, Typas A, Patil KR (2021) Bioaccumulation of therapeutic drugs by human gut bacteria. *Nature* 597:533–538
42. Vila AV, Collij V, Sanna S, Sinha T, Imhann F, Bourgonje AR, Mujagic Z, Jonkers DMAE, Masclee Ad AM, Fu J, Kurilshikov A, Wijmenga C, Zhernakova A, Weersma RK (2020) Impact of commonly used drugs on the composition and metabolic function of the gut microbiota. *Nat Commun* 11:362. <https://doi.org/10.1038/s41467-019-14177-z>
43. Alvarez-Silva C, Kashani A, Hansen TH, Pinna NK, Anjana RM, Dutta A, Saxena S, Støy J, Kampmann U, Nielsen T, Jørgensen T, Gnanaprakash V, Gnanavadeivel RK, Sukumaran A, Rani CSS, Færch K, Radha V, Balasubramanyam M, Nair GB, Das B, Vestergaard H, Hansen T, Mande SS, Mohan V, Arumugam M, Pedersen O (2021) Trans-ethnic gut microbiota signatures of type 2 diabetes in Denmark and India. *Genome Med* 13(1):37
44. Mora MR, Dando R (2021) The sensory properties and metabolic impact of natural and synthetic sweeteners. *Compr Rev Food Sci Food Saf* 20:1554–1583
45. Dai T, Wang M, Wang P, Dai L, Dai R, Meng Q (2021) Inhibition effects of eight anti-coronavirus drugs on glycosides metabolism and glycosidases in human gut microflora. *Pharmazie* 76:195–201. <https://doi.org/10.1691/ph.2021.01005>
46. Swanson HI (2015) Drug metabolism by the host and gut microbiota: a partnership or rivalry? *Drug Metab Dispos* 43:1499–1504. <https://doi.org/10.1124/dmd.115.065714>
47. Wilkinson EM, Ilhan ZE, Herbst-Kralovetz MM (2018) Microbiota-drug interactions: impact on metabolism and efficacy of therapeutics. *Maturitas* 112:53–63. <https://doi.org/10.1016/j.maturitas.2018.03.012>
48. Hitchings R, Kelly L (2019) Predicting and understanding the human microbiome's impact on pharmacology. *Trends Pharmacol Sci* 40(7):495–505. <https://doi.org/10.1016/j.tips.2019.04.014>
49. Weersma RK, Zhernakova A, Fu J (2020) Interaction between drugs and the gut microbiome. *Gut* 69(8):1510–1519. <https://doi.org/10.1136/gutjnl-2019-320204>
50. Dhurjad P, Dhavaliker C, Gupta K, Sonti R (2022) Exploring drug metabolism by the gut microbiota: modes of metabolism and experimental approaches. *Drug Metab Dispos* 50(3):224–234. <https://doi.org/10.1124/dmd.121.000669>
51. Wallace BD, Wang H, Lane KT, Scott JE, Orans J, Koo JS, Venkatesh MK, Jobin C, Yeh LA, Mani S, Redinbo MR (2010) Alleviating cancer drug toxicity by inhibiting a bacterial enzyme. *Science* 330:831–835. <https://doi.org/10.1126/science.1191175>; [pmid:21051639](https://pubmed.ncbi.nlm.nih.gov/21051639/)
52. Clayton TA, Baker D, Lindon JC, Everett JR, Nicholson JK (2009) Pharmaco-metabonomic identification of a significant host-microbiome metabolic interaction affecting human drug metabolism. *Proc Natl Acad Sci* 106:14728–14733. <https://doi.org/10.1073/pnas.0904489106>
53. Schluter J, Peled JU, Taylor BP, Markey KA, Smith M, Taur Y, Niehus R, Staffas A, Dai A, Fontana E, Amoretti LA, Wright RJ, Morjaria S, Fenelus M, Pessin MS, Chao NJ, Lew M, Bohannon L, Bush A, Sung AD, Hohl TM, Perales MA, van den Brink MRM, Xavier JB (2020) The gut microbiota is associated with immune cell dynamics in humans. *Nature* 588(7837):303–307
