Martin F Polz

List of Publications by Citations

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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	Bias in template-to-product ratios in multitemplate PCR. *Applied and Environmental Microbiology*, **1998**, 64, 3724-30	4.8	1017
110	Divergence and redundancy of 16S rRNA sequences in genomes with multiple rrn operons. *Journal of Bacteriology*, **2004**, 186, 2629-35	3.5	457
109	PCR-induced sequence artifacts and bias: insights from comparison of two 16S rRNA clone libraries constructed from the same sample. *Applied and Environmental Microbiology*, **2005**, 71, 8966-9	4.8	436
108	Function and functional redundancy in microbial systems. *Nature Ecology and Evolution*, **2018**, 2, 936-943	12.3	423
107	Fine-scale phylogenetic architecture of a complex bacterial community. *Nature*, **2004**, 430, 551-4	50.4	407
106	Resource partitioning and sympatric differentiation among closely related bacterioplankton. *Science*, **2008**, 320, 1081-5	33.3	389
105	Population genomics of early events in the ecological differentiation of bacteria. *Science*, **2012**, 336, 48-51	33.3	366
104	Heteroduplexes in mixed-template amplifications: formation, consequence and elimination by Ureconditioning PCRU *Nucleic Acids Research*, **2002**, 30, 2083-8	20.1	354
103	The bacterial species challenge: making sense of genetic and ecological diversity. *Science*, **2009**, 323, 741-6	33.3	322
102	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. *Systematic Biology*, **2000**, 49, 539-62	8.4	316
101	Genotypic diversity within a natural coastal bacterioplankton population. *Science*, **2005**, 307, 1311-3	33.3	288
100	Horizontal gene transfer and the evolution of bacterial and archaeal population structure. *Trends in Genetics*, **2013**, 29, 170-5	8.5	273
99	Rapid chemotactic response enables marine bacteria to exploit ephemeral microscale nutrient patches. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 4209-14	11.5	267
98	Explaining microbial genomic diversity in light of evolutionary ecology. *Nature Reviews Microbiology* , **2014**, 12, 263-73	22.2	231
97	Diversity and dynamics of a north atlantic coastal Vibrio community. *Applied and Environmental Microbiology*, **2004**, 70, 4103-10	4.8	224
96	Public good dynamics drive evolution of iron acquisition strategies in natural bacterioplankton populations. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 20059-64	11.5	213
95	Associations and dynamics of Vibrionaceae in the environment, from the genus to the population level. *Frontiers in Microbiology*, **2014**, 5, 38	5.7	208

94	Ecological populations of bacteria act as socially cohesive units of antibiotic production and resistance. *Science*, **2012**, 337, 1228-31	33.3	202
93	Microbial interactions lead to rapid micro-scale successions on model marine particles. *Nature Communications*, **2016**, 7, 11965	17.4	183
92	A simple and efficient method for concentration of ocean viruses by chemical flocculation. *Environmental Microbiology Reports*, **2011**, 3, 195-202	3.7	176
91	Conservation of the chitin utilization pathway in the Vibrionaceae. *Applied and Environmental Microbiology*, **2008**, 74, 44-51	4.8	149
90	Patterns and mechanisms of genetic and phenotypic differentiation in marine microbes. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2006**, 361, 2009-21	5.8	145
89	Effects of temperature and salinity on Vibrio vulnificus population dynamics as assessed by quantitative PCR. *Applied and Environmental Microbiology*, **2004**, 70, 5469-76	4.8	138
88	Microbial community assembly and evolution in subseafloor sediment. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 2940-2945	11.5	120
87	Ordering microbial diversity into ecologically and genetically cohesive units. *Trends in Microbiology*, **2014**, 22, 235-47	12.4	120
86	Competition-dispersal tradeoff ecologically differentiates recently speciated marine bacterioplankton populations. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 5622-7	11.5	117
85	DNA phosphorothioation is widespread and quantized in bacterial genomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 2963-8	11.5	113
84	A major lineage of non-tailed dsDNA viruses as unrecognized killers of marine bacteria. *Nature*, **2018**, 554, 118-122	50.4	109
83	Evaluation of 23S rRNA PCR primers for use in phylogenetic studies of bacterial diversity. *Applied and Environmental Microbiology*, **2006**, 72, 2221-5	4.8	104
82	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, 2791-800	4.8	98
81	Genome sequence of Vibrio splendidus: an abundant planctonic marine species with a large genotypic diversity. *Environmental Microbiology*, **2009**, 11, 1959-70	5.2	88
80	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	12.5	82
79	Adaptive radiation by waves of gene transfer leads to fine-scale resource partitioning in marine microbes. *Nature Communications*, **2016**, 7, 12860	17.4	81
78	Microbial taxonomy in the post-genomic era: rebuilding from scratch?. *Archives of Microbiology*, **2015**, 197, 359-70	3	78
77	High overall diversity and dominance of microdiverse relationships in salt marsh sulphate-reducing bacteria. *Environmental Microbiology*, **2004**, 6, 686-98	5.2	75

