

Georg Zeller

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

72
papers

15,148
citations

41
h-index

80
g-index

80
ext. papers

19,955
ext. citations

18.6
avg, IF

5.69
L-index

#	Paper	IF	Citations
72	Identifying temporal and spatial patterns of variation from multimodal data using MEFISTO.. <i>Nature Methods</i> , 2022 ,	21.6	5
71	A faecal microbiota signature with high specificity for pancreatic cancer.. <i>Gut</i> , 2022 ,	19.2	5
70	Microbiota-dependent activation of the myeloid calcineurin-NFAT pathway inhibits B7H3- and B7H4-dependent anti-tumor immunity in colorectal cancer.. <i>Immunity</i> , 2022 ,	32.3	2
69	Calorie restriction improves metabolic state independently of gut microbiome composition: a randomized dietary intervention trial.. <i>Genome Medicine</i> , 2022 , 14, 30	14.4	2
68	Critical Assessment of Metagenome Interpretation: the second round of challenges.. <i>Nature Methods</i> , 2022 ,	21.6	14
67	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021 , 27, 1885-1892	50.5	19
66	Unravelling the collateral damage of antibiotics on gut bacteria. <i>Nature</i> , 2021 , 599, 120-124	50.4	21
65	Microbiome meta-analysis and cross-disease comparison enabled by the SIAMCAT machine learning toolbox. <i>Genome Biology</i> , 2021 , 22, 93	18.3	26
64	Bedeutung des Darmmikrobioms bei der Organtransplantation. <i>Der Nephrologe</i> , 2021 , 16, 154-159	0.1	
63	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. <i>Frontiers in Microbiology</i> , 2021 , 12, 635781	5.7	18
62	Commensal Clostridiales strains mediate effective anti-cancer immune response against solid tumors. <i>Cell Host and Microbe</i> , 2021 , 29, 1573-1588.e7	23.4	9
61	mOTUs: Profiling Taxonomic Composition, Transcriptional Activity and Strain Populations of Microbial Communities. <i>Current Protocols</i> , 2021 , 1, e218		2
60	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. <i>Nature Microbiology</i> , 2021 , 6, 196-208	26.6	44
59	Analysis of 1321 Eubacterium rectale genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. <i>Genome Biology</i> , 2020 , 21, 138	18.3	27
58	Metabolic models predict bacterial passengers in colorectal cancer. <i>Cancer & Metabolism</i> , 2020 , 8, 3	5.4	14
57	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,	6.7	8
56	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	20.1	21

55	The gut microbiome in solid organ transplantation. <i>Pediatric Transplantation</i> , 2020 , 24, e13866	1.8	5
54	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	10	18
53	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019 , 10, 1014	17.4	134
52	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	50.5	289
51	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. <i>Nature Medicine</i> , 2019 , 25, 679-689	50.5	353
50	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019 , 179, 1068-1083.e21	56.2	113
49	Extensive transmission of microbes along the gastrointestinal tract. <i>ELife</i> , 2019 , 8,	8.9	158
48	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018 , 3, 8-16	26.6	387
47	Extensive impact of non-antibiotic drugs on human gut bacteria. <i>Nature</i> , 2018 , 555, 623-628	50.4	834
46	Nutritional preferences of human gut bacteria reveal their metabolic idiosyncrasies. <i>Nature Microbiology</i> , 2018 , 3, 514-522	26.6	119
45	Mikrobielle Biomarker zur Krebsfrüherkennung. <i>Tumor Diagnostik Und Therapie</i> , 2018 , 39, 55-62	0.1	
44	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017 , 35, 1069-1076	44.5	355
43	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , 2017 , 13, 960	12.2	69
42	CART-a chemical annotation retrieval toolkit. <i>Bioinformatics</i> , 2016 , 32, 2869-71	7.2	5
41	Gut Microbiota Linked to Sexual Preference and HIV Infection. <i>EBioMedicine</i> , 2016 , 5, 135-46	8.8	230
40	Colorectal Cancer and the Human Gut Microbiome: Reproducibility with Whole-Genome Shotgun Sequencing. <i>PLoS ONE</i> , 2016 , 11, e0155362	3.7	147
39	MOCAT2: a metagenomic assembly, annotation and profiling framework. <i>Bioinformatics</i> , 2016 , 32, 2520-3.2	3.2	117
38	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , 2016 , 352, 586-9	33.3	326

