Review

From-Toilet-to-Freezer: A Review on Requirements for an Automatic Protocol to Collect and Store Human Fecal Samples for Research Purposes

Frances Widjaja *[ID] and Ivonne M. C. M. Rietjens

Division of Toxicology, Wageningen University & Research, 6708 WE Wageningen, The Netherlands; ivonne.rietjens@wur.nl
* Correspondence: frances1.widjaja@wur.nl

Abstract: The composition, viability and metabolic functionality of intestinal microbiota play an important role in human health and disease. Studies on intestinal microbiota are often based on fecal samples, because these can be sampled in a non-invasive way, although procedures for sampling, processing and storage vary. This review presents factors to consider when developing an automated protocol for sampling, processing and storing fecal samples: donor inclusion criteria, urine–feces separation in smart toilets, homogenization, aliquoting, usage or type of buffer to dissolve and store fecal material, temperature and time for processing and storage and quality control. The lack of standardization and low-throughput of state-of-the-art fecal collection procedures promote a more automated protocol. Based on this review, an automated protocol is proposed. Fecal samples should be collected and immediately processed under anaerobic conditions at either room temperature (RT) for a maximum of 4 h or at 4 °C for no more than 24 h. Upon homogenization, preferably in the absence of added solvent to allow addition of a buffer of choice at a later stage, aliquots obtained should be stored at either −20 °C for up to a few months or −80 °C for a longer period—up to 2 years. Protocols for quality control should characterize microbial composition and viability as well as metabolic functionality.

Keywords: human; gut microbiota; in vitro; protocol; fecal samples; collection; storage

1. Introduction

Intestinal microbiota are important for host health because they play a role in a variety of physiological and metabolic pathways that influence health and disease [1–5]. Table S1 (Supplementary Material) provides an overview of literature studies reporting the relationship between fecal microbiota and health or disease at phylum, family, genus and species levels. This includes studies on the role of gut microbiota in sleep apnea, type 2 diabetes (T2D), inflammatory bowel disease (IBD), irritable bowel syndrome (IBS), anorexia, obesity, colorectal cancer (CRC), autism, Parkinson's disease and hepatic encephalopathy. For instance, the genus *Roseburia* sp. has been correlated with the health benefits of fiber consumption due to its ability, together with other commensal bacteria, to produce short-chain fatty acids (SCFAs) [6]. In reverse, the absence or decline of the same bacteria could indicate disease symptoms such as pouchitis for patients with ulcerative colitis (UC) [7]. Another example includes *Parvimonas micra*, *Fusobacterium nucleatum* and *Lachnoclostridium* sp. that are commonly used in detection of colorectal cancer (CRC) [8].

In addition to composition, the viability and metabolic functionality of the fecal microbiota, including the chemical reactions that these microbes are able to perform or facilitate, also play a role in health and disease [9–12]. Table S2 (Supplementary Material) provides an overview of chemical conversions catalyzed by the microbiota. Gut microbiota, for example, play an important role in bile acid metabolism and homeostasis, while changes in bile acid profiles and size of the bile acid pool have been reported to show associations

with diseases such as obesity, bile acid diarrhea (BAD), IBS, IBD, T2D, *C. difficile* infection (CDI) and hepatocellular carcinoma [13–16].

Studies on intestinal microbiota are often based on fecal samples because (i) microbiota present in fecal samples closely resemble those in colonic samples [17], where >70% of the intestinal bacteria reside [18,19], and (ii) human feces can be easily obtained in a non-invasive manner [20]. This implies that studying fecal samples to obtain insight into the role of the intestinal microbiota in health and disease requires adequate sampling, processing and storage. In order to facilitate high-throughput collection and storage, an automatic protocol to collect and store human fecal samples for research purposes would be recommended. The current mini-review presents an overview of data currently available on requirements to consider when developing such a protocol. Publications were systematically reviewed for different topics to be considered when collecting and storing human fecal samples for research purposes, starting from the fecal material donor, the toilet itself, the conditions required for fecal collection, processing, storage and, lastly, the quality control.

2. Differences Amongst Reported Human Fecal Microbiota Protocols

Despite the importance and relevance of human fecal microbiota studies, laboratories worldwide perform their fecal collection, processing and storage in a different manner, as previously summarized [21–24]. While it is customary to change protocols based on individual research needs, from comparison of these protocols, the critical steps to be considered become clear. Available data also suggest what would be the optimal requirements for each of these critical steps in order to define a harmonized automated protocol. These critical steps and their relevant parameters and requirements are discussed in the following sections in sequential order.

2.1. Criteria for Human Fecal Material Donors

Before a study begins, a section of the human population is targeted as fecal material donor (i.e., inclusion criteria). These candidates are often invited to fill up a questionnaire on their health status, diet, lifestyle, gastrointestinal issues, antibiotic and medication usage and other factors, which can be used to screen their suitability as fecal donors (i.e., exclusion criteria). This step has been previously documented in detail [25,26] but not all studies describe how to ensure that fecal donors truthfully answer the questionnaire rather than provide answers that allow them to donate their fecal materials [26]. In addition, the categories and the extent of such exclusion criteria differs per research group. For instance, while travel history, gastrointestinal diseases, pregnancy and recent antibiotic usage are commonly included [27–29], screening based on respiratory diseases, positive tests for certain bacterial or viral infections and mental health condition is uncommon [25]. Nevertheless, data collected on screened fecal donors would never fully capture the entire extent of an individual's lifestyle, consequently being a black box in downstream data analysis. In addition, most studies do not disclose their screening criteria, making it difficult to reproduce or compare results. Therefore, required criteria for participants' information should be written as formal guideline such as those published by The Organization for Economic Co-operation and Development (OECD), the World Health Organization (WHO) or the European Food Safety Authority (EFSA).

In addition to the inclusion/exclusion criteria, the number of recruited fecal donor participants varies, with, for instance, ≤30 individual [30–32] or significantly greater than 30 individuals [33–35] recruited in previous studies. While a low number of human fecal participants may often be sufficient to reach the study's objective, and a high number of participants can increase results' representativeness, recruiting a high number of participants and manually processing the fecal samples are laborious in studies with very high numbers of fecal donors [22,36,37], expressing the need for a higher-throughput processing stream.

2.2. Urine–Feces Separation

The first critical factor in a high-throughput automated protocol would be the urine–feces separation. Smart toilets that separate urine from feces already exist, mainly for collecting user's health information, developing sustainable cities, mineral recollection and usage in emergency camps [38–45]. Some toilets are equipped to meet women's and men's different preferences on urine excretion angle, due to different physiology such as height and length of feet [46], and contain sensors that allow self-analysis of human excreta as personalized health monitoring systems [42,44,46]. Different technologies have been used to separate urine and feces such as a vacuum suction pump with two separate holes [47], a bi-sloped conveyor belt to two different tanks [38], a urine diverting pedestal [41], a three-chamber septic tank (Aquatron separation technique (Aquatron, Västerås, Sweden)) [40] and an urine diversion equipped with a sensor such as the Beevi Toilet (Ulsan, Republic of Korea) developed by Science Walden [43]. However, all these technologies are not yet widely applied by research groups performing human gut microbiota studies, implying that most fecal donor participants still have to defecate in a normal toilet without urine–feces separation. While it is possible to defecate without urinating, it is difficult because, once the stronger anal sphincter relaxes, the weaker urinary sphincter also relaxes, which allows urine to pass at the same time as stool excretion [48]. Thus, for efficient urine–feces separation, application of a smart toilet that can automatically separate urine and feces during human fecal excreta collection seems a prerequisite. Nevertheless, in many places where research takes place, such a device may not be a realistic option and one would have to turn to simpler solutions.

2.3. Collection of the Fecal Sample

Collection of the fecal sample from the smart toilet should preferably also be performed in an automatic way, eliminating the need for the donor to collect and transfer the sample by him/herself. For example, Zymo feces catcher (Zymo Research, Kempen, Germany), Fisherbrand™ Commode Speciment Collection System (Fisherbrand™, Landsmeer, The Netherlands) and Fe-Col® Faecal Sample Collection Kits (Alpha Laboratories, Eastleigh, Hampshire, UK) still require manual transfer. The question to be answered then is whether to collect the sample as a whole or to store it in aliquots. Given that stools as such are generally large compared to the amount of material needed for subsequent analyses, aliquoting is implied. Aliquoting avoids multiple freeze–thaw cycles that cause DNA degradation [22], and innovations such as CryoXtractR (Eppendorf, Hamburg, Germany) were developed to facilitate this aliquoting [49]. While the effect of one freeze–thawing cycle on stool microbiota composition is not significant, it is important to note that subsequent freeze–thawing cycles may reduce the overall levels of viable bacteria [50]. Therefore, fecal sample processing protocols should divide specimens into smaller aliquots as a precautionary principle (i.e., avoiding DNA degradation and limiting the decrease in viability) and as a pragmatic approach (i.e., resulting in shorter thawing time at room temperature (RT)).

The need to aliquot also brings the question as to the need for homogenization. There are conflicting opinions related to how homogenized or well-mixed collected fecal specimens already are or whether they should be processed to homogenize their content. One study determined the effect of stool structure on microbial composition by comparing the inner and outer layers of the samples, as well as stool water content, and found minor differences in microbial composition and species abundance between both layers and between different water percentages [23]. Yet the use or omission of bead-beating to homogenize stool samples resulted in aliquots with different proportions of Gram-positive and Gram-negative bacteria [23,24,51]. In contrast, large inconsistency of taxa within an individual stool was found, possibly due to spatial variation of microenvironments [52]. Another study argued that stools with hard and lump consistency showed more diverse microbial composition across different collection sites in a single bowel movement [22,52–54], and the outer part and inner part of stool contain a different ratio of aerobes/anaerobes due to oxygen concentration gradient [22]. These results suggest that stool homogenization under

anaerobic conditions is essential to level out intra-sample variation. Stool homogenization is also crucial for metabolomic (metabolite) analysis but not for microbiome (microbiota) analysis because different sampling regions did not show differences in microbial community alpha diversity, while some identified that metabolites varied significantly across different sampling regions [55]. Considering that homogenization might be crucial for particularly hard and lumpy stool (Type 1–2 according to the Bristol stool chart) [56] but remains an unpleasant task to be manually performed and that metabolomics studies might require fecal homogenization to reduce unnecessary variability, automated homogenizer equipment [57] should be used such as a meat grinder, fecal matter blender [58] or sewage grinder system [59], preferably under anaerobic conditions to avoid preferential loss of obligate anaerobic bacteria.

2.4. Anaerobic Conditions

Anaerobic bacteria account for most of the fecal bacteria and are 100–1000 times more numerous in the intestinal microbiota pool than aerobic bacteria [60,61] but may die during sample preparation due to delay between stool collection and transport to anaerobic laboratory conditions [58,62]. Some studies prevent this loss of anaerobes by storing stools in a closed box with direct exposure to an anaerobic system such as Anaerocult^{TM} A (Merck, Darmstadt, Germany) to ensure an oxygen-free environment before transferring the fecal-containing box into an anaerobic chamber [63,64]. Another system called Exakt Pak canister (Inmark Packaging, Austell, GA, USA) was used to collect stool but there was no indication that the system contained an anaerobic environment [65]. One study performed bacterial enumeration with a different anaerobic system called GasPak generator (Becton Dickinson, Sparks, NJ, USA) [58]. They reported that the time between sample collection and sample processing was an important parameter and that this time should be as short as possible because bacterial culturability showed no discordance when samples were exposed to oxygen for less than two minutes; accordingly, the rest of the work was performed in the anaerobic chamber [58]. In addition, bacterial culturability increased when antioxidant solutions were used [58]. A recently patented fecal sampling device enables anaerobic and hygienic self-collection of stool samples for further processing without opening the device, preventing contact with the fecal donor and sample exposure to the environment [66]. All in all, these studies point to the need for an anaerobic environment for collecting fecal bacteria and a quick transport from toilet to the anaerobic laboratory conditions, which may best be achieved by using a vacuum toilet as used in other fields such as commercial aircraft [67]. This technology could automatically transport the feces to a compartment that can be made anaerobic. Alternatively, the patented stool self-collection device could achieve this objective [66], although at present it is not yet commercially available and the collection is not high-throughput.

2.5. Buffer or No Buffer in Fecal Material Processing

The usage of buffer or solution used to dissolve and subsequently store fecal material differs per study. A previous study summarized an extensive list of different buffer types and protocols used that appeared to depend on the type of experiments performed such as metabolomics, 16 s rRNA sequencing, metatranscriptomics or quantification of bacterial enzyme activities [21]. In addition, when freezing samples for storage at low temperature, usage of 10–20% (*v/v*) glycerol as cryoprotectant was encouraged to preserve bacteria because freeze–thawing compromises cell viability [21,68]. Yet another study advocated against dissolving fecal materials in 10% (*v/v*) glycerol for downstream lyophilization because it leads to an insufficiently dry and sticky product [69]. High concentrations of cryoprotectants such as glycerol and dimethylsulfoxide may penetrate cell membranes and compromise original biological and metabolic characteristics of fecal materials, leading to alternative cryoprotectants such as maltodextrin and trehalose [69], although the effect of cryoprotectant penetration on bacterial viability remains to be elucidated [68]. In addition, although glycerol might protect cell viability upon freezing [68], upon thawing, it may

cause medium enrichment, leading to an increase in certain bacteria and, consequently, changing the original composition or viability of microbiota [70].

In addition to cryprotectants, the inclusion of stabilizers such as RNAlater (Sigma-Aldrich, St. Louis, MO, USA) is debatable. On the one hand, RNAlater is known to protect stool RNA and DNA from rapid degradation, even after up to five years of storage [22,71]. However, the usage of RNAlater was negatively recommended as a storage medium of stool samples for microbial and metabolomic analysis due to a significant level of variation [55]. While RNAlater or other non-lytic or lytic buffers may protect microbial DNA, usage of such buffers may greatly decrease the viability of living cells and hamper subsequent culturing and colonizing studies [72,73].

All in all, rapid deep-freezing to −80 °C without buffer was strongly suggested as the best practice [70,74] because there was no alteration in microbial community with respect to composition between samples from direct freezing without buffer at −80 °C, 24 h storage at −20 °C and 24 h storage at 4 °C or RT [75] and no alteration in bacterial viability upon direct freezing to −70 °C without cryoprotectant [70]. Ultimately, regardless of the use of buffer or not, direct stool freezing is a common crucial step in fecal material processing to conserve fecal microbiota composition, viability and metabolic functionality. Given that the buffer requirements may vary with the subsequent type of analysis and certain preservative buffers might cause divergence compared to samples directly stored to −80 °C [76], it would be best to store the samples without buffer. Upon defreezing, the buffer of choice for subsequent steps can be added by each respective researcher, depending on the nature of their study.

2.6. Temperature and Time for Processing and Storage of Fecal Material

When considering the optimal temperature and time for processing and storage of fecal material, it is difficult to pick the exact combination because each study performs their stability test in a different manner. Despite the variability of storage conditions, available data support that colder storage temperature and shorter storage times are better for conserving microbial stability. Yet, in the case of manual fecal collection and sampling, "as cold and quickly as possible" is often not "as cold and quickly as optimal" due to logistical constrains. Storage time particularly plays an important role in intra-individual feces variation studies, where the stability of fecal microbiota of an individual is studied over time [77]. Table 1 shows available studies with temperature ranges from −80 °C to RT and time ranges from 15 min to 5 years for processing and storage. From this overview, it follows that fecal samples should be processed at either RT for at most 4 h or at 4 °C for no more than 24 h. Later, the aliquots should be stored at either −20 °C for up to a few months or −80 °C for longer periods—up to 2 years.

Table 1. Overview of processing and storage temperature and time across different studies. The coloring indicates whether the conditions indicated resulted in stable samples (green shading) or in samples that showed variability due to sample instability or deterioration (red shading). When this information was absent, no shading is included.

Processing			
Temperature	Time	Remarks	Reference
RT	3 h	After defecation. Stability not indicated.	[62]
20 ± 2 °C	<24 h	Non-significant effects at <24 h, but deletrious effects above this temperature.	[69]
>20 °C	>24 h	Samples should not be exposed to >20 °C if time from transformation to transplants exceeds 24 h.	
37 °C	>24 h	Extinction and proliferation of genus specific to each individual. Metabolomic fingerprints deviates even more as time increases.	

Table 1. *Cont.*

		Processing	
RT	4 h	After stool sample collection, it is acceptable for samples to reach the lab in this condition without preservation [54,78,79].	
4 °C	24 to 48 h	Keep the sample in cold storage when transported from participant to laboratory staff handling.	
RT (with stabilizer)	Up to 4 weeks	Stabilizers such as RNALater, 95% ethanol, Omnigene-Gut (DNA Genotek, Stittsville, Ottawa, ON, Canada) and FTA card (Sigma-Aldrich, St. Louis, MO, USA) can protect stool DNA from degradation [80].	[22]
4 °C (without stabilizer)	Up to a week	Fecal materials are processed without stabilizer [80].	
RT	Short-term	Short-term RT storage showed minimal effect on microbiome and metabolome profiles.	[55]
		Storage	
Temperature	Time	Remarks	Reference
−20 °C	Until further use	Storage condition. Stability not indicated.	[62]
4 °C	Short-term	Ideal for short shipment.	
−80 °C then rapid thaw at 37 °C	3 months	Stable fecal sample transplants in maltodextrin–trehalose solutions within this observation period.	[69]
RT	Greater than 15 min	Storage with or without buffer showed considerable divergence compared to −80 °C samples.	
4 °C	24 h	Does not alter microbiota compared to −80 °C samples.	[74]
−20 °C	72 h	Does not alter microbiota compared to −80 °C samples.	
−80 °C	n.a.	Freezing significantly decreases overall viability to around 25% but does not significantly change viable microbiota composition compared to fresh anaerobically processed specimen.	[50]
−80 °C (with stabilizer)	5 years	Long term stool storage with RNAlater had only limited effects on human fecal microbiota composition.	[71]
−20 to −80 °C	As soon as possible	Once samples reach the laboratory, they should be stored in this condition. Stability not indicated.	
−20 °C	A few months	Stable composition in microbial community.	[22]
−80 °C	2 years to long-term storage	Stable composition in microbial community.	

2.7. Parameters to Evaluate Stability upon Storage with Respect to Composition, Viability and Metabolic Functionality

The correlation between composition and metabolic functionality of gut microbiota with host health and disease are widely studied (Tables S1 and S2—Supplementary Materials). An additional parameter relevant for characterizing the suitability of fecal sampling and storage conditions would be the viability of the isolated fecal bacteria. This especially holds for studies where one wants to isolate specific strains and/or investigate the origin of a specific metabolic reaction or pathway. Table S1 shows correlation of gut microbiota at phylum, family, genus and species level, which are the levels mostly studied for characterizing

microbiota composition. Fecal microbiota composition is often performed with 16 s rRNA down to the genus level [81], yet this is shown to not be sufficiently deep in some studies where differences of specific microbiota occur at species or even sub-species level, requiring a deeper sequencing technique such as metagenomics [82]. Ideally, composition, viability and metabolic functionality of fecal microbiota should be tested because, when the bacteria are present, they might not always be viable and/or have their full metabolic capacity [11]. To test viability, one may use flow cytometry, to discriminate live and dead cells, and/or stool culturing on different media and under various conditions, to quantify the number of cultivable species [83]. Table S2 presents an overview of the many reactions that gut microbiota facilitate, which can be characterized by the catalytic efficiency measured with selected model compounds [84] or through metabolomics [85]. As quality control for the temporal stability [86] of gut microbiota over processing and storage conditions, composition, viability and metabolic functionality should be evaluated to avoid conclusions that can be mistaken for significant effects of a study. These studies will also facilitate a better characterization of the interindividual variability in composition, viability and metabolic functionality that may otherwise also act as a confounder in subsequent studies.

3. Conclusions and Future Perspectives

Studies on the gut microbiome protocols report a wide variety in the methods for human fecal sample collection, processing and storage. Only a limited number of studies exist on the actual stability of the fecal gut microbiota under different collection, processing or storage conditions in terms of either the microbial composition, viability or metabolic functionality. The aim of the present mini-review was to present an overview of the currently available data on collection and storage of fecal samples and consequences for stability of the samples, in order to define the requirements for an automated protocol to collect and store human fecal samples for research purposes in order to facilitate the process from toilet to freezer.

At the current state of the art, some tools for human fecal sample collection and processing are already available, such as fecal collection containers with a spoon [87], where processing is later performed in an anaerobic chamber [69]. Although this method is not standardized and is low-throughput, various research laboratories continue using this manual procedure in collecting human fecal materials because of different reasons such as financial (cheaper than machine at current status), time (relatively faster than learning how to use a new machine) and reproducibility (major change in current method decreases comparability with previously obtained results).

An automated protocol is, however, preferable because of the following considerations: (1) Post-defecation conditions are never 100% anaerobic, allowing exposure to air. For an automatic smart toilet combined with vacuum flush [88], this exposure-to-air period may be significantly reduced compared to manual collection by participants without the use of an anaerobic liquid or system [22]; (2) Fecal material processing often takes longer than 1 h after defecation to freezer due to transportation, homogenization and aliquoting [21,22], making it too laborious for a high-throughput study objective. Moreover, afterwards, aliquots need to be thawed, mixed with buffer of choice, centrifuged and filtered before analysis, adding to the extra processing time.

Based on the requirements above and Table 1, a plausible design for an automated fecal collection process is illustrated in Figure 1 and includes the following: (1) toilet with urine and feces separation; (2) once stool is excreted at RT within 10–15 min, stool should be vacuum flushed to the anaerobic chamber [22,54,78,79]; (3) within the anaerobic chamber, temperature should be set to 4 °C when fecal samples are homogenized and aliquoted within ≤1 h [75,76,89,90]; (4) still within the anaerobic chamber, aliquots are transferred to built-in freezer in the same device; (5) transfer of frozen samples to freezer within 10–15 min; (6) usage of −20 °C and −80 °C freezers for short term (2–3 months) and long-term (2 years) storage, respectively; (7) composition should be characterized by at least 16 S RNA analysis but, preferably, by deeper sequencing techniques, viability by flow cytometry

or stool culturing in different conditions and metabolic functionality by an as-yet undefined but generally to be accepted set of fingerprinting metabolic conversions, reflecting the major types of biochemical conversions know to be catalyzed by the intestinal microbiota.
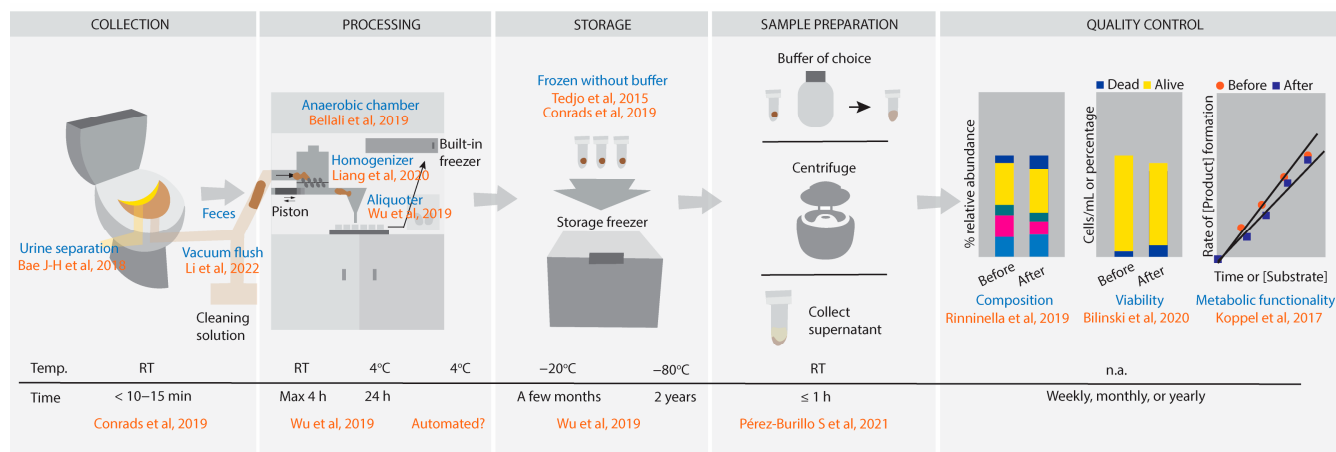

Figure 1. Automated protocol of fecal sample collection from toilet to freezer: collection, processing, storage and quality control [1,21,22,47,55,58,67,74,75,83,91]. The colors in bacterial composition, quality control are meant for illustrative purpose. Colours are only for illustration of different bacterial composition.

Although every study is different and a 'one-size-fits-all' protocol cannot exist [21], an automated protocol for the step of human fecal collection can increase the efficiency and allow gut microbiota studies to recruit more participants. The automated protocol/technology should be compact and portable so that it can be installed in research facilities but also be brought home when participants cannot come to the research facilities. Altogether, the overview of current practices for collection, processing and storage of fecal samples for studies on the composition, viability and metabolic functionality of the human intestinal microbiota, provides guidance of requirements for an automated protocol/technology to ensure fecal microbiota stability across processing and storage conditions.

References

1. Rinninella, E.; Raoul, P.; Cintoni, M.; Franceschi, F.; Miggiano, G.A.D.; Gasbarrini, A.; Mele, M.C. What is the healthy gut microbiota composition? A changing ecosystem across age, environment, diet, and diseases. *Microorganisms* **2019**, *7*, 14. [CrossRef] [PubMed]
2. Haller, D. *The Gut Microbiome in Health and Disease*; Springer: Berlin/Heidelberg, Germany, 2018.
3. Koleva, P.T.; Kim, J.S.; Scott, J.A.; Kozyrskyj, A.L. Microbial programming of health and disease starts during fetal life. *Birth Defects Res. Part C Embryo Today Rev.* **2015**, *105*, 265–277. [CrossRef]
4. Scotti, E.; Boué, S.; Sasso, G.L.; Zanetti, F.; Belcastro, V.; Poussin, C.; Sierro, N.; Battey, J.; Gimalac, A.; Ivanov, N.V. Exploring the microbiome in health and disease: Implications for toxicology. *Toxicol. Res. Appl.* **2017**, *1*, 2397847317741884. [CrossRef]
5. Afzaal, M.; Saeed, F.; Shah, Y.A.; Hussain, M.; Rabail, R.; Socol, C.T.; Hassoun, A.; Pateiro, M.; Lorenzo, J.M.; Rusu, A.V. Human gut microbiota in health and disease: Unveiling the relationship. *Front. Microbiol.* **2022**, *13*, 999001. [CrossRef] [PubMed]
6. Tamanai-Shacoori, Z.; Smida, I.; Bousarghin, L.; Loreal, O.; Meuric, V.; Fong, S.B.; Bonnaure-Mallet, M.; Jolivet-Gougeon, A. Roseburia spp.: A marker of health? *Future Microbiol.* **2017**, *12*, 157–170. [CrossRef]
7. Machiels, K.; Sabino, J.; Vandermosten, L.; Joossens, M.; Arijs, I.; de Bruyn, M.; Eeckhaut, V.; Van Assche, G.; Ferrante, M.; Verhaegen, J. Specific members of the predominant gut microbiota predict pouchitis following colectomy and IPAA in UC. *Gut* **2017**, *66*, 79–88. [CrossRef]
8. Zou, J.; Xiao, Z.; Wu, Y.; Yang, J.; Cui, N. Noninvasive fecal testing for colorectal cancer. *Clin. Chim. Acta* **2022**, *524*, 123–131. [CrossRef]
9. Koppel, N.; Maini Rekdal, V.; Balskus, E.P. Chemical transformation of xenobiotics by the human gut microbiota. *Science* **2017**, *356*, eaag2770. [CrossRef]
10. Yan, S.; Huang, J.; Chen, Z.; Jiang, Z.; Li, X.; Chen, Z. Metabolomics in gut microbiota: Applications and challenges. *Science Bulletin* **2016**, *61*, 1151–1153. [CrossRef]
11. Adak, A.; Khan, M.R. An insight into gut microbiota and its functionalities. *Cell. Mol. Life Sci.* **2019**, *76*, 473–493. [CrossRef]
12. Mullish, B.H.; Pechlivanis, A.; Barker, G.F.; Thursz, M.R.; Marchesi, J.R.; McDonald, J.A. Functional microbiomics: Evaluation of gut microbiota-bile acid metabolism interactions in health and disease. *Methods* **2018**, *149*, 49–58. [CrossRef] [PubMed]
13. Joyce, S.A.; Gahan, C.G. Bile acid modifications at the microbe-host interface: Potential for nutraceutical and pharmaceutical interventions in host health. *Annu. Rev. Food Sci. Technol.* **2016**, *7*, 313–333. [CrossRef]
14. Hara, E. Relationship between obesity, gut microbiome and hepatocellular carcinoma development. *Dig. Dis.* **2015**, *33*, 346–350. [CrossRef] [PubMed]
15. Wewalka, M.; Patti, M.-E.; Barbato, C.; Houten, S.M.; Goldfine, A.B. Fasting serum taurine-conjugated bile acids are elevated in type 2 diabetes and do not change with intensification of insulin. *J. Clin. Endocrinol. Metab.* **2014**, *99*, 1442–1451. [CrossRef] [PubMed]
16. Prinz, P.; Hofmann, T.; Ahnis, A.; Elbelt, U.; Goebel-Stengel, M.; Klapp, B.F.; Rose, M.; Stengel, A. Plasma bile acids show a positive correlation with body mass index and are negatively associated with cognitive restraint of eating in obese patients. *Front. Neurosci.* **2015**, *9*, 199. [CrossRef]
17. Behr, C.; Sperber, S.; Jiang, X.; Strauss, V.; Kamp, H.; Walk, T.; Herold, M.; Beekmann, K.; Rietjens, I.M.C.M.; Van Ravenzwaay, B. Microbiome-related metabolite changes in gut tissue, cecum content and feces of rats treated with antibiotics. *Toxicol. Appl. Pharmacol.* **2018**, *355*, 198–210. [CrossRef]
18. Ley, R.E.; Peterson, D.A.; Gordon, J.I. Ecological and evolutionary forces shaping microbial diversity in the human intestine. *Cell* **2006**, *124*, 837–848. [CrossRef]
19. Giuffrè, M.; Campigotto, M.; Campisciano, G.; Comar, M.; Crocè, L.S. A story of liver and gut microbes: How does the intestinal flora affect liver disease? A review of the literature. *Am. J. Physiol.-Gastrointest. Liver Physiol.* **2020**, *318*, G889–G906. [CrossRef]
20. Chiou, K.L.; Bergey, C.M. Methylation-based enrichment facilitates low-cost, noninvasive genomic scale sequencing of populations from feces. *Sci. Rep.* **2018**, *8*, 1975. [CrossRef]
21. Pérez-Burillo, S.; Molino, S.; Navajas-Porras, B.; Valverde-Moya, Á.J.; Hinojosa-Nogueira, D.; López-Maldonado, A.; Pastoriza, S.; Rufián-Henares, J.Á. An in vitro batch fermentation protocol for studying the contribution of food to gut microbiota composition and functionality. *Nat. Protoc.* **2021**, *16*, 3186–3209. [CrossRef]
22. Wu, W.-K.; Chen, C.-C.; Panyod, S.; Chen, R.-A.; Wu, M.-S.; Sheen, L.-Y.; Chang, S.-C. Optimization of fecal sample processing for microbiome study—The journey from bathroom to bench. *J. Formos. Med. Assoc.* **2019**, *118*, 545–555. [CrossRef]
23. Santiago, A.; Panda, S.; Mengels, G.; Martinez, X.; Azpiroz, F.; Dore, J.; Guarner, F.; Manichanh, C. Processing faecal samples: A step forward for standards in microbial community analysis. *BMC Microbiol.* **2014**, *14*, 112. [CrossRef] [PubMed]
24. Costea, P.I.; Zeller, G.; Sunagawa, S.; Pelletier, E.; Alberti, A.; Levenez, F.; Tramontano, M.; Driessen, M.; Hercog, R.; Jung, F.-E. Towards standards for human fecal sample processing in metagenomic studies. *Nat. Biotechnol.* **2017**, *35*, 1069–1076. [CrossRef] [PubMed]
25. Kassam, Z.; Dubois, N.; Ramakrishna, B.; Ling, K.; Qazi, T.; Smith, M.; Kelly, C.R.; Fischer, M.; Allegretti, J.R.; Budree, S. Donor screening for fecal microbiota transplantation. *N. Engl. J. Med.* **2019**, *381*, 2070–2072. [CrossRef] [PubMed]
26. Chen, J.; Zaman, A.; Ramakrishna, B.; Olesen, S.W. Stool banking for fecal microbiota transplantation: Methods and operations at a large stool bank. *Front. Cell. Infect. Microbiol.* **2021**, *11*, 622949. [CrossRef]

27. van Dongen, K.C.; Belzer, C.; Bakker, W.; Rietjens, I.M.; Beekmann, K. Inter-and Intraindividual Differences in the Capacity of the Human Intestinal Microbiome in Fecal Slurries to Metabolize Fructoselysine and Carboxymethyllysine. *J. Agric. Food Chem.* **2022**, *70*, 11759–11768. [CrossRef]

28. Wang, Q.; Spenkelink, B.; Boonpawa, R.; Rietjens, I.M. Use of physiologically based pharmacokinetic modeling to predict human gut microbial conversion of daidzein to S-Equol. *J. Agric. Food Chem.* **2021**, *70*, 343–352. [CrossRef]

29. Wei, J.; Dai, W.; Pan, X.; Zhong, Y.; Xu, N.; Ye, P.; Wang, J.; Li, J.; Yang, F.; Luo, J. Identifying the Novel Gut Microbial Metabolite Contributing to Metabolic Syndrome in Children Based on Integrative Analyses of Microbiome-Metabolome Signatures. *Microbiol. Spectr.* **2023**, *11*, e03771-22. [CrossRef]

30. Wang, L.; Christophersen, C.T.; Sorich, M.J.; Gerber, J.P.; Angley, M.T.; Conlon, M.A. Low relative abundances of the mucolytic bacterium Akkermansia muciniphila and *Bifidobacterium* spp. in feces of children with autism. *Appl. Environ. Microbiol.* **2011**, *77*, 6718–6721. [CrossRef]

31. Moreno-Indias, I.; Sánchez-Alcoholado, L.; Pérez-Martínez, P.; Andrés-Lacueva, C.; Cardona, F.; Tinahones, F.; Queipo-Ortuño, M.I. Red wine polyphenols modulate fecal microbiota and reduce markers of the metabolic syndrome in obese patients. *Food Funct.* **2016**, *7*, 1775–1787. [CrossRef]

32. Bartosch, S.; Fite, A.; Macfarlane, G.T.; McMurdo, M.E. Characterization of bacterial communities in feces from healthy elderly volunteers and hospitalized elderly patients by using real-time PCR and effects of antibiotic treatment on the fecal microbiota. *Appl. Environ. Microbiol.* **2004**, *70*, 3575–3581. [CrossRef] [PubMed]

33. Fernandes, J.; Wang, A.; Su, W.; Rozenbloom, S.R.; Taibi, A.; Comelli, E.M.; Wolever, T.M. Age, dietary fiber, breath methane, and fecal short chain fatty acids are interrelated in Archaea-positive humans. *J. Nutr.* **2013**, *143*, 1269–1275. [CrossRef] [PubMed]

34. Wong, M.C.; Ching, J.Y.; Chan, V.C.; Lam, T.Y.; Shum, J.P.; Luk, A.K.; Wong, S.S.; Ng, S.C.; Ng, S.S.; Wu, J.C. Diagnostic accuracy of a qualitative fecal immunochemical test varies with location of neoplasia but not number of specimens. *Clin. Gastroenterol. Hepatol.* **2015**, *13*, 1472–1479. [CrossRef] [PubMed]

35. Levi, Z.; Rozen, P.; Hazazi, R.; Vilkin, A.; Waked, A.; Maoz, E.; Birkenfeld, S.; Leshno, M.; Niv, Y. A quantitative immunochemical fecal occult blood test for colorectal neoplasia. *Ann. Intern. Med.* **2007**, *146*, 244–255. [CrossRef]

36. Karu, N.; Deng, L.; Slae, M.; Guo, A.C.; Sajed, T.; Huynh, H.; Wine, E.; Wishart, D.S. A review on human fecal metabolomics: Methods, applications and the human fecal metabolome database. *Anal. Chim. Acta* **2018**, *1030*, 1–24. [CrossRef]

37. Kaisar, M.M.; Brienen, E.A.; Djuardi, Y.; Sartono, E.; Yazdanbakhsh, M.; Verweij, J.J.; Supali, T.; Van Lieshout, L. Improved diagnosis of Trichuris trichiura by using a bead-beating procedure on ethanol preserved stool samples prior to DNA isolation and the performance of multiplex real-time PCR for intestinal parasites. *Parasitology* **2017**, *144*, 965–974. [CrossRef]

38. Hashemi, S.; Han, M.; Kim, T.; Kim, Y. (Eds.) Innovative toilet technologies for smart and green cities. In Proceedings of the 8th Conference International Forum on Urbanism (IFoU), Incheon, Republic of Korea, 2–24 June 2015.

39. Magri, M.E.; Philippi, L.S.r.; Vinnerås, B. Inactivation of pathogens in feces by desiccation and urea treatment for application in urine-diverting dry toilets. *Appl. Environ. Microbiol.* **2013**, *79*, 2156–2163. [CrossRef]

40. Vinnerås, B.; Jönsson, H. The performance and potential of faecal separation and urine diversion to recycle plant nutrients in household wastewater. *Bioresour. Technol.* **2002**, *84*, 275–282. [CrossRef]

41. Zakaria, F.; Ćurko, J.; Muratbegovic, A.; Garcia, H.A.; Hooijmans, C.M.; Brdjanovic, D. Evaluation of a smart toilet in an emergency camp. *Int. J. Disaster Risk Reduct.* **2018**, *27*, 512–523. [CrossRef]

42. Mbonu, C.; Kilanko, O.; Kilanko, M.; Babalola, P. Smart Toilets and Toilet Gadgets in Sustainable Smart Cities: An Overview of Personal Health Monitoring. In *Advanced Manufacturing in Biological, Petroleum, and Nanotechnology Processing: Application Tools for Design, Operation, Cost Management, and Environmental Remediation*; Springer: Berlin/Heidelberg, Germany, 2022; pp. 143–156.

43. Eom, Y.S.; Oh, H.; Cho, J.; Kim, J. Social acceptance and willingness to pay for a smart Eco-toilet system producing a Community-based bioenergy in Korea. *Sustain. Energy Technol. Assess.* **2021**, *47*, 101400. [CrossRef]

44. Zhang, Z.; Shi, Q.; He, T.; Guo, X.; Dong, B.; Lee, J.; Lee, C. Artificial intelligence of toilet (AI-Toilet) for an integrated health monitoring system (IHMS) using smart triboelectric pressure sensors and image sensor. *Nano Energy* **2021**, *90*, 106517. [CrossRef]

45. Ge, T.J.; Chan, C.T.; Lee, B.J.; Liao, J.C.; Park, S.-m. Smart toilets for monitoring COVID-19 surges: Passive diagnostics and public health. *NPJ Digit. Med.* **2022**, *5*, 39. [CrossRef]

46. Park, S.-m.; Won, D.D.; Lee, B.J.; Escobedo, D.; Esteva, A.; Aalipour, A.; Ge, T.J.; Kim, J.H.; Suh, S.; Choi, E.H. A mountable toilet system for personalized health monitoring via the analysis of excreta. *Nat. Biomed. Eng.* **2020**, *4*, 624–635. [CrossRef] [PubMed]

47. Bae, J.-H.; Lee, H.-K. User health information analysis with a urine and feces separable smart toilet system. *IEEE Access* **2018**, *6*, 78751–78765. [CrossRef]

48. Shafik, A. A concept of the anatomy of the anal sphincter mechanism and the physiology of defecation. *Dis. Colon Rectum* **1987**, *30*, 970–982. [CrossRef] [PubMed]

49. Mathieson, W.; Sanchez, I.; Mommaerts, K.; Frasquilho, S.; Betsou, F. An independent evaluation of the CryoXtract Instruments' CXT350 frozen sample aliquotter using tissue and fecal biospecimens. *Biopreserv. Biobank.* **2016**, *14*, 2–8. [CrossRef] [PubMed]

50. Papanicolas, L.E.; Choo, J.M.; Wang, Y.; Leong, L.E.; Costello, S.P.; Gordon, D.L.; Wesselingh, S.L.; Rogers, G.B. Bacterial viability in faecal transplants: Which bacteria survive? *EBioMedicine* **2019**, *41*, 509–516. [CrossRef]

51. Salonen, A.; Nikkilä, J.; Jalanka-Tuovinen, J.; Immonen, O.; Rajilić-Stojanović, M.; Kekkonen, R.A.; Palva, A.; de Vos, W.M. Comparative analysis of fecal DNA extraction methods with phylogenetic microarray: Effective recovery of bacterial and archaeal DNA using mechanical cell lysis. *J. Microbiol. Methods* **2010**, *81*, 127–134. [CrossRef]

52. Gorzelak, M.A.; Gill, S.K.; Tasnim, N.; Ahmadi-Vand, Z.; Jay, M.; Gibson, D.L. Methods for improving human gut microbiome data by reducing variability through sample processing and storage of stool. *PLoS ONE* **2015**, *10*, e0134802. [CrossRef]

53. Wu, G.D.; Lewis, J.D.; Hoffmann, C.; Chen, Y.-Y.; Knight, R.; Bittinger, K.; Hwang, J.; Chen, J.; Berkowsky, R.; Nessel, L. Sampling and pyrosequencing methods for characterizing bacterial communities in the human gut using 16S sequence tags. *BMC Microbiol.* **2010**, *10*, 206. [CrossRef]

54. Wesolowska-Andersen, A.; Bahl, M.I.; Carvalho, V.; Kristiansen, K.; Sicheritz-Pontén, T.; Gupta, R.; Licht, T.R. Choice of bacterial DNA extraction method from fecal material influences community structure as evaluated by metagenomic analysis. *Microbiome* **2014**, *2*, 19. [CrossRef] [PubMed]

55. Liang, Y.; Dong, T.; Chen, M.; He, L.; Wang, T.; Liu, X.; Chang, H.; Mao, J.-H.; Hang, B.; Snijders, A.M. Systematic analysis of impact of sampling regions and storage methods on fecal gut microbiome and metabolome profiles. *Msphere* **2020**, *5*, e00763-00719. [CrossRef] [PubMed]

56. Amarenco, G. Bristol Stool Chart: Prospective and monocentric study of "stools introspection" in healthy subjects. *Prog. En Urol. J. De L'association Fr. D'urologie Et De La Soc. Fr. D'urologie* **2014**, *24*, 708–713.

57. Irmscher, S.B.; Gibis, M.; Herrmann, K.; Kohlus, R.; Weiss, J. Development of a novel homogenizer using the vane pump-grinder technology for the production of meat batter. *J. Food Eng.* **2016**, *169*, 10–17. [CrossRef]

58. Bellali, S.; Lagier, J.-C.; Raoult, D.; Bou Khalil, J. Among live and dead bacteria, the optimization of sample collection and processing remains essential in recovering gut microbiota components. *Front. Microbiol.* **2019**, *10*, 1606. [CrossRef]

59. Lehne, G.; Müller, A.; Schwedes, J. Mechanical disintegration of sewage sludge. *Water Sci. Technol.* **2001**, *43*, 19–26. [CrossRef]

60. Loesche, W.J. Oxygen sensitivity of various anaerobic bacteria. *Appl. Microbiol.* **1969**, *18*, 723–727. [CrossRef]

61. Finegold, S.M. Anaerobic infections in humans: An overview. *Anaerobe* **1995**, *1*, 3–9. [CrossRef]

62. Van der Waaij, L.; Mesander, G.; Limburg, P.; Van der Waaij, D. Direct flow cytometry of anaerobic bacteria in human feces. *Cytom. J. Int. Soc. Anal. Cytol.* **1994**, *16*, 270–279. [CrossRef]

63. Marteau, P.; Pochart, P.; Doré, J.; Béra-Maillet, C.; Bernalier, A.; Corthier, G. Comparative study of bacterial groups within the human cecal and fecal microbiota. *Appl. Environ. Microbiol.* **2001**, *67*, 4939–4942. [CrossRef]

64. Heilig, H.G.; Zoetendal, E.G.; Vaughan, E.E.; Marteau, P.; Akkermans, A.D.; de Vos, W.M. Molecular diversity of *Lactobacillus* spp. and other lactic acid bacteria in the human intestine as determined by specific amplification of 16S ribosomal DNA. *Appl. Environ. Microbiol.* **2002**, *68*, 114–123. [CrossRef] [PubMed]

65. Vogtmann, E.; Chen, J.; Amir, A.; Shi, J.; Abnet, C.C.; Nelson, H.; Knight, R.; Chia, N.; Sinha, R. Comparison of collection methods for fecal samples in microbiome studies. *Am. J. Epidemiol.* **2017**, *185*, 115–123. [CrossRef] [PubMed]

66. Schwintner, C.; Affagard, H.; Joël, D. Microorganism Sampling Method, Microorganism Sampling Device and Sampling Kit Comprising Such a Sampling Device. U.S. Patent 11,013,498, 25 May 2021.