76	Trophic ecology of massive shrimp aggregations at a Mid-Atlantic Ridge hydrothermal vent site. *Limnology and Oceanography*, **1998**, 43, 1631-1638	4.8	75
75	Oysters and Vibrios as a Model for Disease Dynamics in Wild Animals. *Trends in Microbiology*, **2016**, 24, 568-580	12.4	71
74	Chemoautotrophic, sulfur-oxidizing symbiotic bacteria on marine nematodes: Morphological and biochemical characterization. *Microbial Ecology*, **1992**, 24, 313-29	4.4	70
73	Vibrio crassostreae, a benign oyster colonizer turned into a pathogen after plasmid acquisition. *ISME Journal*, **2017**, 11, 1043-1052	11.9	69
72	Comparative biochemical characterization of three exolytic oligoalginate lyases from Vibrio splendidus reveals complementary substrate scope, temperature, and pH adaptations. *Applied and Environmental Microbiology*, **2014**, 80, 4207-14	4.8	68
71	Metapopulation structure of Vibrionaceae among coastal marine invertebrates. *Environmental Microbiology*, **2011**, 13, 265-275	5.2	65
70	Adaptation and spectral tuning in divergent marine proteorhodopsins from the eastern Mediterranean and the Sargasso Seas. *ISME Journal*, **2007**, 1, 48-55	11.9	63
69	High resolution time series reveals cohesive but short-lived communities in coastal plankton. *Nature Communications*, **2018**, 9, 266	17.4	62
68	A Reverse Ecology Approach Based on a Biological Definition of Microbial Populations. *Cell*, **2019**, 178, 820-834.e14	56.2	60
67	Verrucomicrobia use hundreds of enzymes to digest the algal polysaccharide fucoidan. *Nature Microbiology*, **2020**, 5, 1026-1039	26.6	57
66	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, 5100-3	4.8	47
65	Widespread distribution of prophage-encoded virulence factors in marine Vibrio communities. *Scientific Reports*, **2018**, 8, 9973	4.9	47
64	Accurate Quantification of Laminarin in Marine Organic Matter with Enzymes from Marine Microbes. *Applied and Environmental Microbiology*, **2017**, 83,	4.8	45
63	Reproducibility of Vibrionaceae population structure in coastal bacterioplankton. *ISME Journal*, **2013**, 7, 509-19	11.9	45
62	Diversity and heterogeneity of epibiotic bacterial communities on the marine nematode Eubostrichus dianae. *Applied and Environmental Microbiology*, **1999**, 65, 4271-5	4.8	44
61	Merging taxonomy with ecological population prediction in a case study of Vibrionaceae. *Applied and Environmental Microbiology*, **2011**, 77, 7195-206	4.8	42
60	Binding of harvested bacterial exopolymers to the surface of calcite. *Environmental Science & Technology*, **2005**, 39, 8770-5	10.3	40
59	A genomic comparison of 13 symbiotic Vibrio fischeri isolates from the perspective of their host source and colonization behavior. *ISME Journal*, **2016**, 10, 2907-2917	11.9	40

