

# Paul Wilmes

## List of Publications by Year in descending order

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Version: 2024-02-01

127  
papers

15,332  
citations

36303

51  
h-index

20358

116  
g-index

152  
all docs

152  
docs citations

152  
times ranked

21628  
citing authors

#	ARTICLE	IF	CITATIONS
1	Treg induction by a rationally selected mixture of Clostridia strains from the human microbiota. <i>Nature</i> , 2013, 500, 232-236.	27.8	2,339
2	A Dietary Fiber-Deprived Gut Microbiota Degrades the Colonic Mucus Barrier and Enhances Pathogen Susceptibility. <i>Cell</i> , 2016, 167, 1339-1353.e21.	28.9	1,882
3	Generation of genome-scale metabolic reconstructions for 773 members of the human gut microbiota. <i>Nature Biotechnology</i> , 2017, 35, 81-89.	17.5	629
4	Challenges in microbial ecology: building predictive understanding of community function and dynamics. <i>ISME Journal</i> , 2016, 10, 2557-2568.	9.8	570
5	Global diversity and biogeography of bacterial communities in wastewater treatment plants. <i>Nature Microbiology</i> , 2019, 4, 1183-1195.	13.3	491
6	A microfluidics-based in vitro model of the gastrointestinal human-microbe interface. <i>Nature Communications</i> , 2016, 7, 11535.	12.8	466
7	Human Gut Microbiome: Function Matters. <i>Trends in Microbiology</i> , 2018, 26, 563-574.	7.7	458
8	The nasal and gut microbiome in Parkinson's disease and idiopathic rapid eye movement sleep behavior disorder. <i>Movement Disorders</i> , 2018, 33, 88-98.	3.9	428
9	VizBin - an application for reference-independent visualization and human-augmented binning of metagenomic data. <i>Microbiome</i> , 2015, 3, 1.	11.1	352
10	The application of two-dimensional polyacrylamide gel electrophoresis and downstream analyses to a mixed community of prokaryotic microorganisms. <i>Environmental Microbiology</i> , 2004, 6, 911-920.	3.8	347
11	Metaproteomics: studying functional gene expression in microbial ecosystems. <i>Trends in Microbiology</i> , 2006, 14, 92-97.	7.7	326
12	Extensive transmission of microbes along the gastrointestinal tract. <i>ELife</i> , 2019, 8, .	6.0	313
13	Characterization of Extracellular Polymeric Substances from Acidophilic Microbial Biofilms. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2916-2922.	3.1	239
14	Integrated multi-omics of the human gut microbiome in a case study of familial type 1 diabetes. <i>Nature Microbiology</i> , 2017, 2, 16180.	13.3	233
15	Systematic Design of 18S rRNA Gene Primers for Determining Eukaryotic Diversity in Microbial Consortia. <i>PLoS ONE</i> , 2014, 9, e95567.	2.5	218
16	Colonization and Succession within the Human Gut Microbiome by Archaea, Bacteria, and Microeukaryotes during the First Year of Life. <i>Frontiers in Microbiology</i> , 2017, 8, 738.	3.5	207
17	Birth mode is associated with earliest strain-conferred gut microbiome functions and immunostimulatory potential. <i>Nature Communications</i> , 2018, 9, 5091.	12.8	190
18	From meta-omics to causality: experimental models for human microbiome research. <i>Microbiome</i> , 2013, 1, 14.	11.1	173