54. Meinel W, Sczesny S, Brigelius-Flohé R, Blaut M, Glatt H (2009) Impact of gut microbiota on intestinal and hepatic levels of phase 2 xenobiotic-metabolizing enzymes in the rat. *Drug Metab Dispos* 37(6):1179–1186
55. Zierer J, Jackson MA, Kastenmüller G, Mangino M, Long T, Telenti A, Mohnhey RP, Small KS, Bell JT, Steves CJ, Valdes AM, Spector TD, Menni C (2018) The fecal metabolome as a functional readout of the gut microbiome. *Nat Genet* 50(6):790–795
56. Chaudhari SN, Luo JN, Harris DA, Aliakbarian H, Yao L, Paik D, Subramaniam R, Adhikari AA, Vernon AH, Kiliç A, Weiss ST, Huh JR, Sheu EG, Devlin AS (2021) A microbial metabolite remodels the gut-liver axis following bariatric surgery. *Cell Host Microbe* 29(3):408–424.e7
57. Wilson ID, Nicholson JK (2017) Gut microbiome interactions with drug metabolism, efficacy, and toxicity. *Transl Res* 179:204–222
58. Colotti G, Rinaldi T (2020) The central role of gut microbiota in drug metabolism and personalized medicine. *Future Med Chem* 12(13):1197–1200
59. Pellock SJ, Redinbo RM (2017) Glucuronides in the gut: sugar-driven symbioses between microbe and host. *J Biol Chem* 292(21):8569–8576
60. Pollet RM, D'Agostino EH, Walton WG, Xu Y, Little MS, Biernat KA, Pellock SJ, Patterson LM, Creekmore BC, Isenberg

- HN, Bahethi RR, Bhatt AP, Liu J, Gharaibeh RZ, Redinbo MR (2017) An Atlas of  $\beta$ -glucuronidases in the human intestinal microbiome. *Structure* 25(7):967–977
61. Claus SP, Guillo H, Ellero-Simatos S (2016) The gut microbiota: a major player in the toxicity of environmental pollutants? *NPJ Biofilms Microbiomes* 2:16003. <https://doi.org/10.1038/npjbiofilms.2016.3>
62. Kim JK, Choi MS, Jeong JJ, Lim SM, Kim IS, Yoo HH, Kim DH (2018) Effect of probiotics on pharmacokinetics of orally administered acetaminophen in mice. *Drug Metab Dispos* 46(2):122–130
63. Clarke G, Sandhu KV, Griffin BT, Dinan TG, Cryan JF, Hyland NP (2019) Gut reactions: breaking down xenobiotic–microbiome interactions. *Pharmacol Rev* 71:198–224
64. Boelsterli UA, Redinbo MR, Saitta KS (2013) Multiple NSAID-induced hits injure the small intestine: underlying mechanisms and novel strategies. *Toxicol Sci* 131(2):654–667. <https://doi.org/10.1093/toxsci/kfs310>
65. Saitta KS, Zhang C, Lee KK, Fujimoto K, Redinbo MR, Boelsterli UA (2014) Bacterial  $\beta$ -glucuronidase inhibition protects mice against enteropathy induced by indomethacin, ketoprofen or diclofenac: mode of action and pharmacokinetics. *Xenobiotica* 44:28–35
66. Gong S, Feng Y, Zeng Y, Zhang H, Pan M, He F, Wu R, Chen J, Lu J, Zhang S, Yuan S, Chen X (2021) Gut microbiota accelerates cisplatin-induced acute liver injury associated with robust inflammation and oxidative stress in mice. *J Transl Med* 19:147. <https://doi.org/10.1186/s12967-021-02814-5>