67. Li, P.; Zhang, T.T.; Zhang, Y. Measuring the flushing-generated flow and aerosols in lavatory of commercial aircraft. *Build. Environ.* **2022**, *214*, 108948. [CrossRef]

68. Postgate, J.; Hunter, J. On the survival of frozen bacteria. *Microbiology* **1961**, *26*, 367–378. [CrossRef] [PubMed]

69. Burz, S.D.; Abraham, A.-L.; Fonseca, F.; David, O.; Chapron, A.; Béguet-Crespel, F.; Cénard, S.; Le Roux, K.; Patrascu, O.; Levenez, F. A guide for ex vivo handling and storage of stool samples intended for fecal microbiota transplantation. *Sci. Rep.* **2019**, *9*, 8897. [CrossRef] [PubMed]

70. Achá, S.; Kühn, I.; Mbazima, G.; Colque-Navarro, P.; Möllby, R. Changes of viability and composition of the Escherichia coli flora in faecal samples during long time storage. *J. Microbiol. Methods* **2005**, *63*, 229–238. [CrossRef]

71. Tap, J.; Cools-Portier, S.; Pavan, S.; Druesne, A.; Öhman, L.; Törnblom, H.; Simren, M.; Derrien, M. Effects of the long-term storage of human fecal microbiota samples collected in RNAlater. *Sci. Rep.* **2019**, *9*, 601. [CrossRef]

72. Goldman, S.L.; Sanders, J.G.; Yan, W.; Denice, A.; Cornwall, M.; Ivey, K.N.; Taylor, E.N.; Gunderson, A.R.; Sheehan, M.J.; Mjungu, D. Culture-enriched community profiling improves resolution of the vertebrate gut microbiota. *Mol. Ecol. Resour.* **2022**, *22*, 122–136. [CrossRef]

73. Hale, V.L.; Tan, C.L.; Knight, R.; Amato, K.R. Effect of preservation method on spider monkey (*Ateles geoffroyi*) fecal microbiota over 8 weeks. *J. Microbiol. Methods* **2015**, *113*, 16–26. [CrossRef]

74. Conrads, G.; Abdelbary, M.M. Challenges of next-generation sequencing targeting anaerobes. *Anaerobe* **2019**, *58*, 47–52. [CrossRef]

75. Tedjo, D.I.; Jonkers, D.M.; Savelkoul, P.H.; Masclee, A.A.; van Best, N.; Pierik, M.J.; Penders, J. The effect of sampling and storage on the fecal microbiota composition in healthy and diseased subjects. *PLoS ONE* **2015**, *10*, e0126685. [CrossRef]

76. Choo, J.M.; Leong, L.E.; Rogers, G.B. Sample storage conditions significantly influence faecal microbiome profiles. *Sci. Rep.* **2015**, *5*, 16350. [CrossRef]

77. Hisada, T.; Endoh, K.; Kuriki, K. Inter- and intra-individual variations in seasonal and daily stabilities of the human gut microbiota in Japanese. *Arch. Microbiol.* **2015**, *197*, 919–934. [CrossRef]

78. Carroll, I.M.; Ringel-Kulka, T.; Siddle, J.P.; Klaenhammer, T.R.; Ringel, Y. Characterization of the fecal microbiota using high-throughput sequencing reveals a stable microbial community during storage. *PLoS ONE* **2012**, *7*, e46953. [CrossRef] [PubMed]

79. Dore, J.; Ehrlich, S.; Levenez, F.; Pelletier, E.; Alberti, A.; Bertrand, L.; Bork, P.; Costea, P.; Sunagawa, S.; Guarner, F. IHMS Sop 02 V1: Standard operating procedure for fecal samples self-collection. *Int. Hum. Microbiome Stand* **2015**, *2*, 1–13.

80. Song, S.J.; Amir, A.; Metcalf, J.L.; Amato, K.R.; Xu, Z.Z.; Humphrey, G.; Knight, R. Preservation methods differ in fecal microbiome stability, affecting suitability for field studies. *mSystems* **2016**, *1*, e00021-16. [CrossRef] [PubMed]

81. Kennedy, N.A.; Walker, A.W.; Berry, S.H.; Duncan, S.H.; Farquarson, F.M.; Louis, P.; Thomson, J.M.; Consortium, U.I.G.; Satsangi, J.; Flint, H.J.; et al. The impact of different DNA extraction kits and laboratories upon the assessment of human gut microbiota composition by 16S rRNA gene sequencing. *PLoS ONE* **2014**, *9*, e88982. [CrossRef]

82. Shah, N.; Tang, H.; Doak, T.G.; Ye, Y. Comparing bacterial communities inferred from 16S rRNA gene sequencing and shotgun metagenomics. In *Pacific Symposium on Biocomputing 2011*; Altman, R.B., Dunker, A.K., Hunter, L., Murray, T.A., Klein, T.E., Eds.; World Scientific: Kohala Coast, HI, USA, 2011; pp. 165–176. [CrossRef]

83. Bilinski, J.; Dziurzynski, M.; Grzesiowski, P.; Podsiadly, E.; Stelmaszczyk-Emmel, A.; Dzieciatkowski, T.; Dziewit, L.; Basak, G.W. Multimodal approach to assessment of Fecal Microbiota donors based on three complementary methods. *J. Clin. Med.* **2020**, *9*, 2036. [CrossRef]

84. Wilson, I.D.; Nicholson, J.K. Gut microbiome interactions with drug metabolism, efficacy, and toxicity. *Transl. Res.* **2017**, *179*, 204–222. [CrossRef]

85. Zierer, J.; Jackson, M.A.; Kastenmüller, G.; Mangino, M.; Long, T.; Telenti, A.; Mohney, R.P.; Small, K.S.; Bell, J.T.; Steves, C.J. The fecal metabolome as a functional readout of the gut microbiome. *Nat. Genet.* **2018**, *50*, 790–795. [CrossRef]

86. Vandeputte, D.; Tito, R.Y.; Vanleeuwen, R.; Falony, G.; Raes, J. Practical considerations for large-scale gut microbiome studies. *FEMS Microbiol. Rev.* **2017**, *41* (Suppl. S1), S154–S167. [CrossRef] [PubMed]

87. Mathay, C.; Hamot, G.; Henry, E.; Georges, L.; Bellora, C.; Lebrun, L.; de Witt, B.; Ammerlaan, W.; Buschart, A.; Wilmes, P.; et al. Method optimization for fecal sample collection and fecal DNA extraction. *Biopreserv. Biobank.* **2015**, *13*, 79–93. [CrossRef]

88. Otterpohl, R. Options for alternative types of sewerage and treatment systems directed to improvement of the overall performance. *Water Sci. Technol.* **2002**, *45*, 149–158. [CrossRef] [PubMed]

89. Kim, D.; Hofstaedter, C.E.; Zhao, C.; Mattei, L.; Tanes, C.; Clarke, E.; Lauder, A.; Sherrill-Mix, S.; Chehoud, C.; Kelsen, J. Optimizing methods and dodging pitfalls in microbiome research. *Microbiome* **2017**, *5*, 52. [CrossRef] [PubMed]

90. Franzosa, E.A.; Morgan, X.C.; Segata, N.; Waldron, L.; Reyes, J.; Earl, A.M.; Giannoukos, G.; Boylan, M.R.; Ciulla, D.; Gevers, D. Relating the metatranscriptome and metagenome of the human gut. *Proc. Natl. Acad. Sci. USA* **2014**, *111*, E2329–E2338. [CrossRef]

91. Bikov, A.; Szabo, H.; Piroska, M.; Kunos, L.; Szily, M.; Ligeti, B.; Makra, N.; Szabo, D.; Tarnoki, D.L.; Tarnoki, A.D. Gut Microbiome in Patients with Obstructive Sleep Apnoea. *Appl. Sci.* **2022**, *12*, 2007. [CrossRef]

92. Doumatey, A.P.; Adeyemo, A.; Zhou, J.; Lei, L.; Adebamowo, S.N.; Adebamowo, C.; Rotimi, C.N. Gut microbiome profiles are associated with type 2 diabetes in urban Africans. *Front. Cell. Infect. Microbiol.* **2020**, *10*, 63. [CrossRef]

93. Ogilvie, L.A.; Jones, B.V. Dysbiosis modulates capacity for bile acid modification in the gut microbiomes of patients with inflammatory bowel disease: A mechanism and marker of disease? *Gut* **2012**, *61*, 1642–1643. [CrossRef] [PubMed]

94. Hustoft, T.; Hausken, T.; Ystad, S.; Valeur, J.; Brokstad, K.; Hatlebakk, J.; Lied, G.A. Effects of varying dietary content of fermentable short-chain carbohydrates on symptoms, fecal microenvironment, and cytokine profiles in patients with irritable bowel syndrome. *Neurogastroenterol. Motil.* **2017**, *29*, e12969. [CrossRef]

95. Landini, L.; Dadson, P.; Gallo, F.; Honka, M.-J.; Cena, H. Microbiota in Anorexia Nervosa–Potential for Treatment. *Nutr. Res. Rev.* **2022**, 1–51. [CrossRef]

96. Ruiz, A.; Cerdó, T.; Jáuregui, R.; Pieper, D.H.; Marcos, A.; Clemente, A.; García, F.; Margolles, A.; Ferrer, M.; Campoy, C.; et al. One-year calorie restriction impacts gut microbial composition but not its metabolic performance in obese adolescents. *Environ. Microbiol.* **2017**, *19*, 1536–1551. [CrossRef]

97. Zhang, Y.-K.; Zhang, Q.; Wang, Y.-L.; Zhang, W.-Y.; Hu, H.-Q.; Wu, H.-Y.; Sheng, X.-Z.; Luo, K.-J.; Zhang, H.; Wang, M.; et al. A Comparison study of age and colorectal cancer-related gut bacteria. *Front. Cell. Infect. Microbiol.* **2021**, *11*, 606490. [CrossRef]

98. Zhuang, Z.-Q.; Shen, L.-L.; Li, W.-W.; Fu, X.; Zeng, F.; Gui, L.; Lü, Y.; Cai, M.; Zhu, C.; Tan, Y.-L.; et al. Gut microbiota is altered in patients with Alzheimer's disease. *J. Alzheimers Dis.* **2018**, *63*, 1337–1346. [CrossRef]

99. Ding, H.; Yi, X.; Zhang, X.; Wang, H.; Liu, H.; Mou, W.-W. Imbalance in the gut microbiota of children with autism spectrum disorders. *Front. Cell. Infect. Microbiol.* **2021**, *11*, 572752. [CrossRef]

100. Li, Z.; Lu, G.; Li, Z.; Wu, B.; Luo, E.; Qiu, X.; Guo, J.; Xia, Z.; Zheng, C.; Su, Q.; et al. Altered actinobacteria and firmicutes phylum associated epitopes in patients with Parkinson's disease. *Front. Immunol.* **2021**, *12*, 632482. [CrossRef]

101. Otaka, M.; Kikuchi-Hayakawa, H.; Ogura, J.; Ishikawa, H.; Yomogida, Y.; Ota, M.; Hidese, S.; Ishida, I.; Aida, M.; Matsuda, K.; et al. Effect of *Lacticaseibacillus paracasei* strain Shirota on improvement in depressive symptoms, and its association with abundance of Actinobacteria in gut microbiota. *Microorganisms* **2021**, *9*, 1026. [CrossRef]

102. Jia, W.; Rajani, C.; Kaddurah-Daouk, R.; Li, H. Expert insights: The potential role of the gut microbiome-bile acid-brain axis in the development and progression of Alzheimer's disease and hepatic encephalopathy. *Med. Res. Rev.* **2020**, *40*, 1496–1507. [CrossRef]

103. Valentini, F.; Evangelisti, M.; Arpinelli, M.; Di Nardo, G.; Borro, M.; Simmaco, M.; Villa, M.P. Gut microbiota composition in children with obstructive sleep apnoea syndrome: A pilot study. *Sleep Med.* **2020**, *76*, 140–147. [CrossRef] [PubMed]

104. Larsen, N.; Vogensen, F.K.; Van Den Berg, F.W.; Nielsen, D.S.; Andreasen, A.S.; Pedersen, B.K.; Al-Soud, W.A.; Sørensen, S.J.; Hansen, L.H.; Jakobsen, M. Gut microbiota in human adults with type 2 diabetes differs from non-diabetic adults. *PLoS ONE* **2010**, *5*, e9085. [CrossRef] [PubMed]

105. Knox, N.C.; Forbes, J.D.; Peterson, C.-L.; Van Domselaar, G.; Bernstein, C.N. The gut microbiome in inflammatory bowel disease: Lessons learned from other immune-mediated inflammatory diseases. *Off. J. Am. Coll. Gastroenterol. ACG* **2019**, *114*, 1051–1070. [CrossRef] [PubMed]

106. Duan, R.; Zhu, S.; Wang, B.; Duan, L. Alterations of gut microbiota in patients with irritable bowel syndrome based on 16S rRNA-targeted sequencing: A systematic review. *Clin. Transl. Gastroenterol.* **2019**, *10*, e00012. [CrossRef]

107. Wan, Y.; Yuan, J.; Li, J.; Li, H.; Yin, K.; Wang, F.; Li, D. Overweight and underweight status are linked to specific gut microbiota and intestinal tricarboxylic acid cycle intermediates. *Clin. Nutr.* **2020**, *39*, 3189–3198. [CrossRef]

108. Xu, P.; Li, M.; Zhang, J.; Zhang, T. Correlation of intestinal microbiota with overweight and obesity in Kazakh school children. *BMC Microbiol.* **2012**, *12*, 283. [CrossRef]

109. Gagnière, J.; Raisch, J.; Veziant, J.; Barnich, N.; Bonnet, R.; Buc, E.; Bringer, M.-A.; Pezet, D.; Bonnet, M. Gut microbiota imbalance and colorectal cancer. *World J. Gastroenterol.* **2016**, *22*, 501–518. [CrossRef]

110. Doifode, T.; Giridharan, V.V.; Generoso, J.S.; Bhatti, G.; Collodel, A.; Schulz, P.E.; Forlenza, O.V.; Barichello, T. The impact of the microbiota-gut-brain axis on Alzheimer's disease pathophysiology. *Pharmacol. Res.* **2021**, *164*, 105314. [CrossRef]

111. Strati, F.; Cavalieri, D.; Albanese, D.; De Felice, C.; Donati, C.; Hayek, J.; Jousson, O.; Leoncini, S.; Renzi, D.; Calabrò, A.; et al. New evidences on the altered gut microbiota in autism spectrum disorders. *Microbiome* **2017**, *5*, 24. [CrossRef]

112. Lin, C.-H.; Chen, C.-C.; Chiang, H.-L.; Liou, J.-M.; Chang, C.-M.; Lu, T.-P.; Chuang, E.Y.; Tai, Y.-C.; Cheng, C.; Lin, H.-Y.; et al. Altered gut microbiota and inflammatory cytokine responses in patients with Parkinson's disease. *J. Neuroinflammation* **2019**, *16*, 129. [CrossRef]

113. Barandouzi, Z.A.; Starkweather, A.R.; Henderson, W.A.; Gyamfi, A.; Cong, X.S. Altered composition of gut microbiota in depression: A systematic review. *Front. Psychiatry* **2020**, *11*, 541. [CrossRef]

114. Sung, C.M.; Lin, Y.-F.; Chen, K.-F.; Ke, H.-M.; Huang, H.-Y.; Gong, Y.-N.; Tsai, W.-S.; You, J.-F.; Lu, M.J.; Cheng, H.-T.; et al. Predicting clinical outcomes of cirrhosis patients with hepatic encephalopathy from the fecal microbiome. *Cell. Mol. Gastroenterol. Hepatol.* **2019**, *8*, 301–318.e2. [CrossRef]

115. James, M.M.; Pal, N.; Sharma, P.; Kumawat, M.; Shubham, S.; Verma, V.; Tiwari, R.R.; Singh, B.; Nagpal, R.; Sarma, D.K.; et al. Role of butyrogenic Firmicutes in type-2 diabetes. *J. Diabetes Metab. Disord.* **2022**, *21*, 1873–1882. [CrossRef]

116. Matsuoka, K.; Kanai, T. (Eds.) The gut microbiota and inflammatory bowel disease. In *Semin in Immunopathol*; Springer: Berlin/Heidelberg, Germany, 2015.

117. Kassinen, A.; Krogius-Kurikka, L.; Mäkivuokko, H.; Rinttilä, T.; Paulin, L.; Corander, J.; Malinen, E.; Apajalahti, J.; Palva, A. The fecal microbiota of irritable bowel syndrome patients differs significantly from that of healthy subjects. *Gastroenterology* **2007**, *133*, 24–33. [CrossRef] [PubMed]

118. Koliada, A.; Syzenko, G.; Moseiko, V.; Budovska, L.; Puchkov, K.; Perederiy, V.; Gavalko, Y.; Dorofeyev, A.; Romanenko, M.; Tkach, S.; et al. Association between body mass index and Firmicutes/Bacteroidetes ratio in an adult Ukrainian population. *BMC Microbiol.* **2017**, *17*, 120. [CrossRef] [PubMed]

119. Turnbaugh, P.J.; Ley, R.E.; Mahowald, M.A.; Magrini, V.; Mardis, E.R.; Gordon, J.I. An obesity-associated gut microbiome with increased capacity for energy harvest. *Nature* **2006**, *444*, 1027–1031. [CrossRef]

120. Wang, T.; Cai, G.; Qiu, Y.; Fei, N.; Zhang, M.; Pang, X.; Jia, W.; Cai, S.; Zhao, L. Structural segregation of gut microbiota between colorectal cancer patients and healthy volunteers. *ISME J.* **2012**, *6*, 320–329. [CrossRef]

121. Vogt, N.M.; Kerby, R.L.; Dill-McFarland, K.A.; Harding, S.J.; Merluzzi, A.P.; Johnson, S.C.; Carlsson, C.M.; Asthana, S.; Zetterberg, H.; Blennow, K.; et al. Gut microbiome alterations in Alzheimer's disease. *Sci. Rep.* **2017**, *7*, 13537. [CrossRef]

122. Li, Y.; Li, R.; Du, Y.; Xu, X.; Xue, Y.; Gao, D.; Gao, T.; Sheng, Z.; Zhang, L.; Tuo, H. Features of gut microbiota in patients with idiopathic Parkinson's disease. *Zhonghua Yi Xue Za Zhi* **2020**, *100*, 1017–1022.

123. Huang, Y.; Shi, X.; Li, Z.; Shen, Y.; Shi, X.; Wang, L.; Li, G.; Yuan, Y.; Wang, J.; Zhang, Y.; et al. Possible association of Firmicutes in the gut microbiota of patients with major depressive disorder. *Neuropsychiatr. Dis. Treat.* **2018**, 3329–3337. [CrossRef]

124. Zuo, Z.; Fan, H.; Tang, X.D.; Chen, Y.M.; Xun, L.T.; Li, Y.; Song, Z.; Zhai, H. Effect of different treatments and alcohol addiction on gut microbiota in minimal hepatic encephalopathy patients. *Exp. Ther. Med.* **2017**, *14*, 4887–4895. [CrossRef]

125. Li, Q.; Xu, T.; Shao, C.; Gao, W.; Wang, M.; Dong, Y.; Wang, X.; Lu, F.; Li, D.; Tan, H.; et al. Obstructive sleep apnea is related to alterations in fecal microbiome and impaired intestinal barrier function. *Sci. Rep.* **2023**, *13*, 778. [CrossRef]

126. Wei, B.; Wang, Y.; Xiang, S.; Jiang, Y.; Chen, R.; Hu, N. Alterations of gut microbiome in patients with type 2 diabetes mellitus who had undergone cholecystectomy. *Am. J. Physiol.-Endocrinol. Metab.* **2021**, *320*, E113–E121. [CrossRef]

127. Sheehan, D.; Moran, C.; Shanahan, F. The microbiota in inflammatory bowel disease. *J. Gastroenterol.* **2015**, *50*, 495–507. [CrossRef] [PubMed]

128. Mei, L.; Zhou, J.; Su, Y.; Mao, K.; Wu, J.; Zhu, C.; He, L.; Cui, Y. Gut microbiota composition and functional prediction in diarrhea-predominant irritable bowel syndrome. *BMC Gastroenterol.* **2021**, *21*, 105. [CrossRef] [PubMed]

129. Gao, X.; Zhang, M.; Xue, J.; Huang, J.; Zhuang, R.; Zhou, X.; Zhang, H.; Fu, Q.; Hao, Y. Body mass index differences in the gut microbiota are gender specific. *Front. Microbiol.* **2018**, *9*, 1250. [CrossRef] [PubMed]

130. Crovesy, L.; Masterson, D.; Rosado, E.L. Profile of the gut microbiota of adults with obesity: A systematic review. *Eur. J. Clin. Nutr.* **2020**, *74*, 1251–1262. [CrossRef] [PubMed]

131. Vogtmann, E.; Hua, X.; Zeller, G.; Sunagawa, S.; Voigt, A.Y.; Hercog, R.; Goedert, J.J.; Shi, J.; Bork, P.; Sinha, R. Colorectal cancer and the human gut microbiome: Reproducibility with whole-genome shotgun sequencing. *PLoS ONE* **2016**, *11*, e0155362. [CrossRef]

132. Bello-Medina, P.C.; Hernández-Quiroz, F.; Pérez-Morales, M.; González-Franco, D.A.; Cruz-Pauseno, G.; García-Mena, J.; Díaz-Cintra, S.; Pacheco-López, G. Spatial memory and gut microbiota alterations are already present in early adulthood in a pre-clinical transgenic model of Alzheimer's disease. *Front. Neurosci.* **2021**, *15*, 595583. [CrossRef]

133. Ho, L.K.H.; Tong, V.J.W.; Syn, N.; Nagarajan, N.; Tham, E.H.; Tay, S.K.; Shorey, S.; Tambyah, P.A.; Law, E.C.N. Gut microbiota changes in children with autism spectrum disorder: A systematic review. *Gut Pathog.* **2020**, *12*, 6. [CrossRef]

134. Lin, A.; Zheng, W.; He, Y.; Tang, W.; Wei, X.; He, R.; Huang, W.; Su, Y.; Huang, Y.; Zhou, H.; et al. Gut microbiota in patients with Parkinson's disease in southern China. *Park. Relat. Disord.* **2018**, *53*, 82–88. [CrossRef]

135. Rai, R.; Saraswat, V.A.; Dhiman, R.K. Gut microbiota: Its role in hepatic encephalopathy. *J. Clin. Exp. Hepatol.* **2015**, *5*, S29–S36. [CrossRef]

136. Zhang, Z.; Tian, T.; Chen, Z.; Liu, L.; Luo, T.; Dai, J. Characteristics of the gut microbiome in patients with prediabetes and type 2 diabetes. *PeerJ* **2021**, *9*, e10952. [CrossRef]

137. Shin, N.-R.; Whon, T.W.; Bae, J.-W. Proteobacteria: Microbial signature of dysbiosis in gut microbiota. *Trends Biotechnol.* **2015**, *33*, 496–503. [CrossRef] [PubMed]

138. Barandouzi, Z.A.; Lee, J.; del Carmen Rosas, M.; Chen, J.; Henderson, W.A.; Starkweather, A.R.; Cong, X.S. Associations of neurotransmitters and the gut microbiome with emotional distress in mixed type of irritable bowel syndrome. *Sci. Rep.* **2022**, *12*, 1648. [CrossRef] [PubMed]

139. Huey, S.L.; Jiang, L.; Fedarko, M.W.; McDonald, D.; Martino, C.; Ali, F.; Russell, D.G.; Udipi, S.A.; Thorat, A.; Thakker, V.; et al. Nutrition and the gut microbiota in 10- to 18-month-old children living in urban slums of Mumbai, India. *Msphere* **2020**, *5*, e00731-20. [CrossRef]

140. Abdullah, B.; Daud, S.; Aazmi, M.S.; Idorus, M.Y.; Mahamooth, M.I.J. Gut microbiota in pregnant Malaysian women: A comparison between trimesters, body mass index and gestational diabetes status. *BMC Pregnancy Childbirth* **2022**, *22*, 152. [CrossRef] [PubMed]

141. Liu, W.; Zhang, R.; Shu, R.; Yu, J.; Li, H.; Long, H.; Jin, S.; Li, S.; Hu, Q.; Yao, F.; et al. Study of the relationship between microbiome and colorectal cancer susceptibility using 16SrRNA sequencing. *BioMed Res. Int.* **2020**, *2020*, 7828392. [CrossRef]

142. Franceschi, F.; Ojetti, V.; Candelli, M.; Covino, M.; Cardone, S.; Potenza, A.; Simeoni, B.; Gabrielli, M.; Sabia, L.; Gasbarrini, G.; et al. Microbes and Alzheimer'disease: Lessons from *H. pylori* and GUT microbiota. *Eur. Rev. Med. Pharmacol. Sci.* **2019**, *23*, 426–430.

143. Plaza-Díaz, J.; Gómez-Fernández, A.; Chueca, N.; Torre-Aguilar MJdl Gil, Á.; Perez-Navero, J.L.; Flores-Rojas, K.; Martín-Borreguero, P.; Solis-Urra, P.; Ruiz-Ojeda, F.J.; Garcia, F.; et al. Autism spectrum disorder (ASD) with and without mental regression is associated with changes in the fecal microbiota. *Nutrients* **2019**, *11*, 337. [CrossRef]

144. Zapała, B.; Stefura, T.; Wójcik-Pędziwiatr, M.; Kabut, R.; Bałajewicz-Nowak, M.; Milewicz, T.; Dudek, A.; Stój, A.; Rudzińska-Bar, M. Differences in the composition of gut microbiota between patients with parkinson's disease and healthy controls: A cohort study. *J. Clin. Med.* **2021**, *10*, 5698. [CrossRef]

145. Simpson, C.A.; Mu, A.; Haslam, N.; Schwartz, O.S.; Simmons, J.G. Feeling down? A systematic review of the gut microbiota in anxiety/depression and irritable bowel syndrome. *J. Affect. Disord.* **2020**, *266*, 429–446. [CrossRef]

146. Galli, J.; Calò, L.; Posteraro, B.; Rossi, G.; Sterbini, F.P.; Paludetti, G.; Sanguinetti, M. Pediatric oropharyngeal microbiome: Mapping in chronic tonsillitis and tonsillar hypertrophy. *Int. J. Pediatr. Otorhinolaryngol.* **2020**, *139*, 110478. [CrossRef]

147. Zhang, F.; Wang, M.; Yang, J.; Xu, Q.; Liang, C.; Chen, B.; Zhang, J.; Yang, Y.; Wang, H.; Shang, Y.; et al. Response of gut microbiota in type 2 diabetes to hypoglycemic agents. *Endocrine* **2019**, *66*, 485–493. [CrossRef]

148. Damman, C.J.; Miller, S.I.; Surawicz, C.M.; Zisman, T.L. The microbiome and inflammatory bowel disease: Is there a therapeutic role for fecal microbiota transplantation? *Off. J. Am. Coll. Gastroenterol. ACG* **2012**, *107*, 1452–1459. [CrossRef]

149. Pimentel, M.; Lembo, A. Microbiome and its role in irritable bowel syndrome. *Dig. Dis. Sci.* **2020**, *65*, 829–839. [CrossRef] [PubMed]

150. Ghosh, T.S.; Sen Gupta, S.; Bhattacharya, T.; Yadav, D.; Barik, A.; Chowdhury, A.; Das, B.; Mande, S.S.; Nair, G.B. Gut microbiomes of Indian children of varying nutritional status. *PLoS ONE* **2014**, *9*, e95547. [CrossRef] [PubMed]

151. Graessler, J.; Qin, Y.; Zhong, H.; Zhang, J.; Licinio, J.; Wong, M.-L.; Xu, A.; Chavakis, T.; Bornstein, A.B.; Ehrhart-Bornstein, M.; et al. Metagenomic sequencing of the human gut microbiome before and after bariatric surgery in obese patients with type 2 diabetes: Correlation with inflammatory and metabolic parameters. *Pharm. J.* **2013**, *13*, 514–522. [CrossRef]

152. Yang, Y.; Cai, Q.; Shu, X.O.; Steinwandel, M.D.; Blot, W.J.; Zheng, W.; Long, J. Prospective study of oral microbiome and colorectal cancer risk in low-income and African American populations. *Int. J. Cancer* **2019**, *144*, 2381–2389. [CrossRef] [PubMed]

153. Kaiyrlykyzy, A.; Kozhakhmetov, S.; Babenko, D.; Zholdasbekova, G.; Alzhanova, D.; Olzhayev, F.; Baibulatova, A.; Kushugulova, A.R.; Askarova, S. Study of gut microbiota alterations in Alzheimer's dementia patients from Kazakhstan. *Sci. Rep.* **2022**, *12*, 15115. [CrossRef] [PubMed]

154. Zhang, Q.; Zou, R.; Guo, M.; Duan, M.; Li, Q.; Zheng, H. Comparison of gut microbiota between adults with autism spectrum disorder and obese adults. *PeerJ* **2021**, *9*, e10946. [CrossRef]

155. Lubomski, M.; Xu, X.; Holmes, A.J.; Muller, S.; Yang, J.Y.; Davis, R.L.; Sue, C.M. The gut microbiome in Parkinson's disease: A longitudinal study of the impacts on disease progression and the use of device-assisted therapies. *Front. Aging Neurosci.* **2022**, *14*, 875261. [CrossRef]

156. Paudel, D.; Uehara, O.; Giri, S.; Yoshida, K.; Morikawa, T.; Kitagawa, T.; Matsuoka, H.; Miura, H.; Toyofuku, A.; Kuramitsu, Y.; et al. Effect of psychological stress on the oral-gut microbiota and the potential oral-gut-brain axis. *JPN Dent. Sci. Rev.* **2022**, *58*, 365–375. [CrossRef]

157. Ling, Z.; Liu, X.; Cheng, Y.; Jiang, X.; Jiang, H.; Wang, Y.; Li, L. Decreased diversity of the oral microbiota of patients with hepatitis B virus-induced chronic liver disease: A pilot project. *Sci. Rep.* **2015**, *5*, 17098. [CrossRef] [PubMed]

158. Anderson, J.R.; Carroll, I.; Azcarate-Peril, M.A.; Rochette, A.D.; Heinberg, L.J.; Peat, C.; Steffen, F.; Manderino, L.M.; Mitchell, J.; Gunstad, J. A preliminary examination of gut microbiota, sleep, and cognitive flexibility in healthy older adults. *Sleep Med.* **2017**, *38*, 104–107. [CrossRef] [PubMed]

159. Salguero, M.V.; Al-Obaide, M.A.; Singh, R.; Siepmann, T.; Vasylyeva, T.L. Dysbiosis of Gram-negative gut microbiota and the associated serum lipopolysaccharide exacerbates inflammation in type 2 diabetic patients with chronic kidney disease. *Exp. Ther. Med.* **2019**, *18*, 3461–3469. [CrossRef] [PubMed]

160. Salem, F.; Kindt, N.; Marchesi, J.R.; Netter, P.; Lopez, A.; Kokten, T.; Danese, S.; Jouzeau, J.-Y.; Peyrin-Biroulet, L.; Moulin, D. Gut microbiome in chronic rheumatic and inflammatory bowel diseases: Similarities and differences. *United Eur. Gastroenterol. J.* **2019**, *7*, 1008–1032. [CrossRef]

161. Barandouzi, Z.A.; Lee, J.; Maas, K.; Starkweather, A.R.; Cong, X.S. Altered gut microbiota in irritable bowel syndrome and its association with food components. *J. Pers. Med.* **2021**, *11*, 35. [CrossRef]

162. de Clercq, N.C.; Frissen, M.N.; Davids, M.; Groen, A.K.; Nieuwdorp, M. Weight gain after fecal microbiota transplantation in a patient with recurrent underweight following clinical recovery from anorexia nervosa. *Psychother. Psychosom.* **2019**, *88*, 58–60. [CrossRef]

163. Barlow, G.M.; Yu, A.; Mathur, R. Role of the gut microbiome in obesity and diabetes mellitus. *Nutr. Clin. Pract.* **2015**, *30*, 787–797. [CrossRef]

164. Huang, R.; He, K.; Duan, X.; Xiao, J.; Wang, H.; Xiang, G. Changes of intestinal microflora in colorectal cancer patients after surgical resection and chemotherapy. *Comput. Math. Methods Med.* **2022**, *2022*, 1940846. [CrossRef]

165. Askarova, S.; Umbayev, B.; Masoud, A.-R.; Kaiyrlykyzy, A.; Safarova, Y.; Tsoy, A.; Olzhayev, F.; Kushugulova, A. The links between the gut microbiome, aging, modern lifestyle and Alzheimer's disease. *Front. Cell. Infect. Microbiol.* **2020**, *10*, 104. [CrossRef]

166. De Angelis, M.; Piccolo, M.; Vannini, L.; Siragusa, S.; De Giacomo, A.; Serrazzanetti, D.I.; Cristofori, F.; Guerzoni, M.E.; Gobbetti, M.; Francavilla, R. Fecal microbiota and metabolome of children with autism and pervasive developmental disorder not otherwise specified. *PLoS ONE* **2013**, *8*, e76993. [CrossRef]

167. Hemmings, S.M.; Malan-Muller, S.; van den Heuvel, L.L.; Demmitt, B.A.; Stanislawski, M.A.; Smith, D.G.; Bohr, A.D.; Stamper, C.E.; Hyde, E.R.; Morton, J.T.; et al. The microbiome in posttraumatic stress disorder and trauma-exposed controls: An exploratory study. *Psychosom. Med.* **2017**, *79*, 936. [CrossRef] [PubMed]

168. Li, M.; Li, K.; Tang, S.; Lv, Y.; Wang, Q.; Wang, Z.; Luo, B.; Niu, J.; Zhu, Y.; Guo, W.; et al. Restoration of the gut microbiota is associated with a decreased risk of hepatic encephalopathy after TIPS. *JHEP Rep.* **2022**, *4*, 100448. [CrossRef] [PubMed]

169. Nogal, A.; Valdes, A.M.; Menni, C. The role of short-chain fatty acids in the interplay between gut microbiota and diet in cardio-metabolic health. *Gut Microbes* **2021**, *13*, 1897212. [CrossRef] [PubMed]

170. Deledda, A.; Palmas, V.; Heidrich, V.; Fosci, M.; Lombardo, M.; Cambarau, G.; Lai, A.; Melis, M.; Loi, E.; Loviselli, A.; et al. Dynamics of Gut Microbiota and Clinical Variables after Ketogenic and Mediterranean Diets in Drug-Naïve Patients with Type 2 Diabetes Mellitus and Obesity. *Metabolites* **2022**, *12*, 1092. [CrossRef]

171. Chang, C.-C.; Liu, C.-Y.; Su, I.-C.; Lee, Y.-J.; Yeh, H.-J.; Chen, W.-C.; Yu, C.-J.; Kao, W.-Y.; Liu, Y.-C.; Huang, C.-J. Functional Plasmon-Activated Water Increases Akkermansia muciniphila Abundance in Gut Microbiota to Ameliorate Inflammatory Bowel Disease. *Int. J. Mol. Sci.* **2022**, *23*, 11422. [CrossRef] [PubMed]

172. Wang, Q.-S.; Wang, Y.-L.; Zhang, W.-Y.; Li, K.-D.; Luo, X.-F.; Cui, Y.-L. Puerarin from *Pueraria lobata* alleviates the symptoms of irritable bowel syndrome-diarrhea. *Food Funct.* **2021**, *12*, 2211–2224. [CrossRef]

173. Han, D.-S.; Wu, W.-K.; Liu, P.-Y.; Yang, Y.-T.; Hsu, H.-C.; Kuo, C.-H.; Wu, M.-S.; Wang, T.-G. Differences in the gut microbiome and reduced fecal butyrate in elders with low skeletal muscle mass. *Clin. Nutr.* **2022**, *41*, 1491–1500. [CrossRef]

174. Zhang, M.; Chen, J.; Yang, M.; Qian, C.; Liu, Y.; Qi, Y.; Feng, R.; Yang, M.; Liu, W.; Ma, J. Low Doses of Sucralose Alter Fecal Microbiota in High-Fat Diet-Induced Obese Rats. *Front. Nutr.* **2021**, *8*, 1151. [CrossRef]

175. Ubeda, C.; Vázquez-Carretero, M.D.; Luque-Tirado, A.; Ríos-Reina, R.; Rubio-Sánchez, R.; Franco-Macías, E.; García-Miranda, P.; Calonge, M.L.; Peral, M.J. Fecal Volatile Organic Compounds and Microbiota Associated with the Progression of Cognitive Impairment in Alzheimer's Disease. *Int. J. Mol. Sci.* **2022**, *24*, 707. [CrossRef]

176. Li, N.; Chen, H.; Cheng, Y.; Xu, F.; Ruan, G.; Ying, S.; Tang, W.; Chen, L.; Chen, M.; Lv, L.; et al. Fecal microbiota transplantation relieves gastrointestinal and autism symptoms by improving the gut microbiota in an open-label study. *Front. Cell. Infect. Microbiol.* **2021**, *11*, 948.

177. Nishiwaki, H.; Hamaguchi, T.; Ito, M.; Ishida, T.; Maeda, T.; Kashihara, K.; Tsuboi, Y.; Ueyama, J.; Shimamura, T.; Mori, H.; et al. Short-chain fatty acid-producing gut microbiota is decreased in Parkinson's disease but not in rapid-eye-movement sleep behavior disorder. *mSystems* **2020**, *5*, e00797-20. [CrossRef] [PubMed]

178. Park, M.; Choi, J.; Lee, H.-J. Flavonoid-rich orange juice intake and altered gut microbiome in young adults with depressive symptom: A randomized controlled study. *Nutrients* **2020**, *12*, 1815. [CrossRef] [PubMed]

179. Wang, L.; Wan, Y.-J.Y. The role of gut microbiota in liver disease development and treatment. *Liver Res.* **2019**, *3*, 3–18. [CrossRef] [PubMed]

180. Xu, H.; Li, X.; Zheng, X.; Xia, Y.; Fu, Y.; Li, X.; Qian, Y.; Zou, J.; Zhao, A.; Guan, J.; et al. Pediatric obstructive sleep apnea is associated with changes in the oral microbiome and urinary metabolomics profile: A pilot study. *J. Clin. Sleep Med.* **2018**, *14*, 1559–1567. [CrossRef]

181. Bailey, M.J.; Naik, N.N.; Wild, L.E.; Patterson, W.B.; Alderete, T.L. Exposure to air pollutants and the gut microbiota: A potential link between exposure, obesity, and type 2 diabetes. *Gut Microbes* **2020**, *11*, 1188–1202. [CrossRef]

182. Humbel, F.; Rieder, J.H.; Franc, Y.; Juillerat, P.; Scharl, M.; Misselwitz, B.; Schreiner, P.; Begré, S.; Rogler, G.; von Känel, R.; et al. Association of alterations in intestinal microbiota with impaired psychological function in patients with inflammatory bowel diseases in remission. *Clin. Gastroenterol. Hepatol.* **2020**, *18*, 2019–2029.e11. [CrossRef]

183. Jalanka, J.; Lam, C.; Bennett, A.; Hartikainen, A.; Crispie, F.; Finnegan, L.A.; Cotter, P.D.; Spiller, R. Colonic gene expression and fecal microbiota in diarrhea-predominant irritable bowel syndrome: Increased toll-like receptor 4 but minimal inflammation and no response to mesalazine. *J. Neurogastroenterol. Motil.* **2021**, *27*, 279. [CrossRef]

184. Eggers, S.; Safdar, N.; Sethi, A.K.; Suen, G.; Peppard, P.E.; Kates, A.E.; Skarlupka, J.H.; Kanarek, M.; Malecki, K.M. Urinary lead concentration and composition of the adult gut microbiota in a cross-sectional population-based sample. *Environ. Int.* **2019**, *133*, 105122. [CrossRef]

185. Palmas, V.; Pisanu, S.; Madau, V.; Casula, E.; Deledda, A.; Cusano, R.; Uva, P.; Vascellari, S.; Loviselli, A.; Manzin, A.; et al. Gut microbiota markers associated with obesity and overweight in Italian adults. *Sci. Rep.* **2021**, *11*, 5532. [CrossRef]

186. Chen, W.; Liu, F.; Ling, Z.; Tong, X.; Xiang, C. Human intestinal lumen and mucosa-associated microbiota in patients with colorectal cancer. *PLoS ONE* **2012**, *7*, e39743. [CrossRef]

187. Kobayashi, Y.; Sugahara, H.; Shimada, K.; Mitsuyama, E.; Kuhara, T.; Yasuoka, A.; Kondo, T.; Abe, K.; Xiao, J.-Z. Therapeutic potential of *Bifidobacterium breve* strain A1 for preventing cognitive impairment in Alzheimer's disease. *Sci. Rep.* **2017**, *7*, 13510. [CrossRef]

188. Williams, B.L.; Hornig, M.; Parekh, T.; Lipkin, W.I. Application of novel PCR-based methods for detection, quantitation, and phylogenetic characterization of *Sutterella* species in intestinal biopsy samples from children with autism and gastrointestinal disturbances. *mBio* **2012**, *3*, e00261-11. [CrossRef] [PubMed]

189. Johnson, M.E.; Stringer, A.; Bobrovskaya, L. Rotenone induces gastrointestinal pathology and microbiota alterations in a rat model of Parkinson's disease. *Neurotoxicology* **2018**, *65*, 174–185. [CrossRef]

190. Zheng, S.; Zhu, Y.; Wu, W.; Zhang, Q.; Wang, Y.; Wang, Z.; Yang, F. A correlation study of intestinal microflora and first-episode depression in Chinese patients and healthy volunteers. *Brain Behav.* **2021**, *11*, e02036. [CrossRef]

191. Bajaj, J.S.; Ridlon, J.M.; Hylemon, P.B.; Thacker, L.R.; Heuman, D.M.; Smith, S.; Sikaroodi, M.; Gillevet, P.M. Linkage of gut microbiome with cognition in hepatic encephalopathy. *Am. J. Physiol. Gastrointest. Liver Physiol.* **2012**, *302*, G168–G175. [CrossRef]

192. Bikov, A.; Dragonieri, S.; Csoma, B.; Mazzuca, C.; Finamore, P.; Rocchi, G.; Putignani, L.; Guarino, M.; Scarlata, S. The Role of Gut Bacteriome in Asthma, Chronic Obstructive Pulmonary Disease and Obstructive Sleep Apnoea. *Microorganisms* **2022**, *10*, 2457. [CrossRef]

193. Fugmann, M.; Breier, M.; Rottenkolber, M.; Banning, F.; Ferrari, U.; Sacco, V.; Grallert, H.; Parhofer, K.G.; Seissler, J.; Clavel, T.; et al. The stool microbiota of insulin resistant women with recent gestational diabetes, a high risk group for type 2 diabetes. *Sci. Rep.* **2015**, *5*, 13212. [CrossRef]

194. Alam, M.T.; Amos, G.C.; Murphy, A.R.; Murch, S.; Wellington, E.M.; Arasaradnam, R.P. Microbial imbalance in inflammatory bowel disease patients at different taxonomic levels. *Gut Pathog.* **2020**, *12*, 1. [CrossRef]

195. Peter, J.; Fournier, C.; Durdevic, M.; Knoblich, L.; Keip, B.; Dejaco, C.; Trauner, M.; Moser, G. A microbial signature of psychological distress in irritable bowel syndrome. *Psychosom. Med.* **2018**, *80*, 698. [CrossRef]

196. Aguilar, T.; Nava, G.M.; Olvera-Ramírez, A.M.; Ronquillo, D.; Camacho, M.; Zavala, G.A.; Caamaño, M.C.; Acevedo-Whitehouse, K.; Rosado, J.L.; García, O.P. Gut bacterial families are associated with body composition and metabolic risk markers in school-aged children in rural Mexico. *Child. Obes.* **2020**, *16*, 358–366. [CrossRef]

197. Cho, K.Y. Lifestyle modifications result in alterations in the gut microbiota in obese children. *BMC Microbiol.* **2021**, *21*, 10. [CrossRef] [PubMed]

198. Lauka, L.; Reitano, E.; Carra, M.C.; Gaiani, F.; Gavriilidis, P.; Brunetti, F.; De'angelis, G.L.; Sobhani, I.; De'angelis, N. Role of the intestinal microbiome in colorectal cancer surgery outcomes. *World J. Surg. Oncol.* **2019**, *17*, 204. [CrossRef] [PubMed]

199. Pulikkan, J.; Maji, A.; Dhakan, D.B.; Saxena, R.; Mohan, B.; Anto, M.M.; Agarwal, N.; Grace, T.; Sharma, V.K. Gut microbial dysbiosis in Indian children with autism spectrum disorders. *Microb. Ecol.* **2018**, *76*, 1102–1114. [CrossRef] [PubMed]

200. Vidal-Martinez, G.; Chin, B.; Camarillo, C.; Herrera, G.V.; Yang, B.; Sarosiek, I.; Perez, R.G. A pilot microbiota study in Parkinson's disease patients versus control subjects, and effects of FTY720 and FTY720-mitoxy therapies in parkinsonian and multiple system atrophy mouse models. *J. Park. Dis.* **2020**, *10*, 185–192. [CrossRef]

201. Zheng, P.; Yang, J.; Li, Y.; Wu, J.; Liang, W.; Yin, B.; Tan, X.; Huang, Y.; Chai, T.; Zhang, H.; et al. Gut microbial signatures can discriminate unipolar from bipolar depression. *Adv. Sci.* **2020**, *7*, 1902862. [CrossRef]

202. Bajaj, J.S.; Heuman, D.M.; Sanyal, A.J.; Hylemon, P.B.; Sterling, R.K.; Stravitz, R.T.; Fuchs, M.; Ridlon, J.M.; Daita, K.; Monteith, P.; et al. Modulation of the metabiome by rifaximin in patients with cirrhosis and minimal hepatic encephalopathy. *PLoS ONE* **2013**, *8*, e60042. [CrossRef]

203. Farré, N.; Farré, R.; Gozal, D. Sleep apnea morbidity: A consequence of microbial-immune cross-talk? *Chest* **2018**, *154*, 754–759. [CrossRef]

204. Gonai, M.; Shigehisa, A.; Kigawa, I.; Kurasaki, K.; Chonan, O.; Matsuki, T.; Yoshida, Y.; Aida, M.; Hamano, K.; Terauchi, Y. Galacto-oligosaccharides ameliorate dysbiotic *Bifidobacteriaceae* decline in Japanese patients with type 2 diabetes. *Benef. Microbes* **2017**, *8*, 705–716. [CrossRef]

205. Teofani, A.; Marafini, I.; Laudisi, F.; Pietrucci, D.; Salvatori, S.; Unida, V.; Biocca, S.; Monteleone, G.; Desideri, A. Intestinal taxa abundance and diversity in inflammatory bowel disease patients: An analysis including covariates and confounders. *Nutrients* **2022**, *14*, 260. [CrossRef]

206. Pittayanon, R.; Lau, J.T.; Yuan, Y.; Leontiadis, G.I.; Tse, F.; Surette, M.; Moayyedi, P. Gut microbiota in patients with irritable bowel syndrome—A systematic review. *Gastroenterology* **2019**, *157*, 97–108. [CrossRef]

207. Nakayama, J.; Watanabe, K.; Jiang, J.; Matsuda, K.; Chao, S.-H.; Haryono, P.; La-Ongkham, O.; Sarwoko, M.-A.; Sujaya, I.N.; Zhao, L.; et al. Diversity in gut bacterial community of school-age children in Asia. *Sci. Rep.* **2015**, *5*, 8397. [CrossRef] [PubMed]

208. Lane, M.; Howland, G.; West, M.; Hockey, M.; Marx, W.; Loughman, A.; O'hely, M.; Jacka, F.; Rocks, T. The effect of ultra-processed very low-energy diets on gut microbiota and metabolic outcomes in individuals with obesity: A systematic literature review. *Obes. Res. Clin. Pract.* **2020**, *14*, 197–204. [CrossRef] [PubMed]

209. Youssef, O.; Lahti, L.; Kokkola, A.; Karla, T.; Tikkanen, M.; Ehsan, H.; Carpelan-Holmström, M.; Koskensalo, S.; Böhling, T.; Rautelin, H.; et al. Stool microbiota composition differs in patients with stomach, colon, and rectal neoplasms. *Dig. Dis. Sci.* **2018**, *63*, 2950–2958. [CrossRef] [PubMed]

210. Nagpal, R.; Neth, B.J.; Wang, S.; Craft, S.; Yadav, H. Modified Mediterranean-ketogenic diet modulates gut microbiome and short-chain fatty acids in association with Alzheimer's disease markers in subjects with mild cognitive impairment. *EBioMedicine* **2019**, *47*, 529–542. [CrossRef]

211. Xie, X.; Li, L.; Wu, X.; Hou, F.; Chen, Y.; Shi, L.; Liu, Q.; Zhu, K.; Jiang, Q.; Feng, Y.; et al. Alteration of the fecal microbiota in Chinese children with autism spectrum disorder. *Autism Res.* **2022**, *15*, 996–1007. [CrossRef]

212. Shen, T.; Yue, Y.; He, T.; Huang, C.; Qu, B.; Lv, W.; Lai, H.Y. The association between the gut microbiota and Parkinson's disease, a meta-analysis. *Front. Aging Neurosci.* **2021**, *13*, 636545. [CrossRef]

213. Knuesel, T.; Mohajeri, M.H. The role of the gut microbiota in the development and progression of major depressive and bipolar disorder. *Nutrients* **2022**, *14*, 37. [CrossRef] [PubMed]

214. Bajaj, J.S.; Salzman, N.H.; Acharya, C.; Sterling, R.K.; White, M.B.; Gavis, E.A.; Fagan, A.; Hayward, M.; Holtz, M.L.; Matherly, S.; et al. Fecal microbial transplant capsules are safe in hepatic encephalopathy: A phase 1, randomized, placebo-controlled trial. *Hepatology* **2019**, *70*, 1690–1703. [CrossRef]

215. Muñiz Pedrogo, D.A.; Chen, J.; Hillmann, B.; Jeraldo, P.; Al-Ghalith, G.; Taneja, V.; Davis, J.M.; Knights, D.; Nelson, H.; A Faubion, W.; et al. An increased abundance of Clostridiaceae characterizes arthritis in inflammatory bowel disease and rheumatoid arthritis: A cross-sectional study. *Inflamm. Bowel Dis.* **2019**, *25*, 902–913. [CrossRef]

216. Ricci, C.; Rizzello, F.; Valerii, M.C.; Spisni, E.; Gionchetti, P.; Turroni, S.; Candela, M.; D'amico, F.; Spigarelli, R.; Bellocchio, I.; et al. Geraniol treatment for irritable bowel syndrome: A double-blind randomized clinical trial. *Nutrients* **2022**, *14*, 4208. [CrossRef]

217. Hourigan, S.; Grigoryan, Z.; Kim, S.; Chirumamilla, S.; Rabizadeh, S.; Golub, J.; Saeed, S.A.; Elson, C.O.; Oliva-Hemker, M.; Sears, C.L.; et al. Decreased Diversity of the Fecal Microbiome in Pediatric Carriage of *Clostridium difficile*. *Gastroenterology* **2014**, *146*, S-13. [CrossRef]

218. Golloso-Gubat, M.J.; Ducarmon, Q.R.; Tan, R.C.A.; Zwittink, R.D.; Kuijper, E.J.; Nacis, J.S.; Santos, N.L.C. Gut microbiota and dietary intake of normal-weight and overweight Filipino children. *Microorganisms* **2020**, *8*, 1015. [CrossRef] [PubMed]

219. Peters, B.A.; Dominianni, C.; Shapiro, J.A.; Church, T.R.; Wu, J.; Miller, G.; Yuen, E.; Freiman, H.; Lustbader, I.; Salik, J.; et al. The gut microbiota in conventional and serrated precursors of colorectal cancer. *Microbiome* **2016**, *4*, 69. [CrossRef] [PubMed]

220. Hung, C.-C.; Chang, C.-C.; Huang, C.-W.; Nouchi, R.; Cheng, C.-H. Gut microbiota in patients with Alzheimer's disease spectrum: A systematic review and meta-analysis. *Aging* **2022**, *14*, 477. [CrossRef] [PubMed]

221. Srikantha, P.; Mohajeri, M.H. The possible role of the microbiota-gut-brain-axis in autism spectrum disorder. *Int. J. Mol. Sci.* **2019**, *20*, 2115. [CrossRef]

222. Painold, A.; Mörkl, S.; Kashofer, K.; Halwachs, B.; Dalkner, N.; Bengesser, S.; Birner, A.; Fellendorf, F.; Platzer, M.; Queissner, R.; et al. A step ahead: Exploring the gut microbiota in inpatients with bipolar disorder during a depressive episode. *Bipolar Disord.* **2019**, *21*, 40–49. [CrossRef]

223. Haraguchi, M.; Miuma, S.; Masumoto, H.; Ichikawa, T.; Kanda, Y.; Sasaki, R.; Fukushima, M.; Miyaaki, H.; Taura, N.; Nakao, K. Bacteroides in colonic mucosa-associated microbiota affects the development of minimal hepatic encephalopathy in patients with cirrhosis. *Hepatol. Int.* **2019**, *13*, 482–489. [CrossRef]

224. Durgan, D.J.; Ganesh, B.P.; Cope, J.L.; Ajami, N.J.; Phillips, S.C.; Petrosino, J.F.; Hollister, E.B.; Bryan, R.M., Jr. Role of the gut microbiome in obstructive sleep apnea–induced hypertension. *Hypertension* **2016**, *67*, 469–474. [CrossRef]

225. Liu, H.; Zhang, H.; Wang, X.; Yu, X.; Hu, C.; Zhang, X. The family Coriobacteriaceae is a potential contributor to the beneficial effects of Roux-en-Y gastric bypass on type 2 diabetes. *Surg. Obes. Relat. Dis.* **2018**, *14*, 584–593. [CrossRef]

226. Abecia, L.; Hoyles, L.; Khoo, C.; Frantz, N.; McCartney, A.L. Effects of a novel galactooligosaccharide on the faecal microbiota of healthy and inflammatory bowel disease cats during a randomized, double-blind, cross-over feeding study. *Int. J. Probiotics Prebiotics* **2010**, *5*, 61–68.

