

Martin F Polz

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.

111
papers

10,381
citations

47
h-index

101
g-index

113
ext. papers

13,046
ext. citations

11.5
avg, IF

6.38
L-index

#	Paper	IF	Citations
111	Resolving the structure of phage-bacteria interactions in the context of natural diversity.. <i>Nature Communications</i> , 2022 , 13, 372	17.4	3
110	Successional dynamics and alternative stable states in a saline activated sludge microbial community over 9 years. <i>Microbiome</i> , 2021 , 9, 199	16.6	4
109	Rapid evolutionary turnover of mobile genetic elements drives bacterial resistance to phages. <i>Science</i> , 2021 , 374, 488-492	33.3	13
108	Microbiome assembly for sulfonamide subsistence and the transfer of genetic determinants. <i>ISME Journal</i> , 2021 , 15, 2817-2829	11.9	2
107	Reply to Shaw: Challenges for enrichment analysis of AMR gene-bearing plasmids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	
106	Conjugative plasmids interact with insertion sequences to shape the horizontal transfer of antimicrobial resistance genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	39
105	Reply to Partridge et al.: Complementary bioinformatics and experimental approaches to investigate the transfer of AMR genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	
104	Degradation of host translational machinery drives tRNA acquisition in viruses. <i>Cell Systems</i> , 2021 , 12, 771-779.e5	10.6	6
103	Prokaryotic viruses impact functional microorganisms in nutrient removal and carbon cycle in wastewater treatment plants. <i>Nature Communications</i> , 2021 , 12, 5398	17.4	4
102	Coastal Bacterial Community Response to Glacier Melting in the Western Antarctic Peninsula. <i>Microorganisms</i> , 2021 , 9,	4.9	6
101	Redox-informed models of global biogeochemical cycles. <i>Nature Communications</i> , 2020 , 11, 5680	17.4	9
100	The genetic law of the minimum. <i>Science</i> , 2020 , 370, 655-656	33.3	1
99	Diarrhoeal events can trigger long-term <i>Clostridium difficile</i> colonization with recurrent blooms. <i>Nature Microbiology</i> , 2020 , 5, 642-650	26.6	9
98	Culture-independent tracking of <i>Vibrio cholerae</i> lineages reveals complex spatiotemporal dynamics in a natural population. <i>Environmental Microbiology</i> , 2020 , 22, 4244-4256	5.2	7
97	How can microbial population genomics inform community ecology?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020 , 375, 20190253	5.8	13
96	Using Colonization Assays and Comparative Genomics To Discover Symbiosis Behaviors and Factors in <i>Vibrio fischeri</i> . <i>MBio</i> , 2020 , 11,	7.8	7
95	Verrucomicrobia use hundreds of enzymes to digest the algal polysaccharide fucoidan. <i>Nature Microbiology</i> , 2020 , 5, 1026-1039	26.6	57

94	Genomic Features for Desiccation Tolerance and Sugar Biosynthesis in the Extremophile sp. UTEX B3054. <i>Frontiers in Microbiology</i> , 2019 , 10, 950	5.7	6
93	Polyclonal symbiont populations in hydrothermal vent tubeworms and the environment. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019 , 286, 20181281	4.4	10
92	A Reverse Ecology Approach Based on a Biological Definition of Microbial Populations. <i>Cell</i> , 2019 , 178, 820-834.e14	56.2	60
91	Interactions in self-assembled microbial communities saturate with diversity. <i>ISME Journal</i> , 2019 , 13, 1602-1617	11.9	26
90	Maintenance of Sympatric and Allopatric Populations in Free-Living Terrestrial Bacteria. <i>MBio</i> , 2019 , 10,	7.8	10
89	Bacterial community structure in a sympagic habitat expanding with global warming: brackish ice brine at 85-90 °N. <i>ISME Journal</i> , 2019 , 13, 316-333	11.9	11
88	Summer phyto- and bacterioplankton communities during low and high productivity scenarios in the Western Antarctic Peninsula. <i>Polar Biology</i> , 2019 , 42, 159-169	2	12
87	Function and functional redundancy in microbial systems. <i>Nature Ecology and Evolution</i> , 2018 , 2, 936-943	12.3	423
86	Evolution of a Vegetarian Vibrio: Metabolic Specialization of <i>Vibrio breoganii</i> to Macroalgal Substrates. <i>Journal of Bacteriology</i> , 2018 , 200,	3.5	9
85	Streamlining standard bacteriophage methods for higher throughput. <i>MethodsX</i> , 2018 , 5, 159-172	1.9	22
84	High resolution time series reveals cohesive but short-lived communities in coastal plankton. <i>Nature Communications</i> , 2018 , 9, 266	17.4	62
83	A major lineage of non-tailed dsDNA viruses as unrecognized killers of marine bacteria. <i>Nature</i> , 2018 , 554, 118-122	50.4	109
82	Ancestral gene acquisition as the key to virulence potential in environmental <i>Vibrio</i> populations. <i>ISME Journal</i> , 2018 , 12, 2954-2966	11.9	20
81	Inter-individual variability in copepod microbiomes reveals bacterial networks linked to host physiology. <i>ISME Journal</i> , 2018 , 12, 2103-2113	11.9	27
80	Viruses of the Nahant Collection, characterization of 251 marine Vibrionaceae viruses. <i>Scientific Data</i> , 2018 , 5, 180114	8.2	17
79	Widespread distribution of prophage-encoded virulence factors in marine <i>Vibrio</i> communities. <i>Scientific Reports</i> , 2018 , 8, 9973	4.9	47
78	Accurate Quantification of Laminarin in Marine Organic Matter with Enzymes from Marine Microbes. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	45
77	Microbial community assembly and evolution in subseafloor sediment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 2940-2945	11.5	120