67. Selwyn FP, Cui JY, Klaassen CD (2015) RNA-seq quantification of hepatic drug processing genes in germ-free mice. *Drug Metab Dispos* 43:1572–1580
68. Wang J, Yadav V, Smart AL, Tajiri S, Basit AW (2015) Stability of peptide drugs in the colon. *Eur J Pharm Sci* 78:31–36. <https://doi.org/10.1016/j.ejps.2015.06.018>
69. Tozaki H, Emi Y, Horisaka E, Fujita T, Yamamoto A, Muranishi S (1997) Degradation of insulin and calcitonin and their protection by various protease inhibitors in rat caecal contents: implications in peptide delivery to the colon. *J Pharm Pharmacol* 49:164–168. <https://doi.org/10.1111/j.2042-7158.1997.tb06773.x>
70. Kriaa A, Jablaoui A, Mkaouer H, Akermi N, Maguin E, Rhimi M (2020) Serine proteases at the cutting edge of IBD: focus on gastrointestinal inflammation. *FASEB J* 34:7270–7282
71. Choi KY, Swierczewska M, Lee S, Chen X (2012) Protease-activated drug development. *Theranostics* 2:156–178
72. Poreba M (2019) Recent advances in the development of legumain-selective chemical probes and peptide prodrugs. *Biol Chem* 400:1529–1550
73. Poreba M (2020) Protease-activated prodrugs: strategies, challenges, and future directions. *FEBS J* 287:1936–1969
74. Kallemeijn WW, Witte MD, Wennekes T, Aerts JM (2014) Mechanism-based inhibitors of glycosidases: design and applications. *Adv Carbohydr Chem Biochem* 71:297–338. <https://doi.org/10.1016/B978-0-12-800128-8.00004-2>
75. Kaoutari AEI, Armougom F, Gordon JI, Raoult D, Henrissat B (2013) The abundance and variety of carbohydrate active enzymes in the human gut microbiota. *Nat Rev Microbiol* 11:497–504. <https://doi.org/10.1038/nrmicro3050>
76. Wallace BD, Roberts AB, Pollet RM, Ingle JD, Biernat KA, Pellock SJ, Venkatesh MK, Guthrie L, O'Neal SK, Robinson SJ, Dollinger M, Figueroa E, McShane SR, Cohen RD, Jin J, Frye SV, Zamboni WC, Pepe-Ranney C, Mani S, Kelly L, Redinbo MR (2015) Structure and inhibition of microbiome  $\beta$ -glucuronidases essential to the alleviation of cancer drug toxicity. *Chem Biol* 22:1238–1249. <https://doi.org/10.1016/j.chembiol.2015.08.005>
77. Testa B and Mayer JM 2003 Miscellaneous reactions of hydration and dehydration. In: Kolitzus, Bounds PL (ed) *Hydrolysis in drug and prodrug metabolism*. WILEY-VCH-VHCA, 664–732.
78. Stringer AM, Gibson RJ, Bowen JM, Logan RM, Ashton K, Yeoh AS, Al-Dasooqi N, Keefe DM (2009) Irinotecan-induced mucositis manifesting as diarrhoea corresponds with an amended intestinal flora and mucin profile. *Int J Exp Pathol* 90(5):489–499
79. Smith NF, Figg WD, Sparreboom A (2006) Pharmacogenetics of irinotecan metabolism and transport: an update. *Toxicol In Vitro* 20(2):163–175
80. Kehrer DF, Sparreboom A, Verweij J, de Bruijn P, Nierop CA, van de Schraaf J, Ruijgrok EJ, de Jonge MJ (2001) Modulation of irinotecan-induced diarrhea by cotreatment with neomycin in cancer patients. *Clin Cancer Res* 7(5):1136–1141
81. Gibson RJ, Bowen JM, Inglis MR, Cummins AG, Keefe DM (2003) Irinotecan causes severe small intestinal damage, as well as colonic damage, in the rat with implanted breast cancer. *J Gastroenterol Hepatol* 18(9):1095–1100