227. Krogius-Kurikka, L.; Lyra, A.; Malinen, E.; Aarnikunnas, J.; Tuimala, J.; Paulin, L.; Mäkivuokko, H.; Kajander, K.; Palva, A. Microbial community analysis reveals high level phylogenetic alterations in the overall gastrointestinal microbiota of diarrhoea-predominant irritable bowel syndrome sufferers. *BMC Gastroenterol.* **2009**, *9*, 95. [CrossRef] [PubMed]

228. Mörkl, S.; Lackner, S.; Müller, W.; Gorkiewicz, G.; Kashofer, K.; Oberascher, A.; Painold, A.; Holl, A.; Holzer, P.; Meinitzer, A.; et al. Gut microbiota and body composition in anorexia nervosa inpatients in comparison to athletes, overweight, obese, and normal weight controls. *Int. J. Eat. Disord.* **2017**, *50*, 1421–1431. [CrossRef] [PubMed]

229. Alderete, T.L.; Jones, R.B.; Chen, Z.; Kim, J.S.; Habre, R.; Lurmann, F.; Gilliland, F.D.; Goran, M.I. Exposure to traffic-related air pollution and the composition of the gut microbiota in overweight and obese adolescents. *Environ. Res.* **2018**, *161*, 472–478. [CrossRef]

230. Wang, M.; Cao, J.; Gong, C.; Amakye, W.K.; Yao, M.; Ren, J. Exploring the microbiota-Alzheimer's disease linkage using short-term antibiotic treatment followed by fecal microbiota transplantation. *Brain Behav. Immun.* **2021**, *96*, 227–238. [CrossRef]

231. Chen, K.; Fu, Y.; Wang, Y.; Liao, L.; Xu, H.; Zhang, A.; Zhang, J.; Fan, L.; Ren, J.; Fang, B. Therapeutic effects of the in vitro cultured human gut microbiota as transplants on altering gut microbiota and improving symptoms associated with autism spectrum disorder. *Microb. Ecol.* **2020**, *80*, 475–486. [CrossRef]

232. Zhang, L.-N.; Yuan, W.-L.; Ye, M.; Yin, L.; Wang, S.-J. Changes in the intestinal microbiota of patients with Parkinson's disease and their clinical significance. *Int. J. Clin. Pharmacol. Ther.* **2022**, *61*, 48–58. [CrossRef]

233. Lin, Y.; Yan, G.; Feng, F.; Wang, M.; Long, F. Characterization of intestinal microbiota and serum metabolites in patients with mild hepatic encephalopathy. *Open Life Sci.* **2022**, *17*, 139–154. [CrossRef]

234. Hu, C.; Wang, P.; Yang, Y.; Li, J.; Jiao, X.; Yu, H.; Wei, Y.; Li, J.; Qin, Y. Chronic intermittent hypoxia participates in the pathogenesis of atherosclerosis and perturbs the formation of intestinal microbiota. *Front. Cell. Infect. Microbiol.* **2021**, *11*, 560201. [CrossRef]

235. Zhao, Z.; Chen, Y.; Li, X.; Zhu, L.; Wang, X.; Li, L.; Sun, H.; Han, X.; Li, J. Myricetin relieves the symptoms of type 2 diabetes mice and regulates intestinal microflora. *Biomed. Pharmacother.* **2022**, *153*, 113530. [CrossRef]

236. Regner, E.H.; Ohri, N.; Stahly, A.; Gerich, M.E.; Fennimore, B.P.; Ir, D.; Jubair, W.K.; Görg, C.; Siebert, J.; Robertson, C.E.; et al. Functional intraepithelial lymphocyte changes in inflammatory bowel disease and spondyloarthritis have disease specific correlations with intestinal microbiota. *Arthritis Res. Ther.* **2018**, *20*, 149. [CrossRef]

237. Ng, S.C.; Lam, E.F.C.; Lam, T.T.Y.; Chan, Y.; Law, W.; Tse, P.C.H.; A Kamm, M.; Sung, J.J.Y.; Chan, F.K.L.; Wu, J.C.Y. Effect of probiotic bacteria on the intestinal microbiota in irritable bowel syndrome. *J. Gastroenterol. Hepatol.* **2013**, *28*, 1624–1631. [CrossRef] [PubMed]

238. Brandwein, M.; Katz, I.; Katz, A.; Kohen, R. Beyond the gut: Skin microbiome compositional changes are associated with BMI. *Hum. Microbiome J.* **2019**, *13*, 100063. [CrossRef]

239. Palomo-Buitrago, M.E.; Sabater-Masdeu, M.; Moreno-Navarrete, J.M.; Caballano-Infantes, E.; Arnoriaga-Rodríguez, M.; Coll, C.; Ramió, L.; Palomino-Schätzlein, M.; Gutiérrez-Carcedo, P.; Pérez-Brocal, V.; et al. Glutamate interactions with obesity, insulin resistance, cognition and gut microbiota composition. *Acta Diabetol.* **2019**, *56*, 569–579. [CrossRef] [PubMed]

240. Tang, Q.; Liu, R.; Chu, G.; Wang, Y.; Cui, H.; Zhang, T.; Bi, K.; Gao, P.; Song, Z.; Li, Q. A Comprehensive Analysis of Microflora and Metabolites in the Development of Ulcerative Colitis into Colorectal Cancer Based on the Lung–Gut Correlation Theory. *Molecules* **2022**, *27*, 5838. [CrossRef]

241. Ling, Z.; Zhu, M.; Yan, X.; Cheng, Y.; Shao, L.; Liu, X.; Jiang, R.; Wu, S. Structural and functional dysbiosis of fecal microbiota in Chinese patients with Alzheimer's disease. *Front. Cell Dev. Biol.* **2021**, *8*, 634069. [CrossRef]

242. Wallen, Z.D.; Appah, M.; Dean, M.N.; Sesler, C.L.; Factor, S.A.; Molho, E.; Zabetian, C.P.; Standaert, D.G.; Payami, H. Characterizing dysbiosis of gut microbiome in PD: Evidence for overabundance of opportunistic pathogens. *NPJ Park. Dis.* **2020**, *6*, 11. [CrossRef]

243. Chen, Y.-h.; Xue, F.; Yu, S.-f.; Li, X.-s.; Liu, L.; Jia, Y.-y.; Yan, W.-j.; Tan, Q.-r.; Wang, H.-n.; Peng, Z.-w. Gut microbiota dysbiosis in depressed women: The association of symptom severity and microbiota function. *J. Affect. Disord.* **2021**, *282*, 391–400. [CrossRef]

244. Yan, R.; Wang, K.; Wang, Q.; Jiang, H.; Lu, Y.; Chen, X.; Zhang, H.; Su, X.; Du, Y.; Chen, L.; et al. Probiotic *Lactobacillus casei* Shirota prevents acute liver injury by reshaping the gut microbiota to alleviate excessive inflammation and metabolic disorders. *Microb. Biotechnol.* **2022**, *15*, 247–261. [CrossRef]

245. Wang, Y.; Luo, X.; Mao, X.; Tao, Y.; Ran, X.; Zhao, H.; Xiong, J.; Li, L. Gut microbiome analysis of type 2 diabetic patients from the Chinese minority ethnic groups the Uygurs and Kazaks. *PLoS ONE* **2017**, *12*, e0172774. [CrossRef]

246. Lee, S.M.; Kim, N.; Yoon, H.; Kim, Y.S.; Choi, S.I.; Park, J.H.; Lee, D.H. Compositional and functional changes in the gut microbiota in irritable bowel syndrome patients. *Gut Liver* **2021**, *15*, 253. [CrossRef]

247. Lv, Y.; Qin, X.; Jia, H.; Chen, S.; Sun, W.; Wang, X. The association between gut microbiota composition and BMI in Chinese male college students, as analysed by next-generation sequencing. *Br. J. Nutr.* **2019**, *122*, 986–995. [CrossRef] [PubMed]

248. Xu, P.; Wang, J.; Hong, F.; Wang, S.; Jin, X.; Xue, T.; Jia, L.; Zhai, Y. Melatonin prevents obesity through modulation of gut microbiota in mice. *J. Pineal Res.* **2017**, *62*, e12399. [CrossRef] [PubMed]

249. Luo, J.; Zhang, C.; Liu, R.; Gao, L.; Ou, S.; Liu, L.; Peng, X. *Ganoderma lucidum* polysaccharide alleviating colorectal cancer by alteration of special gut bacteria and regulation of gene expression of colonic epithelial cells. *J. Funct. Foods* **2018**, *47*, 127–135. [CrossRef]

250. Sheng, C.; Yang, K.; He, B.; Du, W.; Cai, Y.; Han, Y. Combination of gut microbiota and plasma amyloid-β as a potential index for identifying preclinical Alzheimer's disease: A cross-sectional analysis from the SILCODE study. *Alzheimers Res. Ther.* **2022**, *14*, 35. [CrossRef]

251. Liu, S.; Li, E.; Sun, Z.; Fu, D.; Duan, G.; Jiang, M.; Yu, Y.; Mei, L.; Yang, P.; Tang, Y.; et al. Altered gut microbiota and short chain fatty acids in Chinese children with autism spectrum disorder. *Sci. Rep.* **2019**, *9*, 287. [CrossRef]

252. Murros, K.E. Hydrogen sulfide produced by gut bacteria may induce Parkinson's disease. *Cells* **2022**, *11*, 978. [CrossRef]

253. Rhee, S.J.; Kim, H.; Lee, Y.; Lee, H.J.; Park, C.H.K.; Yang, J.; Kim, Y.-K.; Ahn, Y.M. The association between serum microbial DNA composition and symptoms of depression and anxiety in mood disorders. *Sci. Rep.* **2021**, *11*, 13987. [CrossRef]

254. Szabo, H.; Piroska, M.; Hernyes, A.; Zoldi, L.; Juhasz, J.; Ligeti, B.; Makra, N.; Szabo, D.; Bikov, A.; Kunos, L.; et al. The Relationship between Atherosclerosis and Gut Microbiome in Patients with Obstructive Sleep Apnoea. *Appl. Sci.* **2022**, *12*, 11484. [CrossRef]

255. Baldelli, V.; Scaldaferri, F.; Putignani, L.; Del Chierico, F. The role of Enterobacteriaceae in gut microbiota dysbiosis in inflammatory bowel diseases. *Microorganisms* **2021**, *9*, 697. [CrossRef]

256. Carroll, I.M.; Ringel-Kulka, T.; Siddle, J.P.; Ringel, Y. Alterations in composition and diversity of the intestinal microbiota in patients with diarrhea-predominant irritable bowel syndrome. *Neurogastroenterol. Motil.* **2012**, *24*, 521-e248. [CrossRef]

257. Million, M.; Diallo, A.; Raoult, D. Gut microbiota and malnutrition. *Microb. Pathog.* **2017**, *106*, 127–138. [CrossRef] [PubMed]

258. Sánchez-Alcoholado, L.; Ordóñez, R.; Otero, A.; Plaza-Andrade, I.; Laborda-Illanes, A.; Medina, J.A.; Ramos-Molina, B.; Gómez-Millán, J.; Queipo-Ortuño, M.I. Gut microbiota-mediated inflammation and gut permeability in patients with obesity and colorectal cancer. *Int. J. Mol. Sci.* **2020**, *21*, 6782. [CrossRef]

259. Zhuang, Z.; Yang, R.; Wang, W.; Qi, L.; Huang, T. Associations between gut microbiota and Alzheimer's disease, major depressive disorder, and schizophrenia. *J. Neuroinflammation* **2020**, *17*, 288. [CrossRef]

260. Lou, M.; Cao, A.; Jin, C.; Mi, K.; Xiong, X.; Zeng, Z.; Pan, X.; Qie, J.; Qiu, S.; Niu, Y.; et al. Deviated and early unsustainable stunted development of gut microbiota in children with autism spectrum disorder. *Gut* **2022**, *71*, 1588–1599. [CrossRef]

261. Pietrucci, D.; Cerroni, R.; Unida, V.; Farcomeni, A.; Pierantozzi, M.; Mercuri, N.B.; Biocca, S.; Stefani, A.; Desideri, A. Dysbiosis of gut microbiota in a selected population of Parkinson's patients. *Park. Relat. Disord.* **2019**, *65*, 124–130. [CrossRef] [PubMed]

262. Jiang, H.; Ling, Z.; Zhang, Y.; Mao, H.; Ma, Z.; Yin, Y.; Wang, W.; Tang, W.; Tan, Z.; Shi, J.; et al. Altered fecal microbiota composition in patients with major depressive disorder. *Brain Behav. Immun.* **2015**, *48*, 186–194. [CrossRef] [PubMed]

263. Maki, K.A.; Burke, L.A.; Calik, M.W.; Watanabe-Chailland, M.; Sweeney, D.; Romick-Rosendale, L.E.; Green, S.J.; Fink, A.M. Sleep fragmentation increases blood pressure and is associated with alterations in the gut microbiome and fecal metabolome in rats. *Physiol. Genom.* **2020**, *52*, 280–292. [CrossRef]

264. Li, P.; Lu, B.; Gong, J.; Li, L.; Chen, G.; Zhang, J.; Chen, Y.; Tian, X.; Han, B.; Guo, Y.; et al. Chickpea extract ameliorates metabolic syndrome symptoms via restoring intestinal ecology and metabolic profile in type 2 diabetic rats. *Mol. Nutr. Food Res.* **2021**, *65*, 2100007. [CrossRef]

265. Chen, L.; Wang, W.; Zhou, R.; Ng, S.C.; Li, J.; Huang, M.; Zhou, F.; Wang, X.; Shen, B.; Kamm, M.A.; et al. Characteristics of fecal and mucosa-associated microbiota in Chinese patients with inflammatory bowel disease. *Medicine* **2014**, *93*, e51. [CrossRef]

266. Foley, K.P.; Zlitni, S.; Duggan, B.M.; Barra, N.G.; Anhê, F.F.; Cavallari, J.F.; Henriksbo, B.D.; Chen, C.Y.; Huang, M.; Lau, T.C.; et al. Gut microbiota impairs insulin clearance in obese mice. *Mol. Metab.* **2020**, *42*, 101067. [CrossRef]

267. Wu, N.; Yang, X.; Zhang, R.; Li, J.; Xiao, X.; Hu, Y.; Chen, Y.; Yang, F.; Lu, N.; Wang, Z.; et al. Dysbiosis signature of fecal microbiota in colorectal cancer patients. *Microb. Ecol.* **2013**, *66*, 462–470. [CrossRef] [PubMed]

268. Hou, M.; Xu, G.; Ran, M.; Luo, W.; Wang, H. APOE-ε4 carrier status and gut microbiota dysbiosis in patients with Alzheimer disease. *Front. Neurosci.* **2021**, *15*, 619051. [CrossRef] [PubMed]

269. Liu, R.T.; Rowan-Nash, A.D.; Sheehan, A.E.; Walsh, R.F.; Sanzari, C.M.; Korry, B.J.; Belenky, P. Reductions in anti-inflammatory gut bacteria are associated with depression in a sample of young adults. *Brain Behav. Immun.* **2020**, *88*, 308–324. [CrossRef]

270. Mancini, A.; Campagna, F.; Amodio, P.; Tuohy, K.M. Gut: Liver: Brain axis: The microbial challenge in the hepatic encephalopathy. *Food Funct.* **2018**, *9*, 1373–1388. [CrossRef] [PubMed]

271. Moreno-Indias, I.; Torres, M.; Montserrat, J.M.; Sanchez-Alcoholado, L.; Cardona, F.; Tinahones, F.J.; Gozal, D.; Poroyko, V.A.; Navajas, D.; Queipo-Ortuño, M.I.; et al. Intermittent hypoxia alters gut microbiota diversity in a mouse model of sleep apnoea. *Eur. Respir. J.* **2015**, *45*, 1055–1065. [CrossRef] [PubMed]

272. Vals-Delgado, C.; Alcala-Diaz, J.F.; Molina-Abril, H.; Roncero-Ramos, I.; Caspers, M.P.; Schuren, F.H.; Broek, T.J.V.D.; Luque, R.; Perez-Martinez, P.; Katsiki, N.; et al. An altered microbiota pattern precedes Type 2 diabetes mellitus development: From the CORDIOPREV study. *J. Adv. Res.* **2022**, *35*, 99–108. [CrossRef]

273. Pozuelo, M.; Panda, S.; Santiago, A.; Mendez, S.; Accarino, A.; Santos, J.; Guarner, F.; Azpiroz, F.; Manichanh, C. Reduction of butyrate-and methane-producing microorganisms in patients with Irritable Bowel Syndrome. *Sci. Rep.* **2015**, *5*, 12693. [CrossRef]

274. Nakayama, J.; Yamamoto, A.; Palermo-Conde, L.A.; Higashi, K.; Sonomoto, K.; Tan, J.; Lee, Y.-K. Impact of westernized diet on gut microbiota in children on Leyte Island. *Front. Microbiol.* **2017**, *8*, 197. [CrossRef]

275. Zhang, H.; DiBaise, J.K.; Zuccolo, A.; Kudrna, D.; Braidotti, M.; Yu, Y.; Parameswaran, P.; Crowell, M.D.; Wing, R.; Rittmann, B.E.; et al. Human gut microbiota in obesity and after gastric bypass. *Proc. Natl. Acad. Sci. USA* **2009**, *106*, 2365–2370. [CrossRef]

276. Zackular, J.P.; Baxter, N.T.; Iverson, K.D.; Sadler, W.D.; Petrosino, J.F.; Chen, G.Y.; Schloss, P.D. The gut microbiome modulates colon tumorigenesis. *mBio* **2013**, *4*, e00692-13. [CrossRef]

277. Jung, J.H.; Kim, G.; Byun, M.S.; Lee, J.H.; Yi, D.; Park, H.; Lee, D.Y.; The KBASE Research Group. Gut microbiome alterations in preclinical Alzheimer's disease. *PLoS ONE* **2022**, *17*, e0278276. [CrossRef] [PubMed]

278. Bedarf, J.R.; Hildebrand, F.; Coelho, L.P.; Sunagawa, S.; Bahram, M.; Goeser, F.; Bork, P.; Wüllner, U. Functional implications of microbial and viral gut metagenome changes in early stage L-DOPA-naïve Parkinson's disease patients. *Genome Med.* **2017**, *9*, 39. [CrossRef] [PubMed]

279. Tan, J.; Li, X.; Zhu, Y.; Sullivan, M.A.; Deng, B.; Zhai, X.; Lu, Y. Antidepressant shugan jieyu capsule alters gut microbiota and intestinal microbiome function in rats with chronic unpredictable mild stress-induced depression. *Front. Pharmacol.* **2022**, *13*, 828595. [CrossRef] [PubMed]

280. Yuan, J. Fecal microbiota and metabolome characteristics in cirrhotic patients accompanied with hepatic encephalopathy. *Res. Sq.* **2019**. [CrossRef]

281. Davies, N.; O'Sullivan, J.M.; Plank, L.D.; Murphy, R. Gut microbial predictors of type 2 diabetes remission following bariatric surgery. *Obes. Surg.* **2020**, *30*, 3536–3548. [CrossRef] [PubMed]

282. Willing, B.P.; Dicksved, J.; Halfvarson, J.; Andersson, A.F.; Lucio, M.; Zheng, Z.; Järnerot, G.; Tysk, C.; Jansson, J.K.; Engstrand, L. A pyrosequencing study in twins shows that gastrointestinal microbial profiles vary with inflammatory bowel disease phenotypes. *Gastroenterology* **2010**, *139*, 1844–1854.e1. [CrossRef] [PubMed]

283. Hollister, E.B.; Cain, K.C.; Shulman, R.J.; Jarrett, M.E.; Burr, R.L.; Ko, C.; Zia, J.; Han, C.J.; Heitkemper, M.M. Relationships of microbiome markers with extra-intestinal, psychological distress and gastrointestinal symptoms, and quality of life in women with irritable bowel syndrome. *J. Clin. Gastroenterol.* **2020**, *54*, 175. [CrossRef]

284. Romo-Vaquero, M.; Cortés-Martín, A.; Loria-Kohen, V.; Ramírez-de-Molina, A.; García-Mantrana, I.; Collado, M.C.; Espín, J.C.; Selma, M.V. Deciphering the human gut microbiome of urolithin metabotypes: Association with enterotypes and potential cardiometabolic health implications. *Mol. Nutr. Food Res.* **2019**, *63*, 1800958. [CrossRef]

285. Wang, Y.; Wan, X.; Wu, X.; Zhang, C.; Liu, J.; Hou, S. Eubacterium rectale contributes to colorectal cancer initiation via promoting colitis. *Gut Pathog.* **2021**, *13*, 2. [CrossRef]

286. Zhang, L.; Wang, Y.; Xiayu, X.; Shi, C.; Chen, W.; Song, N.; Fu, X.; Zhou, R.; Xu, Y.-F.; Huang, L.; et al. Altered gut microbiota in a mouse model of Alzheimer's disease. *J. Alzheimers Dis.* **2017**, *60*, 1241–1257. [CrossRef]

287. Vascellari, S.; Melis, M.; Palmas, V.; Pisanu, S.; Serra, A.; Perra, D.; Santoru, M.L.; Oppo, V.; Cusano, R.; Uva, P.; et al. Clinical phenotypes of Parkinson's disease associate with distinct gut microbiota and metabolome enterotypes. *Biomolecules* **2021**, *11*, 144. [CrossRef] [PubMed]

288. Pourdeh, E.F.; Ulker, I. Do all Bariatric Surgery Methods Have the Same Effects on the Gut Microbiota? In *Bariatric Surgery-Past and Present*; IntechOpen: London, UK, 2022.

289. Villanueva-Millan, M.J.; Leite, G.; Wang, J.; Morales, W.; Parodi, G.; Pimentel, M.L.; Barlow, G.M.; Mathur, R.; Rezaie, A.; Sanchez, M.; et al. Methanogens and hydrogen sulfide producing bacteria guide distinct gut microbe profiles and irritable bowel syndrome subtypes. *Am. J. Gastroenterol.* **2022**, *117*, 2055–2066. [CrossRef] [PubMed]

290. Moreno-Indias, I.; Sánchez-Alcoholado, L.; García-Fuentes, E.; Cardona, F.; Queipo-Ortuño, M.I.; Tinahones, F.J. Insulin resistance is associated with specific gut microbiota in appendix samples from morbidly obese patients. *Am. J. Transl. Res.* **2016**, *8*, 5672. [PubMed]

291. Taddese, R.; Garza, D.R.; Ruiter, L.N.; de Jonge, M.I.; Belzer, C.; Aalvink, S.; Nagtegaal, I.D.; Dutilh, B.E.; Boleij, A. Growth rate alterations of human colorectal cancer cells by 157 gut bacteria. *Gut Microbes* **2020**, *12*, 1799733. [CrossRef]

292. Mancuso, C.; Santangelo, R. Alzheimer's disease and gut microbiota modifications: The long way between preclinical studies and clinical evidence. *Pharmacol. Res.* **2018**, *129*, 329–336. [CrossRef]

293. Abrishamkar, P.; Rodriguez, C.V.B.; Choudry, B.; Or, S. Antidepressant usage is associated with alterations in gut microbiota diversity and abundance in Parkinson's Disease patients. *Undergrad. J. Exp. Microbiol. Immunol.* **2022**, *8*, 1–13.

294. Luo, F.; Fang, C. Association between gut microbiota and post-stroke depression in Chinese population: A meta-analysis. *Heliyon* **2022**, *8*, e12605. [CrossRef]

295. Shin, N.R.; Gu, N.; Choi, H.S.; Kim, H. Combined effects of Scutellaria baicalensis with metformin on glucose tolerance of patients with type 2 diabetes via gut microbiota modulation. *Am. J. Physiol.-Endocrinol. Metab.* **2020**, *318*, E52–E61. [CrossRef]

296. Liu, B.; Zhang, Y.; Wang, R.; An, Y.; Gao, W.; Bai, L.; Li, Y.; Zhao, S.; Fan, J.; Liu, E. Western diet feeding influences gut microbiota profiles in apoE knockout mice. *Lipids Health Dis.* **2018**, *17*, 159. [CrossRef]

297. Coker, O.O.; Nakatsu, G.; Dai, R.Z.; Wu, W.K.K.; Wong, S.H.; Ng, S.C.; Chan, F.K.L.; Sung, J.J.Y.; Yu, J. Enteric fungal microbiota dysbiosis and ecological alterations in colorectal cancer. *Gut* **2019**, *68*, 654–662. [CrossRef]

298. Moreno-Indias, I.; Torres, M.; Sanchez-Alcoholado, L.; Cardona, F.; Almendros, I.; Gozal, D.; Montserrat, J.M.; Queipo-Ortuño, M.I.; Farré, R. Normoxic recovery mimicking treatment of sleep apnea does not reverse intermittent hypoxia-induced bacterial dysbiosis and low-grade endotoxemia in mice. *Sleep* **2016**, *39*, 1891–1897. [CrossRef] [PubMed]

299. Han, L.; Li, T.; Du, M.; Chang, R.; Zhan, B.; Mao, X. Beneficial effects of potentilla discolor bunge water extract on inflammatory cytokines release and gut microbiota in high-fat diet and streptozotocin-induced type 2 diabetic mice. *Nutrients* **2019**, *11*, 670. [CrossRef] [PubMed]

300. Soltys, K.; Stuchlikova, M.; Hlavaty, T.; Gaalova, B.; Budis, J.; Gazdarica, J.; Krajcovicova, A.; Zelinkova, Z.; Szemes, T.; Kuba, D.; et al. Seasonal changes of circulating 25-hydroxyvitamin D correlate with the lower gut microbiome composition in inflammatory bowel disease patients. *Sci. Rep.* **2020**, *10*, 6024. [CrossRef] [PubMed]

301. Wang, X.; Qi, Q.; Wang, Y.; Wu, H.; Jin, X.; Yao, H.; Jin, D.; Liu, Y.; Wang, C. Gut microbiota was modulated by moxibustion stimulation in rats with irritable bowel syndrome. *Chin. Med.* **2018**, *13*, 63. [CrossRef]

302. Monira, S.; Nakamura, S.; Gotoh, K.; Izutsu, K.; Watanabe, H.; Alam, N.H.; Endtz, H.P.; Cravioto, A.; Ali, S.I.; Nakaya, T.; et al. Gut microbiota of healthy and malnourished children in Bangladesh. *Front. Microbiol.* **2011**, *2*, 228. [CrossRef]

303. Li, L.; Li, R.; Zhu, R.; Chen, B.; Tian, Y.; Zhang, H.; Xia, B.; Jia, Q.; Wang, L.; Zhao, D.; et al. Salvianolic acid B prevents body weight gain and regulates gut microbiota and LPS/TLR4 signaling pathway in high-fat diet-induced obese mice. *Food Funct.* **2020**, *11*, 8743–8756. [CrossRef] [PubMed]

304. Wu, M.; Wu, Y.; Deng, B.; Li, J.; Cao, H.; Qu, Y.; Qian, X.; Zhong, G. Isoliquiritigenin decreases the incidence of colitis-associated colorectal cancer by modulating the intestinal microbiota. *Oncotarget* **2016**, *7*, 85318. [CrossRef]

305. Shen, L.; Liu, L.; Ji, H.-F. Alzheimer's disease histological and behavioral manifestations in transgenic mice correlate with specific gut microbiome state. *J. Alzheimers Dis.* **2017**, *56*, 385–390. [CrossRef]

306. Coretti, L.; Cristiano, C.; Florio, E.; Scala, G.; Lama, A.; Keller, S.; Cuomo, M.; Russo, R.; Pero, R.; Paciello, O.; et al. Sex-related alterations of gut microbiota composition in the BTBR mouse model of autism spectrum disorder. *Sci. Rep.* **2017**, *7*, 45356. [CrossRef]

307. Sun, J.; Li, H.; Jin, Y.; Yu, J.; Mao, S.; Su, K.-P.; Ling, Z.; Liu, J. Probiotic Clostridium butyricum ameliorated motor deficits in a mouse model of Parkinson's disease via gut microbiota-GLP-1 pathway. *Brain Behav. Immun.* **2021**, *91*, 703–715. [CrossRef]

308. Duan, J.; Huang, Y.; Tan, X.; Chai, T.; Wu, J.; Zhang, H.; Li, Y.; Hu, X.; Zheng, P.; Ji, P.; et al. Characterization of gut microbiome in mice model of depression with divergent response to escitalopram treatment. *Transl. Psychiatry* **2021**, *11*, 303. [CrossRef] [PubMed]

309. Zhang, C.; Chen, F.; Shen, Y.; Chen, Y.; Ma, J. Sleep apnea is associated with the increase of certain genera of Ruminococcaceae and Lachnospiraceae in the gut microbiome of hypertensive patients. *Expert Rev. Respir. Med.* **2022**, *16*, 1247–1256. [CrossRef] [PubMed]

310. Zhao, L.; Lou, H.; Peng, Y.; Chen, S.; Zhang, Y.; Li, X. Comprehensive relationships between gut microbiome and faecal metabolome in individuals with type 2 diabetes and its complications. *Endocrine* **2019**, *66*, 526–537. [CrossRef]

311. Maukonen, J.; Kolho, K.-L.; Paasela, M.; Honkanen, J.; Klemetti, P.; Vaarala, O.; Saarela, M. Altered fecal microbiota in paediatric inflammatory bowel disease. *J. Crohn's Colitis* **2015**, *9*, 1088–1095. [CrossRef]

312. Schulz, N.; Belheouane, M.; Dahmen, B.; Ruan, V.A.; Specht, H.E.; Dempfle, A.; Herpertz-Dahlmann, B.; Baines, J.F.; Seitz, J. Gut microbiota alteration in adolescent anorexia nervosa does not normalize with short-term weight restoration. *Int. J. Eat. Disord.* **2021**, *54*, 969–980. [CrossRef] [PubMed]

313. Ma, L.; Ni, Y.; Wang, Z.; Tu, W.; Ni, L.; Zhuge, F.; Zheng, A.; Hu, L.; Zhao, Y.; Zheng, L.; et al. Spermidine improves gut barrier integrity and gut microbiota function in diet-induced obese mice. *Gut Microbes* **2020**, *12*, 1832857. [CrossRef] [PubMed]

314. Hexun, Z.; Miyake, T.; Maekawa, T.; Mori, H.; Yasukawa, D.; Ohno, M.; Nishida, A.; Andoh, A.; Tani, M. High abundance of lachnospiraceae in the human gut microbiome is related to high immunoscores in advanced colorectal cancer. *Cancer Immunol. Immunother.* **2023**, *72*, 315–326. [CrossRef]

315. Ding, X.; Xu, Y.; Zhang, X.; Zhang, L.; Duan, G.; Song, C.; Li, Z.; Yang, Y.; Wang, Y.; Wang, X.; et al. Gut microbiota changes in patients with autism spectrum disorders. *J. Psychiatr. Res.* **2020**, *129*, 149–159. [CrossRef]

316. Hill-Burns, E.M.; Debelius, J.W.; Morton, J.T.; Wissemann, W.T.; Lewis, M.R.; Wallen, Z.D.; Peddada, S.D.; Factor, S.A.; Molho, E.; Zabetian, C.P.; et al. Parkinson's disease and Parkinson's disease medications have distinct signatures of the gut microbiome. *Mov. Disord.* **2017**, *32*, 739–749. [CrossRef]

317. Zhang, H.-h.; Liu, J.; Lv, Y.-j.; Jiang, Y.-l.; Pan, J.-x.; Zhu, Y.-j.; Huang, M.-g.; Zhang, S.-k. Changes in intestinal microbiota of type 2 diabetes in mice in response to dietary supplementation with instant tea or matcha. *Can. J. Diabetes* **2020**, *44*, 44–52. [CrossRef]

318. Guo, H.; Yu, L.; Tian, F.; Chen, W.; Zhai, Q. The Potential Therapeutic Role of Lactobacillaceae rhamnosus for Treatment of Inflammatory Bowel Disease. *Foods* **2023**, *12*, 692. [CrossRef] [PubMed]

319. Taverniti, V.; Guglielmetti, S. Methodological issues in the study of intestinal microbiota in irritable bowel syndrome. *World J. Gastroenterol. WJG* **2014**, *20*, 8821. [PubMed]

320. Ye, J.; Zhao, Y.; Chen, X.; Zhou, H.; Yang, Y.; Zhang, X.; Huang, Y.; Zhang, N.; Lui, E.M.; Xiao, M. Pu-erh tea ameliorates obesity and modulates gut microbiota in high fat diet fed mice. *Food Res. Int.* **2021**, *144*, 110360. [CrossRef] [PubMed]

321. Zhao, L.; Zhang, X.; Zuo, T.; Yu, J. The composition of colonic commensal bacteria according to anatomical localization in colorectal cancer. *Engineering* **2017**, *3*, 90–97. [CrossRef]

322. Fu, S.-C.; Lee, C.-H.; Wang, H. Exploring the association of autism spectrum disorders and constipation through analysis of the gut microbiome. *Int. J. Environ. Res. Public Health* **2021**, *18*, 667. [CrossRef]

323. Hopfner, F.; Künstner, A.; Müller, S.H.; Künzel, S.; Zeuner, K.E.; Margraf, N.G.; Deuschl, G.; Baines, J.F.; Kuhlenbäumer, G. Gut microbiota in Parkinson disease in a northern German cohort. *Brain Res.* **2017**, *1667*, 41–45. [CrossRef]

324. Chevalier, G.; Siopi, E.; Guenin-Macé, L.; Pascal, M.; Laval, T.; Rifflet, A.; Boneca, I.G.; Demangel, C.; Colsch, B.; Pruvost, A.; et al. Effect of gut microbiota on depressive-like behaviors in mice is mediated by the endocannabinoid system. *Nat. Commun.* **2020**, *11*, 6363. [CrossRef]

325. Zhang, C.; Zhang, T.; Lu, W.; Duan, X.; Luo, X.; Liu, S.; Chen, Y.; Li, Y.; Chen, J.; Liao, J.; et al. Altered airway microbiota composition in patients with pulmonary hypertension. *Hypertension* **2020**, *76*, 1589–1599. [CrossRef]

326. Balmasova, I.P.; Olekhnovich, E.I.; Klimina, K.M.; Korenkova, A.A.; Vakhitova, M.T.; Babaev, E.A.; Ovchinnikova, L.A.; Lomakin, Y.A.; Smirnov, I.V.; Tsarev, V.N.; et al. Drift of the subgingival periodontal microbiome during chronic periodontitis in Type 2 diabetes mellitus patients. *Pathogens* **2021**, *10*, 504. [CrossRef]

327. Hourigan, S.; Chen, L.; Grigoryan, Z.; Laroche, G.; Weidner, M.; Sears, C.; Oliva-Hemker, M. Microbiome changes associated with sustained eradication of *Clostridium difficile* after single faecal microbiota transplantation in children with and without inflammatory bowel disease. *Aliment. Pharmacol. Ther.* **2015**, *42*, 741–752. [CrossRef]

328. Shin, S.; Cho, K.Y. Altered gut microbiota and shift in Bacteroidetes between young obese and normal-weight Korean children: A cross-sectional observational study. *BioMed Res. Int.* **2020**, *2020*. [CrossRef]

329. Wang, P.; Ding, S.; Sun, L.; Feng, Y.; Guo, K.; Zhu, Y.; Huang, D.; Ruan, S. Characteristics and differences of gut microbiota in patients with different traditional Chinese medicine syndromes of colorectal cancer and normal population. *J. Cancer* **2020**, *11*, 7357. [CrossRef] [PubMed]

330. Chen, L.; Xu, X.; Wu, X.; Cao, H.; Li, X.; Hou, Z.; Wang, B.; Liu, J.; Ji, X.; Zhang, P.; et al. A comparison of the composition and functions of the oral and gut microbiotas in Alzheimer's patients. *Front. Cell. Infect. Microbiol.* **2022**, *1241*, 942460. [CrossRef] [PubMed]

331. Shen, L. Gut, oral and nasal microbiota and Parkinson's disease. *Microb. Cell Factories* **2020**, *19*, 50. [CrossRef] [PubMed]

332. Tien, N.T.T. Analysis of the Gut Microbiota of Japanese Alzheimer's Disease Patients and Characterization of Their Butyrate-Producing Bacteria. 2018. Available online: https://ousar.lib.okayama-u.ac.jp/files/public/5/56307/20181212153730430590/K0 005847_Fulltext.pdf (accessed on 23 September 2023).

333. Chen, Z.; Xie, Y.; Zhou, F.; Zhang, B.; Wu, J.; Yang, L.; Xu, S.; Stedtfeld, R.; Chen, Q.; Liu, J.; et al. Featured gut microbiomes associated with the progression of chronic hepatitis B disease. *Front. Microbiol.* **2020**, *11*, 383. [CrossRef]

334. Gonzalez-Mercado, V.J.; Lim, J.; Saligan, L.N.; Perez, N.; Rodriguez, C.; Bernabe, R.; Ozorio, S.; Pedro, E.; Sepehri, F.; Aouizerat, B. Gut microbiota and depressive symptoms at the end of CRT for rectal cancer: A cross-sectional pilot study. *Depress. Res. Treat.* **2021**, *2021*, 7967552. [CrossRef]

335. Zhang, Y.; Lu, S.; Yang, Y.; Wang, Z.; Wang, B.; Zhang, B.; Yu, J.; Lu, W.; Pan, M.; Zhao, J.; et al. The diversity of gut microbiota in type 2 diabetes with or without cognitive impairment. *Aging Clin. Exp. Res.* **2021**, *33*, 589–601. [CrossRef]

336. Knights, D.; Lassen, K.G.; Xavier, R.J. Advances in inflammatory bowel disease pathogenesis: Linking host genetics and the microbiome. *Gut* **2013**, *62*, 1505–1510. [CrossRef]

337. Yun, Y.; Kim, H.-N.; Lee, E.-J.; Ryu, S.; Chang, Y.; Shin, H.; Kim, H.-L.; Kim, T.H.; Yoo, K.; Kim, H.Y. Fecal and blood microbiota profiles and presence of nonalcoholic fatty liver disease in obese versus lean subjects. *PLoS ONE* **2019**, *14*, e0213692. [CrossRef]

338. Kim, M.-H.; Yun, K.E.; Kim, J.; Park, E.; Chang, Y.; Ryu, S.; Kim, H.-L.; Kim, H.-N. Gut microbiota and metabolic health among overweight and obese individuals. *Sci. Rep.* **2020**, *10*, 19417. [CrossRef]

339. Park, J.-Y.; Choi, J.; Lee, Y.; Lee, J.-E.; Lee, E.-H.; Kwon, H.-J.; Yang, J.; Jeong, B.-R.; Kim, Y.-K.; Han, P.-L. Metagenome analysis of bodily microbiota in a mouse model of Alzheimer disease using bacteria-derived membrane vesicles in blood. *Exp. Neurobiol.* **2017**, *26*, 369. [CrossRef] [PubMed]

340. Li, F.; Wang, P.; Chen, Z.; Sui, X.; Xie, X.; Zhang, J. Alteration of the fecal microbiota in North-Eastern Han Chinese population with sporadic Parkinson's disease. *Neurosci. Lett.* **2019**, *707*, 134297. [CrossRef] [PubMed]

341. Tsai, C.-F.; Chuang, C.-H.; Wang, Y.-P.; Lin, Y.-B.; Tu, P.-C.; Liu, P.-Y.; Wu, P.-S.; Lin, C.-Y.; Lu, C.-L. Differences in gut microbiota correlate with symptoms and regional brain volumes in patients with late-life depression. *Front. Aging Neurosci.* **2022**, *14*, 885393. [CrossRef] [PubMed]

342. Xiang, K.; Zhang, J.-J.; Xu, Y.-Y.; Zhong, X.; Ni, J.; Pan, H.-F. Genetically predicted causality of 28 gut microbiome families and type 2 diabetes mellitus risk. *Front. Endocrinol.* **2022**, *13*, 9. [CrossRef] [PubMed]

343. Danilova, N.; Abdulkhakov, S.; Grigoryeva, T.; Dubinkina, V.; Odintsova, V.; Tyakht, A.; Pavlenko, A.; Odintsova, A.; Abdulkhakov, R.; Govorun, V. P794 Alterations of intestinal microbiota in ulcerative colitis. *J. Crohn's Colitis* **2017**, *11* (Suppl. S1), S486. [CrossRef]

344. Chen, H.; Ou, R.; Tang, N.; Su, W.; Yang, R.; Yu, X.; Zhang, G.; Jiao, J.; Zhou, X. Alternation of the gut microbiota in irritable bowel syndrome: An integrated analysis based on multicenter amplicon sequencing data. *J. Transl. Med.* **2023**, *21*, 117. [CrossRef]

345. Smitka, K.; Prochazkova, P.; Roubalova, R.; Dvorak, J.; Papezova, H.; Hill, M.; Pokorny, J.; Kittnar, O.; Bilej, M.; Tlaskalova-Hogenova, H. Current aspects of the role of autoantibodies directed against appetite-regulating hormones and the gut microbiome in eating disorders. *Front. Endocrinol.* **2021**, *12*, 613983. [CrossRef]

346. Aranaz, P.; Ramos-Lopez, O.; Cuevas-Sierra, A.; Martinez, J.A.; Milagro, F.I.; Riezu-Boj, J.I. A predictive regression model of the obesity-related inflammatory status based on gut microbiota composition. *Int. J. Obes.* **2021**, *45*, 2261–2268. [CrossRef]

347. Long, S.; Yang, Y.; Shen, C.; Wang, Y.; Deng, A.; Qin, Q.; Qiao, L. Metaproteomics characterizes human gut microbiome function in colorectal cancer. *NPJ Biofilms Microbiomes* **2020**, *6*, 14. [CrossRef]

348. Petrov, V.A.; Saltykova, I.V.; Zhukova, I.A.; Alifirova, V.M.; Zhukova, N.G.; Dorofeeva, Y.B.; Tyakht, A.V.; Kovarsky, B.A.; Alekseev, D.G.; Kostryukova, E.S.; et al. Analysis of gut microbiota in patients with Parkinson's disease. *Bull. Exp. Biol. Med.* **2017**, *162*, 734–737. [CrossRef]

349. Fontana, A.; Manchia, M.; Panebianco, C.; Paribello, P.; Arzedi, C.; Cossu, E.; Garzilli, M.; Montis, M.A.; Mura, A.; Pisanu, C.; et al. Exploring the role of gut microbiota in major depressive disorder and in treatment resistance to antidepressants. *Biomedicines* **2020**, *8*, 311. [CrossRef]

350. Ponziani, F.R.; Bhoori, S.; Castelli, C.; Putignani, L.; Rivoltini, L.; Del Chierico, F.; Sanguinetti, M.; Morelli, D.; Sterbini, F.P.; Petito, V.; et al. Hepatocellular carcinoma is associated with gut microbiota profile and inflammation in nonalcoholic fatty liver disease. *Hepatology* **2019**, *69*, 107–120. [CrossRef]

351. Zhang, F.; Chen, D.; Zhang, L.; Zhao, Q.; Ma, Y.; Zhang, X.; Zhao, S.; Chen, C. Diaphragma juglandis extracts modifies the gut microbiota during prevention of type 2 diabetes in rats. *J. Ethnopharmacol.* **2022**, *283*, 114484. [CrossRef] [PubMed]

352. Wang, K.; Guo, J.; Chang, X.; Gui, S. Painong-San extract alleviates dextran sulfate sodium-induced colitis in mice by modulating gut microbiota, restoring intestinal barrier function and attenuating TLR4/NF-κB signaling cascades. *J. Pharm. Biomed. Anal.* **2022**, *209*, 114529. [CrossRef] [PubMed]

353. Sampsell, K.; Wang, W.; Ohland, C.; Mager, L.F.; Pett, N.; Lowry, D.E.; Sales, K.M.; McNeely, M.L.; McCoy, K.D.; Culos-Reed, S.N.; et al. Exercise and Prebiotic Fiber Provide Gut Microbiota-Driven Benefit in a Survivor to Germ-Free Mouse Translational Model of Breast Cancer. *Cancers* **2022**, *14*, 2722. [CrossRef] [PubMed]

354. Maya-Lucas, O.; Murugesan, S.; Nirmalkar, K.; Alcaraz, L.D.; Hoyo-Vadillo, C.; Pizano-Zárate, M.L.; García-Mena, J. The gut microbiome of Mexican children affected by obesity. *Anaerobe* **2019**, *55*, 11–23. [CrossRef] [PubMed]

355. Zhang, Q.; Zuo, Z.; Zhuang, J.; Qu, Z.; Han, S.; Jin, W.; Liu, J.; Han, S. Prediction model of poorly differentiated colorectal cancer (CRC) based on gut bacteria. *BMC Microbiol.* **2022**, *22*, 312.