76	A Mobile Element in mutS Drives Hypermutation in a Marine Vibrio. <i>MBio</i> , 2017 , 8,	7.8	14
75	Natural resource landscapes of a marine bacterium reveal distinct fitness-determining genes across the genome. <i>Environmental Microbiology</i> , 2017 , 19, 2422-2433	5.2	5
74	Exploiting fine-scale genetic and physiological variation of closely related microbes to reveal unknown enzyme functions. <i>Journal of Biological Chemistry</i> , 2017 , 292, 13056-13067	5.4	10
73	Direct single-cell biomass estimates for marine bacteria via Archimedes's principle. <i>ISME Journal</i> , 2017 , 11, 825-828	11.9	33
72	<i>Vibrio crassostreae</i> , a benign oyster colonizer turned into a pathogen after plasmid acquisition. <i>ISME Journal</i> , 2017 , 11, 1043-1052	11.9	69
71	Physiological and gene expression responses to nitrogen regimes and temperatures in <i>Mastigocladus</i> sp. strain CHP1, a predominant thermotolerant cyanobacterium of hot springs. <i>Systematic and Applied Microbiology</i> , 2017 , 40, 102-113	4.2	9
70	Endemicity of the cosmopolitan mesophilic chemolithoautotroph <i>Sulfurimonas</i> at deep-sea hydrothermal vents. <i>ISME Journal</i> , 2017 , 11, 909-919	11.9	19
69	Bacterial evolution: Genomics of metabolic trade-offs. <i>Nature Microbiology</i> , 2016 , 1, 16181	26.6	23
68	Microbial interactions lead to rapid micro-scale successions on model marine particles. <i>Nature Communications</i> , 2016 , 7, 11965	17.4	183
67	Adaptive radiation by waves of gene transfer leads to fine-scale resource partitioning in marine microbes. <i>Nature Communications</i> , 2016 , 7, 12860	17.4	81
66	Evidence for Ecological Flexibility in the Cosmopolitan Genus. <i>Frontiers in Microbiology</i> , 2016 , 7, 1874	5.7	37
65	Population genomics of the symbiotic plasmids of sympatric nitrogen-fixing <i>Rhizobium</i> species associated with <i>Phaseolus vulgaris</i> . <i>Environmental Microbiology</i> , 2016 , 18, 2660-76	5.2	34
64	A Small Number of Phylogenetically Distinct Clonal Complexes Dominate a Coastal <i>Vibrio cholerae</i> Population. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 5576-86	4.8	19
63	Oysters and <i>Vibrios</i> as a Model for Disease Dynamics in Wild Animals. <i>Trends in Microbiology</i> , 2016 , 24, 568-580	12.4	71
62	A genomic comparison of 13 symbiotic <i>Vibrio fischeri</i> isolates from the perspective of their host source and colonization behavior. <i>ISME Journal</i> , 2016 , 10, 2907-2917	11.9	40
61	Eco-Evolutionary Dynamics of Episomes among Ecologically Cohesive Bacterial Populations. <i>MBio</i> , 2015 , 6, e00552-15	7.8	18
60	Endosymbionts escape dead hydrothermal vent tubeworms to enrich the free-living population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 11300-5	11.5	39
59	Microbial Speciation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2015 , 7, a018143	10.2	39

