

# 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	Microdiversity characterizes prevalent phylogenetic clades in the glacier-fed stream microbiome. <i>ISME Journal</i> , 2022, 16, 666-675.	9.8	28
2	Toward hypothesis-driven, personalized microbiome screening. <i>Cell Reports Methods</i> , 2022, 2, 100139.	2.9	3
3	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
4	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
5	The gut microbial metabolite formate exacerbates colorectal cancer progression. <i>Nature Metabolism</i> , 2022, 4, 458-475.	11.9	97
6	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
7	Evolution of the murine gut resistome following broad-spectrum antibiotic treatment. <i>Nature Communications</i> , 2022, 13, 2296.	12.8	16
8	The microbiome of cryospheric ecosystems. <i>Nature Communications</i> , 2022, 13, .	12.8	20
9	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
10	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
11	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
12	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
13	SARS-CoV-2 transmission risk from asymptomatic carriers: Results from a mass screening programme in Luxembourg. <i>Lancet Regional Health - Europe</i> , The, 2021, 4, 100056.	5.6	68
14	Unification of functional annotation descriptions using text mining. <i>Biological Chemistry</i> , 2021, 402, 983-990.	2.5	6
15	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
16	Generalisation of COVID-19 incidences provides a biased view of the actual epidemiological situation. <i>Lancet Regional Health - Europe</i> , The, 2021, 5, 100116.	5.6	1
17	Challenges, Strategies, and Perspectives for Reference-Independent Longitudinal Multi-Omic Microbiome Studies. <i>Frontiers in Genetics</i> , 2021, 12, 666244.	2.3	8
18	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

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19	Mantis: flexible and consensus-driven genome annotation. <i>GigaScience</i> , 2021, 10, .	6.4	22
20	Functional meta-omics provide critical insights into long- and short-read assemblies. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	6
21	Genome Sequencing of SARS-CoV-2 Allows Monitoring of Variants of Concern through Wastewater. <i>Water (Switzerland)</i> , 2021, 13, 3018.	2.7	21
22	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	30.7	170
23	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	12.8	34
24	The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. <i>Microbiome</i> , 2021, 9, 243.	11.1	36
25	Systematic characterization of human gut microbiome-secreted molecules by integrated multi-omics. <i>ISME Communications</i> , 2021, 1, 82.	4.2	3
26	The microbiome-gut-brain axis in acute and chronic brain diseases. <i>Current Opinion in Neurobiology</i> , 2020, 61, 1-9.	4.2	105
27	Integration of time-series meta-omics data reveals how microbial ecosystems respond to disturbance. <i>Nature Communications</i> , 2020, 11, 5281.	12.8	57
28	Systems biology of acidophile biofilms for efficient metal extraction. <i>Scientific Data</i> , 2020, 7, 215.	5.3	7
29	Patterns and Drivers of Extracellular Enzyme Activity in New Zealand Glacier-Fed Streams. <i>Frontiers in Microbiology</i> , 2020, 11, 591465.	3.5	18
30	Dichloromethane Degradation Pathway from Unsequenced Hyphomicrobium sp. MC8b Rapidly Explored by Pan-Proteomics. <i>Microorganisms</i> , 2020, 8, 1876.	3.6	6
31	<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
32	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
33	Building an international consortium for tracking coronavirus health status. <i>Nature Medicine</i> , 2020, 26, 1161-1165.	30.7	23
34	Parkinson's disease-associated alterations of the gut microbiome predict disease-relevant changes in metabolic functions. <i>BMC Biology</i> , 2020, 18, 62.	3.8	122
35	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
36	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