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19	Proteogenomic basis for ecological divergence of closely related bacteria in natural acidophilic microbial communities. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2383-2390.	7.1	171
20	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
21	The human gut microbiome in health: establishment and resilience of microbiota over a lifetime. Environmental Microbiology, 2016, 18, 2103-2116.	3.8	169
22	The extracellular RNA complement of <i>Escherichia coli</i> . MicrobiologyOpen, 2015, 4, 252-266.	3.0	162
23	A decade of metaproteomics: Where we stand and what the future holds. Proteomics, 2015, 15, 3409-3417.	2.2	161
24	The Complex Exogenous RNA Spectra in Human Plasma: An Interface with Human Gut Biota?. PLoS ONE, 2012, 7, e51009.	2.5	160
25	Community proteogenomics highlights microbial strain-variant protein expression within activated sludge performing enhanced biological phosphorus removal. ISME Journal, 2008, 2, 853-864.	9.8	156
26	Metaproteomics Provides Functional Insight into Activated Sludge Wastewater Treatment. PLoS ONE, 2008, 3, e1778.	2.5	145
27	IMP: a pipeline for reproducible reference-independent integrated metagenomic and metatranscriptomic analyses. Genome Biology, 2016, 17, 260.	8.8	141
28	A year of monitoring 20 mesophilic full-scale bioreactors reveals the existence of stable but different core microbiomes in bio-waste and wastewater anaerobic digestion systems. Biotechnology for Biofuels, 2018, 11, 196.	6.2	138
29	Microbiome in Colorectal Cancer: How to Get from Meta-omics to Mechanism?. Trends in Microbiology, 2020, 28, 401-423.	7.7	135
30	Parkinson's disease-associated alterations of the gut microbiome predict disease-relevant changes in metabolic functions. BMC Biology, 2020, 18, 62.	3.8	122
31	Ninety-nine <i>de novo</i> assembled genomes from the moose ( <i>Alces alces</i> ) rumen microbiome provide new insights into microbial plant biomass degradation. ISME Journal, 2017, 11, 2538-2551.	9.8	120
32	Sources and Functions of Extracellular Small RNAs in Human Circulation. Annual Review of Nutrition, 2016, 36, 301-336.	10.1	110
33	Glutathione Restricts Serine Metabolism to Preserve Regulatory T Cell Function. Cell Metabolism, 2020, 31, 920-936.e7.	16.2	109
34	Dark matter in host-microbiome metabolomics: Tackling the unknowns—A review. Analytica Chimica Acta, 2018, 1037, 13-27.	5.4	108
35	The microbiome-gut-brain axis in acute and chronic brain diseases. Current Opinion in Neurobiology, 2020, 61, 1-9.	4.2	105
36	A biomolecular isolation framework for eco-systems biology. ISME Journal, 2013, 7, 110-121.	9.8	97

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37	The gut microbial metabolite formate exacerbates colorectal cancer progression. <i>Nature Metabolism</i> , 2022, 4, 458-475.	11.9	97
38	A hundred years of activated sludge: time for a rethink. <i>Frontiers in Microbiology</i> , 2014, 5, 47.	3.5	93
39	The dynamic genetic repertoire of microbial communities. <i>FEMS Microbiology Reviews</i> , 2009, 33, 109-132.	8.6	89
40	Comparative integrated omics: identification of key functionalities in microbial community-wide metabolic networks. <i>Npj Biofilms and Microbiomes</i> , 2015, 1, 15007.	6.4	82
41	PathoFact: a pipeline for the prediction of virulence factors and antimicrobial resistance genes in metagenomic data. <i>Microbiome</i> , 2021, 9, 49.	11.1	81
42	Natural acidophilic biofilm communities reflect distinct organismal and functional organization. <i>ISME Journal</i> , 2009, 3, 266-270.	9.8	79
43	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. <i>Nature Communications</i> , 2014, 5, 5603.	12.8	75
44	Condensing the omics fog of microbial communities. <i>Trends in Microbiology</i> , 2013, 21, 325-333.	7.7	74
45	Multi-omics Reveals the Lifestyle of the Acidophilic, Mineral-Oxidizing Model Species <i>Leptospirillum ferriphilum</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	71
46	Microbial community proteomics: elucidating the catalysts and metabolic mechanisms that drive the Earth's biogeochemical cycles. <i>Current Opinion in Microbiology</i> , 2009, 12, 310-317.	5.1	70
47	Lipid-based biofuel production from wastewater. <i>Current Opinion in Biotechnology</i> , 2014, 30, 9-16.	6.6	69
48	Measuring soil sustainability via soil resilience. <i>Science of the Total Environment</i> , 2018, 626, 1484-1493.	8.0	69
49	SARS-CoV-2 transmission risk from asymptomatic carriers: Results from a mass screening programme in Luxembourg. <i>Lancet Regional Health - Europe</i> , 2021, 4, 100056.	5.6	68
50	Ecological distribution and population physiology defined by proteomics in a natural microbial community. <i>Molecular Systems Biology</i> , 2010, 6, 374.	7.2	63
51	The RNA Complement of Outer Membrane Vesicles From <i>Salmonella enterica</i> Serovar Typhimurium Under Distinct Culture Conditions. <i>Frontiers in Microbiology</i> , 2018, 9, 2015.	3.5	62
52	Using metabolic networks to resolve ecological properties of microbiomes. <i>Current Opinion in Systems Biology</i> , 2018, 8, 73-80.	2.6	61
53	Integrated In Vitro and In Silico Modeling Delineates the Molecular Effects of a Synbiotic Regimen on Colorectal-Cancer-Derived Cells. <i>Cell Reports</i> , 2019, 27, 1621-1632.e9.	6.4	59
54	Deep neural networks outperform human expert's capacity in characterizing bioleaching bacterial biofilm composition. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2019, 22, e00321.	4.4	57