82. Flint HJ, Scott KP, Duncan SH, Louis P, Forano E (2012) Microbial degradation of complex carbohydrates in the gut. *Microbes* 3:289–306
83. Ulmer JE, Vilén EM, Namburi RB, Benjdia A, Beneteau J, Malleron A, Bonnaffé D, Driguez PA, Descroix K, Lassalle G, Le Narvor C, Sandström C, Spillmann D, Berteau O (2014) Characterization of glycosaminoglycan (GAG) sulfatases from the human gut symbiont *Bacteroides thetaiotaomicron* reveals the first GAG-specific bacterial endosulfatase. *J Biol Chem* 289:24289–24303. <https://doi.org/10.1074/jbc.M114.573303>
84. Flint HJ, Duncan SH, Scott KP, Louis P (2017) Interactions and competition within the microbial community of the human colon: links between diet and health. *Environ Microbiol* 9:1101–1111
85. Lukatela G, Krauss N, Theis K, Selmer T, Gieselmann V, von Figura K, Saenger W (1998) Crystal structure of human arylsulfatase A: the aldehyde function and the metal ion at the active site suggest a novel mechanism for sulfate ester hydrolysis. *Biochemistry* 37:3654–3664. <https://doi.org/10.1021/bi9714924>
86. Roberts AB, Wallace BD, Venkatesh K, Mani S, Redinbo MR (2013) Molecular insights into microbial  $\beta$ -glucuronidase inhibition to abrogate CPT-11 toxicity. *Mol Pharmacol* 84(2):208–217. <https://doi.org/10.1124/mol.113.085852>
87. Weinshilboum R, Otterness D (1994) Sulfotransferase enzymes. In: Kauffman FC (ed) *Conjugation-deconjugation reactions in drug metabolism and toxicity*. Handbook of experimental pharmacology. Springer-Verlag, New York, vol 112:45–78
88. Nagata K, Yamazoe Y (2000) Pharmacogenetics of sulfotransferase. *Annu Rev Pharmacol Toxicol* 40(1):159–176
89. Biernat KA, Pellock SJ, Bhatt AP, Bivins MM, Walton WG, Tran BNT, Wei L, Snider MC, Cesmat AP, Tripathy A, Erie DA, Redinbo MR (2019) Structure, function, and inhibition of drug reactivating human gut microbial  $\beta$ -glucuronidases. *Sci Rep* 9:825
90. Ervin SM, Simpson JB, Gibbs ME, Creekmore BC, Lim L, Walton WG, Gharaibeh RZ, Redinbo MR (2020) Structural insights into endobiotic reactivation by human gut microbiome-encoded sulfatases. *Biochemistry* 59(40):3939–3950
91. Choi MS, Yu JS, Yoo HH, Kim DH (2018) The role of gut microbiota in the pharmacokinetics of antihypertensive drugs. *Pharmacol Res* 130:164–171
92. Magdalou J, Gigueux SF, Ouzzine M, Testa B (2003) Biotransformation reactions. In *The practice of medicinal chemistry* <https://doi.org/10.1016/B978-012744481-9/50035-0>
93. Monohoe DR, Garge N, Zhang X, Sun W, O'Connell TM, Bunger MK, Bultman SJ (2011) The microbiome and butyrate regulate energy metabolism and autophagy in the mammalian colon. *Cell Metab* 13(5):517–526. <https://doi.org/10.1016/j.cmet.2011.02.018>

94. Rafii F, Hall JD, Cerniglia CE (1997) Mutagenicity of azo dyes used in foods, drugs and cosmetics before and after reduction by *Clostridium* species from the human intestinal tract. *Food Chem Toxicol* 35:897–901. [https://doi.org/10.1016/S0278-6915\(97\)00060-4](https://doi.org/10.1016/S0278-6915(97)00060-4)
