

# Georg Zeller

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

23,247  
citations

41258

49  
h-index

82410

72  
g-index

80  
all docs

80  
docs citations

80  
times ranked

31515  
citing authors

#	ARTICLE	IF	CITATIONS
1	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	13.7	5,800
2	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	6.0	2,137
3	Extensive impact of non-antibiotic drugs on human gut bacteria. <i>Nature</i> , 2018, 555, 623-628.	13.7	1,339
4	Potential of fecal microbiota for early-stage detection of colorectal cancer. <i>Molecular Systems Biology</i> , 2014, 10, 766.	3.2	991
5	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	6.0	912
6	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. <i>Nature Medicine</i> , 2019, 25, 679-689.	15.2	734
7	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	5.9	717
8	Common Sequence Polymorphisms Shaping Genetic Diversity in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007, 317, 338-342.	6.0	689
9	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013, 10, 1177-1184.	9.0	679
10	Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. <i>Nature Medicine</i> , 2019, 25, 667-678.	15.2	602
11	Genomewide SNP variation reveals relationships among landraces and modern varieties of rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12273-12278.	3.3	581
12	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	9.4	581
13	Systematic evaluation of spliced alignment programs for RNA-seq data. <i>Nature Methods</i> , 2013, 10, 1185-1191.	9.0	467
14	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , 2016, 352, 586-589.	6.0	461
15	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	9.0	442
16	Dual roles of the nuclear cap-binding complex and SERRATE in pre-mRNA splicing and microRNA processing in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8795-8800.	3.3	378
17	Gut Microbiota Linked to Sexual Preference and HIV Infection. <i>EBioMedicine</i> , 2016, 5, 135-146.	2.7	328
18	Extensive transmission of microbes along the gastrointestinal tract. <i>ELife</i> , 2019, 8, .	2.8	313

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19	Accurate and universal delineation of prokaryotic species. <i>Nature Methods</i> , 2013, 10, 881-884.	9.0	311
20	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019, 10, 1014.	5.8	298
21	Stress-induced changes in the <i>Arabidopsis thaliana</i> transcriptome analyzed using whole-genome tiling arrays. <i>Plant Journal</i> , 2009, 58, 1068-1082.	2.8	273
22	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	13.5	268
23	Colorectal Cancer and the Human Gut Microbiome: Reproducibility with Whole-Genome Shotgun Sequencing. <i>PLoS ONE</i> , 2016, 11, e0155362.	1.1	249
24	A spatial and temporal map of <i>C. elegans</i> gene expression. <i>Genome Research</i> , 2011, 21, 325-341.	2.4	241
25	Nutritional preferences of human gut bacteria reveal their metabolic idiosyncrasies. <i>Nature Microbiology</i> , 2018, 3, 514-522.	5.9	196
26	Prediction of Drug Combinations by Integrating Molecular and Pharmacological Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002323.	1.5	173
27	MOCAT2: a metagenomic assembly, annotation and profiling framework. <i>Bioinformatics</i> , 2016, 32, 2520-2523.	1.8	172
28	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	170
29	Unravelling the collateral damage of antibiotics on gut bacteria. <i>Nature</i> , 2021, 599, 120-124.	13.7	159
30	Temporal and technical variability of human gut metagenomes. <i>Genome Biology</i> , 2015, 16, 73.	3.8	143
31	Novel Drug Candidates for the Treatment of Metastatic Colorectal Cancer through Global Inverse Gene-Expression Profiling. <i>Cancer Research</i> , 2014, 74, 5690-5699.	0.4	142
32	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. <i>Nature Microbiology</i> , 2021, 6, 196-208.	5.9	138
33	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	9.0	133
34	Biosynthetic potential of the global ocean microbiome. <i>Nature</i> , 2022, 607, 111-118.	13.7	128
35	Microbiome meta-analysis and cross-disease comparison enabled by the SIAMCAT machine learning toolbox. <i>Genome Biology</i> , 2021, 22, 93.	3.8	122
36	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , 2017, 13, 960.	3.2	115