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55	Integration of time-series meta-omics data reveals how microbial ecosystems respond to disturbance. <i>Nature Communications</i> , 2020, 11, 5281.	12.8	57
56	Genetic and metabolic links between the murine microbiome and memory. <i>Microbiome</i> , 2020, 8, 53.	11.1	56
57	Sequential Isolation of Metabolites, RNA, DNA, and Proteins from the Same Unique Sample. <i>Methods in Enzymology</i> , 2013, 531, 219-236.	1.0	54
58	Mechanisms of Persistence of the Ammonia-Oxidizing Bacteria <i>Nitrosomonas</i> to the Biocide Free Nitrous Acid. <i>Environmental Science &amp; Technology</i> , 2018, 52, 5386-5397.	10.0	52
59	Method Optimization for Fecal Sample Collection and Fecal DNA Extraction. <i>Biopreservation and Biobanking</i> , 2015, 13, 79-93.	1.0	48
60	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	3.7	47
61	Integrative omics analysis of the termite gut system adaptation to <i>Miscanthus</i> diet identifies lignocellulose degradation enzymes. <i>Communications Biology</i> , 2020, 3, 275.	4.4	47
62	Roles of bacteriophages, plasmids and CRISPR immunity in microbial community dynamics revealed using time-series integrated meta-omics. <i>Nature Microbiology</i> , 2021, 6, 123-135.	13.3	47
63	Alignment-free Visualization of Metagenomic Data by Nonlinear Dimension Reduction. <i>Scientific Reports</i> , 2014, 4, 4516.	3.3	46
64	Integrated omics for the identification of key functionalities in biological wastewater treatment microbial communities. <i>Microbial Biotechnology</i> , 2015, 8, 363-368.	4.2	46
65	Small RNA profiling of low biomass samples: identification and removal of contaminants. <i>BMC Biology</i> , 2018, 16, 52.	3.8	46
66	Towards exposure of elusive metabolic mixed-culture processes: the application of metaproteomic analyses to activated sludge. <i>Water Science and Technology</i> , 2006, 54, 217-226.	2.5	44
67	<i>In situ</i> phenotypic heterogeneity among single cells of the filamentous bacterium <i>Candidatus</i> <i>Microthrix parvicella</i> . <i>ISME Journal</i> , 2016, 10, 1274-1279.	9.8	43
68	Phenotypic differentiation of gastrointestinal microbes is reflected in their encoded metabolic repertoires. <i>Microbiome</i> , 2015, 3, 55.	11.1	41
69	The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. <i>Microbiome</i> , 2021, 9, 243.	11.1	36
70	Weak Iron Oxidation by <i>Sulfobacillus thermosulfidooxidans</i> Maintains a Favorable Redox Potential for Chalcopyrite Bioleaching. <i>Frontiers in Microbiology</i> , 2018, 9, 3059.	3.5	35
71	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	12.8	34
72	The Gut Microbiota and Hematopoietic Stem Cell Transplantation: Challenges and Potentials. <i>Journal of Innate Immunity</i> , 2019, 11, 405-415.	3.8	33