356. Jones, J.; Reinke, S.N.; Mousavi-Derazmahalleh, M.; Palmer, D.J.; Christophersen, C.T. Changes to the gut microbiome in young children showing early behavioral signs of autism. *Front. Microbiol.* **2022**, *13*, 905901. [CrossRef]

357. Romano, S.; Savva, G.M.; Bedarf, J.R.; Charles, I.G.; Hildebrand, F.; Narbad, A. Meta-analysis of the Parkinson's disease gut microbiome suggests alterations linked to intestinal inflammation. *NPJ Park. Dis.* **2021**, *7*, 27. [CrossRef]

358. Liu, X.; Li, X.; Teng, T.; Jiang, Y.; Xiang, Y.; Fan, L.; Yu, Y.; Zhou, X.; Xie, P. Comparative analysis of gut microbiota and fecal metabolome features among multiple depressive animal models. *J. Affect. Disord.* **2022**, *314*, 103–111. [CrossRef]

359. Jian, J.; Nie, M.T.; Xiang, B.; Qian, H.; Yin, C.; Zhang, X.; Zhang, M.; Zhu, X.; Xie, W.-F. Rifaximin ameliorates non-alcoholic steatohepatitis in mice through regulating gut microbiome-related bile acids. *Front. Pharmacol.* **2022**, *13*, 1099. [CrossRef] [PubMed]

360. Maskarinec, G.; Raquinio, P.; Kristal, B.S.; Setiawan, V.W.; Wilkens, L.R.; Franke, A.A.; Lim, U.; Le Marchand, L.; Randolph, T.W.; Lampe, J.W.; et al. The gut microbiome and type 2 diabetes status in the Multiethnic Cohort. *PLoS ONE* **2021**, *16*, e0250855. [CrossRef] [PubMed]

361. Rengarajan, S.; Vivio, E.E.; Parkes, M.; Peterson, D.A.; Roberson, E.D.; Newberry, R.D.; Ciorba, M.A.; Hsieh, C.-S. Dynamic immunoglobulin responses to gut bacteria during inflammatory bowel disease. *Gut Microbes* **2020**, *11*, 405–420. [CrossRef]

362. Shivakumar, N.; Sivadas, A.; Devi, S.; Jahoor, F.; McLaughlin, J.; Smith, C.P.; Kurpad, A.V.; Mukhopadhyay, A. Gut microbiota profiles of young South Indian children: Child sex-specific relations with growth. *PLoS ONE* **2021**, *16*, e0251803. [CrossRef] [PubMed]

363. Schott, E.M.; Farnsworth, C.W.; Grier, A.; Lillis, J.A.; Soniwala, S.; Dadourian, G.H.; Bell, R.D.; Doolittle, M.L.; Villani, D.A.; Awad, H.; et al. Targeting the gut microbiome to treat the osteoarthritis of obesity. *JCI Insight* **2018**, *3*, e95997. [CrossRef] [PubMed]

364. Cheng, Y.; Ling, Z.; Li, L. The intestinal microbiota and colorectal cancer. *Front. Immunol.* **2020**, *11*, 615056. [CrossRef]

365. Li, P.; Killinger, B.A.; Ensink, E.; Beddows, I.; Yilmaz, A.; Lubben, N.; Lamp, J.; Schilthuis, M.; Vega, I.E.; Woltjer, R.; et al. Gut microbiota dysbiosis is associated with elevated bile acids in Parkinson's disease. *Metabolites* **2021**, *11*, 29. [CrossRef] [PubMed]

366. Gu, Y.; Chen, H.; Li, X.; Li, D.; Sun, Y.; Yang, L.; Ma, Y.; Chen, E.C.Y. *Lactobacillus paracasei* IMC 502 ameliorates type 2 diabetes by mediating gut microbiota–SCFA–hormone/inflammation pathway in mice. *J. Sci. Food Agric.* **2023**, *103*, 2949–2959. [CrossRef] [PubMed]

367. Morgan, X.C.; Tickle, T.L.; Sokol, H.; Gevers, D.; Devaney, K.L.; Ward, D.V.; Reyes, J.A.; Shah, S.A.; LeLeiko, N.; Snapper, S.B.; et al. Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. *Genome Biol.* **2012**, *13*, R79. [CrossRef]

368. Clarke, S.F.; Murphy, E.F.; O'sullivan, O.; Ross, R.P.; O'toole, P.W.; Shanahan, F.; Cotter, P.D. Targeting the microbiota to address diet-induced obesity: A time dependent challenge. *PLoS ONE* **2013**, *8*, e65790. [CrossRef]

369. Zhang, M.; Zhao, D.; Zhou, G.; Li, C. Dietary pattern, gut microbiota, and Alzheimer's disease. *J. Agric. Food Chem.* **2020**, *68*, 12800–12809. [CrossRef] [PubMed]

370. Inoue, R.; Sakaue, Y.; Sawai, C.; Sawai, T.; Ozeki, M.; Romero-Pérez, G.A.; Tsukahara, T. A preliminary investigation on the relationship between gut microbiota and gene expressions in peripheral mononuclear cells of infants with autism spectrum disorders. *Biosci. Biotechnol. Biochem.* **2016**, *80*, 2450–2458. [CrossRef] [PubMed]

371. Ren, T.; Gao, Y.; Qiu, Y.; Jiang, S.; Zhang, Q.; Zhang, J.; Wang, L.; Zhang, Y.; Wang, L.; Nie, K. Gut microbiota altered in mild cognitive impairment compared with normal cognition in sporadic Parkinson's disease. *Front. Neurol.* **2020**, *11*, 137. [CrossRef] [PubMed]

372. Sun, L.; Ma, L.; Zhang, H.; Cao, Y.; Wang, C.; Hou, N.; Huang, N.; von Deneen, K.M.; Zhao, C.; Shi, Y.; et al. Fto deficiency reduces anxiety-and depression-like behaviors in mice via alterations in gut microbiota. *Theranostics* **2019**, *9*, 721. [CrossRef]

373. Bajaj, J.S. The role of microbiota in hepatic encephalopathy. *Gut Microbes* **2014**, *5*, 397–403. [CrossRef]

374. Palm, N.W.; De Zoete, M.R.; Cullen, T.W.; Barry, N.A.; Stefanowski, J.; Hao, L.; Degnan, P.H.; Hu, J.; Peter, I.; Zhang, W.; et al. Immunoglobulin A coating identifies colitogenic bacteria in inflammatory bowel disease. *Cell* **2014**, *158*, 1000–1010. [CrossRef]

375. Cuevas-Sierra, A.; Riezu-Boj, J.I.; Guruceaga, E.; Milagro, F.I.; Martínez, J.A. Sex-specific associations between gut Prevotellaceae and host genetics on adiposity. *Microorganisms* **2020**, *8*, 938. [CrossRef]

376. Hang, Z.; Lei, T.; Zeng, Z.; Cai, S.; Bi, W.; Du, H. Composition of intestinal flora affects the risk relationship between Alzheimer's disease/Parkinson's disease and cancer. *Biomed. Pharmacother.* **2022**, *145*, 112343. [CrossRef]

377. Sun, H.; You, Z.; Jia, L.; Wang, F. Autism spectrum disorder is associated with gut microbiota disorder in children. *BMC Pediatr.* **2019**, *19*, 516. [CrossRef]

378. Scheperjans, F.; Aho, V.; Pereira, P.A.; Koskinen, K.; Paulin, L.; Pekkonen, E.; Haapaniemi, E.; Kaakkola, S.; Eerola-Rautio, J.; Pohja, M.; et al. Gut microbiota are related to Parkinson's disease and clinical phenotype. *Mov. Disord.* **2015**, *30*, 350–358. [CrossRef]

379. Wu, J.; Li, J.; Gaurav, C.; Muhammad, U.; Chen, Y.; Li, X.; Chen, J.; Wang, Z. CUMS and dexamethasone induce depression-like phenotypes in mice by differentially altering gut microbiota and triggering macroglia activation. *Gen. Psychiatry* **2021**, *34*, e100529. [CrossRef] [PubMed]

380. Bajaj, J.S.; Betrapally, N.S.; Hylemon, P.B.; Heuman, D.M.; Daita, K.; White, M.B.; Unser, A.; Thacker, L.R.; Sanyal, A.J.; Kang, D.J.; et al. Salivary microbiota reflects changes in gut microbiota in cirrhosis with hepatic encephalopathy. *Hepatology* **2015**, *62*, 1260–1271. [CrossRef] [PubMed]

381. Čipčić Paljetak, H.; Barešić, A.; Panek, M.; Perić, M.; Matijašić, M.; Lojkić, I.; Barišić, A.; Vranešić Bender, D.; Ljubas Kelečić, D.; Brinar, M.; et al. Gut microbiota in mucosa and feces of newly diagnosed, treatment-naïve adult inflammatory bowel disease and irritable bowel syndrome patients. *Gut Microbes* **2022**, *14*, 2083419. [CrossRef] [PubMed]

382. Ahasan, M.S.; Waltzek, T.B.; Owens, L.; Ariel, E. Characterisation and comparison of the mucosa-associated bacterial communities across the gastrointestinal tract of stranded green turtles, Chelonia mydas. *AIMS Microbiol.* **2020**, *6*, 361.

383. Orbe-Orihuela, Y.C.; Godoy-Lozano, E.E.; Lagunas-Martínez, A.; Castañeda-Márquez, A.C.; Murga-Garrido, S.; Díaz-Benítez, C.E.; Ochoa-Leyva, A.; Cornejo-Granados, F.; Cruz, M.; Estrada, K.; et al. Association of Gut Microbiota with Dietary-dependent Childhood Obesity. *Arch. Med. Res.* **2022**, *53*, 407–415. [CrossRef]

384. Phipps, O.; Al-Hassi, H.O.; Quraishi, M.N.; Dickson, E.A.; Segal, J.; Steed, H.; Kumar, A.; Acheson, A.G.; Beggs, A.D.; Brookes, M.J. Oral and intravenous iron therapy differentially alter the on-and off-tumor microbiota in anemic colorectal cancer patients. *Cancers* **2021**, *13*, 1341. [CrossRef]

385. Ghyselinck, J.; Verstrepen, L.; Moens, F.; Van Den Abbeele, P.; Bruggeman, A.; Said, J.; Smith, B.; Barker, L.A.; Jordan, C.; Leta, V.; et al. Influence of probiotic bacteria on gut microbiota composition and gut wall function in an in-vitro model in patients with Parkinson's disease. *Int. J. Pharm. X* **2021**, *3*, 100087. [CrossRef]

386. Kelly, J.R.; Borre, Y.; O'Brien, C.; Patterson, E.; El Aidy, S.; Deane, J.; Kennedy, P.J.; Beers, S.; Scott, K.; Moloney, G.; et al. Transferring the blues: Depression-associated gut microbiota induces neurobehavioural changes in the rat. *J. Psychiatr. Res.* **2016**, *82*, 109–118. [CrossRef]

387. Bajaj, J. Potential mechanisms of action of rifaximin in the management of hepatic encephalopathy and other complications of cirrhosis. *Aliment. Pharmacol. Ther.* **2016**, *43*, 11–26. [CrossRef]

388. Eun, C.S.; Kwak, M.-J.; Han, D.S.; Lee, A.R.; Park, D.I.; Yang, S.-K.; Kim, Y.S.; Kim, J.F. Does the intestinal microbial community of Korean Crohn's disease patients differ from that of western patients? *BMC Gastroenterol.* **2016**, *16*, 28. [CrossRef]

389. Tang, B.; Hu, Y.; Chen, J.; Su, C.; Zhang, Q.; Huang, C. Oral and fecal microbiota in patients with diarrheal irritable bowel syndrome. *Heliyon* **2023**, *9*, e13114. [CrossRef] [PubMed]

390. Wang, S.-T.; Meng, X.-Z.; Zhang, J.-H.; Dai, Y.-F.; Shen, Y.; Xu, X.-Y.; Wang, R.-Q.; Li, J.-L. 16S rRNA sequencing analysis of the correlation between the intestinal microbiota and body-mass of grass carp (*Ctenopharyngodon idella*). *Comp. Biochem. Physiol. Part D Genom. Proteom.* **2020**, *35*, 100699. [CrossRef] [PubMed]

391. Yuan, W.; Lu, W.; Wang, H.; Wu, W.; Zhou, Q.; Chen, Y.; Lee, Y.K.; Zhao, J.; Zhang, H.; Chen, W. A multiphase dietetic protocol incorporating an improved ketogenic diet enhances weight loss and alters the gut microbiome of obese people. *Int. J. Food Sci. Nutr.* **2022**, *73*, 238–250. [CrossRef] [PubMed]

392. Yang, J.; McDowell, A.; Kim, E.K.; Seo, H.; Lee, W.H.; Moon, C.-M.; Kym, S.-M.; Lee, D.H.; Park, Y.S.; Jee, Y.-K.; et al. Development of a colorectal cancer diagnostic model and dietary risk assessment through gut microbiome analysis. *Exp. Mol. Med.* **2019**, *51*, 1–15. [CrossRef]

393. Park, S.; Wu, X. Modulation of the Gut Microbiota in Memory Impairment and Alzheimer's Disease via the Inhibition of the Parasympathetic Nervous System. *Int. J. Mol. Sci.* **2022**, *23*, 13574. [CrossRef]

394. Zhu, H.; Zhang, H.; Hou, B.; Xu, B.; Ji, L.; Wu, Y. Curcumin Regulates Gut Microbiota and Exerts a Neuroprotective Effect in the MPTP Model of Parkinson's Disease. *Evid. Based Complement. Alternat. Med.* **2022**, *2022*, 9110560. [CrossRef]

395. Yu, M.; Jia, H.-M.; Qin, L.-L.; Zou, Z.-M. Gut microbiota and gut tissue metabolites involved in development and prevention of depression. *J. Affect. Disord.* **2022**, *297*, 8–17. [CrossRef]

396. Wang, J.Y.; Bajaj, J.S.; Wang, J.B.; Shang, J.; Zhou, X.M.; Guo, X.L.; Zhu, X.; Na Meng, L.; Jiang, H.X.; Mi, Y.Q.; et al. Lactulose improves cognition, quality of life, and gut microbiota in minimal hepatic encephalopathy: A multicenter, randomized controlled trial. *J. Dig. Dis.* **2019**, *20*, 547–556. [CrossRef] [PubMed]

397. Lin, R.; He, X.; Chen, H.; He, Q.; Yao, Z.; Li, Y.; Yang, H.; Simpson, S. Oil tea improves glucose and lipid levels and alters gut microbiota in type 2 diabetic mice. *Nutr. Res.* **2018**, *57*, 67–77. [CrossRef]

398. Dou, X.; Gao, N.; Yan, D.; Shan, A. Sodium butyrate alleviates mouse colitis by regulating gut microbiota dysbiosis. *Animals* **2020**, *10*, 1154. [CrossRef]

399. Lian, Q.; Ding, H.; Zhu, H.; Zhang, C.; Yu, S.; Jie, H.; Zhang, Y.; Wu, B.; Liang, G.; Zhang, G.; et al. Study of Jianpi mixture on intestinal microbiota of diarrhea irritable bowel syndrome mice. *Evid. Based Complement. Alternat. Med.* **2020**, *2020*, 5241308. [CrossRef] [PubMed]

400. Du, R.; Jiao, S.; Dai, Y.; An, J.; Lv, J.; Yan, X.; Wang, J.; Han, B. Probiotic Bacillus amyloliquefaciens C-1 improves growth performance, stimulates GH/IGF-1, and regulates the gut microbiota of growth-retarded beef calves. *Front. Microbiol.* **2018**, *9*, 2006. [CrossRef] [PubMed]

401. Koliarakis, I.; Athanasakis, E.; Sgantzos, M.; Mariolis-Sapsakos, T.; Xynos, E.; Chrysos, E.; Souglakos, J.; Tsiaoussis, J. Intestinal microbiota in colorectal cancer surgery. *Cancers* **2020**, *12*, 3011. [CrossRef] [PubMed]

402. Zhou, Y.; Wang, Y.; Quan, M.; Zhao, H.; Jia, J. Gut microbiota changes and their correlation with cognitive and neuropsychiatric symptoms in Alzheimer's disease. *J. Alzheimers Dis.* **2021**, *81*, 583–595. [CrossRef] [PubMed]

403. Petrak, F.; Herpertz, S.; Hirsch, J.; Röhrig, B.; Donati-Hirsch, I.; Juckel, G.; Meier, J.J.; Gatermann, S. Gut microbiota differs in composition between adults with type 1 diabetes with or without depression and healthy control participants: A case-control study. *BMC Microbiol.* **2022**, *22*, 169. [CrossRef] [PubMed]

404. Badran, M.; Khalyfa, A.; Ericsson, A.; Gozal, D. Fecal microbiota transplantation from mice exposed to chronic intermittent hypoxia elicits sleep disturbances in naïve mice. *Exp. Neurol.* **2020**, *334*, 113439. [CrossRef]

405. De Palma, G.; Lynch, M.D.; Lu, J.; Dang, V.T.; Deng, Y.; Jury, J.; Umeh, G.; Miranda, P.M.; Pastor, M.P.; Sidani, S.; et al. Transplantation of fecal microbiota from patients with irritable bowel syndrome alters gut function and behavior in recipient mice. *Sci. Transl. Med.* **2017**, *9*, eaaf6397. [CrossRef]

406. Bai, J.; Hu, Y.; Bruner, D. Composition of gut microbiota and its association with body mass index and lifestyle factors in a cohort of 7–18 years old children from the American Gut Project. *Pediatr. Obes.* **2019**, *14*, e12480. [CrossRef] [PubMed]

407. Bäuerl, C.; Collado, M.C.; Diaz Cuevas, A.; Viña, J.; Pérez Martínez, G. *Shifts in Gut Microbiota Composition in an APP/PSS1 Transgenic Mouse Model of Alzheimer's Disease during Lifespan*; Blackwell Science Ltd.: Oxford, UK, 2018; pp. 464–471.

408. Jin, M.; Li, J.; Liu, F.; Lyu, N.; Wang, K.; Wang, L.; Liang, S.; Tao, S.; Zhu, B.; Alkasir, R. Analysis of the gut microflora in patients with Parkinson's disease. *Front. Neurosci.* **2019**, *13*, 1184. [CrossRef]

409. Yang, J.; Zhang, Z.; Xie, Z.; Bai, L.; Xiong, P.; Chen, F.; Zhu, T.; Peng, Q.; Wu, H.; Zhou, Y.; et al. Metformin modulates microbiota-derived inosine and ameliorates methamphetamine-induced anxiety and depression-like withdrawal symptoms in mice. *Biomed. Pharmacother.* **2022**, *149*, 112837. [CrossRef]

410. Chassard, C.; Dapoigny, M.; Scott, K.P.; Crouzet, L.; Del'Homme, C.; Marquet, P.; Martin, J.C.; Pickering, G.; Ardid, D.; Eschalier, A.; et al. Functional dysbiosis within the gut microbiota of patients with constipated-irritable bowel syndrome. *Aliment. Pharmacol. Ther.* **2012**, *35*, 828–838. [CrossRef] [PubMed]

411. Morissette, B.; Talbot, G.; Beaulieu, C.; Lessard, M. Growth performance of piglets during the first two weeks of lactation affects the development of the intestinal microbiota. *J. Anim. Physiol. Anim. Nutr.* **2018**, *102*, 525–532. [CrossRef] [PubMed]

412. Liu, B.-N.; Liu, X.-T.; Liang, Z.-H.; Wang, J.-H. Gut microbiota in obesity. *World J. Gastroenterol.* **2021**, *27*, 3837. [CrossRef]

413. Tran, T.T.; Corsini, S.; Kellingray, L.; Hegarty, C.; Le Gall, G.; Narbad, A.; Müller, M.; Tejera, N.; O'Toole, P.W.; Minihane, A.-M.; et al. APOE genotype influences the gut microbiome structure and function in humans and mice: Relevance for Alzheimer's disease pathophysiology. *FASEB J.* **2019**, *33*, 8221. [CrossRef] [PubMed]

414. Onyema Oshim, I.; Regina Agbakoba, N.; Celestine Oguejiofor, O.; Anukam, K.C. Selective Microbial Biomarkers in Type-2 Diabetes with Principal Component Analysis and Receiver-operating Characteristic Curves. *Int. J. Sci. Res. Dent. Med. Sci.* **2021**, *3*, 23–34.

415. Chen, H.; Ou, R.; Tang, N.; Su, W.; Yang, R.; Yu, X.; Zhang, G.; Jiao, J.; Zhou, X. An Integrated Multicenter Amplicon Sequencing Data Reveals New Evidence of the Interaction between the Gut Microbiota and Irritable Bowel Syndrome. *Res. Sq.* **2022**. [CrossRef]

416. Lan, D.; Ji, W.; Lin, B.; Chen, Y.; Huang, C.; Xiong, X.; Fu, M.; Mipam, T.D.; Ai, Y.; Zeng, B.; et al. Correlations between gut microbiota community structures of Tibetans and geography. *Sci. Rep.* **2017**, *7*, 16982. [CrossRef] [PubMed]

417. Liu, J.; Dong, W.; Zhao, J.; Wu, J.; Xia, J.; Xie, S.; Song, X. Gut microbiota profiling variated during colorectal cancer development in mouse. *BMC Genom.* **2022**, *23*, 848. [CrossRef]

418. Tartaglione, A.M.; Villani, A.; Ajmone-Cat, M.A.; Minghetti, L.; Ricceri, L.; Pazienza, V.; De Simone, R.; Calamandrei, G. Maternal immune activation induces autism-like changes in behavior, neuroinflammatory profile and gut microbiota in mouse offspring of both sexes. *Transl. Psychiatry* **2022**, *12*, 384. [CrossRef] [PubMed]

419. Vascellari, S.; Palmas, V.; Melis, M.; Pisanu, S.; Cusano, R.; Uva, P.; Perra, D.; Madau, V.; Sarchioto, M.; Oppo, V.; et al. Gut microbiota and metabolome alterations associated with Parkinson's disease. *mSystems* **2020**, *5*, e00561-20. [CrossRef] [PubMed]

420. Zhang, P.; Zhang, D.; Lai, J.; Fu, Y.; Wu, L.; Huang, H.; Pan, Y.; Jiang, J.; Xi, C.; Che, Z.; et al. Characteristics of the gut microbiota in bipolar depressive disorder patients with distinct weight. *CNS Neurosci. Ther.* **2023**, *29*, 74–83. [CrossRef]

421. Hyun, C.-K. Molecular and pathophysiological links between metabolic disorders and inflammatory bowel diseases. *Int. J. Mol. Sci.* **2021**, *22*, 9139. [CrossRef] [PubMed]

422. Ponziani, F.R.; Pompili, M.; Gasbarrini, A. *Rifaximin Re-Treatment in Patients with Irritable Bowel Syndrome: Feels Like the First Time?* Springer: Berlin/Heidelberg, Germany, 2017; pp. 2220–2222.

423. Coley, E.J.; Hsiao, E.Y. Malnutrition and the microbiome as modifiers of early neurodevelopment. *Trends Neurosci.* **2021**, *44*, 753–764. [CrossRef] [PubMed]

424. Ngowi, E.E.; Wang, Y.Z.; Khattak, S.; Khan, N.H.; Mahmoud, S.S.M.; Helmy, Y.A.S.H.; Jiang, Q.; Li, T.; Duan, S.; Ji, X.; et al. Impact of the factors shaping gut microbiota on obesity. *J. Appl. Microbiol.* **2021**, *131*, 2131–2147. [CrossRef]

425. Raskov, H.; Burcharth, J.; Pommergaard, H.-C. Linking gut microbiota to colorectal cancer. *J. Cancer* **2017**, *8*, 3378. [CrossRef] [PubMed]

426. Liu, J.; Gao, Z.; Liu, C.; Liu, T.; Gao, J.; Cai, Y.; Fan, X. Alteration of Gut Microbiota: New Strategy for Treating Autism Spectrum Disorder. *Front. Cell Dev. Biol.* **2022**, *10*, 192. [CrossRef] [PubMed]

427. Yan, Z.; Li, R.; Shi, W.; Yao, L. Role of the gut-microbiota-metabolite axis in the rotenone model of early-stage Parkinson's Disease. *Metab. Brain Dis.* **2022**, *37*, 2511–2520. [CrossRef]

428. Song, X.; Wang, W.; Ding, S.; Liu, X.; Wang, Y.; Ma, H. Puerarin ameliorates depression-like behaviors of with chronic unpredictable mild stress mice by remodeling their gut microbiota. *J. Affect. Disord.* **2021**, *290*, 353–363. [CrossRef]

429. Lachar, J.; Bajaj, J.S. (Eds.) Changes in the microbiome in cirrhosis and relationship to complications: Hepatic encephalopathy, spontaneous bacterial peritonitis, and sepsis. In *Seminars in Liver Disease*; Thieme Medical Publishers: Leipzig, Germany, 2016.

430. Sanchez-Alcoholado, L.; Castellano-Castillo, D.; Jordán-Martínez, L.; Moreno-Indias, I.; Cardila-Cruz, P.; Elena, D.; Muñoz-Garcia, A.J.; Queipo-Ortuño, M.I.; Jimenez-Navarro, M. Role of gut microbiota on cardio-metabolic parameters and immunity in coronary artery disease patients with and without type-2 diabetes mellitus. *Front. Microbiol.* **2017**, *8*, 1936. [CrossRef]

431. Staudacher, H.M.; Scholz, M.; Lomer, M.C.; Ralph, F.S.; Irving, P.M.; Lindsay, J.O.; Fava, F.; Tuohy, K.; Whelan, K. Gut microbiota associations with diet in irritable bowel syndrome and the effect of low FODMAP diet and probiotics. *Clin. Nutr.* **2021**, *40*, 1861–1870. [CrossRef]

432. Zeng, H.; Ishaq, S.L.; Zhao, F.-Q.; Wright, A.-D.G. Colonic inflammation accompanies an increase of β-catenin signaling and Lachnospiraceae/Streptococcaceae bacteria in the hind gut of high-fat diet-fed mice. *J. Nutr. Biochem.* **2016**, *35*, 30–36. [CrossRef] [PubMed]

433. Wieczorska, K.; Stolarek, M.; Stec, R. The role of the gut microbiome in colorectal cancer: Where are we? Where are we going? *Clin. Colorectal. Cancer* **2020**, *19*, 5–12. [CrossRef] [PubMed]

434. Altaib, H.; Nakamura, K.; Abe, M.; Badr, Y.; Yanase, E.; Nomura, I.; Suzuki, T. Differences in the concentration of the fecal neurotransmitters GABA and glutamate are associated with microbial composition among healthy human subjects. *Microorganisms* **2021**, *9*, 378. [CrossRef] [PubMed]

435. Mohamadkhani, A. Gut microbiota and fecal metabolome perturbation in children with autism spectrum disorder. *Middle East J. Dig. Dis.* **2018**, *10*, 205. [CrossRef]

436. Zhao, H.; Jin, K.; Jiang, C.; Pan, F.; Wu, J.; Luan, H.; Zhao, Z.; Chen, J.; Mou, T.; Wang, Z.; et al. A pilot exploration of multi-omics research of gut microbiome in major depressive disorders. *Transl. Psychiatry* **2022**, *12*, 8. [CrossRef] [PubMed]

437. Rocco, A.; Sgamato, C.; Compare, D.; Coccoli, P.; Nardone, O.M.; Nardone, G. Gut microbes and hepatic encephalopathy: From the old concepts to new perspectives. *Frontiers in Cell and Developmental Biology.* **2021**, *9*, 748253. [CrossRef]

438. Almugadam, B.S.; Liu, Y.; Chen, S.M.; Wang, C.H.; Shao, C.Y.; Ren, B.W.; Tang, L. Alterations of gut microbiota in type 2 diabetes individuals and the confounding effect of antidiabetic agents. *J. Diabetes Res.* **2020**, *2020*, 7253978. [CrossRef]

439. Zhou, X.-Y.; Li, M.; Li, X.; Long, X.; Zuo, X.-L.; Hou, X.-H.; Cong, Y.-Z.; Li, Y.-Q. Visceral hypersensitive rats share common dysbiosis features with irritable bowel syndrome patients. *World J. Gastroenterol.* **2016**, *22*, 5211. [CrossRef]

440. Zhai, S.; Qin, S.; Li, L.; Zhu, L.; Zou, Z.; Wang, L. Dietary butyrate suppresses inflammation through modulating gut microbiota in high-fat diet-fed mice. *FEMS Microbiol. Lett.* **2019**, *366*, fnz153. [CrossRef]

441. Carson, T.L.; Byrd, D.A.; Smith, K.S.; Carter, D.; Abaskaron, M.; Little, R.B.; van Der Pol, W.J.; Lefkowitz, E.J.; Morrow, C.D.; Fruge, A.D.; et al. A case-control study of the association between the gut microbiota and colorectal cancer: Exploring the roles of diet, stress, and race. *Res. Sq.* **2023**. [CrossRef]

442. Zhou, R.; Fan, X.; Schnabl, B. Role of the intestinal microbiome in liver fibrosis development and new treatment strategies. *Transl. Res.* **2019**, *209*, 22–38. [CrossRef] [PubMed]

443. Li, J.; Jia, S.; Yuan, C.; Yu, B.; Zhang, Z.; Zhao, M.; Liu, P.; Li, X.; Cui, B. Jerusalem artichoke inulin supplementation ameliorates hepatic lipid metabolism in type 2 diabetes mellitus mice by modulating the gut microbiota and fecal metabolome. *Food Funct.* **2022**, *13*, 11503–11517. [CrossRef] [PubMed]

444. Zuo, W.; Wang, B.; Bai, X.; Luan, Y.; Fan, Y.; Michail, S.; Sun, F. 16S rRNA and metagenomic shotgun sequencing data revealed consistent patterns of gut microbiome signature in pediatric ulcerative colitis. *Sci. Rep.* **2022**, *12*, 6421. [CrossRef] [PubMed]

445. Setiawan, J.; Chan, N.; Echavez, C.; Mathews, A. Increased body mass is associated with decreased gut microbiome diversity in Parkinson's Disease patients. *Undergrad. J. Exp. Microbiol. Immunol.* **2022**, *8*, 1–13.

446. Fernández, J.; Saettone, P.; Franchini, M.C.; Villar, C.J.; Lombó, F. Antitumor bioactivity and gut microbiota modulation of polyhydroxybutyrate (PHB) in a rat animal model for colorectal cancer. *Int. J. Biol. Macromol.* **2022**, *203*, 638–649. [CrossRef]

447. Nagarajan, A. Characterization of the Metabolic and Cognitive Features of a Novel Alzheimer's Disease Rat Model Along with Investigation of Its Gut Microbiota Change over Time. Master's Thesis, The University of Alabama at Birmingham, Birmingham, AL, USA, 2021.

448. Fattorusso, A.; Di Genova, L.; Dell'Isola, G.B.; Mencaroni, E.; Esposito, S. Autism spectrum disorders and the gut microbiota. *Nutrients* **2019**, *11*, 521. [CrossRef]

449. Liu, M.; Huang, B.; Wang, L.; Lu, Q.; Liu, R. Peanut skin procyanidins ameliorate insulin resistance via modulation of gut microbiota and gut barrier in type 2 diabetic mice. *J. Sci. Food Agric.* **2022**, *102*, 5935–5947. [CrossRef]

450. Cheng, S.; Hu, J.; Wu, X.; Pan, J.-A.; Jiao, N.; Li, Y.; Huang, Y.; Lin, X.; Zou, Y.; Chen, Y.; et al. Altered gut microbiome in FUT2 loss-of-function mutants in support of personalized medicine for inflammatory bowel diseases. *J. Genet. Genom.* **2021**, *48*, 771–780. [CrossRef]

451. Zhao, Q.; Fu, Y.; Zhang, F.; Wang, C.; Yang, X.; Bai, S.; Xue, Y.; Shen, Q. Heat-Treated Adzuki Bean Protein Hydrolysates Reduce Obesity in Mice Fed a High-Fat Diet via Remodeling Gut Microbiota and Improving Metabolic Function. *Mol. Nutr. Food Res.* **2022**, *66*, 2100907. [CrossRef]

452. Park, S.-H.; Lee, J.H.; Shin, J.; Kim, J.-S.; Cha, B.; Lee, S.; Kwon, K.S.; Shin, Y.W.; Choi, S.H. Cognitive function improvement after fecal microbiota transplantation in Alzheimer's dementia patient: A case report. *Curr. Med. Res. Opin.* **2021**, *37*, 1739–1744. [CrossRef]

453. Ma, L.; Zhang, J.; Fujita, Y.; Shinno-Hashimoto, H.; Shan, J.; Wan, X.; Qu, Y.; Chang, L.; Wang, X.; Hashimoto, K. Effects of spleen nerve denervation on depression–like phenotype, systemic inflammation, and abnormal composition of gut microbiota in mice after administration of lipopolysaccharide: A role of brain–spleen axis. *J. Affect. Disord.* **2022**, *317*, 156–165. [CrossRef] [PubMed]

454. Burz, S.D.; Monnoye, M.; Philippe, C.; Farin, W.; Ratziu, V.; Strozzi, F.; Paillarse, J.-M.; Chêne, L.; Blottière, H.M.; Gérard, P. Fecal microbiota transplant from human to mice gives insights into the role of the gut microbiota in non-alcoholic fatty liver disease (NAFLD). *Microorganisms* **2021**, *9*, 199. [CrossRef] [PubMed]

455. Liu, G.; Liang, L.; Yu, G.; Li, Q. Pumpkin polysaccharide modifies the gut microbiota during alleviation of type 2 diabetes in rats. *Int. J. Biol. Macromol.* **2018**, *115*, 711–717. [CrossRef] [PubMed]

456. Yao, C.; Li, Y.; Luo, L.; Xie, F.; Xiong, Q.; Li, T.; Yang, C.; Feng, P.-M. Significant Differences in Gut Microbiota between Irritable Bowel Syndrome with Diarrhea and Healthy Controls in Southwest China. *Dig. Dis. Sci.* **2022**, *68*, 106–127. [CrossRef]

457. Nirmalkar, K.; Murugesan, S.; Pizano-Zárate, M.L.; Villalobos-Flores, L.E.; García-González, C.; Morales-Hernández, R.M.; Nuñez-Hernández, J.A.; Hernández-Quiroz, F.; Romero-Figueroa, M.D.S.; Hernández-Guerrero, C.; et al. Gut microbiota and endothelial dysfunction markers in obese Mexican children and adolescents. *Nutrients* **2018**, *10*, 2009. [CrossRef]

458. Ahn, J.; Sinha, R.; Pei, Z.; Dominianni, C.; Wu, J.; Shi, J.; Goedert, J.J.; Hayes, R.B.; Yang, L. Human gut microbiome and risk for colorectal cancer. *J. Natl. Cancer Inst.* **2013**, *105*, 1907–1911. [CrossRef]

459. Liu, Q.; Xi, Y.; Wang, Q.; Liu, J.; Li, P.; Meng, X.; Liu, K.; Chen, W.; Liu, X.; Liu, Z. Mannan oligosaccharide attenuates cognitive and behavioral disorders in the 5xFAD Alzheimer's disease mouse model via regulating the gut microbiota-brain axis. *Brain Behav. Immun.* **2021**, *95*, 330–343. [CrossRef]

460. Krajmalnik-Brown, R.; Lozupone, C.; Kang, D.-W.; Adams, J.B. Gut bacteria in children with autism spectrum disorders: Challenges and promise of studying how a complex community influences a complex disease. *Microb. Ecol. Health Dis.* **2015**, *26*, 26914. [CrossRef]

461. Sanada, K.; Nakajima, S.; Kurokawa, S.; Barceló-Soler, A.; Ikuse, D.; Hirata, A.; Yoshizawa, A.; Tomizawa, Y.; Salas-Valero, M.; Noda, Y.; et al. Gut microbiota and major depressive disorder: A systematic review and meta-analysis. *J. Affect. Disord.* **2020**, *266*, 1–13. [CrossRef]

462. Gurung, M.; Li, Z.; You, H.; Rodrigues, R.; Jump, D.B.; Morgun, A.; Shulzhenko, N. Role of gut microbiota in type 2 diabetes pathophysiology. *EBioMedicine* **2020**, *51*, 102590. [CrossRef]

463. Pittayanon, R.; Lau, J.T.; Leontiadis, G.I.; Tse, F.; Yuan, Y.; Surette, M.; Moayyedi, P. Differences in Gut Microbiota in Patients with vs without Inflammatory Bowel Diseases: A Systematic Review. *Gastroenterology* **2020**, *158*, 930–946.e1. [CrossRef] [PubMed]

464. Bhattarai, Y.; Muniz Pedrogo, D.A.; Kashyap, P.C. Irritable bowel syndrome: A gut microbiota-related disorder? *Am. J. Physiol.-Gastrointest. Liver Physiol.* **2017**, *312*, G52–G62. [CrossRef] [PubMed]

465. Preidis, G.A.; Ajami, N.J.; Wong, M.C.; Bessard, B.C.; Conner, M.E.; Petrosino, J.F. Composition and function of the undernourished neonatal mouse intestinal microbiome. *J. Nutr. Biochem.* **2015**, *26*, 1050–1057. [CrossRef] [PubMed]

466. Zhou, Q.; Zhang, Y.; Wang, X.; Yang, R.; Zhu, X.; Zhang, Y.; Chen, C.; Yuan, H.; Yang, Z.; Sun, L. Gut bacteria Akkermansia is associated with reduced risk of obesity: Evidence from the American Gut Project. *Nutr. Metab.* **2020**, *17*, 90. [CrossRef] [PubMed]

467. Chattopadhyay, I.; Dhar, R.; Pethusamy, K.; Seethy, A.; Srivastava, T.; Sah, R.; Sharma, J.; Karmakar, S. Exploring the Role of Gut Microbiome in Colon Cancer. *Appl. Biochem. Biotechnol.* **2021**, *193*, 1780–1799. [CrossRef]

468. Kowalski, K.; Mulak, A. Brain-Gut-Microbiota Axis in Alzheimer's Disease. *J. Neurogastroenterol. Motil.* **2019**, *25*, 48–60. [CrossRef]

469. Xu, M.; Xu, X.; Li, J.; Li, F. Association Between Gut Microbiota and Autism Spectrum Disorder: A Systematic Review and Meta-Analysis. *Front. Psychiatry* **2019**, *10*, 473. [CrossRef]

470. Boertien, J.M.; Pereira, P.A.B.; Aho, V.T.E.; Scheperjans, F. Increasing Comparability and Utility of Gut Microbiome Studies in Parkinson's Disease: A Systematic Review. *J. Park. Dis.* **2019**, *9*, S297–S312. [CrossRef]

471. Wong, M.L.; Inserra, A.; Lewis, M.D.; Mastronardi, C.A.; Leong, L.; Choo, J.; Kentish, S.; Xie, P.; Morrison, M.; Wesselingh, S.L.; et al. Inflammasome signaling affects anxiety- and depressive-like behavior and gut microbiome composition. *Mol. Psychiatry* **2016**, *21*, 797–805. [CrossRef]

472. Mashaqi, S.; Kallamadi, R.; Matta, A.; Quan, S.F.; Patel, S.I.; Combs, D.; Estep, L.; Lee-Iannotti, J.; Smith, C.; Parthasarathy, S.; et al. Obstructive Sleep Apnea as a Risk Factor for COVID-19 Severity-The Gut Microbiome as a Common Player Mediating Systemic Inflammation via Gut Barrier Dysfunction. *Cells* **2022**, *11*, 1569. [CrossRef]

473. Zhu, L.; Sha, L.; Li, K.; Wang, Z.; Wang, T.; Li, Y.; Liu, P.; Dong, X.; Dong, Y.; Zhang, X.; et al. Dietary flaxseed oil rich in omega-3 suppresses severity of type 2 diabetes mellitus via anti-inflammation and modulating gut microbiota in rats. *Lipids Health Dis.* **2020**, *19*, 20. [CrossRef] [PubMed]

474. Saulnier, D.M.; Riehle, K.; Mistretta, T.A.; Diaz, M.A.; Mandal, D.; Raza, S.; Weidler, E.M.; Qin, X.; Coarfa, C.; Milosavljevic, A.; et al. Gastrointestinal microbiome signatures of pediatric patients with irritable bowel syndrome. *Gastroenterology* **2011**, *141*, 1782–1791. [CrossRef] [PubMed]

475. Kang, Y.; Li, Y.; Du, Y.; Guo, L.; Chen, M.; Huang, X.; Yang, F.; Hong, J.; Kong, X. Konjaku flour reduces obesity in mice by modulating the composition of the gut microbiota. *Int. J. Obes.* **2019**, *43*, 1631–1643. [CrossRef] [PubMed]

476. Tilg, H.; Adolph, T.E.; Gerner, R.R.; Moschen, A.R. The Intestinal Microbiota in Colorectal Cancer. *Cancer Cell* **2018**, *33*, 954–964. [CrossRef]

477. Santoru, M.L.; Piras, C.; Murgia, A.; Palmas, V.; Camboni, T.; Liggi, S.; Ibba, S.; Lai, M.A.; Orrù, S.; Blois, S.; et al. Cross sectional evaluation of the gut-microbiome metabolome axis in an Italian cohort of IBD patients. *Sci. Rep.* **2017**, *7*, 9523. [CrossRef]

478. Phan, J.; Nair, D.; Jain, S.; Montagne, T.; Flores, D.V.; Nguyen, A.; Dietsche, S.; Gombar, S.; Cotter, P. Alterations in gut microbiome composition and function in irritable bowel syndrome and increased probiotic abundance with daily supplementation. *mSystems* **2021**, *6*, e01215-21. [CrossRef]

479. Nistal, E.; Saenz de Miera, L.E.; Ballesteros Pomar, M.; Sanchez-Campos, S.; Garcia-Mediavilla, M.V.; Alvarez-Cuenllas, B.; Linares, P.; Olcoz, J.L.; Arias-Loste, M.T.; García-Lobo, J.M.; et al. An altered fecal microbiota profile in patients with non-alcoholic fatty liver disease (NAFLD) associated with obesity. *Rev. Esp. Enferm. Dig.* **2019**, *111*, 275–282. [CrossRef]

480. Finegold, S.M.; Dowd, S.E.; Gontcharova, V.; Liu, C.; Henley, K.E.; Wolcott, R.D.; Youn, E.; Summanen, P.H.; Granpeesheh, D.; Dixon, D.; et al. Pyrosequencing study of fecal microflora of autistic and control children. *Anaerobe* **2010**, *16*, 444–453. [CrossRef]

481. Yildiz, S.; Dogan, I.; Dogruman-Al, F.; Nalbantoglu, U.; Ustek, D.; Sarzhanov, F.; Yildirim, S. Association of Enteric Protist Blastocystis spp. and Gut Microbiota with Hepatic Encephalopathy. *J. Gastrointestin. Liver Dis.* **2016**, *25*, 489–497. [CrossRef]