95. Lee SC, Renwick AG (1995) Sulphoxide reduction by rat intestinal flora and by *Escherichia coli* in vitro. *Biochem Pharmacol* 49(11):1567–1576. [https://doi.org/10.1016/0006-2952\(95\)00093-F](https://doi.org/10.1016/0006-2952(95)00093-F)
96. Laue H, Friedrich M, Ruff J, Cook AM (2001) Dissimilatory sulfite reductase (desulfoviridin) of the taurine-degrading, non-sulfate-reducing bacterium *Bilophila wadsworthii* RZATAU contains a fused DsrB-DsrD subunit. *J Bacteriol* 183:1727–1733. <https://doi.org/10.1128/JB.183.5.1727-1733.2001>
97. Haiser HJ, Gootenberg DB, Chatman K, Sirasani G, Balskus EP, Turnbaugh PJ (2013) Predicting and manipulating cardiac drug inactivation by the human gut bacterium *Eggerthella lenta*. *Science* 341:295–298. <https://doi.org/10.1126/science.1235872>
98. Peppercorn MA, Goldman P (1972) The role of intestinal bacteria in the metabolism of salicylazosulfapyridine. *J Pharmacol Exp Ther* 181:555–562
99. Lavrijsen K, van Dyck D, van Houdt J, Hendrickx J, Monbaliu J, Woestenborghs R, Meuldermans W, Heykants J (1995) Reduction of the prodrug loperamide oxide to its active drug loperamide in the gut of rats, dogs, and humans. *Drug Metab Dispos* 23:354–362
100. Guo Y, Lee H, Jeong H (2020) Gut microbiota in reductive drug metabolism. *Prog Mol Biol Transl Sci* 171:61–93
101. Rafii F, Franklin W, Cerniglia CE (1990) Azoreductase activity of anaerobic bacteria isolated from human intestinal microflora. *Appl Environ Microbiol* 56:2146–2151
102. Morrison JM, Wright CM, John GH (2012) Identification, Isolation and characterization of a novel azoreductase from *Clostridium perfringens*. *Anaerobe* 18:229–234
103. Morrison JM, John GH (2015) Non-classical azoreductase secretion in *Clostridium perfringens* in response to sulfonated azo dye exposure. *Anaerobe* 34:34–43
104. Misal SA, Gawai KR (2018) Azoreductase: a key player of xenobiotic metabolism. *Bioresour Bioprocess* 5:17. <https://doi.org/10.1186/s40643-018-0206-8>
105. Chen H, Hopper SL, Cerniglia CE (2005) Biochemical and molecular characterization of an azoreductase from *Staphylococcus aureus*, a tetrameric NADPH-dependent flavoprotein. *Microbiology* 151:1433–1441
106. Wang CJ, Hagemeyer C, Rahman N, Lowe E, Noble M, Coughtrie M, Sim E, Westwood I (2007) Molecular cloning, characterisation and ligand-bound structure of an azoreductase from *Pseudomonas aeruginosa*. *J Mol Biol* 373:1213–1228
107. Qi J, Schlömann M, Tischler D (2016) Biochemical characterization of an azoreductase from *Rhodococcus opacus* ICP possessing methyl red degradation ability. *J Mol Catal B Enzym* 130:9–17
108. Qi J, Anke MK, Szymańska K, Tischler D (2017) Immobilization of *Rhodococcus opacus* ICP azoreductase to obtain azo dye degrading biocatalysts operative at acidic pH. *Int Biodeterior Biodegradation* 118:89–94