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37	Microbiome in Colorectal Cancer: How to Get from Meta-omics to Mechanism?. Trends in Microbiology, 2020, 28, 401-423.	7.7	135
38	Reverse engineering directed gene regulatory networks from transcriptomics and proteomics data of biomining bacterial communities with approximate Bayesian computation and steady-state signalling simulations. BMC Bioinformatics, 2020, 21, 23.	2.6	9
39	Glutathione Restricts Serine Metabolism to Preserve Regulatory T Cell Function. Cell Metabolism, 2020, 31, 920-936.e7.	16.2	109
40	Genetic and metabolic links between the murine microbiome and memory. Microbiome, 2020, 8, 53.	11.1	56
41	IgE-Mediated Peanut Allergy: Current and Novel Predictive Biomarkers for Clinical Phenotypes Using Multi-Omics Approaches. Frontiers in Immunology, 2020, 11, 594350.	4.8	14
42	Optimised biomolecular extraction for metagenomic analysis of microbial biofilms from high-mountain streams. PeerJ, 2020, 8, e9973.	2.0	18
43	Connecting environmental exposure and neurodegeneration using cheminformatics and high resolution mass spectrometry: potential and challenges. Environmental Sciences: Processes and Impacts, 2019, 21, 1426-1445.	3.5	13
44	Sample Preservation and Storage Significantly Impact Taxonomic and Functional Profiles in Metaproteomics Studies of the Human Gut Microbiome. Microorganisms, 2019, 7, 367.	3.6	32
45	Global diversity and biogeography of bacterial communities in wastewater treatment plants. Nature Microbiology, 2019, 4, 1183-1195.	13.3	491
46	Integrated In Vitro and In Silico Modeling Delineates the Molecular Effects of a Synbiotic Regimen on Colorectal-Cancer-Derived Cells. Cell Reports, 2019, 27, 1621-1632.e9.	6.4	59
47	Deep neural networks outperform human expert's capacity in characterizing bioleaching bacterial biofilm composition. Biotechnology Reports (Amsterdam, Netherlands), 2019, 22, e00321.	4.4	57
48	The Gut Microbiota and Hematopoietic Stem Cell Transplantation: Challenges and Potentials. Journal of Innate Immunity, 2019, 11, 405-415.	3.8	33
49	Extensive transmission of microbes along the gastrointestinal tract. ELife, 2019, 8, .	6.0	313
50	Extraction and Analysis of RNA Isolated from Pure Bacteria-Derived Outer Membrane Vesicles. Methods in Molecular Biology, 2018, 1737, 213-230.	0.9	22
51	Mechanisms of Persistence of the Ammonia-Oxidizing Bacteria <i>Nitrosomonas</i> to the Biocide Free Nitrous Acid. Environmental Science & Technology, 2018, 52, 5386-5397.	10.0	52
52	Using metabolic networks to resolve ecological properties of microbiomes. Current Opinion in Systems Biology, 2018, 8, 73-80.	2.6	61
53	Dark matter in host-microbiome metabolomics: Tackling the unknowns – A review. Analytica Chimica Acta, 2018, 1037, 13-27.	5.4	108
54	Measuring soil sustainability via soil resilience. Science of the Total Environment, 2018, 626, 1484-1493.	8.0	69

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55	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
56	Human Gut Microbiome: Function Matters. <i>Trends in Microbiology</i> , 2018, 26, 563-574.	7.7	458
57	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
58	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
59	Birth mode is associated with earliest strain-conferred gut microbiome functions and immunostimulatory potential. <i>Nature Communications</i> , 2018, 9, 5091.	12.8	190
60	Sequential Isolation of DNA, RNA, Protein, and Metabolite Fractions from Murine Organs and Intestinal Contents for Integrated Omics of Host-Microbiota Interactions. <i>Methods in Molecular Biology</i> , 2018, 1841, 279-291.	0.9	5
61	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
62	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	3.7	47
63	Small RNA profiling of low biomass samples: identification and removal of contaminants. <i>BMC Biology</i> , 2018, 16, 52.	3.8	46
64	Automated Microscopic Analysis of Metal Sulfide Colonization by Acidophilic Microorganisms. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	23
65	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. <i>Biotechnology for Biofuels</i> , 2018, 11, 196.	6.2	138
66	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
67	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
68	Engineering Solutions for Representative Models of the Gastrointestinal Human-Microbe Interface. <i>Engineering</i> , 2017, 3, 60-65.	6.7	28
69	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. <i>ISME Journal</i> , 2017, 11, 2538-2551.	9.8	120
70	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
71	ICoVeR – an interactive visualization tool for verification and refinement of metagenomic bins. <i>BMC Bioinformatics</i> , 2017, 18, 233.	2.6	22
72	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

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73	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
74	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
75	First draft genome sequence of a strain belonging to the <i>Zoogloea</i> genus and its gene expression in situ. <i>Standards in Genomic Sciences</i> , 2017, 12, 64.	1.5	8
76	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
77	The human gut microbiome in health: establishment and resilience of microbiota over a lifetime. <i>Environmental Microbiology</i> , 2016, 18, 2103-2116.	3.8	169
78	IMP: a pipeline for reproducible reference-independent integrated metagenomic and metatranscriptomic analyses. <i>Genome Biology</i> , 2016, 17, 260.	8.8	141
79	Challenges in microbial ecology: building predictive understanding of community function and dynamics. <i>ISME Journal</i> , 2016, 10, 2557-2568.	9.8	570
80	Sources and Functions of Extracellular Small RNAs in Human Circulation. <i>Annual Review of Nutrition</i> , 2016, 36, 301-336.	10.1	110
81	<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
82	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
83	A microfluidics-based in vitro model of the gastrointestinal human-microbe interface. <i>Nature Communications</i> , 2016, 7, 11535.	12.8	466
84	A decade of metaproteomics: Where we stand and what the future holds. <i>Proteomics</i> , 2015, 15, 3409-3417.	2.2	161
85	The extracellular RNA complement of <i>Escherichia coli</i> . <i>MicrobiologyOpen</i> , 2015, 4, 252-266.	3.0	162
86	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
87	Phenotypic differentiation of gastrointestinal microbes is reflected in their encoded metabolic repertoires. <i>Microbiome</i> , 2015, 3, 55.	11.1	41
88	Systems Biology of Acidophile Biofilms for Efficient Metal Extraction. <i>Advanced Materials Research</i> , 2015, 1130, 312-315.	0.3	1
89	Method Optimization for Fecal Sample Collection and Fecal DNA Extraction. <i>Biopreservation and Biobanking</i> , 2015, 13, 79-93.	1.0	48
90	VizBin - an application for reference-independent visualization and human-augmented binning of metagenomic data. <i>Microbiome</i> , 2015, 3, 1.	11.1	352