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37	Receptor-type guanylate cyclase is required for carbon dioxide sensation by <i>Caenorhabditis elegans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 254-259.	3.3	113
38	Characterization of drug-induced transcriptional modules: towards drug repositioning and functional understanding. <i>Molecular Systems Biology</i> , 2013, 9, 662.	3.2	110
39	A faecal microbiota signature with high specificity for pancreatic cancer. <i>Gut</i> , 2022, 71, 1359-1372.	6.1	104
40	At-TAX: a whole genome tiling array resource for developmental expression analysis and transcript identification in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2008, 9, R112.	13.9	91
41	Drug discovery in the age of systems biology: the rise of computational approaches for data integration. <i>Current Opinion in Biotechnology</i> , 2012, 23, 609-616.	3.3	86
42	Network Neighbors of Drug Targets Contribute to Drug Side-Effect Similarity. <i>PLoS ONE</i> , 2011, 6, e22187.	1.1	86
43	mGene: Accurate SVM-based gene finding with an application to nematode genomes. <i>Genome Research</i> , 2009, 19, 2133-2143.	2.4	79
44	Analysis of 1321 <i>Eubacterium rectale</i> genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. <i>Genome Biology</i> , 2020, 21, 138.	3.8	72
45	Commensal Clostridiales strains mediate effective anti-cancer immune response against solid tumors. <i>Cell Host and Microbe</i> , 2021, 29, 1573-1588.e7.	5.1	71
46	Global effects of the small RNA biogenesis machinery on the <i>Arabidopsis thaliana</i> transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17466-17473.	3.3	66
47	Quantitative RNA expression analysis with Affymetrix Tiling 1.0R arrays identifies new E2F target genes. <i>Plant Journal</i> , 2009, 57, 184-194.	2.8	65
48	A fair comparison. <i>Nature Methods</i> , 2014, 11, 359-359.	9.0	64
49	Identifying temporal and spatial patterns of variation from multimodal data using MEFISTO. <i>Nature Methods</i> , 2022, 19, 179-186.	9.0	63
50	AGRONOMICS1: A New Resource for <i>Arabidopsis</i> Transcriptome Profiling. <i>Plant Physiology</i> , 2010, 152, 487-499.	2.3	61
51	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2020, 48, D621-D625.	6.5	60
52	Bacterial retrons encode phage-defending tripartite toxin-antitoxin systems. <i>Nature</i> , 2022, 609, 144-150.	13.7	52
53	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. <i>Frontiers in Microbiology</i> , 2021, 12, 635781.	1.5	51
54	Detecting polymorphic regions in <i>Arabidopsis thaliana</i> with resequencing microarrays. <i>Genome Research</i> , 2008, 18, 918-929.	2.4	50

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55	Effects of Weight-Loss Interventions on Short-Chain Fatty Acid Concentrations in Blood and Feces of Adults: A Systematic Review. <i>Advances in Nutrition</i> , 2019, 10, 673-684.	2.9	35
56	Metabolic models predict bacterial passengers in colorectal cancer. <i>Cancer &amp; Metabolism</i> , 2020, 8, 3.	2.4	28
57	mGene.web: a web service for accurate computational gene finding. <i>Nucleic Acids Research</i> , 2009, 37, W312-W316.	6.5	23
58	Comprehensive analysis of <i>Arabidopsis</i> expression level polymorphisms with simple inheritance. <i>Molecular Systems Biology</i> , 2009, 5, 242.	3.2	21
59	Support vector machines-based identification of alternative splicing in <i>Arabidopsis thaliana</i> from whole-genome tiling arrays. <i>BMC Bioinformatics</i> , 2011, 12, 55.	1.2	21
60	Changes in Plasma Short-Chain Fatty Acid Levels after Dietary Weight Loss among Overweight and Obese Adults over 50 Weeks. <i>Nutrients</i> , 2020, 12, 452.	1.7	21
61	Calorie restriction improves metabolic state independently of gut microbiome composition: a randomized dietary intervention trial. <i>Genome Medicine</i> , 2022, 14, 30.	3.6	21
62	The gut microbiome in solid organ transplantation. <i>Pediatric Transplantation</i> , 2020, 24, e13866.	0.5	17
63	Microbiota-dependent activation of the myeloid calcineurin-NFAT pathway inhibits B7H3- and B7H4-dependent anti-tumor immunity in colorectal cancer. <i>Immunity</i> , 2022, 55, 701-717.e7.	6.6	16
64	Oqtans: the RNA-seq workbench in the cloud for complete and reproducible quantitative transcriptome analysis. <i>Bioinformatics</i> , 2014, 30, 1300-1301.	1.8	12
65	CART—a chemical annotation retrieval toolkit. <i>Bioinformatics</i> , 2016, 32, 2869-2871.	1.8	10
66	Next generation genome annotation with mGene.ngs. <i>BMC Bioinformatics</i> , 2010, 11, .	1.2	8
67	mOTUs: Profiling Taxonomic Composition, Transcriptional Activity and Strain Populations of Microbial Communities. <i>Current Protocols</i> , 2021, 1, e218.	1.3	8
68	Transcript normalization and segmentation of tiling array data. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2008, , 527-38.	0.7	8
69	Revealing sequence variation patterns in rice with machine learning methods. <i>BMC Bioinformatics</i> , 2008, 9, .	1.2	1