Corinna Bang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/868180/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Protective and aggressive bacterial subsets and metabolites modify hepatobiliary inflammation and fibrosis in a murine model of PSC. Gut, 2023, 72, 671-685.	12.1	30
2	Circulating microbiome in patients with portal hypertension. Gut Microbes, 2022, 14, 2029674.	9.8	22
3	The fecal mycobiome in non-alcoholic fatty liver disease. Journal of Hepatology, 2022, 76, 788-799.	3.7	66
4	Detection of Cancer Mutations by Urine Liquid Biopsy as a Potential Tool in the Clinical Management of Bladder Cancer Patients. Cancers, 2022, 14, 969.	3.7	2
5	B-cell-depletion reverses dysbiosis of the microbiome in multiple sclerosis patients. Scientific Reports, 2022, 12, 3728.	3.3	10
6	NMR Metabolomics Reveal Urine Markers of Microbiome Diversity and Identify Benzoate Metabolism as a Mediator between High Microbial Alpha Diversity and Metabolic Health. Metabolites, 2022, 12, 308.	2.9	11
7	Bovine milk microbiota: Evaluation of different DNA extraction protocols for challenging samples. MicrobiologyOpen, 2022, 11, e1275.	3.0	6
8	Oral Immune Priming Treatment Alters Microbiome Composition in the Red Flour Beetle Tribolium castaneum. Frontiers in Microbiology, 2022, 13, 793143.	3.5	5
9	Dysbiosis in the Gut Microbiota in Patients with Inflammatory Bowel Disease during Remission. Microbiology Spectrum, 2022, 10, e0061622.	3.0	34
10	Differential Effects of Obesity, Hyperlipidaemia, Dietary Intake and Physical Inactivity on Type I versus Type IV Allergies. Nutrients, 2022, 14, 2351.	4.1	1
11	Long-term instability of the intestinal microbiome is associated with metabolic liver disease, low microbiota diversity, diabetes mellitus and impaired exocrine pancreatic function. Gut, 2021, 70, 522-530.	12.1	96
12	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	21.4	676
13	Carrying asymptomatic gallstones is not associated with changes in intestinal microbiota composition and diversity but cholecystectomy with significant dysbiosis. Scientific Reports, 2021, 11, 6677.	3.3	19
14	Intestinal protozoan infections shape fecal bacterial microbiota in children from Guinea-Bissau. PLoS Neglected Tropical Diseases, 2021, 15, e0009232.	3.0	11
15	Altered Gut Microbial Metabolism of Essential Nutrients in Primary Sclerosing Cholangitis. Gastroenterology, 2021, 160, 1784-1798.e0.	1.3	69
16	Primate phageomes are structured by superhost phylogeny and environment. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	16
17	Short-term physical exercise impacts on the human holobiont obtained by a randomised intervention study. BMC Microbiology, 2021, 21, 162.	3.3	24
18	Microbial Diversity and Abundance of <i>Parabacteroides</i> Mediate the Associations Between Higher Intake of Flavonoid-Rich Foods and Lower Blood Pressure. Hypertension, 2021, 78, 1016-1026.	2.7	14

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19	Genome-wide association study in 8,956 German individuals identifies influence of ABO histo-blood groups on gut microbiome. Nature Genetics, 2021, 53, 147-155.	21.4	101
20	Ecology impacts the decrease of Spirochaetes and Prevotella in the fecal gut microbiota of urban humans. BMC Microbiology, 2021, 21, 276.	3.3	16
21	High-fat meals do not affect thrombin formation and fibrin clot lysis in individuals with obesity during intentional weight loss. Nutrition Research, 2021, 97, 1-10.	2.9	0
22	Targeting the cytoplasmic polyadenylation element-binding protein CPEB4 protects against diet-induced obesity and microbiome dysbiosis. Molecular Metabolism, 2021, 54, 101388.	6.5	8
23	Alterations of the bile microbiome in primary sclerosing cholangitis. Gut, 2020, 69, 665-672.	12.1	80
24	The role of the gut microbiome in the association between habitual anthocyanin intake and visceral abdominal fat in population-level analysis. American Journal of Clinical Nutrition, 2020, 111, 340-350.	4.7	21
25	Postprandial factor VII activation does not increase plasma concentrations of prothrombin fragment 1Â+Â2 in patients with morbid obesity. Thrombosis Research, 2020, 196, 260-267.	1.7	3