109. Qi J, Paul CE, Hollmann F, Tischler D (2017) Changing the electron donor improves azoreductase dye degrading activity at neutral pH. *Enzyme Microb Technol* 100:17–19
110. Oturkar CC, Othman MA, Kulkarni M, Madamwar D, Gawai KR (2013) Synergistic action of flavin containing NADH dependent azoreductase and cytochrome P450 monooxygenase in azoaromatic mineralization. *RSC Adv* 3:3062–3070
111. Liu ZJ, Chen H, Shaw N, Hopper SL, Chen L, Chen S, Cerniglia CE, Wang BC (2007) Crystal structure of an aerobic FMN-dependent azoreductase (AzoA) from *Enterococcus faecalis*. *Arch Biochem Biophys* 463:68–77
112. Matsumoto K, Mukai Y, Ogata D, Shozui F, Nduko JM, Taguchi S, Ooi T (2010) Characterization of thermostable FMN-dependent NADH azoreductase from the moderate thermophile *Geobacillus stearothermophilus*. *Appl Microbiol Biotechnol* 86:1431–1438
113. Liu G, Zhou J, Jin R, Zhou M, Wang J, Lu H, Qu Y (2008) Enhancing survival of *Escherichia coli* by expression of azoreductase AZR possessing quinone reductase activity. *Appl Microbiol Biotechnol* 80:409–416
114. Ryan A, Kaplan E, Nebel JC, Polycarpou E, Crescente V, Lowe E, Preston GM, Sim E (2014) Identification of NAD(P)H quinone oxidoreductase activity in azoreductases from *P aeruginosa* azoreductases and NAD(P)H quinone oxidoreductases belong to the same FMN-dependent superfamily of enzymes. *Plos One* 9:e98551. <https://doi.org/10.1371/journal.pone.0098551>
115. Blumel S, Knackmuss HJ, Stolz A (2002) Molecular cloning and characterization of the gene coding for the aerobic azoreductase from *Xenophilus azovorans* KF46F. *Appl Environ Microbiol* 68:3948–3955
116. Chen H, Feng J, Kweon O, Xu H, Cerniglia CE (2010) Identification and molecular characterization of a novel flavin-free NADPH preferred azoreductase encoded by azo B in *Pigmentiphaga kullae* K24. *BMC Biochem* 11:13
117. Misal SA, Lingojar DP, Shinde RM, Gawai KR (2011) Purification and characterization of azoreductase from alkaliphilic strain *Bacillus badius*. *Process Biochem* 46:1264–1269
118. Misal SA, Humne VT, Lokhande PD, Gawai KR (2015) Biotransformation of nitro aromatic compounds by flavin-free NADH-azoreductase. *J Biorem Biodegrad* 6:2–6
119. Das KM, Farag SA (2000) Current medical therapy of inflammatory bowel disease. *World J Gastroenterol* 6(4):483–489
120. Lautenschlager C, Schmidt C, Fischer D, Stallmach A (2014) Drug delivery strategies in the therapy of inflammatory bowel disease. *Adv Drug Deliv Rev* 71:58–76
121. Nielsen OH, Bandesen S (1983) Kinetics of 5 aminosalicylic acid after jejunal instillation in man. *Br J Clin Pharmacol* 16:738–740
122. Makins RJ, Cowan RE (2001) 5-amino-salicylate in the management of inflammatory bowel disease. *Colorectal Dis* 3:218–222
123. Gwenin CD, Kalaji M, Williams PA, Kay CM (2010) A kinetic analysis of three modified novel nitroreductases. *Biodegradation* 22:463–474
124. Powell N (2020) Nitroreductase in cancer therapy. Available online: <https://nitroreductaseincancertreatment.wordpress.com/nitroreductase/> (accessed on 17 December 2020).
