Dirk Gevers

List of Publications by Year
in descending order

67 papers	37,468 citations	23565 58 h-index	95259 68 g-index
70 all docs	70 docs citations	70 times ranked	44276 citing authors

#	Article	IF	Citations
1	Precise quantification of bacterial strains after fecal microbiota transplantation delineates long-term engraftment and explains outcomes. Nature Microbiology, 2021, 6, 1309-1318.	13.3	60
2	Defined microbiota transplant restores Th17/RORÎ³t⁺regulatory T cell balance in mice colonized with inflammatory bowel disease microbiotas. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21536-21545.	7.1	58
3	Genetic Factors and the Intestinal Microbiome Guide Development of Microbe-Based Therapies for Inflammatory Bowel Diseases. Gastroenterology, 2019, 156, 2174-2189.	1.3	132
4	Transmission of human-associated microbiota along family and social networks. Nature Microbiology, 2019, 4, 964-971.	13.3	149
5	Microbiotas from Humans with Inflammatory Bowel Disease Alter the Balance of Gut Th17 and RORÎ³t+ Regulatory T Cells and Exacerbate Colitis in Mice. Immunity, 2019, 50, 212-224.e4.	14.3	345
6	The classroom microbiome and asthma morbidity in children attending 3 inner-city schools. Journal of Allergy and Clinical Immunology, 2018, 141, 2311-2313.	2.9	24
7	Interplay of host genetics and gut microbiota underlying the onset and clinical presentation of inflammatory bowel disease. Gut, 2018, 67, 108-119.	12.1	590
8	The human gut microbiome in early-onset type 1 diabetes from the TEDDY study. Nature, 2018, 562, 589-594.	27.8	623
9	A Microbiome Foundation for the Study of Crohnâ€™s Disease. Cell Host and Microbe, 2017, 21, 301-304.	11.0	46
10	Ectopic colonization of oral bacteria in the intestine drives T _H 1 cell induction and inflammation. Science, 2017, 358, 359-365.	12.6	612
11	Potential role of intratumor bacteria in mediating tumor resistance to the chemotherapeutic drug gemcitabine. Science, 2017, 357, 1156-1160.	12.6	1,059
12	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. Cell, 2016, 165, 842-853.	28.9	968
13	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science, 2016, 352, 565-569.	12.6	1,398
14	Natural history of the infant gut microbiome and impact of antibiotic treatment on bacterial strain diversity and stability. Science Translational Medicine, 2016, 8, 343ra81.	12.4	763
15	Increased Intestinal Microbial Diversity Following Fecal Microbiota Transplant for Active CrohnÊ¼s Disease. Inflammatory Bowel Diseases, 2016, 22, 2182-2190.	1.9	175
16	Disease-Specific Alterations in the Enteric Virome in Inflammatory Bowel Disease. Cell, 2015, 160, 447-460.	28.9	1,036
17	The Dynamics of the Human Infant Gut Microbiome in Development and in Progression toward Type 1 Diabetes. Cell Host and Microbe, 2015, 17, 260-273.	11.0	1,008
18	Biogeography of the Intestinal Mucosal and Lumenal Microbiome in the Rhesus Macaque. Cell Host and Microbe, 2015, 17, 385-391.	11.0	273

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19	Identifying personal microbiomes using metagenomic codes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2930-8.	7.1	377
20	Host genetic variation impacts microbiome composition across human body sites. Genome Biology, 2015, 16, 191.	8.8	612
21	Detection of low-abundance bacterial strains in metagenomic datasets by eigengenome partitioning. Nature Biotechnology, 2015, 33, 1053-1060.	17.5	144
22	ConStrains identifies microbial strains in metagenomic datasets. Nature Biotechnology, 2015, 33, 1045-1052.	17.5	235
23	The Gut Microbiome Contributes to a Substantial Proportion of the Variation in Blood Lipids. Circulation Research, 2015, 117, 817-824.	4.5	534
24	Complex host genetics influence the microbiome in inflammatory bowel disease. Genome Medicine, 2014, 6, 107.	8.2	322
25	Skin Microbiome Imbalance in Patients with STAT1/STAT3 Defects Impairs Innate Host Defense Responses. Journal of Innate Immunity, 2014, 6, 253-262.	3.8	83
26	Gene-targeted metagenomic analysis of glucan-branching enzyme gene profiles among human and animal fecal microbiota. ISME Journal, 2014, 8, 493-503.	9.8	40
27	Fecal Microbiota Transplant for Relapsing Clostridium difficile Infection Using a Frozen Inoculum From Unrelated Donors: A Randomized, Open-Label, Controlled Pilot Study. Clinical Infectious Diseases, 2014, 58, 1515-1522.	5.8	397
28	The Treatment-Naive Microbiome in New-Onset Crohnâ€™s Disease. Cell Host and Microbe, 2014, 15, 382-392.	11.0	2,582
29	Relating the metatranscriptome and metagenome of the human gut. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2329-38.	7.1	552
30	Gut microbiome composition and function in experimental colitis during active disease and treatment-induced remission. ISME Journal, 2014, 8, 1403-1417.	9.8	352
31	Advancing the Microbiome Research Community. Cell, 2014, 159, 227-230.	28.9	64
32	MetaRef: a pan-genomic database for comparative and community microbial genomics. Nucleic Acids Research, 2014, 42, D617-D624.	14.5	51
33	Pediatric Crohn disease patients exhibit specific ileal transcriptome and microbiome signature. Journal of Clinical Investigation, 2014, 124, 3617-3633.	8.2	431
34	Sequence-Based Discovery ofBradyrhizobium entericain Cord Colitis Syndrome. New England Journal of Medicine, 2013, 369, 517-528.	27.0	148
35	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. Nature Methods, 2013, 10, 57-59.	19.0	3,402
36	The Human Microbiome Project strategy for comprehensive sampling of the human microbiome and why it matters. FASEB Journal, 2013, 27, 1012-1022.	0.5	328

