Georg Zeller

List of Publications by Year
in descending order

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	Identifying temporal and spatial patterns of variation from multimodal data using MEFISTO. Nature Methods, 2022, 19, 179-186.	9.0	63
2	A faecal microbiota signature with high specificity for pancreatic cancer. Gut, 2022, 71, 1359-1372.	6.1	104
3	Microbiota-dependent activation of the myeloid calcineurin-NFAT pathway inhibits B7H3- and B7H4-dependent anti-tumor immunity in colorectal cancer. Immunity, 2022, 55, 701-717.e7.	6.6	16
4	Calorie restriction improves metabolic state independently of gut microbiome composition: a randomized dietary intervention trial. Genome Medicine, 2022, 14, 30.	3.6	21
5	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	9.0	133
6	Biosynthetic potential of the global ocean microbiome. Nature, 2022, 607, 111-118.	13.7	128
7	Bacterial retrons encode phage-defending tripartite toxin–antitoxin systems. Nature, 2022, 609, 144-150.	13.7	52
8	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. Frontiers in Microbiology, 2021, 12, 635781.	1.5	51
9	Microbiome meta-analysis and cross-disease comparison enabled by the SIAMCAT machine learning toolbox. Genome Biology, 2021, 22, 93.	3.8	122
10	Commensal Clostridiales strains mediate effective anti-cancer immune response against solid tumors. Cell Host and Microbe, 2021, 29, 1573-1588.e7.	5.1	71
11	mOTUs: Profiling Taxonomic Composition, Transcriptional Activity and Strain Populations of Microbial Communities. Current Protocols, 2021, 1, e218.	1.3	8
12	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. Nature Microbiology, 2021, 6, 196-208.	5.9	138
13	Unravelling the collateral damage of antibiotics on gut bacteria. Nature, 2021, 599, 120-124.	13.7	159
14	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	15.2	170
15	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. Nucleic Acids Research, 2020, 48, D621-D625.	6.5	60
16	Analysis of 1321 Eubacterium rectale genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. Genome Biology, 2020, 21, 138.	3.8	72
17	Metabolic models predict bacterial passengers in colorectal cancer. Cancer & Metabolism, 2020, 8, 3.	2.4	28
18	Changes in Plasma Short-Chain Fatty Acid Levels after Dietary Weight Loss among Overweight and Obese Adults over 50 Weeks. Nutrients, 2020, 12, 452.	1.7	21

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19	The gut microbiome in solid organ transplantation. Pediatric Transplantation, 2020, 24, e13866.	0.5	17
20	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. Cell, 2019, 179, 1068-1083.e21.	13.5	268
21	Effects of Weight-Loss Interventions on Short-Chain Fatty Acid Concentrations in Blood and Feces of Adults: A Systematic Review. Advances in Nutrition, 2019, 10, 673-684.	2.9	35
22	Microbial abundance, activity and population genomic profiling with mOTUs2. Nature Communications, 2019, 10, 1014.	5.8	298
23	Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. Nature Medicine, 2019, 25, 667-678.	15.2	602
24	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. Nature Medicine, 2019, 25, 679-689.	15.2	734
25	Extensive transmission of microbes along the gastrointestinal tract. ELife, 2019, 8, .	2.8	313
26	Enterotypes in the landscape of gut microbial community composition. Nature Microbiology, 2018, 3, 8-16.	5.9	717
27	Extensive impact of non-antibiotic drugs on human gut bacteria. Nature, 2018, 555, 623-628.	13.7	1,339
28	Nutritional preferences of human gut bacteria reveal their metabolic idiosyncrasies. Nature Microbiology, 2018, 3, 514-522.	5.9	196
29	Towards standards for human fecal sample processing in metagenomic studies. Nature Biotechnology, 2017, 35, 1069-1076.	9.4	581
30	Subspecies in the global human gut microbiome. Molecular Systems Biology, 2017, 13, 960.	3.2	115
31	Colorectal Cancer and the Human Gut Microbiome: Reproducibility with Whole-Genome Shotgun Sequencing. PLoS ONE, 2016, 11, e0155362.	1.1	249
32	MOCAT2: a metagenomic assembly, annotation and profiling framework. Bioinformatics, 2016, 32, 2520-2523.	1.8	172
33	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. Science, 2016, 352, 586-589.	6.0	461
34	CARTâ€"a chemical annotation retrieval toolkit. Bioinformatics, 2016, 32, 2869-2871.	1.8	10
35	Gut Microbiota Linked to Sexual Preference and HIV Infection. EBioMedicine, 2016, 5, 135-146.	2.7	328
36	Structure and function of the global ocean microbiome. Science, 2015, 348, 1261359.	6.0	2,137

