

Martin F Polz

List of Publications by Year in descending order

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Version: 2024-02-01

111
papers

14,658
citations

31902

53
h-index

24915

109
g-index

113
all docs

113
docs citations

113
times ranked

15402
citing authors

#	ARTICLE	IF	CITATIONS
1	Bias in Template-to-Product Ratios in Multitemplate PCR. <i>Applied and Environmental Microbiology</i> , 1998, 64, 3724-3730.	1.4	1,220
2	Function and functional redundancy in microbial systems. <i>Nature Ecology and Evolution</i> , 2018, 2, 936-943.	3.4	912
3	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, 8966-8969.	1.4	522
4	Divergence and Redundancy of 16S rRNA Sequences in Genomes with Multiple <i>rrn</i> Operons. <i>Journal of Bacteriology</i> , 2004, 186, 2629-2635.	1.0	520
5	Population Genomics of Early Events in the Ecological Differentiation of Bacteria. <i>Science</i> , 2012, 336, 48-51.	6.0	484
6	Fine-scale phylogenetic architecture of a complex bacterial community. <i>Nature</i> , 2004, 430, 551-554.	13.7	475
7	Resource Partitioning and Sympatric Differentiation Among Closely Related Bacterioplankton. <i>Science</i> , 2008, 320, 1081-1085.	6.0	472
8	Heteroduplexes in mixed-template amplifications: formation, consequence and elimination by 'reconditioning PCR'. <i>Nucleic Acids Research</i> , 2002, 30, 2083-2088.	6.5	409
9	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, 539-562.	2.7	381
10	The Bacterial Species Challenge: Making Sense of Genetic and Ecological Diversity. <i>Science</i> , 2009, 323, 741-746.	6.0	381
11	Horizontal gene transfer and the evolution of bacterial and archaeal population structure. <i>Trends in Genetics</i> , 2013, 29, 170-175.	2.9	364
12	Microbial interactions lead to rapid micro-scale successions on model marine particles. <i>Nature Communications</i> , 2016, 7, 11965.	5.8	353
13	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, 4209-4214.	3.3	348
14	Genotypic Diversity Within a Natural Coastal Bacterioplankton Population. <i>Science</i> , 2005, 307, 1311-1313.	6.0	331
15	Associations and dynamics of Vibrionaceae in the environment, from the genus to the population level. <i>Frontiers in Microbiology</i> , 2014, 5, 38.	1.5	313
16	Diversity and Dynamics of a North Atlantic Coastal <i>Vibrio</i> Community. <i>Applied and Environmental Microbiology</i> , 2004, 70, 4103-4110.	1.4	310
17	Explaining microbial genomic diversity in light of evolutionary ecology. <i>Nature Reviews Microbiology</i> , 2014, 12, 263-273.	13.6	310
18	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, 20059-20064.	3.3	294

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19	Ecological Populations of Bacteria Act as Socially Cohesive Units of Antibiotic Production and Resistance. <i>Science</i> , 2012, 337, 1228-1231.	6.0	270
20	A simple and efficient method for concentration of ocean viruses by chemical flocculation. <i>Environmental Microbiology Reports</i> , 2011, 3, 195-202.	1.0	245
21	Conservation of the Chitin Utilization Pathway in the <i>Vibrionaceae</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 44-51.	1.4	211
22	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.	3.3	194
23	Competitionâ€“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, 5622-5627.	3.3	187
24	Verrucomicrobia use hundreds of enzymes to digest the algal polysaccharide fucoidan. <i>Nature Microbiology</i> , 2020, 5, 1026-1039.	5.9	182
25	Patterns and mechanisms of genetic and phenotypic differentiation in marine microbes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 2009-2021.	1.8	176
26	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, 5469-5476.	1.4	175
27	Ordering microbial diversity into ecologically and genetically cohesive units. <i>Trends in Microbiology</i> , 2014, 22, 235-247.	3.5	166
28	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, .	3.3	161
29	A major lineage of non-tailed dsDNA viruses as unrecognized killers of marine bacteria. <i>Nature</i> , 2018, 554, 118-122.	13.7	160
30	Microbial taxonomy in the post-genomic era: Rebuilding from scratch?. <i>Archives of Microbiology</i> , 2015, 197, 359-370.	1.0	144
31	Adaptive radiation by waves of gene transfer leads to fine-scale resource partitioning in marine microbes. <i>Nature Communications</i> , 2016, 7, 12860.	5.8	140
32	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, 2963-2968.	3.3	137
33	Evaluation of 23S rRNA PCR Primers for Use in Phylogenetic Studies of Bacterial Diversity. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2221-2225.	1.4	124
34	Oysters and <i>Vibrios</i> as a Model for Disease Dynamics in Wild Animals. <i>Trends in Microbiology</i> , 2016, 24, 568-580.	3.5	124
35	High resolution time series reveals cohesive but short-lived communities in coastal plankton. <i>Nature Communications</i> , 2018, 9, 266.	5.8	122
36	A Reverse Ecology Approach Based on a Biological Definition of Microbial Populations. <i>Cell</i> , 2019, 178, 820-834.e14.	13.5	118