26	Histone variants in archaea and the evolution of combinatorial chromatin complexity. Proceedings of the United States of America, 2020, 117, 33384-33395.	7.1	34
27	The Impact of Oral Sodium Chloride Supplementation on Thrive and the Intestinal Microbiome in Neonates With Small Bowel Ostomies: A Prospective Cohort Study. Frontiers in Immunology, 2020, 11, 1421.	4.8	14
28	A diseaseâ€specific decline of the relative abundance of <i>Bifidobacterium</i> in patients with autoimmune hepatitis. Alimentary Pharmacology and Therapeutics, 2020, 51, 1417-1428.	3.7	55
29	IL-22 Paucity in APECED Is Associated With Mucosal and Microbial Alterations in Oral Cavity. Frontiers in Immunology, 2020, 11, 838.	4.8	14
30	Motor, cognitive and mobility deficits in 1000 geriatric patients: protocol of a quantitative observational study before and after routine clinical geriatric treatment – the ComOn-study. BMC Geriatrics, 2020, 20, 45.	2.7	19
31	Gut mycobiome of primary sclerosing cholangitis patients is characterised by an increase of <i>Trichocladium griseum</i> and <i>Candida</i> species. Gut, 2020, 69, 1890-1892.	12.1	25
32	The Gut Microbiome in Patients With Chronic Pancreatitis Is Characterized by Significant Dysbiosis and Overgrowth by Opportunistic Pathogens. Clinical and Translational Gastroenterology, 2020, 11, e00232.	2.5	49
33	Obese Individuals with and without Type 2 Diabetes Show Different Gut Microbial Functional Capacity and Composition. Cell Host and Microbe, 2019, 26, 252-264.e10.	11.0	274
34	A structured weight loss program increases gut microbiota phylogenetic diversity and reduces levels of Collinsella in obese type 2 diabetics: A pilot study. PLoS ONE, 2019, 14, e0219489.	2.5	82
35	Consistent alterations in faecal microbiomes of patients with primary sclerosing cholangitis independent of associated colitis. Alimentary Pharmacology and Therapeutics, 2019, 50, 580-589.	3.7	67
36	Normal gut microbiome in NMDA receptor encephalitis. Neurology: Neuroimmunology and NeuroInflammation, 2019, 6, .	6.0	10

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37	Helicobacter pylori infection associates with fecal microbiota composition and diversity. Scientific Reports, 2019, 9, 20100.	3.3	49
38	Minor compositional alterations in faecal microbiota after five weeks and five months storage at room temperature on filter papers. Scientific Reports, 2019, 9, 19008.	3.3	7
39	Faecal microbiota composition associates with abdominal pain in the general population. Gut, 2018, 67, gutjnl-2017-314792.	12.1	29
40	Metaorganisms in extreme environments: do microbes play a role in organismal adaptation?. Zoology, 2018, 127, 1-19.	1.2	194
41	Archaea Are Interactive Components of Complex Microbiomes. Trends in Microbiology, 2018, 26, 70-85.	7.7	203
42	Archaea: forgotten players in the microbiome. Emerging Topics in Life Sciences, 2018, 2, 459-468.	2.6	36
43	Microbiomarkers in inflammatory bowel diseases: caveats come with caviar. Gut, 2017, 66, 1734-1738.	12.1	47
44	First Insights into the Diverse Human Archaeome: Specific Detection of Archaea in the Gastrointestinal Tract, Lung, and Nose and on Skin. MBio, 2017, 8, .	4.1	169
45	The Human-Associated Archaeon Methanosphaera stadtmanae Is Recognized through Its RNA and Induces TLR8-Dependent NLRP3 Inflammasome Activation. Frontiers in Immunology, 2017, 8, 1535.	4.8	76
46	Immunogenic properties of the human gut-associated archaeon Methanomassiliicoccus luminyensis and its susceptibility to antimicrobial peptides. PLoS ONE, 2017, 12, e0185919.	2.5	21
47	Archaea associated with human surfaces: not to be underestimated. FEMS Microbiology Reviews, 2015, 39, 631-648.	8.6	88
48	The Intestinal Archaea Methanosphaera stadtmanae and Methanobrevibacter smithii Activate Human Dendritic Cells. PLoS ONE, 2014, 9, e99411.	2.5	127
49	Biofilm formation of mucosa-associated methanoarchaeal strains. Frontiers in Microbiology, 2014, 5, 353.	3.5	27
50	Health- and disease-associated species clusters in complex natural biofilms determine the innate immune response in oral epithelial cells during biofilm maturation. FEMS Microbiology Letters, 2014, 360, 137-143.	1.8	14
51	Effects of Antimicrobial Peptides on Methanogenic Archaea. Antimicrobial Agents and Chemotherapy, 2012, 56, 4123-4130.	3.2	29