58	Microbial taxonomy in the post-genomic era: rebuilding from scratch?. <i>Archives of Microbiology</i> , 2015 , 197, 359-70	3	78
57	Explaining microbial genomic diversity in light of evolutionary ecology. <i>Nature Reviews Microbiology</i> , 2014 , 12, 263-73	22.2	231
56	Ordering microbial diversity into ecologically and genetically cohesive units. <i>Trends in Microbiology</i> , 2014 , 22, 235-47	12.4	120
55	Competition-dispersal tradeoff ecologically differentiates recently speciated marine bacterioplankton populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 5622-7	11.5	117
54	Comparative biochemical characterization of three exolytic oligoalginate lyases from <i>Vibrio splendidus</i> reveals complementary substrate scope, temperature, and pH adaptations. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 4207-14	4.8	68
53	<i>Vibrio metoecus</i> sp. nov., a close relative of <i>Vibrio cholerae</i> isolated from coastal brackish ponds and clinical specimens. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014 , 64, 3208-3214	3.2	24
52	Associations and dynamics of Vibrionaceae in the environment, from the genus to the population level. <i>Frontiers in Microbiology</i> , 2014 , 5, 38	5.7	208
51	Comparative genomics of pathogenic lineages of <i>Vibrio nigripulchritudo</i> identifies virulence-associated traits. <i>ISME Journal</i> , 2013 , 7, 1985-96	11.9	22
50	Reproducibility of Vibrionaceae population structure in coastal bacterioplankton. <i>ISME Journal</i> , 2013 , 7, 509-19	11.9	45
49	Horizontal gene transfer and the evolution of bacterial and archaeal population structure. <i>Trends in Genetics</i> , 2013 , 29, 170-5	8.5	273
48	Public good dynamics drive evolution of iron acquisition strategies in natural bacterioplankton populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 20059-64	11.5	213
47	Population genomics of early events in the ecological differentiation of bacteria. <i>Science</i> , 2012 , 336, 48-51	33.3	366
46	Ecological populations of bacteria act as socially cohesive units of antibiotic production and resistance. <i>Science</i> , 2012 , 337, 1228-31	33.3	202
45	Shape and evolution of the fundamental niche in marine <i>Vibrio</i> . <i>ISME Journal</i> , 2012 , 6, 2168-77	11.9	21
44	High frequency of a novel filamentous phage, VCY ϕ within an environmental <i>Vibrio cholerae</i> population. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 28-33	4.8	21
43	A simple and efficient method for concentration of ocean viruses by chemical flocculation. <i>Environmental Microbiology Reports</i> , 2011 , 3, 195-202	3.7	176
42	A simple and efficient method for concentration of ocean viruses by chemical flocculation. <i>Environmental Microbiology Reports</i> , 2011 , 3, 809-809	3.7	5
41	Metapopulation structure of Vibrionaceae among coastal marine invertebrates. <i>Environmental Microbiology</i> , 2011 , 13, 265-275	5.2	65

40	Merging taxonomy with ecological population prediction in a case study of Vibrionaceae. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 7195-206	4.8	42
39	DNA phosphorothioation is widespread and quantized in bacterial genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 2963-8	11.5	113
38	Diversity of active marine picoeukaryotes in the Eastern Mediterranean Sea unveiled using photosystem-II psbA transcripts. <i>ISME Journal</i> , 2010 , 4, 1044-52	11.9	38
37	O-antigen diversity and lateral transfer of the wbe region among <i>Vibrio splendidus</i> isolates. <i>Environmental Microbiology</i> , 2010 , 12, 2977-87	5.2	24
36	Genome sequence of <i>Vibrio splendidus</i> : an abundant planctonic marine species with a large genotypic diversity. <i>Environmental Microbiology</i> , 2009 , 11, 1959-70	5.2	88
35	The bacterial species challenge: making sense of genetic and ecological diversity. <i>Science</i> , 2009 , 323, 741-6	33.3	322
34	Resource partitioning and sympatric differentiation among closely related bacterioplankton. <i>Science</i> , 2008 , 320, 1081-5	33.3	389
33	Rapid chemotactic response enables marine bacteria to exploit ephemeral microscale nutrient patches. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 4209-14	11.5	267
32	Conservation of the chitin utilization pathway in the Vibrionaceae. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 44-51	4.8	149
31	Adaptation and spectral tuning in divergent marine proteorhodopsins from the eastern Mediterranean and the Sargasso Seas. <i>ISME Journal</i> , 2007 , 1, 48-55	11.9	63
30	Accurately quantifying low-abundant targets amid similar sequences by revealing hidden correlations in oligonucleotide microarray data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 13629-34	11.5	31
29	Extensive variation in intracellular symbiont community composition among members of a single population of the wood-boring bivalve <i>Lyrodus pedicellatus</i> (Bivalvia: Teredinidae). <i>Applied and Environmental Microbiology</i> , 2006 , 72, 412-7	4.8	33
28	Colonization dynamics of altered Schaedler flora is influenced by gender, aging, and <i>Helicobacter hepaticus</i> infection in the intestines of Swiss Webster mice. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 5100-3	4.8	47
27	Evaluation of 23S rRNA PCR primers for use in phylogenetic studies of bacterial diversity. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 2221-5	4.8	104
26	Patterns and mechanisms of genetic and phenotypic differentiation in marine microbes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006 , 361, 2009-21	5.8	145
25	Genotypic diversity within a natural coastal bacterioplankton population. <i>Science</i> , 2005 , 307, 1311-3	33.3	288
24	PCR-induced sequence artifacts and bias: insights from comparison of two 16S rRNA clone libraries constructed from the same sample. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 8966-9	4.8	436
23	Binding of harvested bacterial exopolymers to the surface of calcite. <i>Environmental Science & Technology</i> , 2005 , 39, 8770-5	10.3	40