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37	<i>Vibrio crassostreae</i> , a benign oyster colonizer turned into a pathogen after plasmid acquisition. ISME Journal, 2017, 11, 1043-1052.	4.4	116
38	Spatial Distribution and Stability of the Eight Microbial Species of the Altered Schaedler Flora in the Mouse Gastrointestinal Tract. Applied and Environmental Microbiology, 2004, 70, 2791-2800.	1.4	115
39	Solar disinfection (SODIS): simulation of solar radiation for global assessment and application for point-of-use water treatment in Haiti. Water Research, 2003, 37, 47-54.	5.3	103
40	Comparative Biochemical Characterization of Three Exolytic Oligoalginate Lyases from <i>Vibrio splendidus</i> Reveals Complementary Substrate Scope, Temperature, and pH Adaptations. Applied and Environmental Microbiology, 2014, 80, 4207-4214.	1.4	103
41	Genome sequence of <i>Vibrio splendidus</i> : an abundant planctonic marine species with a large genotypic diversity. Environmental Microbiology, 2009, 11, 1959-1970.	1.8	98
42	Rapid evolutionary turnover of mobile genetic elements drives bacterial resistance to phages. Science, 2021, 374, 488-492.	6.0	96
43	Trophic ecology of massive shrimp aggregations at a Mid-Atlantic Ridge hydrothermal vent site. Limnology and Oceanography, 1998, 43, 1631-1638.	1.6	95
44	Widespread distribution of prophage-encoded virulence factors in marine <i>Vibrio</i> communities. Scientific Reports, 2018, 8, 9973.	1.6	93
45	Chemoautotrophic, sulfur-oxidizing symbiotic bacteria on marine nematodes: Morphological and biochemical characterization. Microbial Ecology, 1992, 24, 313-329.	1.4	85
46	High overall diversity and dominance of microdiverse relationships in salt marsh sulphate-reducing bacteria. Environmental Microbiology, 2004, 6, 686-698.	1.8	84
47	Metapopulation structure of <i>Vibrionaceae</i> among coastal marine invertebrates. Environmental Microbiology, 2011, 13, 265-275.	1.8	76
48	Accurate Quantification of Laminarin in Marine Organic Matter with Enzymes from Marine Microbes. Applied and Environmental Microbiology, 2017, 83, .	1.4	75
49	Population genomics of the symbiotic plasmids of sympatric nitrogen-fixing <i>Rhizobium</i> species associated with <i>Phaseolus vulgaris</i> . Environmental Microbiology, 2016, 18, 2660-2676.	1.8	72
50	Evidence for Ecological Flexibility in the Cosmopolitan Genus <i>Curtobacterium</i> . Frontiers in Microbiology, 2016, 7, 1874.	1.5	66
51	Adaptation and spectral tuning in divergent marine proteorhodopsins from the eastern Mediterranean and the Sargasso Seas. ISME Journal, 2007, 1, 48-55.	4.4	65
52	Microbial Speciation. Cold Spring Harbor Perspectives in Biology, 2015, 7, a018143.	2.3	63
53	Endosymbionts escape dead hydrothermal vent tubeworms to enrich the free-living population. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11300-11305.	3.3	58
54	Phage-host coevolution in natural populations. Nature Microbiology, 2022, 7, 1075-1086.	5.9	58