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73	A Semi-Quantitative, Synteny-Based Method to Improve Functional Predictions for Hypothetical and Poorly Annotated Bacterial and Archaeal Genes. <i>PLoS Computational Biology</i> , 2011, 7, e1002230.	3.2	32
74	Sample Preservation and Storage Significantly Impact Taxonomic and Functional Profiles in Metaproteomics Studies of the Human Gut Microbiome. <i>Microorganisms</i> , 2019, 7, 367.	3.6	32
75	Compositional and functional characterisation of biomass-degrading microbial communities in guts of plant fibre- and soil-feeding higher termites. <i>Microbiome</i> , 2020, 8, 96.	11.1	31
76	<i>Fusobacterium nucleatum</i> Extracellular Vesicles Modulate Gut Epithelial Cell Innate Immunity via FomA and TLR2. <i>Frontiers in Immunology</i> , 2020, 11, 583644.	4.8	29
77	Metabolome-Proteome Differentiation Coupled to Microbial Divergence. <i>MBio</i> , 2010, 1, .	4.1	28
78	Engineering Solutions for Representative Models of the Gastrointestinal Human-Microbe Interface. <i>Engineering</i> , 2017, 3, 60-65.	6.7	28
79	Microdiversity characterizes prevalent phylogenetic clades in the glacier-fed stream microbiome. <i>ISME Journal</i> , 2022, 16, 666-675.	9.8	28
80	Genome Sequence of <i>Candidatus Microthrix parvicella</i> -Bio17-1, a Long-Chain-Fatty-Acid-Accumulating Filamentous Actinobacterium from a Biological Wastewater Treatment Plant. <i>Journal of Bacteriology</i> , 2012, 194, 6670-6671.	2.2	27
81	Integrated meta-omic analyses of the gastrointestinal tract microbiome in patients undergoing allogeneic hematopoietic stem cell transplantation. <i>Translational Research</i> , 2017, 186, 79-94.e1.	5.0	27
82	Persistence of birth mode-dependent effects on gut microbiome composition, immune system stimulation and antimicrobial resistance during the first year of life. <i>ISME Communications</i> , 2021, 1, .	4.2	25
83	Genomic and metabolic adaptations of biofilms to ecological windows of opportunity in glacier-fed streams. <i>Nature Communications</i> , 2022, 13, 2168.	12.8	25
84	Automated Microscopic Analysis of Metal Sulfide Colonization by Acidophilic Microorganisms. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	23
85	Building an international consortium for tracking coronavirus health status. <i>Nature Medicine</i> , 2020, 26, 1161-1165.	30.7	23
86	ICoVeR "an interactive visualization tool for verification and refinement of metagenomic bins. <i>BMC Bioinformatics</i> , 2017, 18, 233.	2.6	22
87	Extraction and Analysis of RNA Isolated from Pure Bacteria-Derived Outer Membrane Vesicles. <i>Methods in Molecular Biology</i> , 2018, 1737, 213-230.	0.9	22
88	Microbial Community Redundancy and Resilience Underpins High-Rate Anaerobic Treatment of Dairy-Processing Wastewater at Ambient Temperatures. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 192.	4.1	22
89	Mantis: flexible and consensus-driven genome annotation. <i>GigaScience</i> , 2021, 10, .	6.4	22
90	Genome Sequencing of SARS-CoV-2 Allows Monitoring of Variants of Concern through Wastewater. <i>Water (Switzerland)</i> , 2021, 13, 3018.	2.7	21

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91	Expressed protein profile of a Tectomicrobium and other microbial symbionts in the marine sponge <i>Aplysina aerophoba</i> as evidenced by metaproteomics. <i>Scientific Reports</i> , 2018, 8, 11795.	3.3	20
92	The microbiome of cryospheric ecosystems. <i>Nature Communications</i> , 2022, 13, .	12.8	20
93	Correlative microscopy for phylogenetic and ultrastructural characterization of microbial communities. <i>Environmental Microbiology Reports</i> , 2012, 4, 36-41.	2.4	19
94	Patterns and Drivers of Extracellular Enzyme Activity in New Zealand Glacier-Fed Streams. <i>Frontiers in Microbiology</i> , 2020, 11, 591465.	3.5	18
95	SARS-CoV-2 transmission in educational settings during an early summer epidemic wave in Luxembourg, 2020. <i>BMC Infectious Diseases</i> , 2021, 21, 417.	2.9	18
96	Optimised biomolecular extraction for metagenomic analysis of microbial biofilms from high-mountain streams. <i>PeerJ</i> , 2020, 8, e9973.	2.0	18
97	Resolving host-microbe interactions in the gut: the promise of in vitro models to complement in vivo research. <i>Current Opinion in Microbiology</i> , 2018, 44, 28-33.	5.1	17
98	Deuterium-exchange metabolomics identifies N-methyl lyso phosphatidylethanolamines as abundant lipids in acidophilic mixed microbial communities. <i>Metabolomics</i> , 2012, 8, 566-578.	3.0	16
99	Evolution of the murine gut resistome following broad-spectrum antibiotic treatment. <i>Nature Communications</i> , 2022, 13, 2296.	12.8	16
100	Glacier shrinkage will accelerate downstream decomposition of organic matter and alters microbiome structure and function. <i>Global Change Biology</i> , 2022, 28, 3846-3859.	9.5	15
101	IgE-Mediated Peanut Allergy: Current and Novel Predictive Biomarkers for Clinical Phenotypes Using Multi-Omics Approaches. <i>Frontiers in Immunology</i> , 2020, 11, 594350.	4.8	14
102	Connecting environmental exposure and neurodegeneration using cheminformatics and high resolution mass spectrometry: potential and challenges. <i>Environmental Sciences: Processes and Impacts</i> , 2019, 21, 1426-1445.	3.5	13
103	Emulating the gut-liver axis: Dissecting the microbiome's effect on drug metabolism using multiorgan-on-chip models. <i>Current Opinion in Endocrine and Metabolic Research</i> , 2021, 18, 94-101.	1.4	12
104	Studying the Parkinson's disease metabolome and exposome in biological samples through different analytical and cheminformatics approaches: a pilot study. <i>Analytical and Bioanalytical Chemistry</i> , 2022, 414, 7399-7419.	3.7	12
105	In praise of open research measures. <i>Nature</i> , 2013, 498, 170-170.	27.8	11
106	Combinatorial analysis reveals highly coordinated early-stage immune reactions that predict later antiviral immunity in mild COVID-19 patients. <i>Cell Reports Medicine</i> , 2022, 3, 100600.	6.5	10
107	Reverse engineering directed gene regulatory networks from transcriptomics and proteomics data of biomining bacterial communities with approximate Bayesian computation and steady-state signalling simulations. <i>BMC Bioinformatics</i> , 2020, 21, 23.	2.6	9
108	Identification, Recovery, and Refinement of Hitherto Undescribed Population-Level Genomes from the Human Gastrointestinal Tract. <i>Frontiers in Microbiology</i> , 2016, 7, 884.	3.5	8