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37	Temporal and technical variability of human gut metagenomes. Genome Biology, 2015, 16, 73.	3.8	143
38	Potential of fecal microbiota for early‑stage detection of colorectal cancer. Molecular Systems Biology, 2014, 10, 766.	3.2	991
39	Oqtans: the RNA-seq workbench in the cloud for complete and reproducible quantitative transcriptome analysis. Bioinformatics, 2014, 30, 1300-1301.	1.8	12
40	A fair comparison. Nature Methods, 2014, 11, 359-359.	9.0	64
41	Novel Drug Candidates for the Treatment of Metastatic Colorectal Cancer through Global Inverse Gene-Expression Profiling. Cancer Research, 2014, 74, 5690-5699.	0.4	142
42	Accurate and universal delineation of prokaryotic species. Nature Methods, 2013, 10, 881-884.	9.0	311
43	Metagenomic species profiling using universal phylogenetic marker genes. Nature Methods, 2013, 10, 1196-1199.	9.0	442
44	Assessment of transcript reconstruction methods for RNA-seq. Nature Methods, 2013, 10, 1177-1184.	9.0	679
45	Systematic evaluation of spliced alignment programs for RNA-seq data. Nature Methods, 2013, 10, 1185-1191.	9.0	467
46	Characterization of drug‑induced transcriptional modules: towards drug repositioning and functional understanding. Molecular Systems Biology, 2013, 9, 662.	3.2	110
47	Drug discovery in the age of systems biology: the rise of computational approaches for data integration. Current Opinion in Biotechnology, 2012, 23, 609-616.	3.3	86
48	A spatial and temporal map of *C. elegans* gene expression. Genome Research, 2011, 21, 325-341.	2.4	241
49	Enterotypes of the human gut microbiome. Nature, 2011, 473, 174-180.	13.7	5,800
50	Support vector machines-based identification of alternative splicing in Arabidopsis thaliana from whole-genome tiling arrays. BMC Bioinformatics, 2011, 12, 55.	1.2	21
51	Receptor-type guanylate cyclase is required for carbon dioxide sensation by *Caenorhabditis elegans*. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 254-259.	3.3	113
52	Prediction of Drug Combinations by Integrating Molecular and Pharmacological Data. PLoS Computational Biology, 2011, 7, e1002323.	1.5	173
53	Network Neighbors of Drug Targets Contribute to Drug Side-Effect Similarity. PLoS ONE, 2011, 6, e22187.	1.1	86
54	Next generation genome annotation with mGene.ngs. BMC Bioinformatics, 2010, 11, .	1.2	8

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55	Global effects of the small RNA biogenesis machinery on the <i>Arabidopsis thaliana</i> transcriptome. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17466-17473.	3.3	66
56	AGRONOMICS1: A New Resource for Arabidopsis Transcriptome Profiling Â Â. Plant Physiology, 2010, 152, 487-499.	2.3	61
57	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	6.0	912
58	mGene: Accurate SVM-based gene finding with an application to nematode genomes. Genome Research, 2009, 19, 2133-2143.	2.4	79
59	Comprehensive analysis of <i>Arabidopsis</i> expression level polymorphisms with simple inheritance. Molecular Systems Biology, 2009, 5, 242.	3.2	21
60	mGene.web: a web service for accurate computational gene finding. Nucleic Acids Research, 2009, 37, W312-W316.	6.5	23
61	Quantitative RNA expression analysis with Affymetrix Tiling 1.0R arrays identifies new E2F target genes. Plant Journal, 2009, 57, 184-194.	2.8	65
62	Stressâ€induced changes in the <i>Arabidopsis thaliana</i> transcriptome analyzed using wholeâ€genome tiling arrays. Plant Journal, 2009, 58, 1068-1082.	2.8	273
63	Genomewide SNP variation reveals relationships among landraces and modern varieties of rice. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12273-12278.	3.3	581
64	Revealing sequence variation patterns in rice with machine learning methods. BMC Bioinformatics, 2008, 9, .	1.2	1
65	At-TAX: a whole genome tiling array resource for developmental expression analysis and transcript identification in Arabidopsis thaliana. Genome Biology, 2008, 9, R112.	13.9	91
66	Dual roles of the nuclear cap-binding complex and SERRATE in pre-mRNA splicing and microRNA processing in <i>Arabidopsis thaliana</i>. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8795-8800.	3.3	378
67	Detecting polymorphic regions in <i>Arabidopsis thaliana</i> with resequencing microarrays. Genome Research, 2008, 18, 918-929.	2.4	50
68	Transcript normalization and segmentation of tiling array data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 527-38.	0.7	8
69	Common Sequence Polymorphisms Shaping Genetic Diversity in <i>Arabidopsis thaliana</i>. Science, 2007, 317, 338-342.	6.0	689