482. Ko, C.Y.; Liu, Q.Q.; Su, H.Z.; Zhang, H.P.; Fan, J.M.; Yang, J.H.; Hu, A.K.; Liu, Y.Q.; Chou, D.; Zeng, Y.M. Gut microbiota in obstructive sleep apnea-hypopnea syndrome: Disease-related dysbiosis and metabolic comorbidities. *Clin. Sci.* **2019**, *133*, 905–917. [CrossRef]

483. Sato, J.; Kanazawa, A.; Ikeda, F.; Yoshihara, T.; Goto, H.; Abe, H.; Komiya, K.; Kawaguchi, M.; Shimizu, T.; Ogihara, T.; et al. Gut dysbiosis and detection of "live gut bacteria" in blood of Japanese patients with type 2 diabetes. *Diabetes Care* **2014**, *37*, 2343–2350. [CrossRef]

484. Takaishi, H.; Matsuki, T.; Nakazawa, A.; Takada, T.; Kado, S.; Asahara, T.; Kamada, N.; Sakuraba, A.; Yajima, T.; Higuchi, H.; et al. Imbalance in intestinal microflora constitution could be involved in the pathogenesis of inflammatory bowel disease. *Int. J. Med. Microbiol.* **2008**, *298*, 463–472. [CrossRef] [PubMed]

485. Tana, C.; Umesaki, Y.; Imaoka, A.; Handa, T.; Kanazawa, M.; Fukudo, S. Altered profiles of intestinal microbiota and organic acids may be the origin of symptoms in irritable bowel syndrome. *Neurogastroenterol. Motil.* **2010**, *22*, 512-e115. [CrossRef] [PubMed]

486. Valentine, G.C.; Hair, A.B.; Martin, C.R. Microbiome and pediatric obesity, malnutrition, and nutrition. *Dev. Microbiome* **2020**, 157–181. [CrossRef]

487. Minato, T.; Maeda, T.; Fujisawa, Y.; Tsuji, H.; Nomoto, K.; Ohno, K.; Hirayama, M. Progression of Parkinson's disease is associated with gut dysbiosis: Two-year follow-up study. *PLoS ONE* **2017**, *12*, e0187307. [CrossRef]

488. Chen, Y.; Ji, F.; Guo, J.; Shi, D.; Fang, D.; Li, L. Dysbiosis of small intestinal microbiota in liver cirrhosis and its association with etiology. *Sci. Rep.* **2016**, *6*, 34055. [CrossRef]

489. Wang, J.; Li, W.; Wang, C.; Wang, L.; He, T.; Hu, H.; Song, J.; Cui, C.; Qiao, J.; Qing, L.; et al. Enterotype Bacteroides Is Associated with a High Risk in Patients with Diabetes: A Pilot Study. *J. Diabetes Res.* **2020**, *2020*, 6047145. [CrossRef] [PubMed]

490. Zhou, Y.; Zhi, F. Lower Level of Bacteroides in the Gut Microbiota Is Associated with Inflammatory Bowel Disease: A Meta-Analysis. *BioMed Res. Int.* **2016**, *2016*, 5828959. [CrossRef] [PubMed]

491. Noor, S.O.; Ridgway, K.; Scovell, L.; Kemsley, E.K.; Lund, E.K.; Jamieson, C.; Johnson, I.T.; Narbad, A. Ulcerative colitis and irritable bowel patients exhibit distinct abnormalities of the gut microbiota. *BMC Gastroenterol.* **2010**, *10*, 134. [CrossRef]

492. Pekmez, C.T.; Dragsted, L.O.; Brahe, L.K. Gut microbiota alterations and dietary modulation in childhood malnutrition–the role of short chain fatty acids. *Clin. Nutr.* **2019**, *38*, 615–630. [CrossRef] [PubMed]

493. Dong, T.S.; Guan, M.; Mayer, E.A.; Stains, J.; Liu, C.; Vora, P.; Jacobs, J.P.; Lagishetty, V.; Chang, L.; Barry, R.L.; et al. Obesity is associated with a distinct brain-gut microbiome signature that connects Prevotella and Bacteroides to the brain's reward center. *Gut Microbes* **2022**, *14*, 2051999. [CrossRef] [PubMed]

494. Ahmed, S.A.; Elhefnawy, A.M.; Azouz, H.G.; Roshdy, Y.S.; Ashry, M.H.; Ibrahim, A.E.; Meheissen, M.A. Study of the gut Microbiome Profile in Children with Autism Spectrum Disorder: A Single Tertiary Hospital Experience. *J. Mol. Neurosci.* **2020**, *70*, 887–896. [CrossRef] [PubMed]

495. Zhang, Y.; Fan, Q.; Hou, Y.; Zhang, X.; Yin, Z.; Cai, X.; Wei, W.; Wang, J.; He, D.; Wang, G.; et al. Bacteroides species differentially modulate depression-like behavior via gut-brain metabolic signaling. *Brain Behav. Immun.* **2022**, *102*, 11–22. [CrossRef] [PubMed]

496. Magzal, F.; Shochat, T.; Haimov, I.; Tamir, S.; Asraf, K.; Tuchner-Arieli, M.; Even, C.; Agmon, M. Increased physical activity improves gut microbiota composition and reduces short-chain fatty acid concentrations in older adults with insomnia. *Sci. Rep.* **2022**, *12*, 2265. [CrossRef] [PubMed]

497. Wei, X.; Tao, J.; Xiao, S.; Jiang, S.; Shang, E.; Zhu, Z.; Qian, D.; Duan, J. Xiexin Tang improves the symptom of type 2 diabetic rats by modulation of the gut microbiota. *Sci. Rep.* **2018**, *8*, 3685. [CrossRef]

498. Liu, C.; Zhan, S.; Tian, Z.; Li, N.; Li, T.; Wu, D.; Zeng, Z.; Zhuang, X. Food Additives Associated with Gut Microbiota Alterations in Inflammatory Bowel Disease: Friends or Enemies? *Nutrients* **2022**, *14*, 3049. [CrossRef]

499. Valdez-Palomares, F.; Nambo-Venegas, R.; Uribe-García, J.; Mendoza-Vargas, A.; Granados-Portillo, O.; Meraz-Cruz, N.; Palacios-González, B. Intestinal microbiota fingerprint in subjects with irritable bowel syndrome responders to a low FODMAP diet. *Food Funct.* **2021**, *12*, 3206–3218. [CrossRef]

500. Zhong, H.; Abdullah Deng, L.; Zhao, M.; Tang, J.; Liu, T.; Zhang, H.; Feng, F. Probiotic-fermented blueberry juice prevents obesity and hyperglycemia in high fat diet-fed mice in association with modulating the gut microbiota. *Food Funct.* **2020**, *11*, 9192–9207. [CrossRef]

501. Sarhadi, V.; Lahti, L.; Saberi, F.; Youssef, O.; Kokkola, A.; Karla, T.; Tikkanen, M.; Rautelin, H.; Puolakkainen, P.; Salehi, R.; et al. Gut Microbiota and Host Gene Mutations in Colorectal Cancer Patients and Controls of Iranian and Finnish Origin. *Anticancer Res.* **2020**, *40*, 1325–1334. [CrossRef]

502. D'Argenio, V.; Veneruso, I.; Gong, C.; Cecarini, V.; Bonfili, L.; Eleuteri, A.M. Gut Microbiome and Mycobiome Alterations in an In Vivo Model of Alzheimer's Disease. *Genes* **2022**, *13*, 1564. [CrossRef]

503. Chi, L.; Khan, I.; Lin, Z.; Zhang, J.; Lee, M.Y.S.; Leong, W.; Hsiao, W.W.; Zheng, Y. Fructo-oligosaccharides from Morinda officinalis remodeled gut microbiota and alleviated depression features in a stress rat model. *Phytomedicine* **2020**, *67*, 153157. [CrossRef] [PubMed]

504. Wang, M.W.; Ma, W.J.; Wang, Y.; Ma, X.H.; Xue, Y.F.; Guan, J.; Chen, X. Comparison of the effects of probiotics, rifaximin, and lactulose in the treatment of minimal hepatic encephalopathy and gut microbiota. *Front. Microbiol.* **2023**, *14*, 1091167. [CrossRef] [PubMed]

505. Le, K.A.; Li, Y.; Xu, X.; Yang, W.; Liu, T.; Zhao, X.; Tang, Y.G.; Cai, D.; Go, V.L.W.; Pandol, S.; et al. Alterations in fecal Lactobacillus and Bifidobacterium species in type 2 diabetic patients in Southern China population. *Front. Physiol.* **2012**, *3*, 496.

506. Fava, F.; Danese, S. Intestinal microbiota in inflammatory bowel disease: Friend of foe? *World J. Gastroenterol.* **2011**, *17*, 557–566. [CrossRef] [PubMed]

507. Iddrisu, I.; Monteagudo-Mera, A.; Poveda, C.; Pyle, S.; Shahzad, M.; Andrews, S.; Walton, G.E. Malnutrition and gut microbiota in children. *Nutrients* **2021**, *13*, 2727. [CrossRef] [PubMed]

508. Million, M.; Maraninchi, M.; Henry, M.; Armougom, F.; Richet, H.; Carrieri, P.; Valero, R.; Raccah, D.; Vialettes, B.; Raoult, D. Obesity-associated gut microbiota is enriched in *Lactobacillus reuteri* and depleted in *Bifidobacterium animalis* and *Methanobrevibacter smithii*. *Int. J. Obes.* **2012**, *36*, 817–825. [CrossRef]

509. Zou, S.; Fang, L.; Lee, M.H. Dysbiosis of gut microbiota in promoting the development of colorectal cancer. *Gastroenterol. Rep.* **2018**, *6*, 1–12. [CrossRef]

510. Aho, V.T.E.; Pereira, P.A.B.; Voutilainen, S.; Paulin, L.; Pekkonen, E.; Auvinen, P.; Scheperjans, F. Gut microbiota in Parkinson's disease: Temporal stability and relations to disease progression. *EBioMedicine* **2019**, *44*, 691–707. [CrossRef]

511. Aizawa, E.; Tsuji, H.; Asahara, T.; Takahashi, T.; Teraishi, T.; Yoshida, S.; Ota, M.; Koga, N.; Hattori, K.; Kunugi, H. Possible association of Bifidobacterium and Lactobacillus in the gut microbiota of patients with major depressive disorder. *J. Affect. Disord.* **2016**, *202*, 254–257. [CrossRef]

512. Xia, X.; Chen, J.; Xia, J.; Wang, B.; Liu, H.; Yang, L.; Wang, Y.; Ling, Z. Role of probiotics in the treatment of minimal hepatic encephalopathy in patients with HBV-induced liver cirrhosis. *J. Int. Med. Res.* **2018**, *46*, 3596–3604. [CrossRef]

513. Berry, D.; Reinisch, W. Intestinal microbiota: A source of novel biomarkers in inflammatory bowel diseases? *Best Pract. Res. Clin. Gastroenterol.* **2013**, *27*, 47–58. [CrossRef] [PubMed]

514. Min, Y.W.; Rezaie, A.; Pimentel, M. Bile acid and gut microbiota in irritable bowel syndrome. *J. Neurogastroenterol. Motil.* **2022**, *28*, 549–561. [CrossRef] [PubMed]

515. Araujo, J.R.; Tomas, J.; Brenner, C.; Sansonetti, P.J. Impact of high-fat diet on the intestinal microbiota and small intestinal physiology before and after the onset of obesity. *Biochimie* **2017**, *141*, 97–106. [CrossRef] [PubMed]

516. Ai, D.; Pan, H.; Li, X.; Gao, Y.; Liu, G.; Xia, L.C. Identifying Gut Microbiota Associated with Colorectal Cancer Using a Zero-Inflated Lognormal Model. *Front. Microbiol.* **2019**, *10*, 826. [CrossRef]

517. Baldini, F.; Hertel, J.; Sandt, E.; Thinnes, C.C.; Neuberger-Castillo, L.; Pavelka, L.; Betsou, F.; Krüger, R.; Thiele, I.; Aguayo, G.; et al. Parkinson's disease-associated alterations of the gut microbiome predict disease-relevant changes in metabolic functions. *BMC Biol.* **2020**, *18*, 62. [CrossRef]

518. Caso, J.R.; MacDowell, K.S.; Gonzalez-Pinto, A.; Garcia, S.; de Diego-Adelino, J.; Carceller-Sindreu, M.; Sarramea, F.; Caballero-Villarraso, J.; Gracia-García, P.; De la Cámara, C.; et al. Gut microbiota, innate immune pathways, and inflammatory control mechanisms in patients with major depressive disorder. *Transl. Psychiatry* **2021**, *11*, 645. [CrossRef]

519. Diaz-Perdigones, C.M.; Munoz-Garach, A.; Alvarez-Bermudez, M.D.; Moreno-Indias, I.; Tinahones, F.J. Gut microbiota of patients with type 2 diabetes and gastrointestinal intolerance to metformin differs in composition and functionality from tolerant patients. *Biomed. Pharmacother.* **2022**, *145*, 112448. [CrossRef]

520. Sokol, H.; Jegou, S.; McQuitty, C.; Straub, M.; Leducq, V.; Landman, C.; Kirchgesner, J.; Le Gall, G.; Bourrier, A.; Nion-Larmurier, I.; et al. Specificities of the intestinal microbiota in patients with inflammatory bowel disease and *Clostridium difficile* infection. *Gut Microbes* **2018**, *9*, 55–60. [CrossRef]

521. Kamil, R.Z.; Murdiati, A.; Juffrie, M.; Nakayama, J.; Rahayu, E.S. Gut microbiota and short-chain fatty acid profile between normal and moderate malnutrition children in Yogyakarta, Indonesia. *Microorganisms* **2021**, *9*, 127. [CrossRef]

522. Zhong, X.; Harrington, J.M.; Millar, S.R.; Perry, I.J.; O'Toole, P.W.; Phillips, C.M. Gut microbiota associations with metabolic health and obesity status in older adults. *Nutrients* **2020**, *12*, 2364. [CrossRef]

523. Ni, J.J.; Li, X.S.; Zhang, H.; Xu, Q.; Wei, X.T.; Feng, G.J.; Zhao, M.; Zhang, Z.J.; Zhang, L.; Shen, G.H.; et al. Mendelian randomization study of causal link from gut microbiota to colorectal cancer. *BMC Cancer* **2022**, *22*, 1371. [CrossRef] [PubMed]

524. Li, W.; Wu, X.; Hu, X.; Wang, T.; Liang, S.; Duan, Y.; Jin, F.; Qin, B. Structural changes of gut microbiota in Parkinson's disease and its correlation with clinical features. *Sci. China Life Sci.* **2017**, *60*, 1223–1233. [CrossRef] [PubMed]

525. Shen, W.; Tao, Y.; Zheng, F.; Zhou, H.; Wu, H.; Shi, H.; Huang, F.; Wu, X. The alteration of gut microbiota in venlafaxine-ameliorated chronic unpredictable mild stress-induced depression in mice. *Behav. Brain Res.* **2023**, *446*, 114399. [CrossRef] [PubMed]

526. Van Meijel, R.L.J.; Venema, K.; Canfora, E.E.; Blaak, E.E.; Goossens, G.H. Mild intermittent hypoxia exposure alters gut microbiota composition in men with overweight and obesity. *Benef. Microbes* **2022**, *13*, 355–363. [CrossRef]

527. Alvarez-Silva, C.; Kashani, A.; Hansen, T.H.; Pinna, N.K.; Anjana, R.M.; Dutta, A.; Saxena, S.; Støy, J.; Kampmann, U.; Nielsen, T.; et al. Trans-ethnic gut microbiota signatures of type 2 diabetes in Denmark and India. *Genome Med.* **2021**, *13*, 37. [CrossRef]

528. Eeckhaut, V.; Machiels, K.; Perrier, C.; Romero, C.; Maes, S.; Flahou, B.; Steppe, M.; Haesebrouck, F.; Sas, B.; Ducatelle, R.; et al. *Butyricicoccus pullicaecorum* in inflammatory bowel disease. *Gut* **2013**, *62*, 1745–1752. [CrossRef]

529. Enqi, W.; Jingzhu, S.; Lingpeng, P.; Yaqin, L. Comparison of the gut microbiota disturbance in rat models of irritable bowel syndrome induced by maternal separation and multiple early-life adversity. *Front. Cell. Infect. Microbiol.* **2021**, *10*, 581974. [CrossRef]

530. Yang, M.; Yin, Y.; Wang, F.; Zhang, H.; Ma, X.; Yin, Y.; Tan, B.; Chen, J. Supplementation with *Lycium barbarum* Polysaccharides Reduce Obesity in High-Fat Diet-Fed Mice by Modulation of Gut Microbiota. *Front. Microbiol.* **2021**, *12*, 719967. [CrossRef]

531. Huang, M.; Liu, K.; Wei, Z.; Feng, Z.; Chen, J.; Yang, J.; Zhong, Q.; Wan, G.; Kong, X.-J. Serum Oxytocin Level Correlates with Gut Microbiome Dysbiosis in Children with Autism Spectrum Disorder. *Front. Neurosci.* **2021**, *15*, 721884. [CrossRef]

532. Qian, Y.; Yang, X.; Xu, S.; Wu, C.; Song, Y.; Qin, N.; Chen, S.-D.; Xiao, Q. Alteration of the fecal microbiota in Chinese patients with Parkinson's disease. *Brain Behav. Immun.* **2018**, *70*, 194–202. [CrossRef]

533. Zhang, Y.-J.; Li, S.; Gan, R.-Y.; Zhou, T.; Xu, D.-P.; Li, H.-B. Impacts of gut bacteria on human health and diseases. *Int. J. Mol. Sci.* **2015**, *16*, 7493–7519. [CrossRef] [PubMed]

534. Radwan, S.; Gilfillan, D.; Eklund, B.; Radwan, H.M.; El Menofy, N.G.; Lee, J.; Kapuscinski, M.; Abdo, Z. A comparative study of the gut microbiome in Egyptian patients with Type I and Type II diabetes. *PLoS ONE* **2020**, *15*, e0238764. [CrossRef] [PubMed]

535. Gallardo-Becerra, L.; Cornejo-Granados, F.; García-López, R.; Valdez-Lara, A.; Bikel, S.; Canizales-Quinteros, S.; López-Contreras, B.E.; Mendoza-Vargas, A.; Nielsen, H.; Ochoa-Leyva, A. Metatranscriptomic analysis to define the Secrebiome, and 16S rRNA profiling of the gut microbiome in obesity and metabolic syndrome of Mexican children. *Microb. Cell Fact.* **2020**, *19*, 61. [CrossRef] [PubMed]

536. Cammann, D.; Lu, Y.; Cummings, M.J.; Zhang, M.L.; Cue, J.M.; Do, J.; Ebersole, J.; Chen, X.; Oh, E.C.; Cummings, J.L.; et al. Genetic correlations between Alzheimer's disease and gut microbiome genera. *Sci. Rep.* **2023**, *13*, 5258. [CrossRef]

537. Wu, T.; Wang, H.; Lu, W.; Zhai, Q.; Zhang, Q.; Yuan, W.; Gu, Z.; Zhao, J.; Zhang, H.; Chen, W. Potential of gut microbiome for detection of autism spectrum disorder. *Microb. Pathog.* **2020**, *149*, 104568. [CrossRef]

538. Zhang, P.; Huang, P.; Du, J.; He, Y.; Liu, J.; He, G.; Cui, S.; Zhang, W.; Li, G.; Chen, S. Specific gut microbiota alterations in essential tremor and its difference from Parkinson's disease. *NPJ Park. Dis.* **2022**, *8*, 98. [CrossRef]

539. Philips, C.A.; Augustine, P.; Ganesan, K.; Ranade, S.; Chopra, V.; Patil, K.; Shende, S.; Ahamed, R.; Kumbar, S.; Rajesh, S.; et al. The role of gut microbiota in clinical complications, disease severity, and treatment response in severe alcoholic hepatitis. *Indian J. Gastroenterol.* **2022**, *41*, 37–51. [CrossRef]

540. Bien, J.; Palagani, V.; Bozko, P. The intestinal microbiota dysbiosis and Clostridium difficile infection: Is there a relationship with inflammatory bowel disease? *Therap. Adv. Gastroenterol.* **2013**, *6*, 53–68. [CrossRef]

541. Salonen, A.; de Vos, W.M.; Palva, A. Gastrointestinal microbiota in irritable bowel syndrome: Present state and perspectives. *Microbiology* **2010**, *156*, 3205–3215. [CrossRef]

542. Gomes, A.C.; Hoffmann, C.; Mota, J.F. The human gut microbiota: Metabolism and perspective in obesity. *Gut Microbes* **2018**, *9*, 308–325. [CrossRef]

543. Sun, J.; Xu, J.; Yang, B.; Chen, K.; Kong, Y.; Fang, N.; Gong, T.; Wang, F.; Ling, Z.; Liu, J. Effect of *Clostridium butyricum* against Microglia-Mediated Neuroinflammation in Alzheimer's Disease via Regulating Gut Microbiota and Metabolites Butyrate. *Mol. Nutr. Food Res.* **2020**, *64*, e1900636. [CrossRef] [PubMed]

544. Parracho, H.M.; Bingham, M.O.; Gibson, G.R.; McCartney, A.L. Differences between the gut microflora of children with autistic spectrum disorders and that of healthy children. *J. Med. Microbiol.* **2005**, *54 Pt 10*, 987–991. [CrossRef] [PubMed]

545. Palacios, N.; Hannoun, A.; Flahive, J.; Ward, D.; Goostrey, K.; Deb, A.; Smith, K.M. Effect of Levodopa Initiation on the Gut Microbiota in Parkinson's Disease. *Front. Neurol.* **2021**, *12*, 574529. [CrossRef] [PubMed]

546. Winter, G.; Hart, R.A.; Charlesworth, R.P.G.; Sharpley, C.F. Gut microbiome and depression: What we know and what we need to know. *Rev. Neurosci.* **2018**, *29*, 629–643. [CrossRef]

547. Afolayan, A.; Adebusoye, L.; Cadmus, E.; Ayeni, F. Insights into the gut microbiota of Nigerian elderly with type 2 diabetes and non-diabetic elderly persons. *Heliyon* **2020**, *6*, e03971. [CrossRef]

548. Chen, D.; Chen, G.; Chen, C.; Zeng, X.; Ye, H. Prebiotics effects in vitro of polysaccharides from tea flowers on gut microbiota of healthy persons and patients with inflammatory bowel disease. *Int. J. Biol. Macromol.* **2020**, *158*, 968–976. [CrossRef]

549. Malinen, E.; Krogius-Kurikka, L.; Lyra, A.; Nikkilä, J.; Jääskeläinen, A.; Rinttilä, T.; Vilpponen-Salmela, T.; von Wright, A.J.; Palva, A. Association of symptoms with gastrointestinal microbiota in irritable bowel syndrome. *World J. Gastroenterol. WJG* **2010**, *16*, 4532. [CrossRef]

550. Gatya, M.; Fibri, D.L.N.; Utami, T.; Suroto, D.A.; Rahayu, E.S. Gut Microbiota Composition in Undernourished Children Associated with Diet and Sociodemographic Factors: A Case–Control Study in Indonesia. *Microorganisms* **2022**, *10*, 1748. [CrossRef]

551. Gomez-Arango, L.F.; Barrett, H.L.; Wilkinson, S.A.; Callaway, L.K.; McIntyre, H.D.; Morrison, M.; Nitert, M.D. Low dietary fiber intake increases Collinsella abundance in the gut microbiota of overweight and obese pregnant women. *Gut Microbes* **2018**, *9*, 189–201. [CrossRef]

552. Sheng, Q.; Du, H.; Cheng, X.; Cheng, X.; Tang, Y.; Pan, L.; Wang, Q.; Lin, J. Characteristics of fecal gut microbiota in patients with colorectal cancer at different stages and different sites. *Oncol. Lett.* **2019**, *18*, 4834–4844. [CrossRef]

553. Huang, B.; Chau, S.W.H.; Liu, Y.; Chan, J.W.Y.; Wang, J.; Ma, S.L.; Zhang, J.; Chan, P.K.S.; Yeoh, Y.K.; Chen, Z.; et al. Gut microbiome dysbiosis across early Parkinson's disease, REM sleep behavior disorder and their first-degree relatives. *Nat. Commun.* **2023**, *14*, 2501. [CrossRef] [PubMed]

554. Yu, X.; Jin, Y.; Zhou, W.; Xiao, T.; Wu, Z.; Su, J.; Gao, H.; Shen, P.; Zheng, B.; Luo, Q.; et al. Rifaximin Modulates the Gut Microbiota to Prevent Hepatic Encephalopathy in Liver Cirrhosis without Impacting the Resistome. *Front. Cell. Infect. Microbiol.* **2021**, *11*, 761192. [CrossRef] [PubMed]

555. Durgan, D.J. Obstructive Sleep Apnea-Induced Hypertension: Role of the Gut Microbiota. *Curr. Hypertens. Rep.* **2017**, *19*, 35. [CrossRef] [PubMed]

556. Huang, X.; Qiu, Y.; Gao, Y.; Zhou, R.; Hu, Q.; He, Z.; Lv, Y.; Wang, X.; Chen, W.; Deng, Y.; et al. Gut microbiota mediate melatonin signalling in association with type 2 diabetes. *Diabetologia* **2022**, *65*, 1627–1641. [CrossRef]

557. Scher, J.U.; Ubeda, C.; Artacho, A.; Attur, M.; Isaac, S.; Reddy, S.M.; Marmon, S.; Neimann, A.; Brusca, S.; Patel, T.; et al. Decreased bacterial diversity characterizes the altered gut microbiota in patients with psoriatic arthritis, resembling dysbiosis in inflammatory bowel disease. *Arthritis Rheumatol.* **2015**, *67*, 128–139. [CrossRef]

558. Monteleone, A.M.; Troisi, J.; Fasano, A.; Dalle Grave, R.; Marciello, F.; Serena, G.; Calugi, S.; Scala, G.; Corrivetti, G.; Cascino, G.; et al. Multi-omics data integration in anorexia nervosa patients before and after weight regain: A microbiome-metabolomics investigation. *Clin. Nutr.* **2021**, *40*, 1137–1146. [CrossRef]

559. Kasai, C.; Sugimoto, K.; Moritani, I.; Tanaka, J.; Oya, Y.; Inoue, H.; Tameda, M.; Shiraki, K.; Ito, M.; Takei, Y.; et al. Comparison of the gut microbiota composition between obese and non-obese individuals in a Japanese population, as analyzed by terminal restriction fragment length polymorphism and next-generation sequencing. *BMC Gastroenterol.* **2015**, *15*, 100. [CrossRef]

560. Andreo-Martinez, P.; Garcia-Martinez, N.; Sanchez-Samper, E.P.; Martinez-Gonzalez, A.E. An approach to gut microbiota profile in children with autism spectrum disorder. *Environ. Microbiol. Rep.* **2020**, *12*, 115–135. [CrossRef]

561. Radjabzadeh, D.; Bosch, J.A.; Uitterlinden, A.G.; Zwinderman, A.H.; Ikram, M.A.; van Meurs, J.B.J.; Luik, A.I.; Nieuwdorp, M.; Lok, A.; van Duijn, C.M.; et al. Gut microbiome-wide association study of depressive symptoms. *Nat. Commun.* **2022**, *13*, 7128. [CrossRef]

562. Mashaqi, S.; Gozal, D. Obstructive Sleep Apnea and Systemic Hypertension: Gut Dysbiosis as the Mediator? *J. Clin. Sleep Med.* **2019**, *15*, 1517–1527. [CrossRef]

563. Gong, X.; Xiong, L.; Bi, C.; Zhang, B. Diosmetin ameliorate type 2 diabetic mellitus by up-regulating Corynebacterium glutamicum to regulate IRS/PI3K/AKT-mediated glucose metabolism disorder in KK-Ay mice. *Phytomedicine* **2021**, *87*, 153582. [CrossRef] [PubMed]

564. Gracey, M.; Suharjono, S.; Sunoto, S.; Stone, D.E. Microbial Contamination of the Gut; another Feature of Malnutrition. *Paediatr. Indones.* **1975**, *15*, 181–190. [CrossRef] [PubMed]

565. Lo, C.I.; Niang, E.H.A.; Ndongo, S.; Raoult, D.; Fournier, P.E.; Fenollar, F. *Corynebacterium bouchesdurhonense* sp. nov., and *Corynebacterium provencense* sp. nov., two new species isolated from obese patients. *New Microbes New Infect.* **2019**, *31*, 100581. [CrossRef]

566. Hasan, R.; Bose, S.; Roy, R.; Paul, D.; Rawat, S.; Nilwe, P.; Chauhan, N.K.; Choudhury, S. Tumor tissue-specific bacterial biomarker panel for colorectal cancer: *Bacteroides massiliensis, Alistipes* species, *Alistipes onderdonkii, Bifidobacterium pseudocatenulatum, Corynebacterium appendicis. Arch. Microbiol.* **2022**, *204*, 348. [CrossRef]

567. Chang, C.H.; Lin, C.H.; Lane, H.Y. d-glutamate and Gut Microbiota in Alzheimer's Disease. *Int. J. Mol. Sci.* **2020**, *21*, 2676. [CrossRef]

568. Aitbali, Y.; Ba-M'hamed, S.; Elhidar, N.; Nafis, A.; Soraa, N.; Bennis, M. Glyphosate based- herbicide exposure affects gut microbiota, anxiety and depression-like behaviors in mice. *Neurotoxicol. Teratol.* **2018**, *67*, 44–49. [CrossRef] [PubMed]

569. Kawaguchi, T.; Suzuki, F.; Imamura, M.; Murashima, N.; Yanase, M.; Mine, T.; Fujisawa, M.; Sato, I.; Yoshiji, H.; Okita, K.; et al. Rifaximin-altered gut microbiota components associated with liver/neuropsychological functions in patients with hepatic encephalopathy: An exploratory data analysis of phase II/III clinical trials. *Hepatol. Res.* **2019**, *49*, 404–418. [CrossRef]

570. Nie, Q.; Hu, J.; Chen, H.; Geng, F.; Nie, S. Arabinoxylan ameliorates type 2 diabetes by regulating the gut microbiota and metabolites. *Food Chem.* **2022**, *371*, 131106. [CrossRef]

571. Gobert, A.P.; Sagrestani, G.; Delmas, E.; Wilson, K.T.; Verriere, T.G.; Dapoigny, M.; Del'homme, C.; Bernalier-Donadille, A. The human intestinal microbiota of constipated-predominant irritable bowel syndrome patients exhibits anti-inflammatory properties. *Sci. Rep.* **2016**, *6*, 39399. [CrossRef]

572. Karlsson, C.L.; Onnerfalt, J.; Xu, J.; Molin, G.; Ahrne, S.; Thorngren-Jerneck, K. The microbiota of the gut in preschool children with normal and excessive body weight. *Obesity* **2012**, *20*, 2257–2261. [CrossRef]

573. Li, C.; Wang, N.; Zheng, G.; Yang, L. Oral Administration of Resveratrol-Selenium-Peptide Nanocomposites Alleviates Alzheimer's Disease-like Pathogenesis by Inhibiting Abeta Aggregation and Regulating Gut Microbiota. *ACS Appl. Mater. Interfaces* **2021**, *13*, 46406–46420. [CrossRef] [PubMed]

574. Heberling, C.A.; Dhurjati, P.S.; Sasser, M. Hypothesis for a systems connectivity model of Autism Spectrum Disorder pathogenesis: Links to gut bacteria, oxidative stress, and intestinal permeability. *Med. Hypotheses* **2013**, *80*, 264–270. [CrossRef] [PubMed]

575. Murros, K.E.; Huynh, V.A.; Takala, T.M.; Saris, P.E.J. Desulfovibrio Bacteria Are Associated with Parkinson's Disease. *Front. Cell. Infect. Microbiol.* **2021**, *11*, 652617. [CrossRef] [PubMed]

576. Liu, L.; Wang, H.; Zhang, H.; Chen, X.; Zhang, Y.; Wu, J.; Zhao, L.; Wang, D.; Pu, J.; Ji, P.; et al. Toward a Deeper Understanding of Gut Microbiome in Depression: The Promise of Clinical Applicability. *Adv. Sci.* **2022**, *9*, e2203707. [CrossRef] [PubMed]

577. Elbere, I.; Silamikelis, I.; Dindune, I.I.; Kalnina, I.; Ustinova, M.; Zaharenko, L.; Silamikele, L.; Rovite, V.; Gudra, D.; Konrade, I.; et al. Baseline gut microbiome composition predicts metformin therapy short-term efficacy in newly diagnosed type 2 diabetes patients. *PLoS ONE* **2020**, *15*, e0241338. [CrossRef] [PubMed]

578. Lopetuso, L.R.; Petito, V.; Graziani, C.; Schiavoni, E.; Sterbini, F.P.; Poscia, A.; Gaetani, E.; Franceschi, F.; Cammarota, G.; Sanguinetti, M.; et al. Gut microbiota in health, diverticular disease, irritable bowel syndrome, and inflammatory bowel diseases: Time for microbial marker of gastrointestinal disorders. *Dig. Dis.* **2018**, *36*, 56–65. [CrossRef] [PubMed]

579. Chumpitazi, B.P.; Hollister, E.B.; Oezguen, N.; Tsai, C.M.; McMeans, A.R.; Luna, R.A.; Savidge, T.C.; Versalovic, J.; Shulman, R.J. Gut microbiota influences low fermentable substrate diet efficacy in children with irritable bowel syndrome. *Gut Microbes* **2014**, *5*, 165–175. [CrossRef]

580. Toe, L.C.; Kerckhof, F.-M.; De Bodt, J.; Morel, F.B.; Ouedraogo, J.-B.; Kolsteren, P.; Van de Wiele, T. A prebiotic-enhanced lipid-based nutrient supplement (LNSp) increases Bifidobacterium relative abundance and enhances short-chain fatty acid production in simulated colonic microbiota from undernourished infants. *FEMS Microbiol. Ecol.* **2020**, *96*, fiaa105. [CrossRef]

581. Naderpoor, N.; Mousa, A.; Gomez-Arango, L.F.; Barrett, H.L.; Dekker Nitert, M.; de Courten, B. Faecal Microbiota Are Related to Insulin Sensitivity and Secretion in Overweight or Obese Adults. *J. Clin. Med.* **2019**, *8*, 452. [CrossRef]

582. Huo, R.X.; Wang, Y.J.; Hou, S.B.; Wang, W.; Zhang, C.Z.; Wan, X.H. Gut mucosal microbiota profiles linked to colorectal cancer recurrence. *World J. Gastroenterol.* **2022**, *28*, 1946–1964. [CrossRef]

583. Chiang, H.L.; Lin, C.H. Altered Gut Microbiome and Intestinal Pathology in Parkinson's Disease. *J. Mov. Disord.* **2019**, *12*, 67–83. [CrossRef] [PubMed]

584. Valles-Colomer, M.; Falony, G.; Darzi, Y.; Tigchelaar, E.F.; Wang, J.; Tito, R.Y.; Schiweck, C.; Kurilshikov, A.; Joossens, M.; Wijmenga, C.; et al. The neuroactive potential of the human gut microbiota in quality of life and depression. *Nat. Microbiol.* **2019**, *4*, 623–632. [CrossRef] [PubMed]

585. Li, Q.; Chang, Y.; Zhang, K.; Chen, H.; Tao, S.; Zhang, Z. Implication of the gut microbiome composition of type 2 diabetic patients from northern China. *Sci. Rep.* **2020**, *10*, 5450. [CrossRef] [PubMed]

586. Blanton, L.V.; Charbonneau, M.R.; Salih, T.; Barratt, M.J.; Venkatesh, S.; Ilkaveya, O.; Subramanian, S.; Manary, M.J.; Trehan, I.; Jorgensen, J.M.; et al. Gut bacteria that rescue growth impairments transmitted by immature microbiota from undernourished children. *Science* **2016**, *351*, 854. [CrossRef] [PubMed]

587. Jiao, N.; Baker, S.S.; Nugent, C.A.; Tsompana, M.; Cai, L.; Wang, Y.; Buck, M.J.; Genco, R.J.; Baker, R.D.; Zhu, R.; et al. Gut microbiome may contribute to insulin resistance and systemic inflammation in obese rodents: A meta-analysis. *Physiol Genom.* **2018**, *50*, 244–254. [CrossRef] [PubMed]

588. Li, B.; He, Y.; Ma, J.; Huang, P.; Du, J.; Cao, L.; Wang, Y.; Xiao, Q.; Tang, H.; Chen, S. Mild cognitive impairment has similar alterations as Alzheimer's disease in gut microbiota. *Alzheimers Dement.* **2019**, *15*, 1357–1366. [CrossRef]

589. Nishiwaki, H.; Ito, M.; Hamaguchi, T.; Maeda, T.; Kashihara, K.; Tsuboi, Y.; Ueyama, J.; Yoshida, T.; Hanada, H.; Takeuchi, I.; et al. Short chain fatty acids-producing and mucin-degrading intestinal bacteria predict the progression of early Parkinson's disease. *NPJ Park. Dis.* **2022**, *8*, 65. [CrossRef]

590. Zhang, Q.; Yun, Y.; An, H.; Zhao, W.; Ma, T.; Wang, Z.; Yang, F. Gut Microbiome Composition Associated With Major Depressive Disorder and Sleep Quality. *Front. Psychiatry* **2021**, *12*, 645045. [CrossRef]

591. Bajaj, J.S.; Hylemon, P.B.; Ridlon, J.M.; Heuman, D.M.; Daita, K.; White, M.B.; Monteith, P.; Noble, N.A.; Sikaroodi, M.; Gillevet, P.M.; et al. Colonic mucosal microbiome differs from stool microbiome in cirrhosis and hepatic encephalopathy and is linked to cognition and inflammation. *Am. J. Physiol. Gastrointest. Liver Physiol.* **2012**, *303*, G675–G685. [CrossRef]

592. Tang, S.S.; Liang, C.H.; Liu, Y.L.; Wei, W.; Deng, X.R.; Shi, X.Y.; Wang, L.M.; Zhang, L.J.; Yuan, H.J. Intermittent hypoxia is involved in gut microbial dysbiosis in type 2 diabetes mellitus and obstructive sleep apnea-hypopnea syndrome. *World J. Gastroenterol.* **2022**, *28*, 2320–2333. [CrossRef]

593. Qin, J.; Li, Y.; Cai, Z.; Li, S.; Zhu, J.; Zhang, F.; Liang, S.; Zhang, W.; Guan, Y.; Shen, D.; et al. A metagenome-wide association study of gut microbiota in type 2 diabetes. *Nature* **2012**, *490*, 55–60. [CrossRef] [PubMed]

594. Zhan, K.; Zheng, H.; Li, J.; Wu, H.; Qin, S.; Luo, L.; Huang, S. Gut microbiota-bile acid crosstalk in diarrhea-irritable bowel syndrome. *BioMed Res. Int.* **2020**, *2020*, 3828249. [CrossRef] [PubMed]

595. Bai, J.; Shen, N.; Liu, Y. Associations between the Gut Microbiome and Migraines in Children Aged 7–18 Years: An Analysis of the American Gut Project Cohort. *Pain Manag. Nurs.* **2023**, *24*, 35–43. [CrossRef] [PubMed]

596. Pinart, M.; Dotsch, A.; Schlicht, K.; Laudes, M.; Bouwman, J.; Forslund, S.K.; Pischon, T.; Nimptsch, K. Gut Microbiome Composition in Obese and Non-Obese Persons: A Systematic Review and Meta-Analysis. *Nutrients* **2021**, *14*, 12. [CrossRef] [PubMed]

597. Bai, X.; Wei, H.; Liu, W.; Coker, O.O.; Gou, H.; Liu, C.; Zhao, L.; Li, C.; Zhou, Y.; Wang, G.; et al. Cigarette smoke promotes colorectal cancer through modulation of gut microbiota and related metabolites. *Gut* **2022**, *71*, 2439–2450. [CrossRef] [PubMed]

598. Wang, M.; Wan, J.; Rong, H.; He, F.; Wang, H.; Zhou, J.; Cai, C.; Wang, Y.; Xu, R.; Yin, Z.; et al. Alterations in Gut Glutamate Metabolism Associated with Changes in Gut Microbiota Composition in Children with Autism Spectrum Disorder. *mSystems* **2019**, *4*, e00321-18. [CrossRef]

599. Lubomski, M.; Davis, R.L.; Sue, C.M. The gut microbiota: A novel therapeutic target in Parkinson's disease? *Park. Relat. Disord.* **2019**, *66*, 265–266. [CrossRef]

600. Philips, C.A.; Ahamed, R.; Rajesh, S.; Singh, S.; Tharakan, A.; Abduljaleel, J.K.; Augustine, P. Clinical outcomes and gut microbiota analysis of severe alcohol-associated hepatitis patients undergoing healthy donor fecal transplant or pentoxifylline therapy: Single-center experience from Kerala. *Gastroenterol. Rep.* **2022**, *10*, goac074. [CrossRef]

601. Xu, T.; Ge, Y.; Du, H.; Li, Q.; Xu, X.; Yi, H.; Wu, X.; Kuang, T.; Fan, G.; Zhang, Y. Berberis kansuensis extract alleviates type 2 diabetes in rats by regulating gut microbiota composition. *J. Ethnopharmacol.* **2021**, *273*, 113995. [CrossRef]

602. Balish, E.; Warner, T. *Enterococcus faecalis* induces inflammatory bowel disease in interleukin-10 knockout mice. *Am. J. Pathol.* **2002**, *160*, 2253–2257. [CrossRef]

603. Ji, M.; Huang, H.; Lan, X. Correlation between intestinal microflora in irritable bowel syndrome and severity. *Dis. Markers* **2022**, *2022*, 1031844. [CrossRef] [PubMed]

604. Lv, Z.; Wang, Y.; Yang, T.; Zhan, X.; Li, Z.; Hu, H.; Li, T.; Chen, J. Vitamin A deficiency impacts the structural segregation of gut microbiota in children with persistent diarrhea. *J. Clin. Biochem. Nutr.* **2016**, *59*, 113–121. [CrossRef] [PubMed]

605. Wu, G.D.; Pan, A.; Zhang, X.; Cai, Y.Y.; Wang, Q.; Huang, F.Q.; Alolga, R.N.; Li, J.; Qi, L.W.; Liu, Q. Cordyceps Improves Obesity and its Related Inflammation via Modulation of *Enterococcus cecorum* Abundance and Bile Acid Metabolism. *Am. J. Chin. Med.* **2022**, *50*, 817–838. [CrossRef]

606. de Almeida, C.V.; Taddei, A.; Amedei, A. The controversial role of *Enterococcus faecalis* in colorectal cancer. *Therap. Adv. Gastroenterol.* **2018**, *11*, 1756284818783606. [CrossRef]

607. Fan, H.X.; Sheng, S.; Zhang, F. New hope for Parkinson's disease treatment: Targeting gut microbiota. *CNS Neurosci. Ther.* **2022**, *28*, 1675–1688. [CrossRef] [PubMed]

608. Jang, H.M.; Kim, J.K.; Joo, M.K.; Shin, Y.J.; Lee, K.E.; Lee, C.K.; Kim, H.J.; Kim, D.H. *Enterococcus faecium* and *Pediococcus acidilactici* deteriorate *Enterobacteriaceae*-induced depression and colitis in mice. *Sci. Rep.* **2022**, *12*, 9389. [CrossRef] [PubMed]

609. Loguercio, C.; Del Vecchio Blanco, C.; Coltorti, M. Enterococcus lactic acid bacteria strain SF68 and lactulose in hepatic encephalopathy: A controlled study. *J. Int. Med. Res.* **1987**, *15*, 335–343. [CrossRef]

610. Forslund, K.; Hildebrand, F.; Nielsen, T.; Falony, G.; Le Chatelier, E.; Sunagawa, S.; Prifti, E.; Vieira-Silva, S.; Gudmundsdottir, V.; Krogh Pedersen, H.; et al. Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. *Nature* **2015**, *528*, 262–266. [CrossRef]

611. Mirsepasi-Lauridsen, H.C.; Vallance, B.A.; Krogfelt, K.A.; Petersen, A.M. Escherichia coli pathobionts associated with inflammatory bowel disease. *Clin. Microbiol. Rev.* **2019**, *32*, e00060-18. [CrossRef]

612. Lee, K.N.; Lee, O.Y. Intestinal microbiota in pathophysiology and management of irritable bowel syndrome. *World J. Gastroenterol. WJG* **2014**, *20*, 8886.

