

# Kevin Vergin

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

5,336  
citations

236925

25  
h-index

414414

32  
g-index

32  
all docs

32  
docs citations

32  
times ranked

4576  
citing authors

#	ARTICLE	IF	CITATIONS
1	SAR11 clade dominates ocean surface bacterioplankton communities. <i>Nature</i> , 2002, 420, 806-810.	27.8	1,005
2	Cultivation of the ubiquitous SAR11 marine bacterioplankton clade. <i>Nature</i> , 2002, 418, 630-633.	27.8	871
3	Abundant SAR11 viruses in the ocean. <i>Nature</i> , 2013, 494, 357-360.	27.8	305
4	Seasonality in Ocean Microbial Communities. <i>Science</i> , 2012, 335, 671-676.	12.6	300
5	Proteorhodopsin in the ubiquitous marine bacterium SAR11. <i>Nature</i> , 2005, 438, 82-85.	27.8	293
6	Seasonal dynamics of SAR11 populations in the euphotic and mesopelagic zones of the northwestern Sargasso Sea. <i>ISME Journal</i> , 2009, 3, 283-295.	9.8	261
7	Temporal and spatial response of bacterioplankton lineages to annual convective overturn at the Bermuda Atlantic Time-series Study site. <i>Limnology and Oceanography</i> , 2005, 50, 1687-1696.	3.1	240
8	Seasonality and vertical structure of microbial communities in an ocean gyre. <i>ISME Journal</i> , 2009, 3, 1148-1163.	9.8	230
9	Unusual bacterioplankton community structure in ultra-oligotrophic Crater Lake. <i>Limnology and Oceanography</i> , 2001, 46, 557-572.	3.1	221
10	The small genome of an abundant coastal ocean methylotroph. <i>Environmental Microbiology</i> , 2008, 10, 1771-1782.	3.8	197
11	Interactions among dissolved organic carbon, microbial processes, and community structure in the mesopelagic zone of the northwestern Sargasso Sea. <i>Limnology and Oceanography</i> , 2004, 49, 1073-1083.	3.1	192
12	High-resolution SAR11 ecotype dynamics at the Bermuda Atlantic Time-series Study site by phylogenetic placement of pyrosequences. <i>ISME Journal</i> , 2013, 7, 1322-1332.	9.8	191
13	<i>Lentisphaera araneosa</i> gen. nov., sp. nov., a transparent exopolymer producing marine bacterium, and the description of a novel bacterial phylum, <i>Lentisphaerae</i> . <i>Environmental Microbiology</i> , 2004, 6, 611-621.	3.8	159
14	Phylogenetic comparisons of a coastal bacterioplankton community with its counterparts in open ocean and freshwater systems. <i>FEMS Microbiology Ecology</i> , 2000, 33, 219-232.	2.7	123
15	Phytoplankton distribution patterns in the northwestern Sargasso Sea revealed by small subunit rRNA genes from plastids. <i>ISME Journal</i> , 2012, 6, 481-492.	9.8	98
16	Spatiotemporal distributions of rare bacterioplankton populations indicate adaptive strategies in the oligotrophic ocean. <i>Aquatic Microbial Ecology</i> , 2013, 71, 1-13.	1.8	90
17	High intraspecific recombination rate in a native population of <i>Candidatus Pelagibacter ubique</i> (SAR11). <i>Environmental Microbiology</i> , 2007, 9, 2430-2440.	3.8	77
18	Polyphyletic photosynthetic reaction centre genes in oligotrophic marine Gammaproteobacteria. <i>Environmental Microbiology</i> , 2007, 9, 1456-1463.	3.8	76

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19	Bacterial community composition determined by culture-independent and -dependent methods during propane-stimulated bioremediation in trichloroethene-contaminated groundwater. <i>Environmental Microbiology</i> , 2005, 7, 165-178.	3.8	63
20	Meta-omic signatures of microbial metal and nitrogen cycling in marine oxygen minimum zones. <i>Frontiers in Microbiology</i> , 2015, 6, 998.	3.5	58
21	Genetic analysis of natural populations of the marine diazotrophic cyanobacterium <i>Trichodesmium</i> . <i>FEMS Microbiology Ecology</i> , 1999, 30, 57-65.	2.7	54
22	Biological cycling of volatile organic carbon by phytoplankton and bacterioplankton. <i>Limnology and Oceanography</i> , 2017, 62, 2650-2661.	3.1	52
23	Streamlined Method to Analyze 16S rRNA Gene Clone Libraries. <i>BioTechniques</i> , 2001, 30, 938-944.	1.8	38
24	Elemental content and stoichiometry of SAR11 chemoheterotrophic marine bacteria. <i>Limnology and Oceanography Letters</i> , 2019, 4, 44-51.	3.9	36
25	Marine bacterioplankton community turnover within seasonally hypoxic waters of a subtropical sound: <i>D</i> 's Hole, Bermuda. <i>Environmental Microbiology</i> , 2015, 17, 3481-3499.	3.8	32
26	Optofluidic Single-Cell Genome Amplification of Sub-micron Bacteria in the Ocean Subsurface. <i>Frontiers in Microbiology</i> , 2018, 9, 1152.	3.5	18
27	Genome Sequences of <i>Oceanicola granulosus</i> HTCC2516 <sup>T</sup> and <i>Oceanicola batsensis</i> HTCC2597 <sup>T</sup> . <i>Journal of Bacteriology</i> , 2010, 192, 3549-3550.	2.2	14
28	Genome Sequence of the Marine Alphaproteobacterium HTCC2150, Assigned to the <i>Roseobacter</i> Clade. <i>Journal of Bacteriology</i> , 2010, 192, 6315-6316.	2.2	10
29	Stable Isotope Probing Identifies Bacterioplankton Lineages Capable of Utilizing Dissolved Organic Matter Across a Range of Bioavailability. <i>Frontiers in Microbiology</i> , 2020, 11, 580397.	3.5	10
30	Bacterial diversity in the bottom boundary layer of the inner continental shelf of Oregon, USA. <i>Aquatic Microbial Ecology</i> , 2011, 64, 15-25.	1.8	10
31	Linkages Among Dissolved Organic Matter Export, Dissolved Metabolites, and Associated Microbial Community Structure Response in the Northwestern Sargasso Sea on a Seasonal Scale. <i>Frontiers in Microbiology</i> , 2022, 13, 833252.	3.5	10
32	Genetic analysis of natural populations of the marine diazotrophic cyanobacterium <i>Trichodesmium</i> . <i>FEMS Microbiology Ecology</i> , 1999, 30, 57-65.	2.7	2