58	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, 11300-5	11.5	39
57	Microbial Speciation. *Cold Spring Harbor Perspectives in Biology*, **2015**, 7, a018143	10.2	39
56	Conjugative plasmids interact with insertion sequences to shape the horizontal transfer of antimicrobial resistance genes. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	39
55	Diversity of active marine picoeukaryotes in the Eastern Mediterranean Sea unveiled using photosystem-II psbA transcripts. *ISME Journal*, **2010**, 4, 1044-52	11.9	38
54	Evidence for Ecological Flexibility in the Cosmopolitan Genus. *Frontiers in Microbiology*, **2016**, 7, 1874	5.7	37
53	Two new Mycobacterium strains and their role in toluene degradation in a contaminated stream. *Applied and Environmental Microbiology*, **1998**, 64, 1715-20	4.8	35
52	Rapid and simple method for the most-probable-number estimation of arsenic-reducing bacteria. *Applied and Environmental Microbiology*, **2001**, 67, 3168-73	4.8	34
51	Population genomics of the symbiotic plasmids of sympatric nitrogen-fixing Rhizobium species associated with Phaseolus vulgaris. *Environmental Microbiology*, **2016**, 18, 2660-76	5.2	34
50	Direct single-cell biomass estimates for marine bacteria via ArchimedesUprinciple. *ISME Journal*, **2017**, 11, 825-828	11.9	33
49	Extensive variation in intracellular symbiont community composition among members of a single population of the wood-boring bivalve Lyrodus pedicellatus (Bivalvia: Teredinidae). *Applied and Environmental Microbiology*, **2006**, 72, 412-7	4.8	33
48	Dynamics of Vibrio Populations and Their Role in Environmental Nutrient Cycling190-203		33
47	Accurately quantifying low-abundant targets amid similar sequences by revealing hidden correlations in oligonucleotide microarray data. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 13629-34	11.5	31
46	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, 6077-86	4.8	28
45	Inter-individual variability in copepod microbiomes reveals bacterial networks linked to host physiology. *ISME Journal*, **2018**, 12, 2103-2113	11.9	27
44	Interactions in self-assembled microbial communities saturate with diversity. *ISME Journal*, **2019**, 13, 1602-1617	11.9	26
43	Vibrio metoecus sp. nov., a close relative of Vibrio cholerae isolated from coastal brackish ponds and clinical specimens. *International Journal of Systematic and Evolutionary Microbiology*, **2014**, 64, 3208-3214	3.2	24
42	O-antigen diversity and lateral transfer of the wbe region among Vibrio splendidus isolates. *Environmental Microbiology*, **2010**, 12, 2977-87	5.2	24
41	Bacterial evolution: Genomics of metabolic trade-offs. *Nature Microbiology*, **2016**, 1, 16181	26.6	23

40	Streamlining standard bacteriophage methods for higher throughput. *MethodsX*, **2018**, 5, 159-172	1.9	22
39	Comparative genomics of pathogenic lineages of Vibrio nigripulchritudo identifies virulence-associated traits. *ISME Journal*, **2013**, 7, 1985-96	11.9	22
38	Illuminating reactive microbial transport in saturated porous media: demonstration of a visualization method and conceptual transport model. *Journal of Contaminant Hydrology*, **2005**, 77, 233-45	3.9	22
37	Combination of competitive quantitative PCR and constant-denaturant capillary electrophoresis for high-resolution detection and enumeration of microbial cells. *Applied and Environmental Microbiology*, **2001**, 67, 3897-903	4.8	22
36	Shape and evolution of the fundamental niche in marine Vibrio. *ISME Journal*, **2012**, 6, 2168-77	11.9	21
35	High frequency of a novel filamentous phage, VCY within an environmental Vibrio cholerae population. *Applied and Environmental Microbiology*, **2012**, 78, 28-33	4.8	21
34	Ancestral gene acquisition as the key to virulence potential in environmental Vibrio populations. *ISME Journal*, **2018**, 12, 2954-2966	11.9	20
33	Endemicity of the cosmopolitan mesophilic chemolithoautotroph Sulfurimonas at deep-sea hydrothermal vents. *ISME Journal*, **2017**, 11, 909-919	11.9	19
32	A Small Number of Phylogenetically Distinct Clonal Complexes Dominate a Coastal Vibrio cholerae Population. *Applied and Environmental Microbiology*, **2016**, 82, 5576-86	4.8	19
31	Eco-Evolutionary Dynamics of Episomes among Ecologically Cohesive Bacterial Populations. *MBio*, **2015**, 6, e00552-15	7.8	18
30	Viruses of the Nahant Collection, characterization of 251 marine Vibrionaceae viruses. *Scientific Data*, **2018**, 5, 180114	8.2	17
29	A(r)Ray of hope in analysis of the function and diversity of microbial communities. *Biological Bulletin*, **2003**, 204, 196-9	1.5	16
28	A Mobile Element in mutS Drives Hypermutation in a Marine Vibrio. *MBio*, **2017**, 8,	7.8	14
27	How can microbial population genomics inform community ecology?. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2020**, 375, 20190253	5.8	13
26	Rapid evolutionary turnover of mobile genetic elements drives bacterial resistance to phages. *Science*, **2021**, 374, 488-492	33.3	13
25	Summer phyto- and bacterioplankton communities during low and high productivity scenarios in the Western Antarctic Peninsula. *Polar Biology*, **2019**, 42, 159-169	2	12
24	Bacterial community structure in a sympagic habitat expanding with global warming: brackish ice brine at 85-90 N. *ISME Journal*, **2019**, 13, 316-333	11.9	11
23	Exploiting fine-scale genetic and physiological variation of closely related microbes to reveal unknown enzyme functions. *Journal of Biological Chemistry*, **2017**, 292, 13056-13067	5.4	10