37	Ocean plankton. Structure and function of the global ocean microbiome. <i>Science</i> , 2015 , 348, 1261359	33.3	1261
36	Temporal and technical variability of human gut metagenomes. <i>Genome Biology</i> , 2015 , 16, 73	18.3	108
35	A fair comparison. <i>Nature Methods</i> , 2014 , 11, 359	21.6	33
34	Novel drug candidates for the treatment of metastatic colorectal cancer through global inverse gene-expression profiling. <i>Cancer Research</i> , 2014 , 74, 5690-9	10.1	84
33	Potential of fecal microbiota for early-stage detection of colorectal cancer. <i>Molecular Systems Biology</i> , 2014 , 10, 766	12.2	575
32	Oqtans: the RNA-seq workbench in the cloud for complete and reproducible quantitative transcriptome analysis. <i>Bioinformatics</i> , 2014 , 30, 1300-1	7.2	10
31	Accurate and universal delineation of prokaryotic species. <i>Nature Methods</i> , 2013 , 10, 881-4	21.6	234
30	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013 , 10, 1196-9	21.6	340
29	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013 , 10, 1177-84	21.6	477
28	Systematic evaluation of spliced alignment programs for RNA-seq data. <i>Nature Methods</i> , 2013 , 10, 1185-9	21.6	371
27	Characterization of drug-induced transcriptional modules: towards drug repositioning and functional understanding. <i>Molecular Systems Biology</i> , 2013 , 9, 662	12.2	86
26	Drug discovery in the age of systems biology: the rise of computational approaches for data integration. <i>Current Opinion in Biotechnology</i> , 2012 , 23, 609-16	11.4	71
25	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011 , 473, 174-80	50.4	4240
24	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	3.6	16
23	A spatial and temporal map of <i>C. elegans</i> gene expression. <i>Genome Research</i> , 2011 , 21, 325-41	9.7	192
22	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, 2549	11.5	87
21	Prediction of drug combinations by integrating molecular and pharmacological data. <i>PLoS Computational Biology</i> , 2011 , 7, e1002323	5	145
20	Network neighbors of drug targets contribute to drug side-effect similarity. <i>PLoS ONE</i> , 2011 , 6, e22187	3.7	75

19	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, 17466-73	11.5	57
18	AGRONOMICS1: a new resource for <i>Arabidopsis</i> transcriptome profiling. <i>Plant Physiology</i> , 2010 , 152, 487-99	6.6	56
17	Integrative analysis of the <i>Caenorhabditis elegans</i> genome by the modENCODE project. <i>Science</i> , 2010 , 330, 1775-87	33.3	744
16	Next generation genome annotation with mGene.ngs. <i>BMC Bioinformatics</i> , 2010 , 11,	3.6	7
15	mGene: accurate SVM-based gene finding with an application to nematode genomes. <i>Genome Research</i> , 2009 , 19, 2133-43	9.7	68
14	Comprehensive analysis of <i>Arabidopsis</i> expression level polymorphisms with simple inheritance. <i>Molecular Systems Biology</i> , 2009 , 5, 242	12.2	20
13	mGene.web: a web service for accurate computational gene finding. <i>Nucleic Acids Research</i> , 2009 , 37, W312-6	20.1	20
12	Quantitative RNA expression analysis with Affymetrix Tiling 1.0R arrays identifies new E2F target genes. <i>Plant Journal</i> , 2009 , 57, 184-94	6.9	56
11	Stress-induced changes in the <i>Arabidopsis thaliana</i> transcriptome analyzed using whole-genome tiling arrays. <i>Plant Journal</i> , 2009 , 58, 1068-82	6.9	249
10	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, 12273-8	11.5	499
9	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	18.3	85
8	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, 8795-800	11.5	297
7	Detecting polymorphic regions in <i>Arabidopsis thaliana</i> with resequencing microarrays. <i>Genome Research</i> , 2008 , 18, 918-29	9.7	46
6	Transcript normalization and segmentation of tiling array data. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2008 , 527-38	1.3	8
5	Common sequence polymorphisms shaping genetic diversity in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007 , 317, 338-42	33.3	596
4	Dissecting the collateral damage of antibiotics on gut microbes		4
3	Microbiome meta-analysis and cross-disease comparison enabled by the SIAMCAT machine-learning toolbox		3
2	Uncharted biosynthetic potential of the ocean microbiome		6

1 Biosynthetic potential of the global ocean microbiome. *Nature*,

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