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37	Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome. PLoS Computational Biology, 2012, 8, e1002358.	3.2	939
38	Microbial Co-occurrence Relationships in the Human Microbiome. PLoS Computational Biology, 2012, 8, e1002606.	3.2	1,268
39	Bioinformatics for the Human Microbiome Project. PLoS Computational Biology, 2012, 8, e1002779.	3.2	73
40	Comparative Genomics of Enterococci: Variation in Enterococcus faecalis, Clade Structure in E. faecium, and Defining Characteristics of E .Â gallinarum and E .Â casseliflavus. MBio, 2012, 3, e00318-11.	4.1	259
41	Genomic analysis identifies association of Fusobacterium with colorectal carcinoma. Genome Research, 2012, 22, 292-298.	5.5	1,587
42	Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. Genome Biology, 2012, 13, R79.	9.6	2,258
43	The interpersonal and intrapersonal diversity of human-associated microbiota in key body sites. Journal of Allergy and Clinical Immunology, 2012, 129, 1204-1208.	2.9	266
44	Non-Invasive Mapping of the Gastrointestinal Microbiota Identifies Children with Inflammatory Bowel Disease. PLoS ONE, 2012, 7, e39242.	2.5	252
45	A Metagenomic Approach to Characterization of the Vaginal Microbiome Signature in Pregnancy. PLoS ONE, 2012, 7, e36466.	2.5	572
46	Next-Generation Sequencing for the Identification of Transplantation-Associated Pathogens. Blood, 2012, 120, LBA-4-LBA-4.	1.4	1
47	Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. Genome Research, 2011, 21, 494-504.	5.5	3,015
48	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	17.5	608
49	The Genome of Th17 Cell-Inducing Segmented Filamentous Bacteria Reveals Extensive Auxotrophy and Adaptations to the Intestinal Environment. Cell Host and Microbe, 2011, 10, 260-272.	11.0	175
50	Distinct microbiome in pouchitis compared to healthy pouches in ulcerative colitis and familial adenomatous polyposis. Inflammatory Bowel Diseases, 2011, 17, 1092-1100.	1.9	67
51	Comparative and Functional Genomics of Rhodococcus opacus PD630 for Biofuels Development. PLoS Genetics, 2011, 7, e1002219.	3.5	109
52	Reducing the Effects of PCR Amplification and Sequencing Artifacts on 16S rRNA-Based Studies. PLoS ONE, 2011, 6, e27310.	2.5	1,891
53	High-Quality Draft Genome Sequences of 28 Enterococcus sp. Isolates. Journal of Bacteriology, 2010, 192, 2469-2470.	2.2	80
54	A Catalog of Reference Genomes from the Human Microbiome. Science, 2010, 328, 994-999.	12.6	621

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55	Resource Partitioning and Sympatric Differentiation Among Closely Related Bacterioplankton. Science, 2008, 320, 1081-1085.	12.6	472
56	Conservation of the Chitin Utilization Pathway in the Vibrionaceae. Applied and Environmental Microbiology, 2008, 74, 44-51.	3.1	211
57	Diversity Analysis of Dairy and Nondairy Lactococcus lactis Isolates, Using a Novel Multilocus Sequence Analysis Scheme and (GTG) ₅ -PCR Fingerprinting. Applied and Environmental Microbiology, 2007, 73, 7128-7137.	3.1	95
58	Nitric oxide reductase (norB) gene sequence analysis reveals discrepancies with nitrite reductase (nir) gene phylogeny in cultivated denitrifiers. Environmental Microbiology, 2007, 9, 1072-1077.	3.8	47
59	Horizontal transfer of tet(M) and erm(B) resistance plasmids from food strains of Lactobacillus plantarum to Enterococcus faecalis JH2-2 in the gastrointestinal tract of gnotobiotic rats. FEMS Microbiology Ecology, 2007, 59, 158-166.	2.7	131
60	The incidence of nirS and nirK and their genetic heterogeneity in cultivated denitrifiers. Environmental Microbiology, 2006, 8, 2012-2021.	3.8	201
61	Re-evaluating prokaryotic species. Nature Reviews Microbiology, 2005, 3, 733-739.	28.6	1,019
62	Towards a prokaryotic genomic taxonomy. FEMS Microbiology Reviews, 2005, 29, 147-167.	8.6	121
63	Gene duplication and biased functional retention of paralogs in bacterial genomes. Trends in Microbiology, 2004, 12, 148-154.	7.7	150
64	Genomic and phenotypic comparison of Bacillus fumarioli isolates from geothermal Antarctic soil and gelatine. Research in Microbiology, 2004, 155, 483-490.	2.1	10
65	In vitro conjugal transfer of tetracycline resistance fromLactobacillusisolates to other Gram-positive bacteria. FEMS Microbiology Letters, 2003, 225, 125-130.	1.8	159
66	Molecular Characterization of tet(M) Genes in Lactobacillus Isolates from Different Types of Fermented Dry Sausage. Applied and Environmental Microbiology, 2003, 69, 1270-1275.	3.1	250
67	Applicability of rep-PCR fingerprinting for identification ofLactobacillusspecies. FEMS Microbiology Letters, 2001, 205, 31-36.	1.8	564