125. Whiteway J, Koziarz P, Veall J, Sandhu N, Kumar P, Hoecher B, Lambert IB (1998) Oxygen-insensitive nitroreductases: analysis of the roles of *nfsA* and *nfsB* in development of resistance to 5-Nitrofurantoin derivatives in *Escherichia coli*. *J Bacteriol* 180:5529–5539
126. Smith AL, Erwin AL, Kline T, Unrath WCT, Nelson K, Weber A, Howald WN (2007) Chloramphenicol is a substrate for a novel nitroreductase pathway in *Haemophilus influenzae*. *Antimicrob Agents Chemother* 51(8):2820–2829
127. Onderdonk AB, Kasper DL, Mansheim BJ, Louie TJ, Gorbach SL, Bartlett JG (1979) Experimental animal models for anaerobic infections. *Rev Infect Dis* 1(2):291–301
128. Harris BE, Manning BW, Federle TW, Diasio RB (1986) Conversion of 5-fluorocytosine to 5-fluorouracil by human intestinal microflora. *Antimicrob Agents Chemother* 29(1):44–48
129. Burapan S, Kim M, Han J (2017) Demethylation of polymethoxyflavones by human gut bacterium *Blautia* sp MRG-PMF1. *Journal of Agricultural and Food Chemistry* 65(8):1620–1629. <https://doi.org/10.1021/acs.jafc.7b00408>

130. Ticak T, Kountz DJ, Girosky KE, Krzycki JA, Ferguson DJ Jr (2014) A nonpyrrolysine member of the widely distributed trimethylamine methyltransferase family is a glycine betaine methyltransferase. *Proc Natl Acad Sci USA* 111:E4668–E4676. <https://doi.org/10.1073/pnas.1409642111>
131. Kumano T, Fujiki E, Hashimoto Y, Kobayashi M (2016) Discovery of a sesamin-metabolizing microorganism and a new enzyme. *Proc Natl Acad Sci USA* 113:9087–9092. <https://doi.org/10.1073/pnas.1605050113>
132. Tailford LE, Owen CD, Walshaw J, Crost EH, Hardy-Goddard J, Le Gall G, de Vos WM, Taylor GL, Juge N (2015) Discovery of intramolecular trans-sialidases in human gut microbiota suggests novel mechanisms of mucosal adaptation. *Nat Commun* 6:7624. <https://doi.org/10.1038/ncomms8624>
133. Yao M, Wu J, Li B, Xiao H, McClements DJ, Li L (2017) Microencapsulation of *Lactobacillus salivarius* Li01 for enhanced storage viability and targeted delivery to gut microbiota. *Food Hydrocolloids* 72:228–236
134. Li M, Li G, Shang Q, Chen X, Liu W, Pi X, Zhu L, Yin Y, Yu G, Wang X (2016) *In vitro* fermentation of alginate and its derivatives by human gut microbiota. *Anaerobe* 39:19–25
135. Li M, Shang Q, Li G, Wang X, Yu G (2017) Degradation of marine algae-derived carbohydrates by bacteroidetes isolated from human gut microbiota. *Mar Drugs* 15(4):92
136. An C, Kuda T, Yazaki T, Takahashi H, Kimura B (2013) Flx pyrosequencing analysis of the effects of the brown-algal fermentable polysaccharides alginate and laminaran on rat cecal microbiotas. *Appl Environ Microbiol* 79:860–866
137. Stender EGP, Andersen CD, Fredslund F, Holck J, Solberg A, Teze D, Peters GHJ, Christensen BE, Aachmann FL, Welner DH, Svensson B (2019) Structural and functional aspects of mannuronic acid-specific PL6 alginate lyase from the human gut microbe *Bacteroides cellulosilyticus*. *J Biol Chem* 294(47):17915–17930
138. Ndeh D, Munoz JM, Cartmell A, Bulmer D, Wills C, Henrissat B, Gray J (2018) The human gut microbe *Bacteroides thetaiotaomicron* encodes the founding member of a novel glycosaminoglycan-degrading polysaccharide lyase family PL29. *J Biol Chem* 293(46):17906–17916
139. Yan F, LaMarre JM, Rohrich R, Wiesner J, Jomaa H, Mankin AS, Fujimori DG (2010) RlmN and Cfr are radical SAM enzymes involved in methylation of ribosomal RNA. *J Am Chem Soc* 132:3953–3964