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91	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
92	RNA in Circulation: Sources and Functions of Extracellular Exogenous RNA in the Blood. , 2015, , 556-564.		1
93	A hundred years of activated sludge: time for a rethink. <i>Frontiers in Microbiology</i> , 2014, 5, 47.	3.5	93
94	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. <i>Nature Communications</i> , 2014, 5, 5603.	12.8	75
95	Systematic Design of 18S rRNA Gene Primers for Determining Eukaryotic Diversity in Microbial Consortia. <i>PLoS ONE</i> , 2014, 9, e95567.	2.5	218
96	Lipid-based biofuel production from wastewater. <i>Current Opinion in Biotechnology</i> , 2014, 30, 9-16.	6.6	69
97	Alignment-free Visualization of Metagenomic Data by Nonlinear Dimension Reduction. <i>Scientific Reports</i> , 2014, 4, 4516.	3.3	46
98	RNA in Circulation: Sources and Functions of Extracellular Exogenous RNA in the Blood. , 2014, , 1-9.		1
99	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
100	Condensing the omics fog of microbial communities. <i>Trends in Microbiology</i> , 2013, 21, 325-333.	7.7	74
101	From meta-omics to causality: experimental models for human microbiome research. <i>Microbiome</i> , 2013, 1, 14.	11.1	173
102	A biomolecular isolation framework for eco-systems biology. <i>ISME Journal</i> , 2013, 7, 110-121.	9.8	97
103	In praise of open research measures. <i>Nature</i> , 2013, 498, 170-170.	27.8	11
104	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
105	Microbiome and type 1 diabetes (revision number 14). , 2013, , .		0
106	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
107	The Complex Exogenous RNA Spectra in Human Plasma: An Interface with Human Gut Biota?. <i>PLoS ONE</i> , 2012, 7, e51009.	2.5	160
108	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

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109	Correlative microscopy for phylogenetic and ultrastructural characterization of microbial communities. <i>Environmental Microbiology Reports</i> , 2012, 4, 36-41.	2.4	19
110	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
111	Three-Dimensional Analysis of Microbial Communities. <i>Microscopy and Microanalysis</i> , 2010, 16, 388-389.	0.4	0
112	Metabolome-Proteome Differentiation Coupled to Microbial Divergence. <i>MBio</i> , 2010, 1, .	4.1	28
113	Proteogenomic basis for ecological divergence of closely related bacteria in natural acidophilic microbial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2383-2390.	7.1	171
114	Ecological distribution and population physiology defined by proteomics in a natural microbial community. <i>Molecular Systems Biology</i> , 2010, 6, 374.	7.2	63
115	Correlative TEM/FISH Imaging of Microbial Communities. <i>Biophysical Journal</i> , 2010, 98, 581a.	0.5	0
116	Characterization of Extracellular Polymeric Substances from Acidophilic Microbial Biofilms. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2916-2922.	3.1	239
117	Natural acidophilic biofilm communities reflect distinct organismal and functional organization. <i>ISME Journal</i> , 2009, 3, 266-270.	9.8	79
118	The dynamic genetic repertoire of microbial communities. <i>FEMS Microbiology Reviews</i> , 2009, 33, 109-132.	8.6	89
119	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
120	Community proteogenomics highlights microbial strain-variant protein expression within activated sludge performing enhanced biological phosphorus removal. <i>ISME Journal</i> , 2008, 2, 853-864.	9.8	156
121	Metaproteomics Provides Functional Insight into Activated Sludge Wastewater Treatment. <i>PLoS ONE</i> , 2008, 3, e1778.	2.5	145
122	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
123	Metaproteomics: studying functional gene expression in microbial ecosystems. <i>Trends in Microbiology</i> , 2006, 14, 92-97.	7.7	326
124	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
125	Mass Screening for SARS-CoV-2 Uncovers Significant Transmission Risk from Asymptomatic Carriers. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
126	The sequential isolation of metabolites, RNA, DNA, and proteins from a single, undivided mixed microbial community sample. <i>Protocol Exchange</i> , 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