22	Polyclonal symbiont populations in hydrothermal vent tubeworms and the environment. *Proceedings of the Royal Society B: Biological Sciences*, **2019**, 286, 20181281	4.4	10
21	Maintenance of Sympatric and Allopatric Populations in Free-Living Terrestrial Bacteria. *MBio*, **2019** , 10,	7.8	10
20	Physiological and gene expression responses to nitrogen regimes and temperatures in Mastigocladus sp. strain CHP1, a predominant thermotolerant cyanobacterium of hot springs. *Systematic and Applied Microbiology*, **2017**, 40, 102-113	4.2	9
19	Redox-informed models of global biogeochemical cycles. *Nature Communications*, **2020**, 11, 5680	17.4	9
18	Diarrhoeal events can trigger long-term Clostridium difficile colonization with recurrent blooms. *Nature Microbiology*, **2020**, 5, 642-650	26.6	9
17	Evolution of a Vegetarian Vibrio: Metabolic Specialization of Vibrio breoganii to Macroalgal Substrates. *Journal of Bacteriology*, **2018**, 200,	3.5	9
16	Culture-independent tracking of Vibrio cholerae lineages reveals complex spatiotemporal dynamics in a natural population. *Environmental Microbiology*, **2020**, 22, 4244-4256	5.2	7
15	Using Colonization Assays and Comparative Genomics To Discover Symbiosis Behaviors and Factors in Vibrio fischeri. *MBio*, **2020**, 11,	7.8	7
14	Genomic Features for Desiccation Tolerance and Sugar Biosynthesis in the Extremophile sp. UTEX B3054. *Frontiers in Microbiology*, **2019**, 10, 950	5.7	6
13	Degradation of host translational machinery drives tRNA acquisition in viruses. *Cell Systems*, **2021**, 12, 771-779.e5	10.6	6
12	Coastal Bacterial Community Response to Glacier Melting in the Western Antarctic Peninsula. *Microorganisms*, **2021**, 9,	4.9	6
11	Natural resource landscapes of a marine bacterium reveal distinct fitness-determining genes across the genome. *Environmental Microbiology*, **2017**, 19, 2422-2433	5.2	5
10	A simple and efficient method for concentration of ocean viruses by chemical flocculation. *Environmental Microbiology Reports*, **2011**, 3, 809-809	3.7	5
9	Successional dynamics and alternative stable states in a saline activated sludge microbial community over 9 years. *Microbiome*, **2021**, 9, 199	16.6	4
8	Prokaryotic viruses impact functional microorganisms in nutrient removal and carbon cycle in wastewater treatment plants. *Nature Communications*, **2021**, 12, 5398	17.4	4
7	Resolving the structure of phage-bacteria interactions in the context of natural diversity.. *Nature Communications*, **2022**, 13, 372	17.4	3
6	Microbiome assembly for sulfonamide subsistence and the transfer of genetic determinants. *ISME Journal*, **2021**, 15, 2817-2829	11.9	2
5	The genetic law of the minimum. *Science*, **2020**, 370, 655-656	33.3	1

4	Resolving the structure of phage-bacteria interactions in the context of natural diversity	1
3	Cell Density Dependent Reduction Kinetics of Hexavalent Uranium by Shewanella oneidensis. *Materials Research Society Symposia Proceedings*, **2002**, 757, II3.12.1	
2	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,	11.5
1	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,	11.5