140. Hashim H, Azmin S, Razlan H, Nw Y, Tan HJ, Manaf MR, Ibrahim NM (2014) Eradication of *Helicobacter pylori* infection improves levodopa action, clinical symptoms and quality of life in patients with Parkinson's disease. *PLoS ONE* 9(11):e112330
141. Kumar K, Jaiswal SK, Dhoke GV, Srivastava GN, Sharma AK, Sharma VK (2018) Mechanistic and structural insight into promiscuity based metabolism of cardiac drug digoxin by gut microbial enzyme. *Journal of Cellular Biochemistry* 119:5287e96
142. Strong HA, Renwick AG, George CF, Liu YF, Hill MJ (1987) The reduction of sulphinpyrazone and sulindac by intestinal bacteria. *Xenobiotica* 17(6):685–696. <https://doi.org/10.3109/00498258709043976>
143. Amadio J, Gordon K, Murphy CD (2010) Biotransformation of flurbiprofen by *Cunninghamella* species. *Appl Environ Microbiol* 76(18):6299–6303. <https://doi.org/10.1128/AEM.01027-10>
144. Raffi F, Cerniglia CE (1995) Reduction of azo dyes and nitroaromatic compounds by bacterial enzymes from the human intestinal tract. *Environmental Health Perspectives* 103(suppl 5):17e9
145. Raffi F, Sutherland JB, Hansen EB Jr, Cerniglia CE (1997) Reduction of nitrazepam by *Clostridium leptum*, a nitroreductase-producing bacterium isolated from the human intestinal tract. *Clin Infect Dis* 25(suppl 2):S121–S122. <https://doi.org/10.1086/516204>
146. Lee Y, Kim AH, Kim E, Lee S, Yu KS, Jang IJ, Chung JY, Cho JY (2021) Changes in the gut microbiome influence the hypoglycemic effect of metformin through the altered metabolism of branched-chain and nonessential amino acids. *Diabetes Res Clin Pract* 178:108985
147. Movva R, Lobb M, Ó Cuív P, Florin THJ, Duley JA, Oancea I (2016) Microbial metabolism of thiopurines: a method to measure thioguanine nucleotides. *J Microbiol Methods*. 128:102–107 <https://doi.org/10.1016/j.mimet.2016.07.017>. Epub 2016 Jul 19. PMID: 27444548.
148. Wu H, Esteve E, Tremaroli V, Khan MT, Caesar R, Manneras-Holm L, Ståhlman M, Olsson LM, Serino M, Planas-Fèlix M, Xifra G, Mercader JM, Torrents D, Burcelin R, Ricart W, Perkins R, Fernández-Real JM, Bäckhed F (2017) Metformin alters the gut microbiome of individuals with treatment-naïve type 2 diabetes, contributing to the therapeutic effects of the drug. *Nat Med* 23:850–858
149. Sun L, Xie C, Wang G, Wu Y, Wu Q, Wang X, Liu J, Deng Y, Xia J, Chen B, Zhang S, Yun C, Lian G, Zhang X, Zhang H, Bisson WH, Shi J, Gao X, Ge P, Liu C, Krausz KW, Nichols RG, Cai J, Rimal B, Patterson AD, Wang X, Gonzalez FJ, Jiang C (2018) Gut microbiota and intestinal FXR mediate the clinical benefits of metformin. *Nat Med* 24:1919–1929
150. Olivares M, Neyrinck AM, Potgens SA, Beaumont M, Salazar N, Cani PD, Bindels LB, Delzenne NM (2018) The DPP-4 inhibitor vildagliptin impacts the gut microbiota and prevents disruption of intestinal homeostasis induced by a Western diet in mice. *Diabetologia* 61(8):1838–1848
151. Lee DM, Battson ML, Jarrell DK, Hou S, Ecton KE, Weir TL, Gentile CL (2018) SGLT2 inhibition via dapagliflozin improves generalized vascular dysfunction and alters the gut microbiota in type 2 diabetic mice. *Cardiovasc Diabetol* 17(1):62
152. Xiao X, Nakatsu G, Jin Y, Wong S, Yu J, Lau JYW (2017) Gut microbiota mediates protection against enteropathy induced by indomethacin. *Sci Rep* 7:40317. <https://doi.org/10.1038/srep40317>
153. Rogers MAM, Aronoff DM (2016) The influence of non-steroidal anti-inflammatory drugs on the gut microbiome. *Clin Microbiol Infect* 22:178.e1–178.e9. <https://doi.org/10.1016/j.cmi.2015.10.003>