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55	Diversity and Heterogeneity of Epibiotic Bacterial Communities on the Marine Nematode <i>Eubostrichus diana</i> . Applied and Environmental Microbiology, 1999, 65, 4271-4275.	1.4	57
56	Dynamics of <i>Vibrio</i> Populations and Their Role in Environmental Nutrient Cycling. , 0, , 190-203.		55
57	Interactions in self-assembled microbial communities saturate with diversity. ISME Journal, 2019, 13, 1602-1617.	4.4	54
58	Inter-individual variability in copepod microbiomes reveals bacterial networks linked to host physiology. ISME Journal, 2018, 12, 2103-2113.	4.4	52
59	Colonization Dynamics of Altered Schaedler Flora Is Influenced by Gender, Aging, and Helicobacter hepaticus Infection in the Intestines of Swiss Webster Mice. Applied and Environmental Microbiology, 2006, 72, 5100-5103.	1.4	50
60	Reproducibility of <i>Vibrionaceae</i> population structure in coastal bacterioplankton. ISME Journal, 2013, 7, 509-519.	4.4	50
61	Merging Taxonomy with Ecological Population Prediction in a Case Study of Vibrionaceae. Applied and Environmental Microbiology, 2011, 77, 7195-7206.	1.4	49
62	A genomic comparison of 13 symbiotic <i>Vibrio fischeri</i> isolates from the perspective of their host source and colonization behavior. ISME Journal, 2016, 10, 2907-2917.	4.4	49
63	Prokaryotic viruses impact functional microorganisms in nutrient removal and carbon cycle in wastewater treatment plants. Nature Communications, 2021, 12, 5398.	5.8	49
64	Resolving the structure of phage-bacteria interactions in the context of natural diversity. Nature Communications, 2022, 13, 372.	5.8	48
65	Direct single-cell biomass estimates for marine bacteria via Archimedes™ principle. ISME Journal, 2017, 11, 825-828.	4.4	47
66	Two New <i>Mycobacterium</i> Strains and Their Role in Toluene Degradation in a Contaminated Stream. Applied and Environmental Microbiology, 1998, 64, 1715-1720.	1.4	47
67	Sequencing-Independent Method To Generate Oligonucleotide Probes Targeting a Variable Region in Bacterial 16S rRNA by PCR with Detachable Primers. Applied and Environmental Microbiology, 2002, 68, 6077-6086.	1.4	45
68	Bacterial evolution: Genomics of metabolic trade-offs. Nature Microbiology, 2016, 1, 16181.	5.9	45
69	Streamlining standard bacteriophage methods for higher throughput. MethodsX, 2018, 5, 159-172.	0.7	45
70	Binding of Harvested Bacterial Exopolymers to the Surface of Calcite. Environmental Science & Technology, 2005, 39, 8770-8775.	4.6	43
71	Diversity of active marine picoeukaryotes in the Eastern Mediterranean Sea unveiled using photosystem-II <i>psbA</i> transcripts. ISME Journal, 2010, 4, 1044-1052.	4.4	43
72	Rapid and Simple Method for the Most-Probable-Number Estimation of Arsenic-Reducing Bacteria. Applied and Environmental Microbiology, 2001, 67, 3168-3173.	1.4	40

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73	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, 412-417.	1.4	39
74	<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.	0.8	39
75	Ancestral gene acquisition as the key to virulence potential in environmental <i>Vibrio</i> populations. <i>ISME Journal</i> , 2018, 12, 2954-2966.	4.4	37
76	Successional dynamics and alternative stable states in a saline activated sludge microbial community over 9 years. <i>Microbiome</i> , 2021, 9, 199.	4.9	33
77	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, 13629-13634.	3.3	32
78	Degradation of host translational machinery drives tRNA acquisition in viruses. <i>Cell Systems</i> , 2021, 12, 771-779.e5.	2.9	32
79	Comparative genomics of pathogenic lineages of <i>Vibrio nigripulchritudo</i> identifies virulence-associated traits. <i>ISME Journal</i> , 2013, 7, 1985-1996.	4.4	30
80	Endemicity of the cosmopolitan mesophilic chemolithoautotroph <i>Sulfurimonas</i> at deep-sea hydrothermal vents. <i>ISME Journal</i> , 2017, 11, 909-919.	4.4	30
81	Polyclonal symbiont populations in hydrothermal vent tubeworms and the environment. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20181281.	1.2	30
82	Antigen diversity and lateral transfer of the <i>wbe</i> region among <i>Vibrio splendidus</i> isolates. <i>Environmental Microbiology</i> , 2010, 12, 2977-2987.	1.8	27
83	High Frequency of a Novel Filamentous Phage, VCY1, within an Environmental <i>Vibrio cholerae</i> Population. <i>Applied and Environmental Microbiology</i> , 2012, 78, 28-33.	1.4	27
84	How can microbial population genomics inform community ecology?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190253.	1.8	27
85	Shape and evolution of the fundamental niche in marine <i>Vibrio</i> . <i>ISME Journal</i> , 2012, 6, 2168-2177.	4.4	26
86	A Mobile Element in <i>mutS</i> Drives Hypermutation in a Marine <i>Vibrio</i> . <i>MBio</i> , 2017, 8, .	1.8	26
87	Redox-informed models of global biogeochemical cycles. <i>Nature Communications</i> , 2020, 11, 5680.	5.8	26
88	Viruses of the Nahant Collection, characterization of 251 marine Vibrionaceae viruses. <i>Scientific Data</i> , 2018, 5, 180114.	2.4	26
89	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, 233-245.	1.6	25
90	Eco-Evolutionary Dynamics of Episomes among Ecologically Cohesive Bacterial Populations. <i>MBio</i> , 2015, 6, e00552-15.	1.8	25