613. Million, M.; Angelakis, E.; Maraninchi, M.; Henry, M.; Giorgi, R.; Valero, R.; Vialettes, B.; Raoult, D. Correlation between body mass index and gut concentrations of *Lactobacillus reuteri*, *Bifidobacterium animalis*, *Methanobrevibacter smithii* and *Escherichia coli*. *Int. J. Obes.* **2013**, *37*, 1460–1466. [CrossRef] [PubMed]

614. Radilla-Vazquez, R.B.; Parra-Rojas, I.; Martinez-Hernandez, N.E.; Marquez-Sandoval, Y.F.; Illades-Aguiar, B.; Castro-Alarcon, N. Gut Microbiota and Metabolic Endotoxemia in Young Obese Mexican Subjects. *Obes. Facts.* **2016**, *9*, 1–11. [CrossRef] [PubMed]

615. Bostanciklioglu, M. The role of gut microbiota in pathogenesis of Alzheimer's disease. *J. Appl. Microbiol.* **2019**, *127*, 954–967. [CrossRef] [PubMed]

616. Carissimi, C.; Laudadio, I.; Palone, F.; Fulci, V.; Cesi, V.; Cardona, F.; Alfonsi, C.; Cucchiara, S.; Isoldi, S.; Stronati, L. Functional analysis of gut microbiota and immunoinflammation in children with autism spectrum disorders. *Dig. Liver Dis.* **2019**, *51*, 1366–1374. [CrossRef]

617. Sun, M.F.; Shen, Y.Q. Dysbiosis of gut microbiota and microbial metabolites in Parkinson's Disease. *Ageing Res. Rev.* **2018**, *45*, 53–61. [CrossRef]

618. Du Toit, A. Gut microbiota and depression. *Nat. Rev. Microbiol.* **2022**, *20*, 190. [CrossRef]

619. Liu, Q.; Duan, Z.P.; Ha, D.K.; Bengmark, S.; Kurtovic, J.; Riordan, S.M. Synbiotic modulation of gut flora: Effect on minimal hepatic encephalopathy in patients with cirrhosis. *Hepatology* **2004**, *39*, 1441–1449. [CrossRef]

620. Bhute, S.S.; Suryavanshi, M.V.; Joshi, S.M.; Yajnik, C.S.; Shouche, Y.S.; Ghaskadbi, S.S. Gut Microbial Diversity Assessment of Indian Type-2-Diabetics Reveals Alterations in Eubacteria, Archaea, and Eukaryotes. *Front. Microbiol.* **2017**, *8*, 214. [CrossRef]

621. Jones, R.B.; Alderete, T.L.; Kim, J.S.; Millstein, J.; Gilliland, F.D.; Goran, M.I. High intake of dietary fructose in overweight/obese teenagers associated with depletion of *Eubacterium* and *Streptococcus* in gut microbiome. *Gut Microbes* **2019**, *10*, 712–719. [CrossRef]

622. Ryu, S.W.; Kim, J.S.; Oh, B.S.; Choi, W.J.; Yu, S.Y.; Bak, J.E.; Park, S.H.; Kang, S.W.; Lee, J.; Jung, W.Y.; et al. Gut Microbiota Eubacterium callanderi Exerts Anti-Colorectal Cancer Activity. *Microbiol. Spectr.* **2022**, *10*, e0253122. [CrossRef]

623. Shabbir, U.; Arshad, M.S.; Sameen, A.; Oh, D.H. Crosstalk between Gut and Brain in Alzheimer's Disease: The Role of Gut Microbiota Modulation Strategies. *Nutrients* **2021**, *13*, 690. [PubMed]

624. Merli, M.; Iebba, V.; Giusto, M. What is new about diet in hepatic encephalopathy. *Metab. Brain Dis.* **2016**, *31*, 1289–1294. [CrossRef] [PubMed]

625. Navab-Moghadam, F.; Sedighi, M.; Khamseh, M.E.; Alaei-Shahmiri, F.; Talebi, M.; Razavi, S.; Amirmozafari, N. The association of type II diabetes with gut microbiota composition. *Microb. Pathog.* **2017**, *110*, 630–636. [CrossRef] [PubMed]

626. Cao, Y.; Shen, J.; Ran, Z.H. Association between *Faecalibacterium prausnitzii* reduction and inflammatory bowel disease: A meta-analysis and systematic review of the literature. *Gastroenterol. Res. Pract.* **2014**, *2014*, 872725. [CrossRef]

627. Maharshak, N.; Ringel, Y.; Katibian, D.; Lundqvist, A.; Sartor, R.B.; Carroll, I.M.; Ringel-Kulka, T. Fecal and mucosa-associated intestinal microbiota in patients with diarrhea-predominant irritable bowel syndrome. *Dig. Dis. Sci.* **2018**, *63*, 1890–1899. [CrossRef]

628. Maioli, T.U.; Borras-Nogues, E.; Torres, L.; Barbosa, S.C.; Martins, V.D.; Langella, P.; Azevedo, V.A.; Chatel, J.-M. Possible Benefits of *Faecalibacterium prausnitzii* for Obesity-Associated Gut Disorders. *Front. Pharmacol.* **2021**, *12*, 740636. [CrossRef]

629. Dikeocha, I.J.; Al-Kabsi, A.M.; Chiu, H.T.; Alshawsh, M.A. *Faecalibacterium prausnitzii* Ameliorates Colorectal Tumorigenesis and Suppresses Proliferation of HCT116 Colorectal Cancer Cells. *Biomedicines* **2022**, *10*, 1128. [CrossRef]

630. Leblhuber, F.; Ehrlich, D.; Steiner, K.; Geisler, S.; Fuchs, D.; Lanser, L.; Kurz, K. The Immunopathogenesis of Alzheimer's Disease Is Related to the Composition of Gut Microbiota. *Nutrients* **2021**, *13*, 361. [CrossRef]

631. Hua, X.; Zhu, J.; Yang, T.; Guo, M.; Li, Q.; Chen, J.; Li, T. The Gut Microbiota and Associated Metabolites Are Altered in Sleep Disorder of Children with Autism Spectrum Disorders. *Front. Psychiatry* **2020**, *11*, 855. [CrossRef]

632. Ye, X.; Wang, D.; Zhu, H.; Wang, D.; Li, J.; Tang, Y.; Wu, J. Gut Microbiota Changes in Patients with Major Depressive Disorder Treated with Vortioxetine. *Front. Psychiatry* **2021**, *12*, 641491. [CrossRef]

633. Bajaj, J.S.; Gillevet, P.M.; Patel, N.R.; Ahluwalia, V.; Ridlon, J.M.; Kettenmann, B.; Schubert, C.M.; Sikaroodi, M.; Heuman, D.M.; Crossey, M.M.E.; et al. A longitudinal systems biology analysis of lactulose withdrawal in hepatic encephalopathy. *Metab. Brain Dis.* **2012**, *27*, 205–215. [CrossRef] [PubMed]

634. Zhang, Y.; Si, X.; Yang, L.; Wang, H.; Sun, Y.; Liu, N. Association between intestinal microbiota and inflammatory bowel disease. *Anim. Model. Exp. Med.* **2022**, *5*, 311–322. [CrossRef] [PubMed]

635. Wiredu Ocansey, D.K.; Hang, S.; Yuan, X.; Qian, H.; Zhou, M.; Valerie Olovo, C.; Zhang, X.; Mao, F. The diagnostic and prognostic potential of gut bacteria in inflammatory bowel disease. *Gut Microbes* **2023**, *15*, 2176118. [CrossRef] [PubMed]

636. Duan, M.; Wang, Y.; Zhang, Q.; Zou, R.; Guo, M.; Zheng, H. Characteristics of gut microbiota in people with obesity. *PLoS ONE* **2021**, *16*, e0255446. [CrossRef]

637. Kelly, D.; Yang, L.; Pei, Z. Gut Microbiota, Fusobacteria, and Colorectal Cancer. *Diseases* **2018**, *6*, 109. [CrossRef]

638. Yan, C.; Diao, Q.; Zhao, Y.; Zhang, C.; He, X.; Huang, R.; Li, Y. Fusobacterium nucleatum infection-induced neurodegeneration and abnormal gut microbiota composition in Alzheimer's disease-like rats. *Front. Neurosci.* **2022**, *16*, 884543. [CrossRef]

639. Talukdar, R.; Sarkar, P.; Jakkampudi, A.; Sarkar, S.; Aslam, M.; Jandhyala, M.; Deepika, G.; Unnisa, M.; Reddy, D.N. The gut microbiome in pancreatogenic diabetes differs from that of Type 1 and Type 2 diabetes. *Sci. Rep.* **2021**, *11*, 10978. [CrossRef]

640. Brand, E.C.; Klaassen, M.A.; Gacesa, R.; Vila, A.V.; Ghosh, H.; De Zoete, M.R.; Boomsma, D.I.; Hoentjen, F.; Horjus Talabur Horje, C.S.; van de Meeberg, P.C.; et al. Healthy cotwins share gut microbiome signatures with their inflammatory bowel disease twins and unrelated patients. *Gastroenterology* **2021**, *160*, 1970–1985. [CrossRef]

641. Selma, M.V.; Romo-Vaquero, M.; Garcia-Villalba, R.; Gonzalez-Sarrias, A.; Tomas-Barberan, F.A.; Espin, J.C. The human gut microbial ecology associated with overweight and obesity determines ellagic acid metabolism. *Food Funct.* **2016**, *7*, 1769–1774. [CrossRef]

642. Romo-Vaquero, M.; Fernandez-Villalba, E.; Gil-Martinez, A.L.; Cuenca-Bermejo, L.; Espin, J.C.; Herrero, M.T.; Selma, M.V. Urolithins: Potential biomarkers of gut dysbiosis and disease stage in Parkinson's patients. *Food Funct.* **2022**, *13*, 6306–6316. [CrossRef]

643. Chen, J.J.; Zheng, P.; Liu, Y.Y.; Zhong, X.G.; Wang, H.Y.; Guo, Y.J.; Xie, P. Sex differences in gut microbiota in patients with major depressive disorder. *Neuropsychiatr. Dis. Treat.* **2018**, *14*, 647–655. [CrossRef] [PubMed]

644. Wasilewska, J.; Klukowski, M.; Debkowska, K.; Kilon, J.; Citko, D.; Flisiak, M.; Oleksinska, M.; Kaczmarski, M. Helicobacter pylori seroprevalence in children with sleep-disordered breathing. *Int. J. Pediatr. Otorhinolaryngol.* **2016**, *87*, 208–212. [CrossRef] [PubMed]

645. Hosseininasab Nodoushan, S.A.; Nabavi, A. The Interaction of *Helicobacter pylori* Infection and Type 2 Diabetes Mellitus. *Adv. Biomed. Res.* **2019**, *8*, 15. [CrossRef] [PubMed]

646. Bai, X.; Jiang, L.; Ruan, G.; Liu, T.; Yang, H. *Helicobacter pylori* may participate in the development of inflammatory bowel disease by modulating the intestinal microbiota. *Chin. Med. J.* **2022**, *135*, 634–638. [CrossRef]

647. Ng, Q.X.; Foo, N.X.; Loke, W.; Koh, Y.Q.; Seah, V.J.M.; Soh, A.Y.S.; Yeo, W.S. Is there an association between *Helicobacter pylori* infection and irritable bowel syndrome? A meta-analysis. *World J. Gastroenterol.* **2019**, *25*, 5702. [CrossRef] [PubMed]

648. Siddiqui, B.; Yakoob, J.; Abbas, Z.; Azmat, R.; Fatima, S.S.; Awan, S. Distribution of *Helicobacter pylori* infection and abnormal body-mass index (BMI) in a developing country. *J. Infect. Dev. Ctries* **2018**, *12*, 342–346. [CrossRef]

649. Dai, K.; Song, Y.; Zhang, D.; Wei, Y.; Jiang, S.; Xu, F.; Wang, H.; Zhang, X.; Shao, X. Thinned peach polyphenols alleviate obesity in high fat mice by affecting gut microbiota. *Food Res. Int.* **2022**, *157*, 111255. [CrossRef]

650. Dahmus, J.D.; Kotler, D.L.; Kastenberg, D.M.; Kistler, C.A. The gut microbiome and colorectal cancer: A review of bacterial pathogenesis. *J. Gastrointest. Oncol.* **2018**, *9*, 769–777. [CrossRef]

651. Doulberis, M.; Kotronis, G.; Gialamprinou, D.; Polyzos, S.A.; Papaefthymiou, A.; Katsinelos, P.; Kountouras, J. Alzheimer's disease and gastrointestinal microbiota; impact of *Helicobacter pylori* infection involvement. *Int. J. Neurosci.* **2021**, *131*, 289–301. [CrossRef]

652. Cao, X.; Lin, P.; Jiang, P.; Li, C. Characteristics of the gastrointestinal microbiome in children with autism spectrum disorder: A systematic review. *Shanghai Arch Psychiatry* **2013**, *25*, 342–353.

653. McGee, D.J.; Lu, X.H.; Disbrow, E.A. Stomaching the Possibility of a Pathogenic Role for Helicobacter pylori in Parkinson's Disease. *J. Park. Dis.* **2018**, *8*, 367–374. [CrossRef] [PubMed]

654. Tsai, C.F.; Chen, M.H.; Wang, Y.P.; Liu, P.Y.; Hou, M.C.; Lee, F.Y.; Lu, C.L. Increased risk of short-term depressive disorder after Helicobacter pylori eradication: A population-based nested cohort study. *Helicobacter* **2021**, *26*, e12824. [CrossRef]

655. Schulz, C.; Schutte, K.; Malfertheiner, P. Does *H. pylori* eradication therapy benefit patients with hepatic encephalopathy?: Systematic review. *J. Clin. Gastroenterol.* **2014**, *48*, 491–499. [CrossRef] [PubMed]

656. Lippert, K.; Kedenko, L.; Antonielli, L.; Kedenko, I.; Gemeier, C.; Leitner, M.; Kautzky-Willer, A.; Paulweber, B.; Hackl, E. Gut microbiota dysbiosis associated with glucose metabolism disorders and the metabolic syndrome in older adults. *Benef. Microbes* **2017**, *8*, 545–556. [CrossRef]

657. Nardone, O.M.; de Sire, R.; Petito, V.; Testa, A.; Villani, G.; Scaldaferri, F.; Castiglione, F. Inflammatory bowel diseases and sarcopenia: The role of inflammation and gut microbiota in the development of muscle failure. *Front. Immunol.* **2021**, *12*, 694217. [CrossRef] [PubMed]

658. Chumpitazi, B.P.; Hoffman, K.L.; Smith, D.P.; McMeans, A.R.; Musaad, S.; Versalovic, J.; Petrosino, J.F.; Shulman, R.J. Fructan-sensitive children with irritable bowel syndrome have distinct gut microbiome signatures. *Aliment. Pharmacol. Ther.* **2021**, *53*, 499–509. [CrossRef] [PubMed]

659. Kobayashi, T.; Osaki, T.; Oikawa, S. Use of T-RFLP and seven restriction enzymes to compare the faecal microbiota of obese and lean Japanese healthy men. *Benef. Microbes* **2015**, *6*, 735–745. [CrossRef] [PubMed]

660. Jia, W.; Rajani, C.; Xu, H.; Zheng, X. Gut microbiota alterations are distinct for primary colorectal cancer and hepatocellular carcinoma. *Protein Cell* **2021**, *12*, 374–393. [CrossRef] [PubMed]

661. Jang, J.H.; Yeom, M.J.; Ahn, S.; Oh, J.Y.; Ji, S.; Kim, T.H.; Park, H.J. Acupuncture inhibits neuroinflammation and gut microbial dysbiosis in a mouse model of Parkinson's disease. *Brain Behav. Immun.* **2020**, *89*, 641–655. [CrossRef]

662. Bloom, P.P.; Luevano, J.M., Jr.; Miller, K.J.; Chung, R.T. Deep stool microbiome analysis in cirrhosis reveals an association between short-chain fatty acids and hepatic encephalopathy. *Ann. Hepatol.* **2021**, *25*, 100333. [CrossRef]

663. Tiwana, H.; Wilson, C.; Walmsley, R.; Wakefield, A.; Smith, M.; Cox, N.; Hudson, M.J.; Ebringer, A. Antibody responses to gut bacteria in ankylosing spondylitis, rheumatoid arthritis, Crohn's disease and ulcerative colitis. *Rheumatol. Int.* **1997**, *17*, 11–16. [CrossRef] [PubMed]

664. Ganji, L.; Alebouyeh, M.; Shirazi, M.H.; Eshraghi, S.S.; Mirshafiey, A.; Daryani, N.E.; Zali, M.R. Dysbiosis of fecal microbiota and high frequency of *Citrobacter*, *Klebsiella* spp., and Actinomycetes in patients with irritable bowel syndrome and gastroenteritis. *Gastroenterol. Hepatol. Bed Bench* **2016**, *9*, 325. [PubMed]

665. Chen, Y.R.; Zheng, H.M.; Zhang, G.X.; Chen, F.L.; Chen, L.D.; Yang, Z.C. High *Oscillospira* abundance indicates constipation and low BMI in the Guangdong Gut Microbiome Project. *Sci. Rep.* **2020**, *10*, 9364. [CrossRef] [PubMed]

666. Wang, Z.; Zhu, H.; Jiang, Q.; Zhu, Y.Z. The gut microbiome as non-invasive biomarkers for identifying overweight people at risk for osteoarthritis. *Microb. Pathog.* **2021**, *157*, 104976. [CrossRef]

667. Cong, J.; Zhu, H.; Liu, D.; Li, T.; Zhang, C.; Zhu, J.; Lv, H.; Liu, K.; Hao, C.; Tian, Z.; et al. A Pilot Study: Changes of Gut Microbiota in Post-surgery Colorectal Cancer Patients. *Front. Microbiol.* **2018**, *9*, 2777. [CrossRef]

668. Yildirim, S.; Nalbantoglu, O.U.; Bayraktar, A.; Ercan, F.B.; Gundogdu, A.; Velioglu, H.A.; Göl, M.F.; Soylu, A.E.; Koç, F.; Gülpınar, E.A.; et al. Stratification of the Gut Microbiota Composition Landscape across the Alzheimer's Disease Continuum in a Turkish Cohort. *mSystems* **2022**, *7*, e0000422. [CrossRef]

669. Ye, F.; Gao, X.; Wang, Z.; Cao, S.; Liang, G.; He, D.; Lv, Z.; Wang, L.; Xu, P.; Zhang, Q. Comparison of gut microbiota in autism spectrum disorders and neurotypical boys in China: A case-control study. *Synth. Syst. Biotechnol.* **2021**, *6*, 120–126. [CrossRef]

670. Wallen, Z.D.; Demirkan, A.; Twa, G.; Cohen, G.; Dean, M.N.; Standaert, D.G.; Sampson, T.R.; Payami, H. Metagenomics of Parkinson's disease implicates the gut microbiome in multiple disease mechanisms. *Nat. Commun.* **2022**, *13*, 6958. [CrossRef]

671. Lin, P.; Ding, B.; Feng, C.; Yin, S.; Zhang, T.; Qi, X.; Lv, H.; Guo, X.; Dong, K.; Zhu, Y.; et al. Prevotella and Klebsiella proportions in fecal microbial communities are potential characteristic parameters for patients with major depressive disorder. *J. Affect. Disord.* **2017**, *207*, 300–304. [CrossRef]

672. Halawa, M.R.; El-Salam, M.A.; Mostafa, B.M.; Sallout, S.S. The Gut Microbiome, *Lactobacillus acidophilus*; Relation with Type 2 Diabetes Mellitus. *Curr. Diabetes Rev.* **2019**, *15*, 480–485. [CrossRef]

673. Wang, W.; Chen, L.; Zhou, R.; Wang, X.; Song, L.; Huang, S.; Wang, G.; Xia, B. Increased proportions of *Bifidobacterium* and the *Lactobacillus* group and loss of butyrate-producing bacteria in inflammatory bowel disease. *J. Clin. Microbiol.* **2014**, *52*, 398–406. [CrossRef]

674. Szablewski, L. Human Gut Microbiota in Health and Alzheimer's Disease. *J. Alzheimers Dis.* **2018**, *62*, 549–560. [CrossRef]

675. De Angelis, M.; Francavilla, R.; Piccolo, M.; De Giacomo, A.; Gobbetti, M. Autism spectrum disorders and intestinal microbiota. *Gut Microbes* **2015**, *6*, 207–213. [CrossRef] [PubMed]

676. Macbeth, W.A.; Kass, E.H.; McDermott, W.V., Jr. Treatment of Hepatic Encephalopathy by Alteration of Intestinal Flora with *Lactobacillus acidophilus*. *Lancet* **1965**, *1*, 399–403. [CrossRef] [PubMed]

677. Tellez Corral, M.A.; Herrera Daza, E.; Cuervo Jimenez, H.K.; Bravo Becerra, M.d.M.; Villamil, J.C.; Hidalgo Martinez, P.; Roa Molina, N.S.; Otero, L.; Cortés, M.E.; Parra Giraldo, C.M. Cryptic Oral Microbiota: What Is Its Role as Obstructive Sleep Apnea-Related Periodontal Pathogens? *Int. J. Environ. Res. Public Health* **2023**, *20*, 1740. [CrossRef] [PubMed]

678. Sobhani, I.; Tap, J.; Roudot-Thoraval, F.; Roperch, J.P.; Letulle, S.; Langella, P.; Corthier, G.; Van Nhieu, J.T.; Furet, J.P. Microbial dysbiosis in colorectal cancer (CRC) patients. *PLoS ONE* **2011**, *6*, e16393. [CrossRef]

679. Wasen, C.; Simonsen, E.; Ekwudo, M.N.; Profant, M.R.; Cox, L.M. The emerging role of the microbiome in Alzheimer's disease. *Int. Rev. Neurobiol.* **2022**, *167*, 101–139.

680. Lee, Y.; Park, J.Y.; Lee, E.H.; Yang, J.; Jeong, B.R.; Kim, Y.K.; Seoh, J.Y.; Lee, S.; Han, P.L.; Kim, E.J. Rapid Assessment of Microbiota Changes in Individuals with Autism Spectrum Disorder Using Bacteria-derived Membrane Vesicles in Urine. *Exp. Neurobiol.* **2017**, *26*, 307–317. [CrossRef]

681. Tetz, G.; Brown, S.M.; Hao, Y.; Tetz, V. Parkinson's disease and bacteriophages as its overlooked contributors. *Sci. Rep.* **2018**, *8*, 10812. [CrossRef]

682. Ganci, M.; Suleyman, E.; Butt, H.; Ball, M. Associations between self-reported psychological symptom severity and gut microbiota: Further support for the microgenderome. *BMC Psychiatry* **2022**, *22*, 307. [CrossRef]

683. Chen, Z.; Radjabzadeh, D.; Chen, L.; Kurilshikov, A.; Kavousi, M.; Ahmadizar, F.; Ikram, M.A.; Uitterlinden, A.G.; Zhernakova, A.; Fu, J.; et al. Association of Insulin Resistance and Type 2 Diabetes with Gut Microbial Diversity: A Microbiome-Wide Analysis from Population Studies. *JAMA Netw. Open* **2021**, *4*, e2118811. [CrossRef] [PubMed]

684. Hu, Y.; Chen, F.; Ye, H.; Lu, B. Integrative analysis of the gut microbiome and metabolome in a rat model with stress induced irritable bowel syndrome. *Sci. Rep.* **2021**, *11*, 17596. [CrossRef] [PubMed]

685. Wang, Y.; Zhang, Y.; Qian, Y.; Xie, Y.H.; Jiang, S.S.; Kang, Z.R.; Chen, Y.; Chen, Z.; Fang, J. Alterations in the oral and gut microbiome of colorectal cancer patients and association with host clinical factors. *Int. J. Cancer* **2021**, *149*, 925–935. [CrossRef] [PubMed]

686. Abraham, D.; Feher, J.; Scuderi, G.L.; Szabo, D.; Dobolyi, A.; Cservenak, M.; Juhasz, J.; Ligeti, B.; Pongor, S.; Gomez-Cabrera, M.C.; et al. Exercise and probiotics attenuate the development of Alzheimer's disease in transgenic mice: Role of microbiome. *Exp. Gerontol.* **2019**, *115*, 122–131. [CrossRef] [PubMed]

687. Abujamel, T.S.; Al-Otaibi, N.M.; Abuaish, S.; AlHarbi, R.H.; Assas, M.B.; Alzahrani, S.A.; Alotaibi, S.M.; El-Ansary, A.; Aabed, K. Different Alterations in Gut Microbiota between Bifidobacterium longum and Fecal Microbiota Transplantation Treatments in Propionic Acid Rat Model of Autism. *Nutrients* **2022**, *14*, 608. [CrossRef]

688. Chen, T.J.; Feng, Y.; Liu, T.; Wu, T.T.; Chen, Y.J.; Li, X.; Li, Q.; Wu, Y.C. Fisetin Regulates Gut Microbiota and Exerts Neuroprotective Effect on Mouse Model of Parkinson's Disease. *Front. Neurosci.* **2020**, *14*, 549037. [CrossRef]

689. Tung, T.H.; Tung, Y.T.; Lin, I.H.; Shih, C.K.; Nguyen, N.T.K.; Shabrina, A.; Huang, S.Y. Fish Oil, but Not Olive Oil, Ameliorates Depressive-Like Behavior and Gut Microbiota Dysbiosis in Rats under Chronic Mild Stress. *Biomolecules* **2019**, *9*, 516. [CrossRef] [PubMed]

690. Lucking, E.F.; O'Connor, K.M.; Strain, C.R.; Fouhy, F.; Bastiaanssen, T.F.S.; Burns, D.P.; Golubeva, A.V.; Stanton, C.; Clarke, G.; Cryan, J.F.; et al. Chronic intermittent hypoxia disrupts cardiorespiratory homeostasis and gut microbiota composition in adult male guinea-pigs. *EBioMedicine* **2018**, *38*, 191–205. [CrossRef]

691. Torquati, L.; Gajanand, T.; Cox, E.R.; Willis, C.R.G.; Zaugg, J.; Keating, S.E.; Coombes, J.S. Effects of exercise intensity on gut microbiome composition and function in people with type 2 diabetes. *Eur. J. Sport Sci.* **2022**, *23*, 530–541. [CrossRef]

692. Ghavami, S.B.; Rostami, E.; Sephay, A.A.; Shahrokh, S.; Balaii, H.; Aghdaei, H.A.; Zali, M.R. Alterations of the human gut *Methanobrevibacter smithii* as a biomarker for inflammatory bowel diseases. *Microb. Pathog.* **2018**, *117*, 285–289. [CrossRef]

693. Huang, H.L.; Chen, H.T.; Luo, Q.L.; Xu, H.M.; He, J.; Li, Y.Q.; Zhou, Y.L.; Yao, F.; Nie, Y.Q.; Zhou, Y.J. Relief of irritable bowel syndrome by fecal microbiota transplantation is associated with changes in diversity and composition of the gut microbiota. *J. Dig. Dis.* **2019**, *20*, 401–408. [CrossRef] [PubMed]

694. Coker, O.O.; Wu, W.K.K.; Wong, S.H.; Sung, J.J.Y.; Yu, J. Altered Gut Archaea Composition and Interaction with Bacteria Are Associated with Colorectal Cancer. *Gastroenterology* **2020**, *159*, 1459–1470.e5. [CrossRef] [PubMed]

695. Garcez, M.L.; Jacobs, K.R.; Guillemin, G.J. Microbiota Alterations in Alzheimer's Disease: Involvement of the Kynurenine Pathway and Inflammation. *Neurotox. Res.* **2019**, *36*, 424–436. [CrossRef] [PubMed]

696. Newell, C.; Bomhof, M.R.; Reimer, R.A.; Hittel, D.S.; Rho, J.M.; Shearer, J. Ketogenic diet modifies the gut microbiota in a murine model of autism spectrum disorder. *Mol. Autism.* **2016**, *7*, 37. [CrossRef] [PubMed]

697. Ortega, M.A.; Alvarez-Mon, M.A.; García-Montero, C.; Fraile-Martinez, O.; Guijarro, L.G.; Lahera, G.; Monserrat, J.; Valls, P.; Mora, F.; Rodríguez-Jiménez, R.; et al. Gut Microbiota Metabolites in Major Depressive Disorder-Deep Insights into Their Pathophysiological Role and Potential Translational Applications. *Metabolites* **2022**, *12*, 50. [CrossRef] [PubMed]

698. Zhang, L.; Zhang, T.; Sun, J.; Huang, Y.; Liu, T.; Ye, Z.; Hu, J.; Zhang, G.; Chen, H.; He, Y.; et al. Calorie restriction ameliorates hyperglycemia, modulates the disordered gut microbiota, and mitigates metabolic endotoxemia and inflammation in type 2 diabetic rats. *J. Endocrinol. Investig.* **2023**, *46*, 699–711. [CrossRef]

699. Pisani, A.; Rausch, P.; Bang, C.; Ellul, S.; Tabone, T.; Marantidis Cordina, C.; Zahra, G.; Franke, A.; Ellul, P. Dysbiosis in the gut microbiota in patients with inflammatory bowel disease during remission. *Microbiol. Spectr.* **2022**, *10*, e00616-22. [CrossRef]

700. Tap, J.; Derrien, M.; Törnblom, H.; Brazeilles, R.; Cools-Portier, S.; Doré, J.; Störsrud, S.; Le Nevé, B.; Öhman, L.; Simrén, M. Identification of an intestinal microbiota signature associated with severity of irritable bowel syndrome. *Gastroenterology* **2017**, *152*, 111–123.e8. [CrossRef]

701. Xu, M.; Mo, X.; Huang, H.; Chen, X.; Liu, H.; Peng, Z.; Chen, L.; Rong, S.; Yang, W.; Xu, S.; et al. Yeast beta-glucan alleviates cognitive deficit by regulating gut microbiota and metabolites in Abeta(1)(−)(42)-induced AD-like mice. *Int. J. Biol. Macromol.* **2020**, *161*, 258–270. [CrossRef]

702. Levi Mortera, S.; Vernocchi, P.; Basadonne, I.; Zandona, A.; Chierici, M.; Durighello, M.; Marzano, V.; Gardini, S.; Gasbarrini, A.; Urbani, A.; et al. A metaproteomic-based gut microbiota profiling in children affected by autism spectrum disorders. *J. Proteom.* **2022**, *251*, 104407. [CrossRef]

703. O'donovan, S.M.; Crowley, E.K.; Brown, J.R.; O'sullivan, O.; O'leary, O.F.; Timmons, S.; Nolan, Y.M.; Clarke, D.J.; Hyland, N.P.; Joyce, S.A.; et al. Nigral overexpression of alpha-synuclein in a rat Parkinson's disease model indicates alterations in the enteric nervous system and the gut microbiome. *Neurogastroenterol. Motil.* **2020**, *32*, e13726. [CrossRef] [PubMed]

704. Iebba, V.; Guerrieri, F.; Di Gregorio, V.; Levrero, M.; Gagliardi, A.; Santangelo, F.; Sobolev, A.P.; Circi, S.; Giannelli, V.; Mannina, L.; et al. Combining amplicon sequencing and metabolomics in cirrhotic patients highlights distinctive microbiota features involved in bacterial translocation, systemic inflammation and hepatic encephalopathy. *Sci. Rep.* **2018**, *8*, 8210. [CrossRef] [PubMed]

705. Tripathi, A.; Melnik, A.V.; Xue, J.; Poulsen, O.; Meehan, M.J.; Humphrey, G.; Jiang, L.; Ackermann, G.; McDonald, D.; Zhou, D.; et al. Intermittent Hypoxia and Hypercapnia, a Hallmark of Obstructive Sleep Apnea, Alters the Gut Microbiome and Metabolome. *mSystems* **2018**, *3*, e00020-18. [CrossRef] [PubMed]

706. Shang, J.; Liu, F.; Zhang, B.; Dong, K.; Lu, M.; Jiang, R.; Xu, Y.; Diao, L.; Zhao, J.; Tang, H. Liraglutide-induced structural modulation of the gut microbiota in patients with type 2 diabetes mellitus. *PeerJ* **2021**, *9*, e11128. [CrossRef]

707. Cremon, C.; Guglielmetti, S.; Gargari, G.; Taverniti, V.; Castellazzi, A.M.; Valsecchi, C.; Tagliacarne, C.; Fiore, W.; Bellini, M.; Bertani, L.; et al. Effect of *Lactobacillus paracasei* CNCM I-1572 on symptoms, gut microbiota, short chain fatty acids, and immune activation in patients with irritable bowel syndrome: A pilot randomized clinical trial. *United Eur. Gastroenterol. J.* **2018**, *6*, 604–613. [CrossRef] [PubMed]

708. Yang, T.W.; Lee, W.H.; Tu, S.J.; Huang, W.C.; Chen, H.M.; Sun, T.H.; Tsai, M.C.; Wang, C.C.; Chen, H.Y.; Huang, C.C.; et al. Enterotype-based Analysis of Gut Microbiota along the Conventional Adenoma-Carcinoma Colorectal Cancer Pathway. *Sci. Rep.* **2019**, *9*, 10923. [CrossRef]

709. Hang, Z.; Cai, S.; Lei, T.; Zhang, X.; Xiao, Z.; Wang, D.; Li, Y.; Bi, W.; Yang, Y.; Deng, S.; et al. Transfer of Tumor-Bearing Mice Intestinal Flora Can Ameliorate Cognition in Alzheimer's Disease Mice. *J. Alzheimers Dis.* **2022**, *86*, 1287–1300. [CrossRef]

710. Zhai, Q.; Cen, S.; Jiang, J.; Zhao, J.; Zhang, H.; Chen, W. Disturbance of trace element and gut microbiota profiles as indicators of autism spectrum disorder: A pilot study of Chinese children. *Environ. Res.* **2019**, *171*, 501–509. [CrossRef]

711. Zhang, M.; Li, A.; Yang, Q.; Li, J.; Wang, L.; Liu, X.; Huang, Y.; Liu, L. Beneficial Effect of Alkaloids from *Sophora alopecuroides* L. on CUMS-Induced Depression Model Mice via Modulating Gut Microbiota. *Front. Cell. Infect. Microbiol.* **2021**, *11*, 665159. [CrossRef]

712. Wang, Y.; Ye, X.; Ding, D.; Lu, Y. Characteristics of the intestinal flora in patients with peripheral neuropathy associated with type 2 diabetes. *J. Int. Med. Res.* **2020**, *48*, 300060520936806. [CrossRef]

713. Zhou, Y.; Zhang, F.; Mao, L.; Feng, T.; Wang, K.; Xu, M.; Lv, B.; Wang, X. Bifico relieves irritable bowel syndrome by regulating gut microbiota dysbiosis and inflammatory cytokines. *Eur. J. Nutr.* **2023**, *62*, 139–155. [CrossRef]

714. Wu, T.R.; Lin, C.S.; Chang, C.J.; Lin, T.L.; Martel, J.; Ko, Y.F.; Ojcius, D.M.; Lu, C.C.; Young, J.D.; Lai, H.C. Gut commensal *Parabacteroides goldsteinii* plays a predominant role in the anti-obesity effects of polysaccharides isolated from *Hirsutella sinensis*. *Gut* **2019**, *68*, 248–262. [CrossRef]

715. Sheng, Q.S.; He, K.X.; Li, J.J.; Zhong, Z.F.; Wang, F.X.; Pan, L.L.; Lin, J.J. Comparison of Gut Microbiome in Human Colorectal Cancer in Paired Tumor and Adjacent Normal Tissues. *Onco Targets Ther.* **2020**, *13*, 635–646. [CrossRef]

716. Sun, Z.Z.; Li, X.Y.; Wang, S.; Shen, L.; Ji, H.F. Bidirectional interactions between curcumin and gut microbiota in transgenic mice with Alzheimer's disease. *Appl. Microbiol. Biotechnol.* **2020**, *104*, 3507–3515. [CrossRef]

717. Gomez-Nguyen, A.; Basson, A.R.; Dark-Fleury, L.; Hsu, K.; Osme, A.; Menghini, P.; Pizarro, T.T.; Cominelli, F. Parabacteroides distasonis induces depressive-like behavior in a mouse model of Crohn's disease. *Brain Behav. Immun.* **2021**, *98*, 245–250. [CrossRef]

718. Guarner, F. The intestinal flora in inflammatory bowel disease: Normal or abnormal? *Curr. Opin. Gastroenterol.* **2005**, *21*, 414–418. [PubMed]

719. Shen, H.; Han, J.; Li, Y.; Lu, C.; Zhou, J.; Li, Y.; Su, X. Different host-specific responses in thyroid function and gut microbiota modulation between diet-induced obese and normal mice given the same dose of iodine. *Appl. Microbiol. Biotechnol.* **2019**, *103*, 3537–3547. [CrossRef] [PubMed]

720. Salminen, A. Activation of aryl hydrocarbon receptor (AhR) in Alzheimer's disease: Role of tryptophan metabolites generated by gut host-microbiota. *J. Mol. Med.* **2023**, *101*, 201–222. [CrossRef]

721. Dogra, N.; Mani, R.J.; Katare, D.P. The Gut-Brain Axis: Two Ways Signaling in Parkinson's Disease. *Cell. Mol. Neurobiol.* **2022**, *42*, 315–332. [CrossRef] [PubMed]

722. Ko, C.Y.; Fan, J.M.; Hu, A.K.; Su, H.Z.; Yang, J.H.; Huang, L.M.; Yan, F.; Zhang, H.; Zeng, Y. Disruption of sleep architecture in *Prevotella* enterotype of patients with obstructive sleep apnea-hypopnea syndrome. *Brain Behav.* **2019**, *9*, e01287. [CrossRef] [PubMed]

723. Leite, A.Z.; Rodrigues, N.C.; Gonzaga, M.I.; Paiolo, J.C.C.; de Souza, C.A.; Stefanutto, N.A.V.; Omori, W.P.; Pinheiro, D.G.; Brisotti, J.L.; Junior, E.M.; et al. Detection of Increased Plasma Interleukin-6 Levels and Prevalence of *Prevotella copri* and *Bacteroides vulgatus* in the Feces of Type 2 Diabetes Patients. *Front. Immunol.* **2017**, *8*, 1107. [CrossRef] [PubMed]

724. Altomare, A.; Putignani, L.; Del Chierico, F.; Cocca, S.; Angeletti, S.; Ciccozzi, M.; Tripiciano, C.; Dalla Piccola, B.; Cicala, M.; Guarino, M.P.L. Gut mucosal-associated microbiota better discloses inflammatory bowel disease differential patterns than faecal microbiota. *Dig. Liver Dis.* **2019**, *51*, 648–656. [CrossRef] [PubMed]

725. Su, T.; Liu, R.; Lee, A.; Long, Y.; Du, L.; Lai, S.; Chen, X.; Wang, L.; Si, J.; Owyang, C.; et al. Altered intestinal microbiota with increased abundance of *Prevotella* is associated with high risk of diarrhea-predominant irritable bowel syndrome. *Gastroenterol. Res. Pract.* **2018**, *2018*, 6961783. [CrossRef] [PubMed]

726. Ericsson, A.C.; Akter, S.; Hanson, M.M.; Busi, S.B.; Parker, T.W.; Schehr, R.J.; Hankins, M.A.; Ahner, C.E.; Davis, J.W.; Franklin, C.L.; et al. Differential susceptibility to colorectal cancer due to naturally occurring gut microbiota. *Oncotarget* **2015**, *6*, 33689–33704. [CrossRef]

727. Guo, M.; Peng, J.; Huang, X.; Xiao, L.; Huang, F.; Zuo, Z. Gut Microbiome Features of Chinese Patients Newly Diagnosed with Alzheimer's Disease or Mild Cognitive Impairment. *J. Alzheimers Dis.* **2021**, *80*, 299–310. [CrossRef]

728. Mertsalmi, T.H.; Aho, V.T.E.; Pereira, P.A.B.; Paulin, L.; Pekkonen, E.; Auvinen, P.; Scheperjans, F. More than constipation–bowel symptoms in Parkinson's disease and their connection to gut microbiota. *Eur. J. Neurol.* **2017**, *24*, 1375–1383. [CrossRef]

729. Dhiman, R.K. Gut microbiota, inflammation and hepatic encephalopathy: A puzzle with a solution in sight. *J. Clin. Exp. Hepatol.* **2012**, *2*, 207–210. [CrossRef] [PubMed]

730. Kobyliak, N.; Falalyeyeva, T.; Mykhalchyshyn, G.; Kyriienko, D.; Komissarenko, I. Effect of alive probiotic on insulin resistance in type 2 diabetes patients: Randomized clinical trial. *Diabetes Metab. Syndr.* **2018**, *12*, 617–624. [CrossRef]

731. Brahe, L.K.; Astrup, A.; Larsen, L.H. Can We Prevent Obesity-Related Metabolic Diseases by Dietary Modulation of the Gut Microbiota? *Adv. Nutr.* **2016**, *7*, 90–101. [CrossRef]

732. Lacroix, S.; Pechereau, F.; Leblanc, N.; Boubertakh, B.; Houde, A.; Martin, C.; Flamand, N.; Silvestri, C.; Raymond, F.; Di Marzo, V.; et al. Rapid and Concomitant Gut Microbiota and Endocannabinoidome Response to Diet-Induced Obesity in Mice. *mSystems.* **2019**, *4*, e00407-19. [CrossRef]

733. Wagner, J.; Short, K.; Catto-Smith, A.G.; Cameron, D.J.; Bishop, R.F.; Kirkwood, C.D. Identification and characterisation of Pseudomonas 16S ribosomal DNA from ileal biopsies of children with Crohn's disease. *PLoS ONE* **2008**, *3*, e3578. [CrossRef] [PubMed]

734. Kerckhoffs, A.P.; Ben-Amor, K.; Samsom, M.; van der Rest, M.E.; de Vogel, J.; Knol, J.; Akkermans, L.M.A. Molecular analysis of faecal and duodenal samples reveals significantly higher prevalence and numbers of *Pseudomonas aeruginosa* in irritable bowel syndrome. *J. Med. Microbiol.* **2011**, *60*, 236–245. [CrossRef]

735. Petriz, B.A.; Castro, A.P.; Almeida, J.A.; Gomes, C.P.; Fernandes, G.R.; Kruger, R.H.; Pereira, R.W.; Franco, O.L. Exercise induction of gut microbiota modifications in obese, non-obese and hypertensive rats. *BMC Genom.* **2014**, *15*, 511. [CrossRef]

736. Gao, Z.; Guo, B.; Gao, R.; Zhu, Q.; Qin, H. Microbiota disbiosis is associated with colorectal cancer. *Front. Microbiol.* **2015**, *6*, 20. [CrossRef] [PubMed]

737. Wu, S.; Liu, X.; Jiang, R.; Yan, X.; Ling, Z. Roles and Mechanisms of Gut Microbiota in Patients with Alzheimer's Disease. *Front. Aging Neurosci.* **2021**, *13*, 650047. [CrossRef] [PubMed]

738. Pulikkan, J.; Mazumder, A.; Grace, T. Role of the Gut Microbiome in Autism Spectrum Disorders. *Adv. Exp. Med. Biol.* **2019**, *1118*, 253–269.

