

# Bernard Berger

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

5,299  
citations

279798

23  
h-index

477307

29  
g-index

30  
all docs

30  
docs citations

30  
times ranked

7192  
citing authors

#	ARTICLE	IF	CITATIONS
1	Term infant formula supplemented with milk-derived oligosaccharides shifts the gut microbiota closer to that of human milk-fed infants and improves intestinal immune defense: a randomized controlled trial. <i>American Journal of Clinical Nutrition</i> , 2022, 115, 142-153.	4.7	19
2	Safety and efficacy of a probiotic-containing infant formula supplemented with 2â€™-fucosyllactose: a double-blind randomized controlled trial. <i>Nutrition Journal</i> , 2022, 21, 11.	3.4	20
3	Human Milk Oligosaccharide-Stimulated Bifidobacterium Species Contribute to Prevent Later Respiratory Tract Infections. <i>Microorganisms</i> , 2021, 9, 1939.	3.6	20
4	Linking Human Milk Oligosaccharides, Infant Fecal Community Types, and Later Risk To Require Antibiotics. <i>MBio</i> , 2020, 11, .	4.1	98
5	Early Effect of Supplemented Infant Formulae on Intestinal Biomarkers and Microbiota: A Randomized Clinical Trial. <i>Nutrients</i> , 2020, 12, 1481.	4.1	23
6	The Mouse Microbiome Is Required for Sex-Specific Diurnal Rhythms of Gene Expression and Metabolism. <i>Cell Metabolism</i> , 2019, 29, 362-382.e8.	16.2	178
7	Antibiotic Treatment Leads to Fecal <i>Escherichia coli</i> and Coliphage Expansion in Severely Malnourished Diarrhea Patients. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2018, 5, 458-460.e6.	4.5	15
8	Bangladeshi children with acute diarrhoea show faecal microbiomes with increased <i>Streptococcus</i> abundance, irrespective of diarrhoea aetiology. <i>Environmental Microbiology</i> , 2018, 20, 2256-2269.	3.8	33
9	Human Milk Oligosaccharides: 2â€™-Fucosyllactose (2â€™-FL) and Lacto-N-Neotetraose (LNnT) in Infant Formula. <i>Nutrients</i> , 2018, 10, 1161.	4.1	208
10	Calypto: a user-friendly web-server for mining and visualizing microbiomeâ€™environment interactions. <i>Bioinformatics</i> , 2017, 33, 782-783.	4.1	627
11	Oral application of <i>Escherichia coli</i> bacteriophage: safety tests in healthy and diarrheal children from Bangladesh. <i>Environmental Microbiology</i> , 2017, 19, 237-250.	3.8	105
12	Oral Phage Therapy of Acute Bacterial Diarrhea With Two Coliphage Preparations: A Randomized Trial in Children From Bangladesh. <i>EBioMedicine</i> , 2016, 4, 124-137.	6.1	370
13	Dynamics of Infant Gut Microbiota Are Influenced by Delivery Mode and Gestational Duration and Are Associated with Subsequent Adiposity. <i>MBio</i> , 2015, 6, .	4.1	271
14	Rate of establishing the gut microbiota in infancy has consequences for future health. <i>Gut Microbes</i> , 2015, 6, 321-325.	9.8	82
15	Effect of <i>Lactobacillus rhamnosus</i> CGMCC1.3724 supplementation on weight loss and maintenance in obese men and women. <i>British Journal of Nutrition</i> , 2014, 111, 1507-1519.	2.3	272
16	Nasopharyngeal Microbiota in Healthy Children and Pneumonia Patients. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1590-1594.	3.9	86
17	Safety analysis of a Russian phage cocktail: From MetaGenomic analysis to oral application in healthy human subjects. <i>Virology</i> , 2013, 443, 187-196.	2.4	211
18	Oral T4-like phage cocktail application to healthy adult volunteers from Bangladesh. <i>Virology</i> , 2012, 434, 222-232.	2.4	201

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19	Colonization-Induced Host-Gut Microbial Metabolic Interaction. MBio, 2011, 2, e00271-10.	4.1	342
20	Characterization of a novel Lactobacillus species closely related to Lactobacillus johnsonii using a combination of molecular and comparative genomics methods. BMC Genomics, 2010, 11, 504.	2.8	29
21	Investigation of the intestinal microbiota in preterm infants using different methods. Anaerobe, 2010, 16, 362-370.	2.1	118
22	Oral supplementation with probiotics in very-low-birth-weight preterm infants: a randomized, double-blind, placebo-controlled trial. American Journal of Clinical Nutrition, 2009, 89, 1828-1835.	4.7	182
23	Identification of Genes Associated with the Long-Gut-Persistence Phenotype of the Probiotic <i>Lactobacillus johnsonii</i> Strain NCC533 Using a Combination of Genomics and Transcriptome Analysis. Journal of Bacteriology, 2008, 190, 3161-3168.	2.2	163
24	The Role of Prophage for Genome Diversification within a Clonal Lineage of Lactobacillus johnsonii : Characterization of the Defective Prophage LJ771. Journal of Bacteriology, 2008, 190, 5806-5813.	2.2	19
25	Gene Expression of Commensal <i>Lactobacillus johnsonii</i> Strain NCC533 during In Vitro Growth and in the Murine Gut. Journal of Bacteriology, 2007, 189, 8109-8119.	2.2	62
26	Similarity and Differences in the Lactobacillus acidophilus Group Identified by Polyphasic Analysis and Comparative Genomics. Journal of Bacteriology, 2007, 189, 1311-1321.	2.2	115
27	The genome sequence of the probiotic intestinal bacterium Lactobacillus johnsonii NCC 533. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 2512-2517.	7.1	476
28	Integration and Distribution of Lactobacillus johnsonii Prophages. Journal of Bacteriology, 2003, 185, 4603-4608.	2.2	54
29	The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation to the human gastrointestinal tract. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14422-14427.	7.1	874
30	Infant Formula With a Specific Blend of Five Human Milk Oligosaccharides Drives the Gut Microbiota Development and Improves Gut Maturation Markers: A Randomized Controlled Trial. Frontiers in Nutrition, 0, 9, .	3.7	26