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109	First draft genome sequence of a strain belonging to the Zoogloea genus and its gene expression in situ. Standards in Genomic Sciences, 2017, 12, 64.	1.5	8
110	Challenges, Strategies, and Perspectives for Reference-Independent Longitudinal Multi-Omic Microbiome Studies. Frontiers in Genetics, 2021, 12, 666244.	2.3	8
111	Systems biology of acidophile biofilms for efficient metal extraction. Scientific Data, 2020, 7, 215.	5.3	7
112	Dichloromethane Degradation Pathway from Unsequenced Hyphomicrobium sp. MC8b Rapidly Explored by Pan-Proteomics. Microorganisms, 2020, 8, 1876.	3.6	6
113	Unification of functional annotation descriptions using text mining. Biological Chemistry, 2021, 402, 983-990.	2.5	6
114	Functional meta-omics provide critical insights into long- and short-read assemblies. Briefings in Bioinformatics, 2021, 22, .	6.5	6
115	Sequential Isolation of DNA, RNA, Protein, and Metabolite Fractions from Murine Organs and Intestinal Contents for Integrated Omics of Host-Microbiota Interactions. Methods in Molecular Biology, 2018, 1841, 279-291.	0.9	5
116	Toward hypothesis-driven, personalized microbiome screening. Cell Reports Methods, 2022, 2, 100139.	2.9	3
117	Systematic characterization of human gut microbiome-secreted molecules by integrated multi-omics. ISME Communications, 2021, 1, 82.	4.2	3
118	Systems Biology of Acidophile Biofilms for Efficient Metal Extraction. Advanced Materials Research, 2015, 1130, 312-315.	0.3	1
119	Generalisation of COVID-19 incidences provides a biased view of the actual epidemiological situation. Lancet Regional Health - Europe, The, 2021, 5, 100116.	5.6	1
120	Mass Screening for SARS-CoV-2 Uncovers Significant Transmission Risk from Asymptomatic Carriers. SSRN Electronic Journal, 0, , .	0.4	1
121	RNA in Circulation: Sources and Functions of Extracellular Exogenous RNA in the Blood. , 2014, , 1-9.		1
122	RNA in Circulation: Sources and Functions of Extracellular Exogenous RNA in the Blood. , 2015, , 556-564.		1
123	Three-Dimensional Analysis of Microbial Communities. Microscopy and Microanalysis, 2010, 16, 388-389.	0.4	0
124	Correlative TEM/FISH Imaging of Microbial Communities. Biophysical Journal, 2010, 98, 581a.	0.5	0
125	Microbiome and type 1 diabetes (revision number 14). , 2013, , .		0
126	The sequential isolation of metabolites, RNA, DNA, and proteins from a single, undivided mixed microbial community sample. Protocol Exchange, 0, , .	0.3	0



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127	Integrated in Vitro and in Silico Modelling Delineates the Molecular Effects of a Symbiotic Regimen on Colorectal Cancer-Derived Cells. SSRN Electronic Journal, 0, , .	0.4	0