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91	A Small Number of Phylogenetically Distinct Clonal Complexes Dominate a Coastal <i>Vibrio cholerae</i> Population. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5576-5586.	1.4	24
92	Evolution of a Vegetarian <i>Vibrio</i> : Metabolic Specialization of <i>Vibrio breoganii</i> to Macroalgal Substrates. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	24
93	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, 3897-3903.	1.4	23
94	Summer phyto- and bacterioplankton communities during low and high productivity scenarios in the Western Antarctic Peninsula. <i>Polar Biology</i> , 2019, 42, 159-169.	0.5	23
95	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.	1.2	22
96	Diarrhoeal events can trigger long-term <i>Clostridium difficile</i> colonization with recurrent blooms. <i>Nature Microbiology</i> , 2020, 5, 642-650.	5.9	21
97	Maintenance of Sympatric and Allopatric Populations in Free-Living Terrestrial Bacteria. <i>MBio</i> , 2019, 10, .	1.8	19
98	A(r)Ray of Hope in Analysis of the Function and Diversity of Microbial Communities. <i>Biological Bulletin</i> , 2003, 204, 196-199.	0.7	18
99	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.	1.6	18
100	Bacterial community structure in a sympagic habitat expanding with global warming: brackish ice brine at 85°N. <i>ISME Journal</i> , 2019, 13, 316-333.	4.4	18
101	Using Colonization Assays and Comparative Genomics To Discover Symbiosis Behaviors and Factors in <i>Vibrio fischeri</i> . <i>MBio</i> , 2020, 11, .	1.8	17
102	Genomic Features for Desiccation Tolerance and Sugar Biosynthesis in the Extremophile <i>Gloeocapsopsis</i> sp. UTEX B3054. <i>Frontiers in Microbiology</i> , 2019, 10, 950.	1.5	15
103	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.	1.8	15
104	Microbiome assembly for sulfonamide subsistence and the transfer of genetic determinants. <i>ISME Journal</i> , 2021, 15, 2817-2829.	4.4	10
105	Coastal Bacterial Community Response to Glacier Melting in the Western Antarctic Peninsula. <i>Microorganisms</i> , 2021, 9, 88.	1.6	10
106	Natural resource landscapes of a marine bacterium reveal distinct fitness-determining genes across the genome. <i>Environmental Microbiology</i> , 2017, 19, 2422-2433.	1.8	8
107	A simple and efficient method for concentration of ocean viruses by chemical flocculation. <i>Environmental Microbiology Reports</i> , 2011, 3, 809-809.	1.0	6
108	The genetic law of the minimum. <i>Science</i> , 2020, 370, 655-656.	6.0	2

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109	Reply to Partridge et al.: Complementary bioinformatics and experimental approaches to investigate the transfer of AMR genes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	2
110	Cell Density Dependent Reduction Kinetics of Hexavalent Uranium by <i>Shewanella oneidensis</i> . Materials Research Society Symposia Proceedings, 2002, 757, II3.12.1.	0.1	1
111	Reply to Shaw: Challenges for enrichment analysis of AMR gene-bearing plasmids. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2104557118.	3.3	0