739. Wang, Y.; Tong, Q.; Ma, S.R.; Zhao, Z.X.; Pan, L.B.; Cong, L.; Han, P.; Peng, R.; Yu, H.; Lin, Y.; et al. Oral berberine improves brain dopa/dopamine levels to ameliorate Parkinson's disease by regulating gut microbiota. *Signal. Transduct. Target Ther.* **2021**, *6*, 77. [CrossRef]

740. Waclawikova, B.; El Aidy, S. Role of Microbiota and Tryptophan Metabolites in the Remote Effect of Intestinal Inflammation on Brain and Depression. *Pharmaceuticals* **2018**, *11*, 63. [CrossRef]

741. Jang, S.; Kim, Y.; Lee, C.; Kwon, B.; Noh, J.; Jee, J.J.; Yoon, S.S.; Koh, H.; Park, S. The effect of formula-based nutritional treatment on colitis in a murine model. *J. Korean Med. Sci.* **2021**, *36*, e342. [CrossRef]

742. Seo, K.H.; Kim, D.H.; Yokoyama, W.H.; Kim, H. Synbiotic Effect of Whole Grape Seed Flour and Newly Isolated Kefir Lactic Acid Bacteria on Intestinal Microbiota of Diet-Induced Obese Mice. *J. Agric. Food Chem.* **2020**, *68*, 13131–13137. [CrossRef]

743. Romero-Garmendia, I.; Garcia-Etxebarria, K. Host Genetics and Microbiota Interactions in Colorectal Cancer: Shared or Independent Risk? *Microorganisms* **2022**, *10*, 2129. [CrossRef] [PubMed]

744. Kim, J.E.; Roh, Y.J.; Choi, Y.J.; Lee, S.J.; Jin, Y.J.; Song, H.J.; Hong, J.T.; Hwang, D.Y. Dysbiosis of Fecal Microbiota in Tg2576 Mice for Alzheimer's Disease during Pathological Constipation. *Int. J. Mol. Sci.* **2022**, *23*, 14928. [CrossRef] [PubMed]

745. Getachew, B.; Tizabi, Y. Effects of C-Terminal Domain of the Heavy Chain of Tetanus Toxin on Gut Microbiota in a Rat Model of Depression. *Clin. Pharmacol. Transl. Med.* **2019**, *3*, 152–159. [PubMed]

746. Faden, H. The Role of Faecalibacterium, Roseburia, and Butyrate in Inflammatory Bowel Disease. *Dig. Dis.* **2022**, *40*, 793–795. [CrossRef] [PubMed]

747. Ruusunen, A.; Rocks, T.; Jacka, F.; Loughman, A. The gut microbiome in anorexia nervosa: Relevance for nutritional rehabilitation. *Psychopharmacology* **2019**, *236*, 1545–1558. [CrossRef] [PubMed]

748. Robinson, H.; Barrett, H.; Gomez-Arango, L.; McIntyre, H.D.; Callaway, L.; Dekker Nitert, M. Ketonuria Is Associated with Changes to the Abundance of Roseburia in the Gut Microbiota of Overweight and Obese Women at 16 Weeks Gestation: A Cross-Sectional Observational Study. *Nutrients* **2019**, *11*, 1836. [CrossRef] [PubMed]

749. Geng, J.; Fan, H.; Tang, X.; Zhai, H.; Zhang, Z. Diversified pattern of the human colorectal cancer microbiome. *Gut Pathog.* **2013**, *5*, 2. [CrossRef]

750. Jiang, L.; Li, J.C.; Tang, B.S.; Guo, J.F. Associations between Gut Microbiota and Parkinson's Disease: A Bidirectional Mendelian Randomization Analysis. *Eur. J. Neurol.* **2023**. [CrossRef]

751. Qu, W.; Liu, S.; Zhang, W.; Zhu, H.; Tao, Q.; Wang, H.; Yan, H. Impact of traditional Chinese medicine treatment on chronic unpredictable mild stress-induced depression-like behaviors: Intestinal microbiota and gut microbiome function. *Food Funct.* **2019**, *10*, 5886–5897. [CrossRef]

752. Henke, M.T.; Kenny, D.J.; Cassilly, C.D.; Vlamakis, H.; Xavier, R.J.; Clardy, J. Ruminococcus gnavus, a member of the human gut microbiome associated with Crohn's disease, produces an inflammatory polysaccharide. *Proc. Natl. Acad. Sci. USA* **2019**, *116*, 12672–12677. [CrossRef]

753. Salas-Perez, F.; Assmann, T.S.; Ramos-Lopez, O.; Martinez, J.A.; Riezu-Boj, J.I.; Milagro, F.I. Crosstalk between Gut Microbiota and Epigenetic Markers in Obesity Development: Relationship between *Ruminococcus*, BMI, and MACROD2/SEL1L2 Methylation. *Nutrients* **2023**, *15*, 1550. [CrossRef] [PubMed]

754. Wang, L.; Christophersen, C.T.; Sorich, M.J.; Gerber, J.P.; Angley, M.T.; Conlon, M.A. Increased abundance of *Sutterella* spp. and *Ruminococcus torques* in feces of children with autism spectrum disorder. *Mol. Autism.* **2013**, *4*, 42. [CrossRef] [PubMed]

755. Lukic, I.; Getselter, D.; Ziv, O.; Oron, O.; Reuveni, E.; Koren, O.; Elliott, E. Antidepressants affect gut microbiota and *Ruminococcus flavefaciens* is able to abolish their effects on depressive-like behavior. *Transl. Psychiatry* **2019**, *9*, 133. [CrossRef] [PubMed]

756. Silamikele, L.; Saksis, R.; Silamikelis, I.; Kotovica, P.P.; Briviba, M.; Kalnina, I.; Kalniņa, Z.; Fridmanis, D.; Kloviņš, J. Spatial variation of the gut microbiome in response to long-term metformin treatment in high-fat diet-induced type 2 diabetes mouse model of both sexes. *Gut Microbes* **2023**, *15*, 2188663. [CrossRef]

757. Ma, H.-Q.; Yu, T.-T.; Zhao, X.-J.; Zhang, Y.; Zhang, H.-J. Fecal microbial dysbiosis in Chinese patients with inflammatory bowel disease. *World J. Gastroenterol.* **2018**, *24*, 1464. [CrossRef]

758. Mohamad, N.E.; Yeap, S.K.; Ky, H.; Liew, N.W.C.; Beh, B.K.; Boo, S.Y.; Ho, W.Y.; Sharifuddin, S.A.; Long, K.; Alitheen, N.B. Pineapple Vinegar Regulates Obesity-Related Genes and Alters the Gut Microbiota in High-Fat Diet (HFD) C57BL/6 Obese Mice. *Evid. Based Complement. Alternat. Med.* **2020**, *2020*, 1257962. [CrossRef]

759. Getachew, B.; Aubee, J.I.; Schottenfeld, R.S.; Csoka, A.B.; Thompson, K.M.; Tizabi, Y. Ketamine interactions with gut-microbiota in rats: Relevance to its antidepressant and anti-inflammatory properties. *BMC Microbiol.* **2018**, *18*, 222. [CrossRef]

760. Zhao, X.; Zhang, Y.; Guo, R.; Yu, W.; Zhang, F.; Wu, F.; Shang, J. The Alteration in Composition and Function of Gut Microbiome in Patients with Type 2 Diabetes. *J. Diabetes Res.* **2020**, *2020*, 8842651. [CrossRef]

761. Cheung, Y.B.; Xu, Y.; Mangani, C.; Fan, Y.-M.; Dewey, K.G.; Salminen, S.J.; Maleta, K.; Ashorn, P. Gut microbiota in Malawian infants in a nutritional supplementation trial. *Trop. Med. Int. Health* **2016**, *21*, 283–290. [CrossRef]

762. Nie, Q.; Chen, H.; Hu, J.; Fan, S.; Nie, S. Dietary compounds and traditional Chinese medicine ameliorate type 2 diabetes by modulating gut microbiota. *Crit. Rev. Food Sci. Nutr.* **2019**, *59*, 848–863. [CrossRef]

763. Correa, T.A.F.; Rogero, M.M.; Hassimotto, N.M.A.; Lajolo, F.M. The Two-Way Polyphenols-Microbiota Interactions and Their Effects on Obesity and Related Metabolic Diseases. *Front. Nutr.* **2019**, *6*, 188. [CrossRef] [PubMed]

764. Kasai, C.; Sugimoto, K.; Moritani, I.; Tanaka, J.; Oya, Y.; Inoue, H.; Tameda, M.; Shiraki, K.; Ito, M.; Takei, Y.; et al. Comparison of human gut microbiota in control subjects and patients with colorectal carcinoma in adenoma: Terminal restriction fragment length polymorphism and next-generation sequencing analyses. *Oncol. Rep.* **2016**, *35*, 325–333. [CrossRef] [PubMed]

765. Chen, H.M.; Kuo, P.H.; Hsu, C.Y.; Chiu, Y.H.; Liu, Y.W.; Lu, M.L.; Chen, C.H. Psychophysiological Effects of Lactobacillus plantarum PS128 in Patients with Major Depressive Disorder: A Preliminary 8-Week Open Trial. *Nutrients* **2021**, *13*, 3731. [CrossRef] [PubMed]

766. Moon, J.Y.; Zolnik, C.P.; Wang, Z.; Qiu, Y.; Usyk, M.; Wang, T.; Kizer, J.R.; Landay, A.L.; Kurland, I.J.; Anastos, K.; et al. Gut microbiota and plasma metabolites associated with diabetes in women with, or at high risk for, HIV infection. *EBioMedicine* **2018**, *37*, 392–400. [CrossRef] [PubMed]

767. Zareef, R.; Younis, N.; Mahfouz, R. Inflammatory bowel disease: A key role for microbiota? *Meta Gene* **2020**, *25*, 100713. [CrossRef]

768. Chen, X.; Zhang, D.; Sun, H.; Jiang, F.; Shen, Y.; Wei, P.; Shen, X. Characterization of the gut microbiota in Chinese children with overweight and obesity using 16S rRNA gene sequencing. *PeerJ* **2021**, *9*, e11439. [CrossRef]

769. Liu, C.; Shao, W.; Gao, M.; Liu, J.; Guo, Q.; Jin, J.; Meng, F. Changes in intestinal flora in patients with type 2 diabetes on a low-fat diet during 6 months of follow-up. *Exp. Ther. Med.* **2020**, *20*, 40. [CrossRef]

770. Zhong, Y.-B.; Kang, Z.-P.; Wang, M.-X.; Long, J.; Wang, H.-Y.; Huang, J.-Q.; Wei, S.-Y.; Zhou, W.; Zhao, H.-M.; Liu, D.-Y. Curcumin ameliorated dextran sulfate sodium-induced colitis via regulating the homeostasis of DCs and Treg and improving the composition of the gut microbiota. *J. Funct. Foods* **2021**, *86*, 104716. [CrossRef]

771. Lin, C.; Li, B.; Tu, C.; Chen, X.; Guo, M. Correlations between Intestinal Microbiota and Clinical Characteristics in Colorectal Adenoma/Carcinoma. *BioMed Res. Int.* **2022**, *2022*, 3140070. [CrossRef]

772. Wu, Y.; Niu, X.; Li, P.; Tong, T.; Wang, Q.; Zhang, M.; Li, Y.; Liu, J.; Li, Z. *Lactobacillaceae* improve cognitive dysfunction via regulating gut microbiota and suppressing Abeta deposits and neuroinflammation in APP/PS1 mice. *Arch. Microbiol.* **2023**, *205*, 118. [CrossRef]

773. Singh, Y.; El-Hadidi, M.; Admard, J.; Wassouf, Z.; Schulze-Hentrich, J.M.; Kohlhofer, U.; Quintanilla-Martinez, L.; Huson, D.; Riess, O.; Casadei, N. Enriched Environmental Conditions Modify the Gut Microbiome Composition and Fecal Markers of Inflammation in Parkinson's Disease. *Front. Neurosci.* **2019**, *13*, 1032. [CrossRef] [PubMed]

774. He, K.; Hu, Y.; Ma, H.; Zou, Z.; Xiao, Y.; Yang, Y.; Feng, M.; Li, X.; Ye, X. Rhizoma Coptidis alkaloids alleviate hyperlipidemia in B6 mice by modulating gut microbiota and bile acid pathways. *Biochim. Biophys. Acta* **2016**, *1862*, 1696–1709. [CrossRef] [PubMed]

775. Katsidzira, L.; Ocvirk, S.; Wilson, A.; Li, J.; Mahachi, C.B.; Soni, D.; DeLany, J.; Nicholson, J.K.; Zoetendal, E.G.; O'keefe, S.J.D. Differences in Fecal Gut Microbiota, Short-Chain Fatty Acids and Bile Acids Link Colorectal Cancer Risk to Dietary Changes Associated with Urbanization among Zimbabweans. *Nutr. Cancer* **2019**, *71*, 1313–1324. [CrossRef]

776. Yao, Y.; Qi, X.; Jia, Y.; Ye, J.; Chu, X.; Wen, Y.; Cheng, B.; Cheng, S.; Liu, L.; Liang, C.; et al. Evaluating the interactive effects of dietary habits and human gut microbiome on the risks of depression and anxiety. *Psychol. Med.* **2022**, *53*, 3047–3055. [CrossRef] [PubMed]

777. Bui, T.I.; Gill, A.L.; Mooney, R.A.; Gill, S.R. Modulation of Gut Microbiota Metabolism in Obesity-Related Type 2 Diabetes Reduces Osteomyelitis Severity. *Microbiol. Spectr.* **2022**, *10*, e0017022. [CrossRef]

778. Azimirad, M.; Krutova, M.; Balaii, H.; Kodori, M.; Shahrokh, S.; Azizi, O.; Yadegar, A.; Aghdaei, H.A.; Zali, M.R. Coexistence of Clostridioides difficile and Staphylococcus aureus in gut of Iranian outpatients with underlying inflammatory bowel disease. *Anaerobe* **2020**, *61*, 102113. [CrossRef] [PubMed]

779. Cani, P.D.; Delzenne, N.M. Interplay between obesity and associated metabolic disorders: New insights into the gut microbiota. *Curr. Opin. Pharmacol.* **2009**, *9*, 737–743. [CrossRef]

780. Pistollato, F.; Sumalla Cano, S.; Elio, I.; Masias Vergara, M.; Giampieri, F.; Battino, M. Role of gut microbiota and nutrients in amyloid formation and pathogenesis of Alzheimer disease. *Nutr. Rev.* **2016**, *74*, 624–634. [CrossRef]

781. Chen, Y.; Xu, J.; Chen, Y. Regulation of Neurotransmitters by the Gut Microbiota and Effects on Cognition in Neurological Disorders. *Nutrients* **2021**, *13*, 2099. [CrossRef]

782. Wilkowska, A.; Szalach, L.P.; Cubala, W.J. Gut Microbiota in Depression: A Focus on Ketamine. *Front. Behav. Neurosci.* **2021**, *15*, 693362. [CrossRef]

783. Sun, X.; Chi, X.; Zhao, Y.; Liu, S.; Xing, H. Characteristics and Clinical Significance of Intestinal Microbiota in Patients with Chronic Hepatitis B Cirrhosis and Type 2 Diabetes Mellitus. *J. Diabetes Res.* **2022**, *2022*, 1826181. [CrossRef]

784. Heidarian, F.; Noormohammadi, Z.; Aghdaei, H.A.; Alebouyeh, M. Relative abundance of *streptococcus* spp. and its association with disease activity in inflammatory bowel disease patients compared with controls. *Arch. Clin. Infect. Dis.* **2017**, *12*, e57291. [CrossRef]

785. Hong, S.N.; Rhee, P.-L. Unraveling the ties between irritable bowel syndrome and intestinal microbiota. *World J. Gastroenterol. WJG* **2014**, *20*, 2470. [CrossRef]

786. Wang, M.; Doenyas, C.; Wan, J.; Zeng, S.; Cai, C.; Zhou, J.; Liu, Y.; Yin, Z.; Zhou, W. Virulence factor-related gut microbiota genes and immunoglobulin A levels as novel markers for machine learning-based classification of autism spectrum disorder. *Comput. Struct. Biotechnol. J.* **2021**, *19*, 545–554. [CrossRef]

787. Li, Z.; Lu, G.; Luo, E.; Wu, B.; Li, Z.; Guo, J.; Xia, Z.; Zheng, C.; Su, Q.; Zeng, Y.; et al. Oral, Nasal, and Gut Microbiota in Parkinson's Disease. *Neuroscience* **2022**, *480*, 65–78. [CrossRef]

788. Smith, R.P.; Easson, C.; Lyle, S.M.; Kapoor, R.; Donnelly, C.P.; Davidson, E.J.; Parikh, E.; Lopez, J.V.; Tartar, J.L. Gut microbiome diversity is associated with sleep physiology in humans. *PLoS ONE* **2019**, *14*, e0222394. [CrossRef]

789. Bai, Z.; Huang, X.; Wu, G.; Ye, H.; Huang, W.; Nie, Q.; Chen, H.; Yin, J.; Chen, Y.; Nie, S. Polysaccharides from red kidney bean alleviating hyperglycemia and hyperlipidemia in type 2 diabetic rats via gut microbiota and lipid metabolic modulation. *Food Chem.* **2023**, *404*, 134598. [CrossRef]

790. Loh, G.; Blaut, M. Role of commensal gut bacteria in inflammatory bowel diseases. *Gut Microbes* **2012**, *3*, 544–555. [CrossRef]

791. Khoo, X.H.; Chong, C.W.; Talha, A.M.; Philip, K.; Teh, C.S.J.; Isa, A.M.; Wong, M.S.; Chew, D.C.H.; Wong, Z.; Jusoh, N.S.; et al. The impact of diet and ethnicity on Gut Microbiota Variation in Irritable Bowel Syndrome: A Multi-centre Study. *J. Gastroenterol. Hepatol.* **2023**, *38*, 1259–1268. [CrossRef]

792. Chavez-Carbajal, A.; Nirmalkar, K.; Perez-Lizaur, A.; Hernandez-Quiroz, F.; Ramirez-Del-Alto, S.; Garcia-Mena, J.; Hernández-Guerrero, C. Gut Microbiota and Predicted Metabolic Pathways in a Sample of Mexican Women Affected by Obesity and Obesity Plus Metabolic Syndrome. *Int. J. Mol. Sci.* **2019**, *20*, 438. [CrossRef]

793. Natalello, G.; Bosello, S.L.; Paroni Sterbini, F.; Posteraro, B.; De Lorenzis, E.; Canestrari, G.B.; Gigante, L.; Verardi, L.; Ferraccioli, G.; Sanguinetti, M.; et al. Gut microbiota analysis in systemic sclerosis according to disease characteristics and nutritional status. *Clin. Exp. Rheumatol.* **2020**, *38* (Suppl. S125), 73–84. [PubMed]

794. Zhang, M.; Lv, Y.; Hou, S.; Liu, Y.; Wang, Y.; Wan, X. Differential Mucosal Microbiome Profiles across Stages of Human Colorectal Cancer. *Life* **2021**, *11*, 831. [CrossRef] [PubMed]

795. Wang, Y.; Shen, R.; Liu, M.; Zhou, Q.; Zhai, Y.-H.; Fan, L.-H.; Lan, Y.-Z.; Zhu, X.-D. Metagenomic analysis of Tongxie Yaofang therapy for rat models of ulcerative colitis with liver depression and spleen deficiency syndrome. *All Life* **2023**, *16*, 1–12. [CrossRef]

796. Bischoff, S.C.; Nguyen, N.K.; Seethaler, B.; Beisner, J.; Kügler, P.; Stefan, T. Gut Microbiota Patterns Predicting Long-Term Weight Loss Success in Individuals with Obesity Undergoing Nonsurgical Therapy. *Nutrients* **2022**, *14*, 3182. [CrossRef] [PubMed]

797. Yang, W.; Shao, L.; Heizhati, M.; Wu, T.; Yao, X.; Wang, Y.; Wang, L.; Li, N. Oropharyngeal Microbiome in Obstructive Sleep Apnea: Decreased Diversity and Abundance. *J. Clin. Sleep Med.* **2019**, *15*, 1777–1788. [CrossRef]

798. Tai, N.; Wong, F.S.; Wen, L. The role of gut microbiota in the development of type 1, type 2 diabetes mellitus and obesity. *Rev. Endocr. Metab. Disord.* **2015**, *16*, 55–65. [CrossRef]

799. Heimesaat, M.M.; Fischer, A.; Siegmund, B.; Kupz, A.; Niebergall, J.; Fuchs, D.; Jahn, H.-K.; Freudenberg, M.; Loddenkemper, C.; Batra, A.; et al. Shift towards pro-inflammatory intestinal bacteria aggravates acute murine colitis via Toll-like receptors 2 and 4. *PLoS ONE* **2007**, *2*, e662. [CrossRef]

800. Verdam, F.J.; Fuentes, S.; de Jonge, C.; Zoetendal, E.G.; Erbil, R.; Greve, J.W.; Buurman, W.A.; de Vos, W.M.; Rensen, S.S. Human intestinal microbiota composition is associated with local and systemic inflammation in obesity. *Obesity* **2013**, *21*, E607-15. [CrossRef]

801. Purcell, R.V.; Visnovska, M.; Biggs, P.J.; Schmeier, S.; Frizelle, F.A. Distinct gut microbiome patterns associate with consensus molecular subtypes of colorectal cancer. *Sci. Rep.* **2017**, *7*, 11590. [CrossRef]

802. Wang, J.; Ye, F.; Cheng, X.; Zhang, X.; Liu, F.; Liu, G.; Ni, M.; Qiao, S.; Zhou, W.; Zhang, Y. The Effects of LW-AFC on Intestinal Microbiome in Senescence-Accelerated Mouse Prone 8 Strain, a Mouse Model of Alzheimer's Disease. *J. Alzheimers Dis.* **2016**, *53*, 907–919. [CrossRef]

803. Afroz, K.F.; Reyes, N.; Young, K.; Parikh, K.; Misra, V.; Alvina, K. Author Correction: Altered gut microbiome and autism like behavior are associated with parental high salt diet in male mice. *Sci. Rep.* **2022**, *12*, 5686. [CrossRef]

804. Zhu, Y.H.; Huan, F.; Wang, J.; Xie, X.; Yu, G.; Wang, X.; Jiang, L.; Gao, R.; Xiao, H.; Ding, H.; et al. 1-Methyl-4-phenyl-1,2,3,6-tetrahydropyridine Induced Parkinson's Disease in Mouse: Potential Association between Neurotransmitter Disturbance and Gut Microbiota Dysbiosis. *ACS Chem. Neurosci.* **2020**, *11*, 3366–3376. [CrossRef]

805. Lai, W.T.; Zhao, J.; Xu, S.X.; Deng, W.F.; Xu, D.; Wang, M.B.; He, F.S.; Liu, Y.H.; Guo, Y.Y.; Ye, S.W.; et al. Shotgun metagenomics reveals both taxonomic and tryptophan pathway differences of gut microbiota in bipolar disorder with current major depressive episode patients. *J. Affect. Disord.* **2021**, *278*, 311–319. [CrossRef]

806. Cai, Y.; Juszczak, H.M.; Cope, E.K.; Goldberg, A.N. The microbiome in obstructive sleep apnea. *Sleep* **2021**, *44*, zsab061. [CrossRef]

807. Zhao, F.; Liu, Q.; Cao, J.; Xu, Y.; Pei, Z.; Fan, H.; Yuan, Y.; Shen, X.; Li, C. A sea cucumber (*Holothuria leucospilota*) polysaccharide improves the gut microbiome to alleviate the symptoms of type 2 diabetes mellitus in Goto-Kakizaki rats. *Food Chem. Toxicol.* **2020**, *135*, 110886. [CrossRef] [PubMed]

808. Li, H.; Christman, L.M.; Li, R.; Gu, L. Synergic interactions between polyphenols and gut microbiota in mitigating inflammatory bowel diseases. *Food Funct.* **2020**, *11*, 4878–4891. [CrossRef] [PubMed]

809. Angelakis, E.; Bachar, D.; Yasir, M.; Musso, D.; Djossou, F.; Melenotte, C.; Robert, C.; Davoust, B.; Gaborit, B.; Azhar, E.; et al. Comparison of the gut microbiota of obese individuals from different geographic origins. *New Microbes New Infect.* **2019**, *27*, 40–47. [CrossRef] [PubMed]

810. Fox, M.; Knorr, D.A.; Haptonstall, K.M. Alzheimer's disease and symbiotic microbiota: An evolutionary medicine perspective. *Ann. N. Y. Acad. Sci.* **2019**, *1449*, 3–24. [CrossRef] [PubMed]

811. Scassellati, C.; Marizzoni, M.; Cattane, N.; Lopizzo, N.; Mombelli, E.; Riva, M.A.; Cattaneo, A. The Complex Molecular Picture of Gut and Oral Microbiota-Brain-Depression System: What We Know and What We Need to Know. *Front. Psychiatry* **2021**, *12*, 722335. [CrossRef]

812. Bajer, L.; Kverka, M.; Kostovcik, M.; Macinga, P.; Dvorak, J.; Stehlikova, Z.; Brezina, J.; Wohl, P.; Spicak, J.; Drastich, P. Distinct gut microbiota profiles in patients with primary sclerosing cholangitis and ulcerative colitis. *World J. Gastroenterol.* **2017**, *23*, 4548. [CrossRef]

813. de Souza, A.Z.; Zambom, A.Z.; Abboud, K.Y.; Reis, S.K.; Tannihao, F.; Guadagnini, D.; Saad, M.J.; Prada, P.O. Oral supplementation with L-glutamine alters gut microbiota of obese and overweight adults: A pilot study. *Nutrition* **2015**, *31*, 884–889. [CrossRef] [PubMed]

814. Shi, F.; Liu, G.; Lin, Y.; Guo, C.L.; Han, J.; Chu, E.S.H.; Shi, C.; Li, Y.; Zhang, H.; Hu, C.; et al. Altered gut microbiome composition by appendectomy contributes to colorectal cancer. *Oncogene* **2023**, *42*, 530–540. [CrossRef] [PubMed]

815. Zhang, M.; Ma, W.; Zhang, J.; He, Y.; Wang, J. Analysis of gut microbiota profiles and microbe-disease associations in children with autism spectrum disorders in China. *Sci. Rep.* **2018**, *8*, 13981. [CrossRef] [PubMed]

816. Hu, S.; Li, A.; Huang, T.; Lai, J.; Li, J.; Sublette, M.E.; Lu, H.; Lu, Q.; Du, Y.; Hu, Z.; et al. Gut Microbiota Changes in Patients with Bipolar Depression. *Adv. Sci.* **2019**, *6*, 1900752. [CrossRef] [PubMed]

817. Salamone, D.; Rivellese, A.A.; Vetrani, C. The relationship between gut microbiota, short-chain fatty acids and type 2 diabetes mellitus: The possible role of dietary fibre. *Acta Diabetol.* **2021**, *58*, 1131–1138. [CrossRef]

818. Zuo, T.; Kamm, M.A.; Colombel, J.-F.; Ng, S.C. Urbanization and the gut microbiota in health and inflammatory bowel disease. *Nat. Rev. Gastroenterol. Hepatol.* **2018**, *15*, 440–452. [CrossRef]

819. Chen, J.; He, X.; Huang, J. Diet effects in gut microbiome and obesity. *J. Food Sci.* **2014**, *79*, R442–R451. [CrossRef]

820. Zhang, W.; Zhang, J.; Liu, T.; Xing, J.; Zhang, H.; Wang, D.; Tang, D. Bidirectional effects of intestinal microbiota and antibiotics: A new strategy for colorectal cancer treatment and prevention. *J. Cancer Res. Clin. Oncol.* **2022**, *148*, 2387–2404. [CrossRef]

821. Allaband, C.; Lingaraju, A.; Martino, C.; Russell, B.; Tripathi, A.; Poulsen, O.; Machado, A.C.D.; Zhou, D.; Xue, J.; Elijah, E.; et al. Intermittent hypoxia and hypercapnia alter diurnal rhythms of luminal gut microbiome and metabolome. *mSystems* **2021**, *6*, e00116-21. [CrossRef]

822. Remely, M.; Hippe, B.; Zanner, J.; Aumueller, E.; Brath, H.; Haslberger, A.G. Gut Microbiota of Obese, Type 2 Diabetic Individuals is Enriched in *Faecalibacterium prausnitzii*, *Akkermansia muciniphila* and *Peptostreptococcus anaerobius* after Weight Loss. *Endocr. Metab. Immune Disord. Drug Targets* **2016**, *16*, 99–106. [CrossRef]

823. Zhang, T.; Ji, X.; Lu, G.; Zhang, F. The potential of *Akkermansia muciniphila* in inflammatory bowel disease. *Appl. Microbiol. Biotechnol.* **2021**, *105*, 5785–5794. [PubMed]

824. Depommier, C.; Everard, A.; Druart, C.; Plovier, H.; Van Hul, M.; Vieira-Silva, S.; Falony, G.; Raes, J.; Maiter, D.; Delzenne, N.M.; et al. Supplementation with *Akkermansia muciniphila* in overweight and obese human volunteers: A proof-of-concept exploratory study. *Nat. Med.* **2019**, *25*, 1096–1103. [PubMed]

825. Osman, M.A.; Neoh, H.-M.; Ab Mutalib, N.-S.; Chin, S.-F.; Mazlan, L.; Raja Ali, R.A.; Zakaria, A.D.; Ngiu, C.S.; Ang, M.Y.; Jamal, R. *Parvimonas micra*, *Peptostreptococcus stomatis*, *Fusobacterium nucleatum* and *Akkermansia muciniphila* as a four-bacteria biomarker panel of colorectal cancer. *Sci. Rep.* **2021**, *11*, 2925. [PubMed]

826. Ou, Z.; Deng, L.; Lu, Z.; Wu, F.; Liu, W.; Huang, D.; Peng, Y. Protective effects of *Akkermansia muciniphila* on cognitive deficits and amyloid pathology in a mouse model of Alzheimer's disease. *Nutr. Diabetes* **2020**, *10*, 12.

827. Fang, X.; Li, F.J.; Hong, D.J. Potential Role of *Akkermansia muciniphila* in Parkinson's Disease and Other Neurological/Autoimmune Diseases. *Curr. Med. Sci.* **2021**, *41*, 1172–1177.

828. Ding, Y.; Bu, F.; Chen, T.; Shi, G.; Yuan, X.; Feng, Z.; Duan, Z.; Wang, R.; Zhang, S.; Wang, Q.; et al. A next-generation probiotic: *Akkermansia muciniphila* ameliorates chronic stress-induced depressive-like behavior in mice by regulating gut microbiota and metabolites. *Appl. Microbiol. Biotechnol.* **2021**, *105*, 8411–8426. [PubMed]

829. Xu, J.; Lian, F.; Zhao, L.; Zhao, Y.; Chen, X.; Zhang, X.; Guo, Y.; Zhang, C.; Zhou, Q.; Xue, Z.; et al. Structural modulation of gut microbiota during alleviation of type 2 diabetes with a Chinese herbal formula. *ISME J.* **2015**, *9*, 552–562.

830. Dziarski, R.; Park, S.Y.; Kashyap, D.R.; Dowd, S.E.; Gupta, D. *Pglyrp*-Regulated Gut Microflora *Prevotella falsenii*, *Parabacteroides distasonis* and *Bacteroides eggerthii* Enhance and *Alistipes finegoldii* Attenuates Colitis in Mice. *PLoS ONE* **2016**, *11*, e0146162.

831. Lotankar, M.; Mokkala, K.; Houttu, N.; Koivuniemi, E.; Sorensen, N.; Nielsen, H.B.; Munukka, E.; Lahti, L.; Laitinen, K. Distinct Diet-Microbiota-Metabolism Interactions in Overweight and Obese Pregnant Women: A Metagenomics Approach. *Microbiol. Spectr.* **2022**, *10*, e0089321.

832. Sun, T.; Liu, S.; Zhou, Y.; Yao, Z.; Zhang, D.; Cao, S.; Wei, Z.; Tan, B.; Li, Y.; Lian, Z.; et al. Evolutionary biologic changes of gut microbiota in an 'adenoma-carcinoma sequence' mouse colorectal cancer model induced by 1, 2-Dimethylhydrazine. *Oncotarget* **2017**, *8*, 444–457.

833. Li, Z.; Zhu, H.; Guo, Y.; Du, X.; Qin, C. Gut microbiota regulate cognitive deficits and amyloid deposition in a model of Alzheimer's disease. *J. Neurochem.* **2020**, *155*, 448–461. [CrossRef] [PubMed]

834. Averina, O.; Kovtun, A.; Danilenko, V. Bacterial Genes of Metabolite Biomarkers of Autism Spectrum Disorders in Gut Microbiota of Young Children: Detection by Real-Time PCR and In Silico Analysis. *Russ. J. Genet.* **2020**, *56*, 1260–1268. [CrossRef]

835. Avagliano, C.; Coretti, L.; Lama, A.; Pirozzi, C.; De Caro, C.; De Biase, D.; Turco, L.; Mollica, M.P.; Paciello, O.; Calignano, A.; et al. Dual-Hit Model of Parkinson's Disease: Impact of Dysbiosis on 6-Hydroxydopamine-Insulted Mice-Neuroprotective and Anti-Inflammatory Effects of Butyrate. *Int. J. Mol. Sci.* **2022**, *23*, 6367. [CrossRef] [PubMed]

836. Liu, P.; Gao, M.; Liu, Z.; Zhang, Y.; Tu, H.; Lei, L.; Wu, P.; Zhang, A.; Yang, C.; Li, G.; et al. Gut Microbiome Composition Linked to Inflammatory Factors and Cognitive Functions in First-Episode, Drug-Naive Major Depressive Disorder Patients. *Front. Neurosci.* **2021**, *15*, 800764. [CrossRef]

837. Han, Y.; Xu, J.; Yan, Y.; Zhao, X. Dynamics of the gut microbiota in rats after hypobaric hypoxia exposure. *PeerJ* **2022**, *10*, e14090. [CrossRef]

838. Kulkarni, P.; Devkumar, P.; Chattopadhyay, I. Could dysbiosis of inflammatory and anti-inflammatory gut bacteria have an implications in the development of type 2 diabetes? A pilot investigation. *BMC Res. Notes* **2021**, *14*, 52.

839. Hou, Y.; Dong, L.; Lu, X.; Shi, H.; Xu, B.; Zhong, W.; Ma, L.; Wang, S.; Yang, C.; He, X.; et al. Distinctions Between Fecal and Intestinal Mucosal Microbiota in Subgroups of Irritable Bowel Syndrome. *Dig. Dis. Sci.* **2022**, *67*, 5580–5592. [CrossRef]

840. Del Chierico, F.; Abbatini, F.; Russo, A.; Quagliariello, A.; Reddel, S.; Capoccia, D.; Caccamo, R.; Ginanni Corradini, S.; Nobili, V.; De Peppo, F.; et al. Gut Microbiota Markers in Obese Adolescent and Adult Patients: Age-Dependent Differential Patterns. *Front. Microbiol.* **2018**, *9*, 1210. [CrossRef]

841. Song, C.H.; Kim, N.; Nam, R.H.; Choi, S.I.; Jang, J.Y.; Lee, H.N. Changes in Gut Microbiome upon Orchiectomy and Testosterone Administration in AOM/DSS-Induced Colon Cancer Mouse Model. *Cancer Res. Treat.* **2023**, *55*, 196–218. [CrossRef]

842. Wagner, V.E.; Dey, N.; Guruge, J.; Hsiao, A.; Ahern, P.P.; Semenkovich, N.P.; Blanton, L.V.; Cheng, J.; Griffin, N.; Stappenbeck, T.S.; et al. Effects of a gut pathobiont in a gnotobiotic mouse model of childhood undernutrition. *Sci. Transl. Med.* **2016**, *8*, 366ra164. [CrossRef]

843. Shen, W.D.; Lin, X.; Liu, H.M.; Li, B.Y.; Qiu, X.; Lv, W.Q.; Zhu, X.Z.; Greenbaum, J.; Liu, R.K.; Shen, J.; et al. Gut microbiota accelerates obesity in peri-/post-menopausal women via *Bacteroides fragilis* and acetic acid. *Int. J. Obes.* **2022**, *46*, 1918–1924. [CrossRef] [PubMed]

844. Wei, Z.; Cao, S.; Liu, S.; Yao, Z.; Sun, T.; Li, Y.; Li, J.; Zhang, D.; Zhou, Y. Could gut microbiota serve as prognostic biomarker associated with colorectal cancer patients' survival? A pilot study on relevant mechanism. *Oncotarget* **2016**, *7*, 46158–46172. [CrossRef] [PubMed]

845. Zou, R.; Xu, F.; Wang, Y.; Duan, M.; Guo, M.; Zhang, Q.; Zhao, H.; Zheng, H. Changes in the Gut Microbiota of Children with Autism Spectrum Disorder. *Autism Res.* **2020**, *13*, 1614–1625. [CrossRef]

846. Luna, R.A.; Foster, J.A. Gut brain axis: Diet microbiota interactions and implications for modulation of anxiety and depression. *Curr. Opin. Biotechnol.* **2015**, *32*, 35–41. [CrossRef]

847. Schafer, D.F.; Jones, E.A. Hepatic encephalopathy and the gamma-aminobutyric-acid neurotransmitter system. *Lancet* **1982**, *1*, 18–20. [CrossRef]

848. Ren, Y.; Hao, L.; Liu, J.; Wang, P.; Ding, Q.; Chen, C.; Song, Y. Alterations in the Gut Microbiota in Pregnant Women with Pregestational Type 2 Diabetes Mellitus. *mSystems* **2023**, *8*, e0114622. [CrossRef] [PubMed]

849. Hu, M.; Caldarelli, G.; Gili, T. Network analysis of a complex disease: The gut microbiota in the inflammatory bowel disease case. *arXiv* **2022**, arXiv:220807763.

850. Di Luccia, B.; Ahern, P.P.; Griffin, N.W.; Cheng, J.; Guruge, J.L.; Byrne, A.E.; Rodionov, D.A.; Leyn, S.A.; Osterman, A.L.; Ahmed, T.; et al. Combined Prebiotic and Microbial Intervention Improves Oral Cholera Vaccination Responses in a Mouse Model of Childhood Undernutrition. *Cell Host Microbe* **2020**, *27*, 899–908.e5. [CrossRef]

851. West, K.A.; Yin, X.; Rutherford, E.M.; Wee, B.; Choi, J.; Chrisman, B.S.; Dunlap, K.L.; Hannibal, R.L.; Hartono, W.; Lin, M.; et al. Multi-angle meta-analysis of the gut microbiome in Autism Spectrum Disorder: A step toward understanding patient subgroups. *Sci. Rep.* **2022**, *12*, 17034. [CrossRef]

852. Bi, M.; Feng, L.; He, J.; Liu, C.; Wang, Y.; Jiang, H.; Liu, S.-J. Emerging insights between gut microbiome dysbiosis and Parkinson's disease: Pathogenic and clinical relevance. *Ageing Res. Rev.* **2022**, *82*, 101759. [CrossRef]

853. Liu, W.; Du, Q.; Han, D.; Zhang, H. The Gut Microbiome and Obstructive Sleep Apnea Syndrome in Children. *Sleep Med.* **2022**, *100*, 462–471. [CrossRef] [PubMed]

854. Wu, X.; Ma, C.; Han, L.; Nawaz, M.; Gao, F.; Zhang, X.; Yu, P.; Zhao, C.; Li, L.; Zhou, A.; et al. Molecular characterisation of the faecal microbiota in patients with type II diabetes. *Curr. Microbiol.* **2010**, *61*, 69–78. [CrossRef] [PubMed]

855. Schirmer, M.; Franzosa, E.A.; Lloyd-Price, J.; McIver, L.J.; Schwager, R.; Poon, T.W.; Ananthakrishnan, A.N.; Andrews, E.; Barron, G.; Lake, K.; et al. Dynamics of metatranscription in the inflammatory bowel disease gut microbiome. *Nat. Microbiol.* **2018**, *3*, 337–346. [CrossRef] [PubMed]

856. Hata, T.; Miyata, N.; Takakura, S.; Yoshihara, K.; Asano, Y.; Kimura-Todani, T.; Yamashita, M.; Zhang, X.T.; Watanabe, N.; Mikami, K. The Gut Microbiome Derived from Anorexia Nervosa Patients Impairs Weight Gain and Behavioral Performance in Female Mice. *Endocrinology* **2019**, *160*, 2441–2452. [CrossRef] [PubMed]

857. Nicolucci, A.C.; Hume, M.P.; Martinez, I.; Mayengbam, S.; Walter, J.; Reimer, R.A. Prebiotics Reduce Body Fat and Alter Intestinal Microbiota in Children Who Are Overweight or with Obesity. *Gastroenterology* **2017**, *153*, 711–722. [CrossRef]

858. Liang, S.; Sin, Z.Y.; Yu, J.; Zhao, S.; Xi, Z.; Bruzzone, R.; Tun, H.M. Multi-cohort analysis of depression-associated gut bacteria sheds insight on bacterial biomarkers across populations. *Cell. Mol. Life Sci.* **2022**, *80*, 9. [CrossRef]

859. Qian, X.; Si, Q.; Lin, G.; Zhu, M.; Lu, J.; Zhang, H.; Wang, G.; Chen, W. *Bifidobacterium adolescentis* Is Effective in Relieving Type 2 Diabetes and May Be Related to Its Dominant Core Genome and Gut Microbiota Modulation Capacity. *Nutrients* **2022**, *14*, 2479. [CrossRef]

860. Kowalska-Duplaga, K.; Gosiewski, T.; Kapusta, P.; Sroka-Oleksiak, A.; Wędrychowicz, A.; Pieczarkowski, S.; Ludwig-Słomczyńska, A.H.; Wołkow, P.P.; Fyderek, K. Differences in the intestinal microbiome of healthy children and patients with newly diagnosed Crohn's disease. *Sci. Rep.* **2019**, *9*, 18880. [CrossRef]

861. Iribarren, C.; Magnusson, M.K.; Vigsnaes, L.K.; Aziz, I.; Amundsen, I.D.; Suligoj, T.; Juge, N.; Patel, P.; Sapnara, M.; Johnsen, L.; et al. The Effects of Human Milk Oligosaccharides on Gut Microbiota, Metabolite Profiles and Host Mucosal Response in Patients with Irritable Bowel Syndrome. *Nutrients* **2021**, *13*, 3836. [CrossRef]

862. Azcarate-Peril, M.A.; Sikes, M.; Bruno-Barcena, J.M. The intestinal microbiota, gastrointestinal environment and colorectal cancer: A putative role for probiotics in prevention of colorectal cancer? *Am. J. Physiol. Gastrointest. Liver Physiol.* **2011**, *301*, G401–G424. [CrossRef]

863. Mulle, J.G.; Sharp, W.G.; Cubells, J.F. The gut microbiome: A new frontier in autism research. *Curr. Psychiatry Rep.* **2013**, *15*, 337. [CrossRef] [PubMed]

864. Alfonsetti, M.; Castelli, V.; d'Angelo, M. Are We What We Eat? Impact of Diet on the Gut–Brain Axis in Parkinson's Disease. *Nutrients* **2022**, *14*, 380. [CrossRef] [PubMed]

865. Guo, Y.; Xie, J.P.; Deng, K.; Li, X.; Yuan, Y.; Xuan, Q.; Xie, J.; He, X.-M.; Wang, Q.; Li, J.-J.; et al. Prophylactic Effects of *Bifidobacterium adolescentis* on Anxiety and Depression-Like Phenotypes after Chronic Stress: A Role of the Gut Microbiota-Inflammation Axis. *Front. Behav. Neurosci.* **2019**, *13*, 126. [CrossRef]

866. Bloom, P.P.; Donlan, J.; Torres Soto, M.; Daidone, M.; Hohmann, E.; Chung, R.T. Fecal microbiota transplant improves cognition in hepatic encephalopathy and its effect varies by donor and recipient. *Hepatol. Commun.* **2022**, *6*, 2079–2089. [CrossRef] [PubMed]

867. Suceveanu, A.I.; Stoian, A.P.; Parepa, I.; Voinea, C.; Hainarosie, R.; Manuc, D.; Nitipir, C.; Mazilu, L.; Suceveanu, A.P. Gut microbiota patterns in obese and type 2 diabetes (T2D) patients from romanian black sea coast region. *Rev. Chim.* **2018**, *69*, 2260–2267. [CrossRef]

868. Lee, K.J.; Tack, J. Altered intestinal microbiota in irritable bowel syndrome. *Neurogastroenterol. Motil.* **2010**, *22*, 493–498. [CrossRef]

869. Wang, Q.; Wang, K.; Wu, W.; Lv, L.; Bian, X.; Yang, L.; Wang, Q.; Li, Y.; Ye, J.; Fang, D.; et al. Administration of *Bifidobacterium bifidum* CGMCC 15068 modulates gut microbiota and metabolome in azoxymethane (AOM)/dextran sulphate sodium (DSS)-induced colitis-associated colon cancer (CAC) in mice. *Appl. Microbiol. Biotechnol.* **2020**, *104*, 5915–5928. [CrossRef]

870. Kim, H.; Kim, S.; Park, S.J.; Park, G.; Shin, H.; Park, M.S.; Kim, J. Administration of *Bifidobacterium bifidum* BGN4 and *Bifidobacterium longum* BORI Improves Cognitive and Memory Function in the Mouse Model of Alzheimer's Disease. *Front. Aging Neurosci.* **2021**, *13*, 709091. [CrossRef]

871. Settanni, C.R.; Bibbò, S.; Ianiro, G.; Rinninella, E.; Cintoni, M.; Mele, M.C.; Cammarota, G.; Gasbarrini, A. Gastrointestinal involvement of autism spectrum disorder: Focus on gut microbiota. *Expert Rev. Gastroenterol. Hepatol.* **2021**, *15*, 599–622. [CrossRef]

872. Bullich, C.; Keshavarzian, A.; Garssen, J.; Kraneveld, A.; Perez-Pardo, P. Gut Vibes in Parkinson's Disease: The Microbiota-Gut-Brain Axis. *Mov. Disord. Clin. Pract.* **2019**, *6*, 639–651. [CrossRef]

873. Soverini, M.; Turroni, S.; Biagi, E.; Quercia, S.; Brigidi, P.; Candela, M.; Rampelli, S. Variation of Carbohydrate-Active Enzyme Patterns in the Gut Microbiota of Italian Healthy Subjects and Type 2 Diabetes Patients. *Front. Microbiol.* **2017**, *8*, 2079. [CrossRef] [PubMed]

874. Conte, M.P.; Schippa, S.; Zamboni, I.; Penta, M.; Chiarini, F.; Seganti, L.; Osborn, J.; Falconieri, P.; Borrelli, O.; Cucchiara, S. Gut-associated bacterial microbiota in paediatric patients with inflammatory bowel disease. *Gut* **2006**, *55*, 1760–1767. [CrossRef] [PubMed]

875. Malinen, E.; Rinttila, T.; Kajander, K.; Matto, J.; Kassinen, A.; Krogius, L.; Saarela, M.; Korpela, R.; Palva, A. Analysis of the fecal microbiota of irritable bowel syndrome patients and healthy controls with real-time PCR. *Am. J. Gastroenterol.* **2005**, *100*, 373–382. [CrossRef] [PubMed]

876. Greathouse, K.L.; White, J.R.; Padgett, R.N.; Perrotta, B.G.; Jenkins, G.D.; Chia, N.; Chen, J. Gut microbiome meta-analysis reveals dysbiosis is independent of body mass index in predicting risk of obesity-associated CRC. *BMJ Open Gastroenterol.* **2019**, *6*, e000247. [CrossRef]

877. Ha, S.; Oh, D.; Lee, S.; Park, J.; Ahn, J.; Choi, S.; Cheon, K.-A. Altered Gut Microbiota in Korean Children with Autism Spectrum Disorders. *Nutrients* **2021**, *13*, 3300. [CrossRef]

878. Bolliri, C.; Fontana, A.; Cereda, E.; Barichella, M.; Cilia, R.; Ferri, V.; Caronni, S.; Calandrella, D.; Morelli, L.; Pezzoli, G. Gut Microbiota in Monozygotic Twins Discordant for Parkinson's Disease. *Ann. Neurol.* **2022**, *92*, 631–636. [CrossRef]

879. Galley, J.D.; Mashburn-Warren, L.; Blalock, L.C.; Lauber, C.L.; Carroll, J.E.; Ross, K.M.; Hobel, C.; Coussons-Read, M.; Schetter, C.D.; Gur, T.L. Maternal anxiety, depression and stress affects offspring gut microbiome diversity and bifidobacterial abundances. *Brain Behav. Immun.* **2023**, *107*, 253–264. [CrossRef]

880. Badran, M.; Khalyfa, A.; Ericsson, A.C.; Puech, C.; McAdams, Z.; Bender, S.B.; Gozal, D. Gut microbiota mediate vascular dysfunction in a murine model of sleep apnoea: Effect of probiotics. *Eur. Respir. J.* **2023**, *61*, 2200002. [CrossRef]

881. Yao, S.; Zhao, Z.; Wang, W.; Liu, X. Bifidobacterium Longum: Protection against Inflammatory Bowel Disease. *J. Immunol. Res.* **2021**, *2021*, 8030297. [CrossRef]

882. Fanigliulo, L.; Comparato, G.; Aragona, G.; Cavallaro, L.; Iori, V.; Maino, M.; Cavestro, G.M.; Soliani, P.; Sianesi, M.; Franzè, A.; et al. Role of gut microflora and probiotic effects in the irritable bowel syndrome. *Acta Biomed.* **2006**, *77*, 85–89.