22	Illuminating reactive microbial transport in saturated porous media: demonstration of a visualization method and conceptual transport model. <i>Journal of Contaminant Hydrology</i> , 2005 , 77, 233-45	4.9	22
21	Effects of temperature and salinity on <i>Vibrio vulnificus</i> population dynamics as assessed by quantitative PCR. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 5469-76	4.8	138
20	Spatial distribution and stability of the eight microbial species of the altered schaedler flora in the mouse gastrointestinal tract. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 2791-800	4.8	98
19	Diversity and dynamics of a north atlantic coastal <i>Vibrio</i> community. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 4103-10	4.8	224
18	Divergence and redundancy of 16S rRNA sequences in genomes with multiple <i>rrn</i> operons. <i>Journal of Bacteriology</i> , 2004 , 186, 2629-35	3.5	457
17	High overall diversity and dominance of microdiverse relationships in salt marsh sulphate-reducing bacteria. <i>Environmental Microbiology</i> , 2004 , 6, 686-98	5.2	75
16	Fine-scale phylogenetic architecture of a complex bacterial community. <i>Nature</i> , 2004 , 430, 551-4	50.4	407
15	A(r)Ray of hope in analysis of the function and diversity of microbial communities. <i>Biological Bulletin</i> , 2003 , 204, 196-9	1.5	16
14	Solar disinfection (SODIS): simulation of solar radiation for global assessment and application for point-of-use water treatment in Haiti. <i>Water Research</i> , 2003 , 37, 47-54	12.5	82
13	Heteroduplexes in mixed-template amplifications: formation, consequence and elimination by reconditioning PCR. <i>Nucleic Acids Research</i> , 2002 , 30, 2083-8	20.1	354
12	Sequencing-independent method to generate oligonucleotide probes targeting a variable region in bacterial 16S rRNA by PCR with detachable primers. <i>Applied and Environmental Microbiology</i> , 2002 , 68, 6077-86	4.8	28
11	Cell Density Dependent Reduction Kinetics of Hexavalent Uranium by <i>Shewanella oneidensis</i> . <i>Materials Research Society Symposia Proceedings</i> , 2002 , 757, 113.12.1		
10	Rapid and simple method for the most-probable-number estimation of arsenic-reducing bacteria. <i>Applied and Environmental Microbiology</i> , 2001 , 67, 3168-73	4.8	34
9	Combination of competitive quantitative PCR and constant-denaturant capillary electrophoresis for high-resolution detection and enumeration of microbial cells. <i>Applied and Environmental Microbiology</i> , 2001 , 67, 3897-903	4.8	22
8	Triploblastic relationships with emphasis on the acoelomates and the position of Gnathostomulida, Cycliophora, Plathelminthes, and Chaetognatha: a combined approach of 18S rDNA sequences and morphology. <i>Systematic Biology</i> , 2000 , 49, 539-62	8.4	316
7	Diversity and heterogeneity of epibiotic bacterial communities on the marine nematode <i>Eubostrichus diana</i> e. <i>Applied and Environmental Microbiology</i> , 1999 , 65, 4271-5	4.8	44
6	Trophic ecology of massive shrimp aggregations at a Mid-Atlantic Ridge hydrothermal vent site. <i>Limnology and Oceanography</i> , 1998 , 43, 1631-1638	4.8	75
5	Bias in template-to-product ratios in multitemplate PCR. <i>Applied and Environmental Microbiology</i> , 1998 , 64, 3724-30	4.8	1017

4	Two new <i>Mycobacterium</i> strains and their role in toluene degradation in a contaminated stream. <i>Applied and Environmental Microbiology</i> , 1998 , 64, 1715-20	4.8	35
3	Chemoautotrophic, sulfur-oxidizing symbiotic bacteria on marine nematodes: Morphological and biochemical characterization. <i>Microbial Ecology</i> , 1992 , 24, 313-29	4.4	70
2	Dynamics of <i>Vibrio</i> Populations and Their Role in Environmental Nutrient Cycling 190-203		33
1	Resolving the structure of phage-bacteria interactions in the context of natural diversity		1