883. Coretti, L.; Paparo, L.; Riccio, M.P.; Amato, F.; Cuomo, M.; Natale, A.; Borrelli, L.; Corrado, G.; De Caro, C.; Comegna, M.; et al. Corrigendum: Gut Microbiota Features in Young Children with Autism Spectrum Disorders. *Front. Microbiol.* **2019**, *10*, 920. [CrossRef] [PubMed]

884. Tian, P.; Zou, R.; Song, L.; Zhang, X.; Jiang, B.; Wang, G.; Lee, Y.-K.; Zhao, J.; Zhang, H.; Chen, W. Ingestion of *Bifidobacterium longum* subspecies infantis strain CCFM687 regulated emotional behavior and the central BDNF pathway in chronic stress-induced depressive mice through reshaping the gut microbiota. *Food Funct.* **2019**, *10*, 7588–7598. [CrossRef] [PubMed]

885. Malaguarnera, M.; Greco, F.; Barone, G.; Gargante, M.P.; Malaguarnera, M.; Toscano, M.A. *Bifidobacterium longum* with fructo-oligosaccharide (FOS) treatment in minimal hepatic encephalopathy: A randomized, double-blind, placebo-controlled study. *Dig. Dis. Sci.* **2007**, *52*, 3259–3265. [CrossRef]

886. Olson, C.A.; Iniguez, A.J.; Yang, G.E.; Fang, P.; Pronovost, G.N.; Jameson, K.G.; Rendon, T.K.; Paramo, J.; Barlow, J.T.; Ismagilov, R.F.; et al. Alterations in the gut microbiota contribute to cognitive impairment induced by the ketogenic diet and hypoxia. *Cell Host Microbe* **2021**, *29*, 1378–1392. [CrossRef]

887. Velizarova, M.; Yanachkova, V.; Boneva, T.; Giragosyan, S.; Mihaleva, I.; Andreeva-Gateva, P.; Svinarov, D.; Dimova, I. Relationship between Vitamin D status and microbiome changes in Bulgarian patients with type 2 diabetes mellitus. *Biotechnol. Biotechnol. Equip.* **2023**, *37*, 2209662. [CrossRef]

888. Devkota, S.; Chang, E.B. Interactions between diet, bile acid metabolism, gut microbiota, and inflammatory bowel diseases. *Dig. Dis.* **2015**, *33*, 351–356. [CrossRef]

889. Jacobs, J.P.; Lagishetty, V.; Hauer, M.C.; Labus, J.S.; Dong, T.S.; Toma, R.; Vuyisich, M.; Naliboff, B.D.; Lackner, J.M.; Gupta, A.; et al. Multi-omics profiles of the intestinal microbiome in irritable bowel syndrome and its bowel habit subtypes. *Microbiome* **2023**, *11*, 5. [CrossRef] [PubMed]

890. Jian, C.; Luukkonen, P.; Sadevirta, S.; Yki-Jarvinen, H.; Salonen, A. Impact of short-term overfeeding of saturated or unsaturated fat or sugars on the gut microbiota in relation to liver fat in obese and overweight adults. *Clin. Nutr.* **2021**, *40*, 207–216. [CrossRef]

891. Verhaar, B.J.H.; Hendriksen, H.M.A.; de Leeuw, F.A.; Doorduijn, A.S.; van Leeuwenstijn, M.; Teunissen, C.E.; Barkhof, F.; Scheltens, P.; Kraaij, R.; van Duijn, C.M.; et al. Gut Microbiota Composition Is Related to AD Pathology. *Front. Immunol.* **2021**, *12*, 794519. [CrossRef]

892. Kittana, M.; Ahmadani, A.; Al Marzooq, F.; Attlee, A. Dietary Fat Effect on the Gut Microbiome, and Its Role in the Modulation of Gastrointestinal Disorders in Children with Autism Spectrum Disorder. *Nutrients* **2021**, *13*, 3818. [CrossRef]

893. Stevens, B.R.; Pepine, C.J.; Richards, E.M.; Kim, S.; Raizada, M.K. Depressive hypertension: A proposed human endotype of brain/gut microbiome dysbiosis. *Am. Heart J.* **2021**, *239*, 27–37. [CrossRef]

894. Di Lodovico, L.; Mondot, S.; Dore, J.; Mack, I.; Hanachi, M.; Gorwood, P. Anorexia nervosa and gut microbiota: A systematic review and quantitative synthesis of pooled microbiological data. *Prog. Neuropsychopharmacol. Biol. Psychiatry* **2021**, *106*, 110114. [CrossRef] [PubMed]

895. Parnell, J.A.; Reimer, R.A. Prebiotic fiber modulation of the gut microbiota improves risk factors for obesity and the metabolic syndrome. *Gut Microbes* **2012**, *3*, 29–34. [CrossRef] [PubMed]

896. Zhang, H.; Chang, Y.; Zheng, Q.; Zhang, R.; Hu, C.; Jia, W. Altered intestinal microbiota associated with colorectal cancer. *Front. Med.* **2019**, *13*, 461–470. [CrossRef] [PubMed]

897. Gonzalez Cordero, E.M.; Cuevas-Budhart, M.A.; Perez Moran, D.; Trejo Villeda, M.A.; Gomez-Del-Pulgar, G.f.-M.M. Relationship Between the Gut Microbiota and Alzheimer's Disease: A Systematic Review. *J. Alzheimers Dis.* **2022**, *87*, 519–528. [CrossRef]

898. Matarazzo, I.; Toniato, E.; Robuffo, I. Psychobiome Feeding Mind: Polyphenolics in Depression and Anxiety. *Curr. Top. Med Chem.* **2018**, *18*, 2108–2115. [CrossRef]

899. Million, M.; Alou, M.T.; Khelaifia, S.; Bachar, D.; Lagier, J.C.; Dione, N.; Brah, S.; Hugon, P.; Lombard, V.; Armougom, F.; et al. Increased Gut Redox and Depletion of Anaerobic and Methanogenic Prokaryotes in Severe Acute Malnutrition. *Sci. Rep.* **2016**, *6*, 26051. [CrossRef]

900. Leung, J.; Burke, B.; Ford, D.; Garvin, G.; Korn, C.; Sulis, C.; Bhadelia, N. Possible association between obesity and *Clostridium difficile* infection. *Emerg. Infect. Dis.* **2013**, *19*, 1791–1798. [CrossRef]

901. Jahani-Sherafat, S.; Azimirad, M.; Alebouyeh, M.; Amoli, H.A.; Hosseini, P.; Ghasemian-Safaei, H.; Moghim, S. The rate and importance of *Clostridium difficile* in colorectal cancer patients. *Gastroenterol. Hepatol. Bed Bench* **2019**, *12*, 358–363.

902. Toh, M.C.; Allen-Vercoe, E. The human gut microbiota with reference to autism spectrum disorder: Considering the whole as more than a sum of its parts. *Microb. Ecol. Health Dis.* **2015**, *26*, 26309. [CrossRef]

903. Evrensel, A.; Ceylan, M.E. The Gut-Brain Axis: The Missing Link in Depression. *Clin. Psychopharmacol. Neurosci.* **2015**, *13*, 239–244. [CrossRef]

904. Riordan, S.M.; Williams, R. Gut flora and hepatic encephalopathy in patients with cirrhosis. *N. Engl. J. Med.* **2010**, *362*, 1140–1142. [CrossRef] [PubMed]

905. Swidsinski, A.; Weber, J.; Loening-Baucke, V.; Hale, L.P.; Lochs, H. Spatial organization and composition of the mucosal flora in patients with inflammatory bowel disease. *J. Clin. Microbiol.* **2005**, *43*, 3380–3389. [CrossRef] [PubMed]

906. Maukonen, J.; Satokari, R.; Matto, J.; Soderlund, H.; Mattila-Sandholm, T.; Saarela, M. Prevalence and temporal stability of selected clostridial groups in irritable bowel syndrome in relation to predominant faecal bacteria. *J. Med. Microbiol.* **2006**, *55 Pt 5*, 625–633. [CrossRef] [PubMed]

907. Collado, M.C.; Isolauri, E.; Laitinen, K.; Salminen, S. Distinct composition of gut microbiota during pregnancy in overweight and normal-weight women. *Am. J. Clin. Nutr.* **2008**, *88*, 894–899. [CrossRef] [PubMed]

908. Kim, E.; Coelho, D.; Blachier, F. Review of the association between meat consumption and risk of colorectal cancer. *Nutr. Res.* **2013**, *33*, 983–994. [CrossRef]

909. Kleessen, B.; Kroesen, A.J.; Buhr, H.J.; Blaut, M. Mucosal and invading bacteria in patients with inflammatory bowel disease compared with controls. *Scand. J. Gastroenterol.* **2002**, *37*, 1034–1041. [CrossRef]

910. Palacios, T.; Coulson, S.; Butt, H.; Vitetta, L. The gastrointestinal microbiota and multi-strain probiotic therapy: In children and adolescent obesity. *Adv. Integr. Med.* **2014**, *1*, 2–8. [CrossRef]

911. Luna, R.A.; Oezguen, N.; Balderas, M.; Venkatachalam, A.; Runge, J.K.; Versalovic, J.; Veenstra-VanderWeele, J.; Anderson, G.M.; Savidge, T.; Williams, K.C. Distinct Microbiome-Neuroimmune Signatures Correlate with Functional Abdominal Pain in Children with Autism Spectrum Disorder. *Cell. Mol. Gastroenterol. Hepatol.* **2017**, *3*, 218–230. [CrossRef]

912. Karnachuk, O.V.; Ikkert, O.P.; Avakyan, M.R.; Knyazev, Y.V.; Volochaev, M.N.; Zyusman, V.S.; Panov, V.L.; Kadnikov, V.V.; Mardanov, A.V.; Ravin, N.V. *Desulfovibrio desulfuricans* AY5 Isolated from a Patient with Autism Spectrum Disorder Binds Iron in Low-Soluble Greigite and Pyrite. *Microorganisms* **2021**, *9*, 2558. [CrossRef]

913. Wu, S.; Hammarstedt-Nordenvall, L.; Jangard, M.; Cheng, L.; Radu, S.A.; Angelidou, P.; Zha, Y.; Hamsten, M.; Engstrand, L.; Du, J.; et al. Tonsillar Microbiota: A Cross-Sectional Study of Patients with Chronic Tonsillitis or Tonsillar Hypertrophy. *Msystems* **2021**, *6*, e01302-20. [CrossRef] [PubMed]

914. El-Salhy, M.; Casen, C.; Valeur, J.; Hausken, T.; Hatlebakk, J.G. Responses to faecal microbiota transplantation in female and male patients with irritable bowel syndrome. *World J. Gastroenterol.* **2021**, *27*, 2219–2237. [CrossRef] [PubMed]

915. McLeod, A.; Penalver Bernabe, B.; Xia, Y.; Sanchez-Flack, J.; Lamar, M.; Schiffer, L.; Castellanos, K.; Fantuzzi, G.; Maki, P.; Fitzgibbon, M.; et al. Comparing the gut microbiome of obese, African American, older adults with and without mild cognitive impairment. *PLoS ONE* **2023**, *18*, e0280211. [CrossRef] [PubMed]

916. Huh, J.W.; Kim, M.J.; Kim, J.; Lee, H.G.; Ryoo, S.B.; Ku, J.L.; Jeong, S.Y.; Park, K.J.; Kim, D.; Kim, J.F.; et al. Enterotypical Prevotella and three novel bacterial biomarkers in preoperative stool predict the clinical outcome of colorectal cancer. *Microbiome* **2022**, *10*, 203. [CrossRef]

917. Bosch, J.A.; Nieuwdorp, M.; Zwinderman, A.H.; Deschasaux, M.; Radjabzadeh, D.; Kraaij, R.; Davids, M.; de Rooij, S.R.; Lok, A. The gut microbiota and depressive symptoms across ethnic groups. *Nat. Commun.* **2022**, *13*, 7129. [CrossRef]

918. Badran, M.; Mashaqi, S.; Gozal, D. The gut microbiome as a target for adjuvant therapy in obstructive sleep apnea. *Expert Opin. Ther. Targets* **2020**, *24*, 1263–1282. [CrossRef]

919. Yu, S.; Ge, X.; Xu, H.; Tan, B.; Tian, B.; Shi, Y.; Dai, Y.; Li, Y.; Hu, S.; Qian, J. Gut microbiome and mycobiome in inflammatory bowel disease patients with Clostridioides difficile infection. *Front. Cell. Infect. Microbiol.* **2023**, *13*, 1129043. [CrossRef]

920. Shin, S.Y.; Park, S.; Moon, J.M.; Kim, K.; Kim, J.W.; Chun, J.; Lee, T.H.; Choi, C.H.; The Microbiome Research Group of the Korean Society for Neurogastroenterology and Motility. Compositional Changes in the Gut Microbiota of Responders and Non-responders to Probiotic Treatment among Patients with Diarrhea-predominant Irritable Bowel Syndrome: A Post Hoc Analysis of a Randomized Clinical Trial. *J. Neurogastroenterol. Motil.* **2022**, *28*, 642–654. [CrossRef]

921. Ondee, T.; Pongpirul, K.; Janchot, K.; Kanacharoen, S.; Lertmongkolaksorn, T.; Wongsaroj, L.; Somboonna, N.; Ngamwongsatit, N.; Leelahavanichkul, A. *Lactiplantibacillus plantarum* dfa1 Outperforms *Enterococcus faecium* dfa1 on Anti-Obesity in High Fat-Induced Obesity Mice Possibly through the Differences in Gut Dysbiosis Attenuation, despite the Similar Anti-Inflammatory Properties. *Nutrients* **2021**, *14*, 80. [CrossRef]

922. Kovtun, A.S.; Averina, O.V.; Alekseeva, M.G.; Danilenko, V.N. Antibiotic resistance genes in the gut microbiota of children with autistic spectrum disorder as possible predictors of the disease. *Microb. Drug Resist.* **2020**, *26*, 1307–1320. [CrossRef]

923. Loguercio, C.; Abbiati, R.; Rinaldi, M.; Romano, A.; Del Vecchio Blanco, C.; Coltorti, M. Long-term effects of *Enterococcus faecium* SF68 versus lactulose in the treatment of patients with cirrhosis and grade 1–2 hepatic encephalopathy. *J. Hepatol.* **1995**, *23*, 39–46. [CrossRef] [PubMed]

924. Munir, S.S.; Sert Kuniyoshi, F.H.; Singh, P.; Covassin, N. Is the Gut Microbiome Implicated in the Excess Risk of Hypertension Associated with Obstructive Sleep Apnea? A Contemporary Review. *Antioxidants* **2023**, *12*, 866. [CrossRef] [PubMed]

925. Tsai, H.-J.; Tsai, W.-C.; Hung, W.-C.; Hung, W.-W.; Chang, C.-C.; Dai, C.-Y.; Tsai, Y.-C. Gut microbiota and subclinical cardiovascular disease in patients with type 2 diabetes mellitus. *Nutrients* **2021**, *13*, 2679. [CrossRef] [PubMed]

926. Rhodes, J.M. The role of Escherichia coli in inflammatory bowel disease. *Gut* **2007**, *56*, 610–612. [CrossRef]

927. Liu, H.N.; Wu, H.; Chen, Y.Z.; Chen, Y.J.; Shen, X.Z.; Liu, T.T. Altered molecular signature of intestinal microbiota in irritable bowel syndrome patients compared with healthy controls: A systematic review and meta-analysis. *Dig. Liver Dis.* **2017**, *49*, 331–337. [CrossRef]

928. Veziant, J.; Villeger, R.; Barnich, N.; Bonnet, M. Gut Microbiota as Potential Biomarker and/or Therapeutic Target to Improve the Management of Cancer: Focus on Colibactin-Producing Escherichia coli in Colorectal Cancer. *Cancers* **2021**, *13*, 2215. [CrossRef] [PubMed]

929. Wu, H.; Wei, J.; Zhao, X.; Liu, Y.; Chen, Z.; Wei, K.; Lu, J.; Chen, W.; Jiang, M.; Li, S.; et al. Neuroprotective effects of an engineered *Escherichia coli* Nissle 1917 on Parkinson's disease in mice by delivering GLP-1 and modulating gut microbiota. *Bioeng. Transl. Med.* **2022**, *8*, e10351. [CrossRef] [PubMed]

930. Yun, S.-W.; Kim, J.-K.; Han, M.; Kim, D.-H. *Lacticaseibacillus paracasei* NK112 mitigates *Escherichia coli*-induced depression and cognitive impairment in mice by regulating IL-6 expression and gut microbiota. *Benef. Microbes* **2021**, *12*, 541–551. [CrossRef]

931. Manzhalii, E.; Moyseyenko, V.; Kondratiuk, V.; Molochek, N.; Falalyeyeva, T.; Kobyliak, N. Effect of a specific Escherichia coli Nissle 1917 strain on minimal/mild hepatic encephalopathy treatment. *World J. Hepatol.* **2022**, *14*, 634–646. [CrossRef]

932. Morales, E.J.D.C. Obstructive Sleep Apnea and the Gut Microbiome. Master's Thesis, The University of Arizona, Tucson, AZ, USA, 2018.

933. Ge, X.; Zhang, A.; Li, L.; Sun, Q.; He, J.; Wu, Y.; Tan, R.; Pan, Y.; Zhao, J.; Xu, Y.; et al. Application of machine learning tools: Potential and useful approach for the prediction of type 2 diabetes mellitus based on the gut microbiome profile. *Exp. Ther. Med.* **2022**, *23*, 305. [CrossRef]

934. Balamurugan, R.; George, G.; Kabeerdoss, J.; Hepsiba, J.; Chandragunasekaran, A.M.; Ramakrishna, B.S. Quantitative differences in intestinal *Faecalibacterium prausnitzii* in obese Indian children. *Br. J. Nutr.* **2010**, *103*, 335–338. [CrossRef]

935. Bojovic, K.; Ignjatovic Eth, I.; Sokovic Bajic, S.; Vojnovic Milutinovic, D.; Tomic, M.; Golic, N.; Tolinački, M. Gut Microbiota Dysbiosis Associated with Altered Production of Short Chain Fatty Acids in Children with Neurodevelopmental Disorders. *Front. Cell. Infect. Microbiol.* **2020**, *10*, 223. [CrossRef] [PubMed]

936. Lu, Q.; Lai, J.; Lu, H.; Ng, C.; Huang, T.; Zhang, H.; Ding, K.; Wang, Z.; Jiang, J.; Hu, J.; et al. Gut Microbiota in Bipolar Depression and Its Relationship to Brain Function: An Advanced Exploration. *Front. Psychiatry* **2019**, *10*, 784. [CrossRef] [PubMed]

937. Sokol, H.; Pigneur, B.; Watterlot, L.; Lakhdari, O.; Bermudez-Humaran, L.G.; Gratadoux, J.J.; Blugeon, S.; Bridonneau, C.; Furet, J.-P.; Corthier, G.; et al. *Faecalibacterium prausnitzii* is an anti-inflammatory commensal bacterium identified by gut microbiota analysis of Crohn disease patients. *Proc. Natl. Acad. Sci. USA* **2008**, *105*, 16731–16736. [CrossRef]

938. Chumpitazi, B.P.; Cope, J.L.; Hollister, E.B.; Tsai, C.M.; McMeans, A.R.; Luna, R.A.; Versalovic, J.; Shulman, R.J. Randomised clinical trial: Gut microbiome biomarkers are associated with clinical response to a low FODMAP diet in children with the irritable bowel syndrome. *Aliment. Pharmacol. Ther.* **2015**, *42*, 418–427. [CrossRef]

939. Ueda, A.; Shinkai, S.; Shiroma, H.; Taniguchi, Y.; Tsuchida, S.; Kariya, T.; Kawahara, T.; Kobayashi, Y.; Kohda, N.; Ushida, K.; et al. Identification of *Faecalibacterium prausnitzii* strains for gut microbiome-based intervention in Alzheimer's-type dementia. *Cell Rep. Med.* **2021**, *2*, 100398. [CrossRef] [PubMed]

940. Unger, M.M.; Spiegel, J.; Dillmann, K.-U.; Grundmann, D.; Philippeit, H.; Bürmann, J.; Faßbender, K.; Schwiertz, A.; Schäfer, K.-H. Short chain fatty acids and gut microbiota differ between patients with Parkinson's disease and age-matched controls. *Park. Relat. Disord.* **2016**, *32*, 66–72. [CrossRef]

941. Zhang, X.; Li, X.; Xu, H.; Fu, Z.; Wang, F.; Huang, W.; Wu, K.; Li, C.; Liu, Y.; Zou, J.; et al. Changes in the oral and nasal microbiota in pediatric obstructive sleep apnea. *J. Oral Microbiol.* **2023**, *15*, 2182571. [CrossRef]

942. Sedighi, M.; Razavi, S.; Navab-Moghadam, F.; Khamseh, M.E.; Alaei-Shahmiri, F.; Mehrtash, A.; Amirmozafari, N. Comparison of gut microbiota in adult patients with type 2 diabetes and healthy individuals. *Microb. Pathog.* **2017**, *111*, 362–369. [CrossRef]

943. Lin, S.; Zhang, X.; Zhu, X.; Jiao, J.; Wu, Y.; Li, Y.; Zhao, L. *Fusobacterium nucleatum* aggravates ulcerative colitis through promoting gut microbiota dysbiosis and dysmetabolism. *J. Periodontol.* **2023**, *94*, 405–418. [CrossRef]

944. Kushak, R.I.; Sengupta, A.; Winter, H.S. Interactions between the intestinal microbiota and epigenome in individuals with autism spectrum disorder. *Dev. Med. Child Neurol.* **2022**, *64*, 296–304. [CrossRef] [PubMed]

945. Kountouras, J.; Polyzos, S.A.; Deretzi, G. *Helicobacter pylori* associated with obstructive sleep apnea might contribute to sleep, cognition, and driving performance disturbances in patients with cirrhosis. *Clin. Gastroenterol. Hepatol.* **2015**, *13*, 1547. [CrossRef] [PubMed]

946. Gupta, S.S.; Mohammed, M.H.; Ghosh, T.S.; Kanungo, S.; Nair, G.B.; Mande, S.S. Metagenome of the gut of a malnourished child. *Gut Pathog.* **2011**, *3*, 7. [CrossRef] [PubMed]

947. Lender, N.; Talley, N.J.; Enck, P.; Haag, S.; Zipfel, S.; Morrison, M.; Holtmann, G.J. Review article: Associations between Helicobacter pylori and obesity—An ecological study. *Aliment. Pharmacol. Ther.* **2014**, *40*, 24–31. [CrossRef]

948. Jahani-Sherafat, S.; Alebouyeh, M.; Moghim, S.; Ahmadi Amoli, H.; Ghasemian-Safaei, H. Role of gut microbiota in the pathogenesis of colorectal cancer; a review article. *Gastroenterol. Hepatol. Bed Bench* **2018**, *11*, 101–109.

949. Elfil, M.; Kamel, S.; Kandil, M.; Koo, B.B.; Schaefer, S.M. Implications of the Gut Microbiome in Parkinson's Disease. *Mov. Disord.* **2020**, *35*, 921–933. [CrossRef]

950. Mobini, R.; Tremaroli, V.; Ståhlman, M.; Karlsson, F.; Levin, M.; Ljungberg, M.; Sohlin, M.; Bertéus Forslund, H.; Perkins, R.; Bäckhed, F. Metabolic effects of *Lactobacillus reuteri* DSM 17938 in people with type 2 diabetes: A randomized controlled trial. *Diabetes Obes. Metab.* **2017**, *19*, 579–589. [CrossRef]

951. Wang, H.; Zhou, C.; Huang, J.; Kuai, X.; Shao, X. The potential therapeutic role of *Lactobacillus reuteri* for treatment of inflammatory bowel disease. *Am. J. Transl. Res.* **2020**, *12*, 1569–1583.

952. Niv, E.; Naftali, T.; Hallak, R.; Vaisman, N. The efficacy of *Lactobacillus reuteri* ATCC 55730 in the treatment of patients with irritable bowel syndrome—A double blind, placebo-controlled, randomized study. *Clin. Nutr.* **2005**, *24*, 925–931. [CrossRef]

953. Bell, H.N.; Rebernick, R.J.; Goyert, J.; Singhal, R.; Kuljanin, M.; Kerk, S.A.; Huang, W.; Das, N.K.; Andren, A.; Solanki, S.; et al. Reuterin in the healthy gut microbiome suppresses colorectal cancer growth through altering redox balance. *Cancer Cell* **2022**, *40*, 185–200.e6. [CrossRef]

954. Liu, G.; Tan, F.H.; Lau, S.A.; Jaafar, M.H.; Chung, F.Y.; Azzam, G.; Liong, M.; Li, Y. Lactic acid bacteria feeding reversed the malformed eye structures and ameliorated gut microbiota profiles of Drosophila melanogaster Alzheimer's disease model. *J. Appl. Microbiol.* **2022**, *132*, 3155–3167. [CrossRef] [PubMed]

955. Sgritta, M.; Dooling, S.W.; Buffington, S.A.; Momin, E.N.; Francis, M.B.; Britton, R.A.; Costa-Mattioli, M. Mechanisms Underlying Microbial-Mediated Changes in Social Behavior in Mouse Models of Autism Spectrum Disorder. *Neuron* **2019**, *101*, 246–259.e6. [CrossRef]

956. Du, Y.; Li, Y.; Xu, X.; Li, R.; Zhang, M.; Cui, Y.; Zhang, L.; Wei, Z.; Wang, S.; Tuo, H. Probiotics for constipation and gut microbiota in Parkinson's disease. *Park. Relat. Disord.* **2022**, *103*, 92–97. [CrossRef] [PubMed]

957. Zhou, H.; Wang, R.; Zhang, S.; Zhang, X.; Zhou, H.; Wen, T.; Wang, J. Depression-like symptoms due to Dcf1 deficiency are alleviated by intestinal transplantation of *Lactobacillus murine* and *Lactobacillus reuteri. Biochem. Biophys. Res. Commun.* **2022**, *593*, 137–143. [CrossRef] [PubMed]

958. Rivera-Flores, R.; Morán-Villota, S.; Cervantes-Barragán, L.; López-Macias, C.; Uribe, M. Manipulation of microbiota with probiotics as an alternative for treatment of hepatic encephalopathy. *Nutrition* **2020**, *73*, 110693. [CrossRef]

959. Zhang, W.-Y.; Zhang, H.-H.; Yu, C.-H.; Fang, J.; Ying, H.-Z. Ethanol extract of *Atractylodis macrocephalae Rhizoma* ameliorates insulin resistance and gut microbiota in type 2 diabetic db/db mice. *J. Funct. Foods* **2017**, *39*, 139–151. [CrossRef]

960. Ghoshal, U.; Shukla, R.; Srivastava, D.; Ghoshal, U.C. Irritable Bowel Syndrome, Particularly the Constipation-Predominant Form, Involves an Increase in *Methanobrevibacter smithii*, Which Is Associated with Higher Methane Production. *Gut Liver* **2016**, *10*, 932–938. [CrossRef]

961. Tidjani Alou, M.; Million, M.; Traore, S.I.; Mouelhi, D.; Khelaifia, S.; Bachar, D.; Caputo, A.; Delerce, J.; Brah, S.; Alhousseini, D.; et al. Gut Bacteria Missing in Severe Acute Malnutrition, Can We Identify Potential Probiotics by Culturomics? *Front. Microbiol.* **2017**, *8*, 899. [CrossRef]

962. Liu, D.; Zhang, S.; Li, S.; Zhang, Q.; Cai, Y.; Li, P.; Li, H.; Shen, B.; Liao, Q.; Hong, Y.; et al. Indoleacrylic acid produced by *Parabacteroides distasonis* alleviates type 2 diabetes via activation of AhR to repair intestinal barrier. *BMC Biol.* **2023**, *21*, 90. [CrossRef]

963. Herndon, C.C.; Wang, Y.P.; Lu, C.L. Targeting the gut microbiota for the treatment of irritable bowel syndrome. *Kaohsiung J. Med. Sci.* **2020**, *36*, 160–170. [CrossRef]

964. Song, H.; Shen, X.; Chu, Q.; Zheng, X. Pomegranate fruit pulp polyphenols reduce diet-induced obesity with modulation of gut microbiota in mice. *J. Sci. Food Agric.* **2022**, *102*, 1968–1977. [CrossRef] [PubMed]

965. Yuan, N.; Li, X.; Wang, M.; Zhang, Z.; Qiao, L.; Gao, Y.; Xu, X.; Zhi, J.; Li, Y.; Li, Z.; et al. Gut Microbiota Alteration Influences Colorectal Cancer Metastasis to the Liver by Remodeling the Liver Immune Microenvironment. *Gut Liver* **2022**, *16*, 575–588. [CrossRef] [PubMed]

966. Averina, O.V.; Kovtun, A.S.; Polyakova, S.I.; Savilova, A.M.; Rebrikov, D.V.; Danilenko, V.N. The bacterial neurometabolic signature of the gut microbiota of young children with autism spectrum disorders. *J. Med. Microbiol.* **2020**, *69*, 558–571. [CrossRef] [PubMed]

967. Wang, L.; Yu, X.; Xu, X.; Ming, J.; Wang, Z.; Gao, B.; Xing, Y.; Zhou, J.; Fu, J.; Liu, T.; et al. The fecal microbiota is already altered in normoglycemic individuals who go on to have type 2 diabetes. *Front. Cell. Infect. Microbiol.* **2021**, *11*, 598672. [CrossRef] [PubMed]

968. Ohkusa, T.; Koido, S. Intestinal microbiota and ulcerative colitis. *J. Infect. Chemother.* **2015**, *21*, 761–768. [CrossRef] [PubMed]

969. Goll, R.; Johnsen, P.H.; Hjerde, E.; Diab, J.; Valle, P.C.; Hilpusch, F.; Cavanagh, J.P. Effects of fecal microbiota transplantation in subjects with irritable bowel syndrome are mirrored by changes in gut microbiome. *Gut Microbes* **2020**, *12*, 1794263. [CrossRef] [PubMed]

970. Dhopatkar, N.; Keeler, J.L.; Mutwalli, H.; Whelan, K.; Treasure, J.; Himmerich, H. Gastrointestinal symptoms, gut microbiome, probiotics and prebiotics in anorexia nervosa: A review of mechanistic rationale and clinical evidence. *Psychoneuroendocrinology* **2023**, *147*, 105959. [CrossRef]

971. Liu, W.; Fang, X.; Zhou, Y.; Dou, L.; Dou, T. Machine learning-based investigation of the relationship between gut microbiome and obesity status. *Microbes Infect.* **2022**, *24*, 104892. [CrossRef]

972. Yoon, H.; Kim, N.; Park, J.H.; Kim, Y.S.; Lee, J.; Kim, H.W.; Choi, Y.J.; Shin, C.M.; Park, Y.S.; Lee, D.H.; et al. Comparisons of Gut Microbiota among Healthy Control, Patients with Conventional Adenoma, Sessile Serrated Adenoma, and Colorectal Cancer. *J. Cancer Prev.* **2017**, *22*, 108–114. [CrossRef]

973. Kong, X.; Liu, J.; Cetinbas, M.; Sadreyev, R.; Koh, M.; Huang, H.; Adeseye, A.; He, P.; Zhu, J.; Russell, H.; et al. New and Preliminary Evidence on Altered Oral and Gut Microbiota in Individuals with Autism Spectrum Disorder (ASD): Implications for ASD Diagnosis and Subtyping Based on Microbial Biomarkers. *Nutrients* **2019**, *11*, 2128. [CrossRef]

974. Kovtun, A.S.; Averina, O.V.; Angelova, I.Y.; Yunes, R.A.; Zorkina, Y.A.; Morozova, A.Y.; Pavlichenko, A.V.; Syunyakov, T.S.; Karpenko, O.A.; Kostyuk, G.P.; et al. Alterations of the Composition and Neurometabolic Profile of Human Gut Microbiota in Major Depressive Disorder. *Biomedicines* **2022**, *10*, 2162. [CrossRef] [PubMed]

975. Alsharairi, N.A. The Therapeutic Role of Short-Chain Fatty Acids Mediated Very Low-Calorie Ketogenic Diet-Gut Microbiota Relationships in Paediatric Inflammatory Bowel Diseases. *Nutrients* **2022**, *14*, 4113. [CrossRef] [PubMed]

976. Petrov, V.; Alifirova, V.; Saltykova, I.; Zhukova, I.; Zhukova, N.; Dorofeeva, Y.B.; Tyakht, A.V.; Altukhov, I.A.; Kostryukova, E.S.; Titova, M.A.; et al. Comparison study of gut microbiota in case of Parkinson's disease and other neurological disorders. *Bull. Sib. Med.* **2017**, *15*, 113–125. [CrossRef]

977. Bakir-Gungor, B.; Hacilar, H.; Jabeer, A.; Nalbantoglu, O.U.; Aran, O.; Yousef, M. Inflammatory bowel disease biomarkers of human gut microbiota selected via different feature selection methods. *PeerJ* **2022**, *10*, e13205. [CrossRef]

978. Lyra, A.; Rinttila, T.; Nikkila, J.; Krogius-Kurikka, L.; Kajander, K.; Malinen, E.; Mättö, J.; Mäkelä, L.; Palva, A. Diarrhoea-predominant irritable bowel syndrome distinguishable by 16S rRNA gene phylotype quantification. *World J. Gastroenterol.* **2009**, *15*, 5936–5945. [CrossRef]

979. Wang, Y.; Lim, Y.Y.; He, Z.; Wong, W.T.; Lai, W.F. Dietary phytochemicals that influence gut microbiota: Roles and actions as anti-Alzheimer agents. *Crit. Rev. Food Sci. Nutr.* **2022**, *62*, 5140–5166. [CrossRef]

980. Wan, Y.; Zuo, T.; Xu, Z.; Zhang, F.; Zhan, H.; Dorothy, C.; Leung, T.-F.; Yeoh, Y.K.; Chan, F.K.L.; Chan, R.; et al. Underdevelopment of the gut microbiota and bacteria species as non-invasive markers of prediction in children with autism spectrum disorder. *Gut* **2022**, *71*, 910–918. [CrossRef]

981. Kwak, M.S.; Cha, J.M.; Shin, H.P.; Jeon, J.W.; Yoon, J.Y. Development of a Novel Metagenomic Biomarker for Prediction of Upper Gastrointestinal Tract Involvement in Patients with Crohn's Disease. *Front. Microbiol.* **2020**, *11*, 1162. [CrossRef]

982. Hynonen, U.; Rasinkangas, P.; Satokari, R.; Paulin, L.; de Vos, W.M.; Pietilä, T.E.; Kant, R.; Palva, A. Isolation and whole genome sequencing of a Ruminococcus-like bacterium, associated with irritable bowel syndrome. *Anaerobe* **2016**, *39*, 60–67. [CrossRef]

983. Togo, A.H.; Diop, A.; Bittar, F.; Maraninchi, M.; Valero, R.; Armstrong, N.; Dubourg, G.; Labas, N.; Richez, M.; Delerce, J.; et al. Correction to: Description of *Mediterraneibacter massiliensis*, gen. nov., sp. nov., a new genus isolated from the gut microbiota of an obese patient and reclassification of *Ruminococcus faecis*, *Ruminococcus lactaris*, *Ruminococcus torques*, *Ruminococcus gnavus* and *Clostridium glycyrrhizinilyticum* as *Mediterraneibacter faecis* comb. nov., *Mediterraneibacter lactaris* comb. nov., *Mediterraneibacter torques* comb. nov., *Mediterraneibacter gnavus* comb. nov. and *Mediterraneibacter glycyrrhizinilyticus* comb. nov. *Antonie Van Leeuwenhoek* **2018**, *111*, 2129–2130.

984. Matto, J.; Maunuksela, L.; Kajander, K.; Palva, A.; Korpela, R.; Kassinen, A.; Saarela, M. Composition and temporal stability of gastrointestinal microbiota in irritable bowel syndrome—A longitudinal study in IBS and control subjects. *FEMS Immunol. Med. Microbiol.* **2005**, *43*, 213–222. [CrossRef]

985. Han, K.; Ji, L.; Wang, C.; Shao, Y.; Chen, C.; Liu, L.; Feng, M.; Yang, F.; Wu, X.; Li, X.; et al. The host genetics affects gut microbiome diversity in Chinese depressed patients. *Front. Genet.* **2022**, *13*, 976814. [CrossRef] [PubMed]

986. Yukawa-Muto, Y.; Kamiya, T.; Fujii, H.; Mori, H.; Toyoda, A.; Sato, I.; Konishi, Y.; Hirayama, A.; Hara, E.; Fukuda, S.; et al. Distinct responsiveness to rifaximin in patients with hepatic encephalopathy depends on functional gut microbial species. *Hepatol. Commun.* **2022**, *6*, 2090–2104. [CrossRef] [PubMed]

987. Huang, Q.Y.; Yao, F.; Zhou, C.R.; Huang, X.Y.; Wang, Q.; Long, H.; Wu, Q.M. Role of gut microbiome in regulating the effectiveness of metformin in reducing colorectal cancer in type 2 diabetes. *World J. Clin. Cases* **2020**, *8*, 6213–6228. [CrossRef]

988. Weingarden, A.R.; Vaughn, B.P. Intestinal microbiota, fecal microbiota transplantation, and inflammatory bowel disease. *Gut Microbes* **2017**, *8*, 238–252. [CrossRef] [PubMed]

989. Beatty, J.K.; Bhargava, A.; Buret, A.G. Post-infectious irritable bowel syndrome: Mechanistic insights into chronic disturbances following enteric infection. *World J. Gastroenterol.* **2014**, *20*, 3976–3985. [CrossRef]

990. Subramanian, S.; Huq, S.; Yatsunenko, T.; Haque, R.; Mahfuz, M.; Alam, M.A.; Benezra, A.; DeStefano, J.; Meier, M.F.; Muegge, B.D.; et al. Persistent gut microbiota immaturity in malnourished Bangladeshi children. *Nature* **2014**, *510*, 417–421. [CrossRef]

991. Mehal, W.Z. The Gordian Knot of dysbiosis, obesity and NAFLD. *Nat. Rev. Gastroenterol. Hepatol.* **2013**, *10*, 637–644. [CrossRef]

992. Gao, R.; Gao, Z.; Huang, L.; Qin, H. Gut microbiota and colorectal cancer. *Eur. J. Clin. Microbiol. Infect. Dis.* **2017**, *36*, 757–769. [CrossRef]

993. Vojdani, A.; Vojdani, E.; Saidara, E.; Kharrazian, D. Reaction of Amyloid-beta Peptide Antibody with Different Infectious Agents Involved in Alzheimer's Disease. *J. Alzheimers Dis.* **2018**, *63*, 847–860. [CrossRef]

994. Mehta, K.K.; Bhat, R.; Markande, A.R. Effects of gut bacteria and their amyloids on mental health and neurodegeneration in Parkinson's disease. *J. Appl. Biol. Biotechnol.* **2023**, *11*, 38–46. [CrossRef]

995. Strugala, G.J.; Rauws, A.G.; Elbers, R. Intestinal first pass metabolism of amygdalin in the rat in vitro. *Biochem. Pharmacol.* **1986**, *35*, 2123–2128. [CrossRef] [PubMed]

996. Manhardt, M.A. Correlation of Injected Amygdalin and Urinary Thiocyanate in JAX C57 BL/KsJ Mice. Master's Thesis, Loyola University Chicago, Chicago, IL, USA, 1981.

997. Niimura, T.; Tokieda, T.; Yamaha, T. Partial purification and some properties of cyclamate sulfamatase. *J. Biochem.* **1974**, *75*, 407–417. [CrossRef] [PubMed]

998. Macfarlane, G.; Allison, C. Utilisation of protein by human gut bacteria. *FEMS Microbiol. Ecol.* **1986**, *2*, 19–24. [CrossRef]

999. Macfarlane, G.; Cummings, J.; Allison, C. Protein degradation by human intestinal bacteria. *Microbiology* **1986**, *132*, 1647–1656. [CrossRef]

1000. Elshahed, M.S.; Miron, A.; Aprotosoaie, A.C.; Farag, M.A. Pectin in diet: Interactions with the human microbiome, role in gut homeostasis, and nutrient-drug interactions. *Carbohydr. Polym.* **2021**, *255*, 117388. [CrossRef]

1001. Romano, K.A.; Vivas, E.I.; Amador-Noguez, D.; Rey, F.E. Intestinal microbiota composition modulates choline bioavailability from diet and accumulation of the proatherogenic metabolite trimethylamine-N-oxide. *mBio* **2015**, *6*, e02481-14. [CrossRef]

1002. Williams, B.B.; Van Benschoten, A.H.; Cimermancic, P.; Donia, M.S.; Zimmermann, M.; Taketani, M.; Ishihara, A.; Kashyap, P.C.; Fraser, J.S.; Fischbach, M.A. Discovery and characterization of gut microbiota decarboxylases that can produce the neurotransmitter tryptamine. *Cell Host Microbe* **2014**, *16*, 495–503. [CrossRef]

1003. Yang, M.; Ma, J.; Ruan, J.; Ye, Y.; Fu, P.P.-C.; Lin, G. Intestinal and hepatic biotransformation of pyrrolizidine alkaloid N-oxides to toxic pyrrolizidine alkaloids. *Arch. Toxicol.* **2019**, *93*, 2197–2209. [CrossRef]

1004. Widjaja, F.; Wesseling, S.; Rietjens, I.M.C.M. Physiologically based kinetic modelling predicts the in vivo relative potency of riddelliine N-oxide compared to riddelliine in rat to be dose dependent. *Arch. Toxicol.* **2022**, *96*, 135–151. [CrossRef]

1005. Juste, C.; Gérard, P. Cholesterol-to-coprostanol conversion by the gut microbiota: What we know, suspect, and ignore. *Microorganisms* **2021**, *9*, 1881. [CrossRef] [PubMed]

1006. Robertson, L.; Chandrasekaran, A.; Reuning, R.; Hui, J.; Rawal, B. Reduction of digoxin to 20R-dihydrodigoxin by cultures of Eubacterium lentum. *Appl. Environ. Microbiol.* **1986**, *51*, 1300–1303. [CrossRef] [PubMed]

1007. Xu, H.; Heinze, T.M.; Chen, S.; Cerniglia, C.E.; Chen, H. Anaerobic metabolism of 1-amino-2-naphthol-based azo dyes (Sudan dyes) by human intestinal microflora. *Appl. Environ. Microbiol.* **2007**, *73*, 7759–7762. [CrossRef] [PubMed]

1008. Gingell, R.; Bridges, J.; Williams, R. The role of the gut flora in the metabolism of prontosil and neoprontosil in the rat. *Xenobiotica* **1971**, *1*, 143–156. [CrossRef]

1009. Klotz, U.; Maier, K.; Fischer, C.; Heinkel, K. Therapeutic efficacy of sulfasalazine and its metabolites in patients with ulcerative colitis and Crohn's disease. *N. Engl. J. Med.* **1980**, *303*, 1499–1502. [CrossRef] [PubMed]

1010. Strong, H.; Renwick, A.; George, C.; Liu, Y.; Hill, M. The reduction of sulphinpyrazone and sulindac by intestinal bacteria. *Xenobiotica* **1987**, *17*, 685–696. [CrossRef]

1011. Xin, Z.; Fengwei, T.; Gang, W.; Xiaoming, L.; Qiuxiang, Z.; Hao, Z.; Wei, C. Isolation, identification and characterization of human intestinal bacteria with the ability to utilize chloramphenicol as the sole source of carbon and energy. *FEMS Microbiol. Ecol.* **2012**, *82*, 703–712. [CrossRef]

1012. LinWu, S.-W.; Syu, C.-J.; Chen, Y.-L.; Wang, A.H.-J.; Peng, F.-C. Characterization of Escherichia coli nitroreductase NfsB in the metabolism of nitrobenzodiazepines. *Biochem. Pharmacol.* **2009**, *78*, 96–103. [CrossRef]

1013. Feng, R.; Shou, J.-W.; Zhao, Z.-X.; He, C.-Y.; Ma, C.; Huang, M.; Fu, J.; Tan, X.-S.; Li, X.-Y.; Wen, B.-Y. Transforming berberine into its intestine-absorbable form by the gut microbiota. *Sci. Rep.* **2015**, *5*, 12155. [CrossRef]

1014. Jourova, L.; Anzenbacher, P.; Matuskova, Z.; Vecera, R.; Strojil, J.; Kolar, M.; Nobilis, M.; Hermanova, P.; Hudcovic, T.; Kozakova, H. Gut microbiota metabolizes nabumetone in vitro: Consequences for its bioavailability in vivo in the rodents with altered gut microbiome. *Xenobiotica* **2019**, *49*, 1296–1302. [CrossRef]

1015. Yan, A.; Culp, E.; Perry, J.; Lau, J.T.; MacNeil, L.T.; Surette, M.G.; Wright, G.D. Transformation of the anticancer drug doxorubicin in the human gut microbiome. *ACS Infect. Dis.* **2018**, *4*, 68–76. [CrossRef] [PubMed]

1016. Mendez-Catala, D.M.; Spenkelink, A.; Rietjens, I.M.; Beekmann, K. An in vitro model to quantify interspecies differences in kinetics for intestinal microbial bioactivation and detoxification of zearalenone. *Toxicol. Rep.* **2020**, *7*, 938–946. [CrossRef] [PubMed]

1017. Bachmann, V.; Kostiuk, B.; Unterweger, D.; Diaz-Satizabal, L.; Ogg, S.; Pukatzki, S. Bile salts modulate the mucin-activated type VI secretion system of pandemic Vibrio cholerae. *PLoS Negl. Trop. Dis.* **2015**, *9*, e0004031. [CrossRef] [PubMed]

1018. Deloménie, C.; Fouix, S.; Longuemaux, S.; Brahimi, N.m.; Bizet, C.; Picard, B.; Denamur, E.; Dupret, J.-M. Identification and functional characterization of arylamine N-acetyltransferases in eubacteria: Evidence for highly selective acetylation of 5-aminosalicylic acid. *J. Bacteriol.* **2001**, *183*, 3417–3427. [CrossRef]

1019. Li, F.; Jin, J.; Rietjens, I.M.; Xing, F. Interindividual differences in in vitro human intestinal microbial conversion of 3-acetyl-DON and 15-acetyl-DON. *Toxins* **2022**, *14*, 199. [CrossRef]

1020. Humblot, C.; Murkovic, M.; Rigottier-Gois, L.; Bensaada, M.; Bouclet, A.; Andrieux, C.; Anba, J.; Rabot, S. β-glucuronidase in human intestinal microbiota is necessary for the colonic genotoxicity of the food-borne carcinogen 2-amino-3-methylimidazo [4, 5-f] quinoline in rats. *Carcinogenesis* **2007**, *28*, 2419–2425. [CrossRef]

1021. van Kessel, S.P.; Frye, A.K.; El-Gendy, A.O.; Castejon, M.; Keshavarzian, A.; van Dijk, G.; El Aidy, S. Gut bacterial tyrosine decarboxylases restrict levels of levodopa in the treatment of Parkinson's disease. *Nat. Commun.* **2019**, *10*, 310. [CrossRef]

1022. Saito, Y.; Sato, T.; Nomoto, K.; Tsuji, H. Identification of phenol-and p-cresol-producing intestinal bacteria by using media supplemented with tyrosine and its metabolites. *FEMS Microbiol. Ecol.* **2018**, *94*, fiy125. [CrossRef]

1023. García-Villalba, R.; Beltrán, D.; Espín, J.C.; Selma, M.V.; Tomás-Barberán, F.A. Time course production of urolithins from ellagic acid by human gut microbiota. *J. Agric. Food Chem.* **2013**, *61*, 8797–8806. [CrossRef]

1024. Goldin, B.R.; Peppercorn, M.A.; Goldman, P. Contributions of host and intestinal microflora in the metabolism of L-dopa by the rat. *J. Pharmacol. Exp. Ther.* **1973**, *186*, 160–166.

1025. Clavel, T.; Henderson, G.; Engst, W.; Dore, J.; Blaut, M. Phylogeny of human intestinal bacteria that activate the dietary lignan secoisolariciresinol diglucoside. *FEMS Microbiol. Ecol.* **2006**, *55*, 471–478. [CrossRef] [PubMed]

1026. Zhang, S.; Mao, B.; Cui, S.; Zhang, Q.; Zhao, J.; Tang, X.; Chen, W. Absorption, metabolism, bioactivity, and biotransformation of epigallocatechin gallate. *Crit. Rev. Food Sci. Nutr.* **2023**, 1–21. [CrossRef]

1027. Malet-Martino, M.-C.; Martino, R.; De Forni, M.; Andremont, A.; Hartmann, O.; Armand, J. Flucytosine conversion to fluorouracil in humans: Does a correlation with gut flora status exist? A report of two cases using fluorine-19 magnetic resonance spectroscopy. *Infection* **1991**, *19*, 178–180. [CrossRef] [PubMed]

1028. Liu, Z.; de Bruijn, W.J.; Bruins, M.E.; Vincken, J.-P. Reciprocal interactions between epigallocatechin-3-gallate (EGCG) and human gut microbiota in vitro. *J. Agric. Food Chem.* **2020**, *68*, 9804–9815. [CrossRef] [PubMed]

1029. Espín, J.C.; González-Sarrías, A.; Tomás-Barberán, F.A. The gut microbiota: A key factor in the therapeutic effects of (poly)phenols. *Biochem. Pharmacol.* **2017**, *139*, 82–93. [CrossRef]

1030. Zheng, X.; Zhao, A.; Xie, G.; Chi, Y.; Zhao, L.; Li, H.; Wang, C.; Bao, Y.; Jia, W.; Luther, M. Melamine-induced renal toxicity is mediated by the gut microbiota. *Sci. Transl. Med.* **2013**, *5*, 172ra122. [CrossRef]

1031. Oku, T.; Nakamura, S. Digestion, absorption, fermentation, and metabolism of functional sugar substitutes and their available energy. *Pure Appl. Chem.* **2002**, *74*, 1253–1261. [CrossRef]