

# Nathan A Ahlgren

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1253048/publications.pdf>

Version: 2024-02-01

25  
papers

3,490  
citations

394421

19  
h-index

610901

24  
g-index

28  
all docs

28  
docs citations

28  
times ranked

3964  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome divergence in two <i>Prochlorococcus</i> ecotypes reflects oceanic niche differentiation. <i>Nature</i> , 2003, 424, 1042-1047.	27.8	1,086
2	VirFinder: a novel k-mer based tool for identifying viral sequences from assembled metagenomic data. <i>Microbiome</i> , 2017, 5, 69.	11.1	433
3	Identifying viruses from metagenomic data using deep learning. <i>Quantitative Biology</i> , 2020, 8, 64-77.	0.5	302
4	Alignment-free $d_2^*$ oligonucleotide frequency dissimilarity measure improves prediction of hosts from metagenomically-derived viral sequences. <i>Nucleic Acids Research</i> , 2017, 45, 39-53.	14.5	245
5	Copper toxicity and cyanobacteria ecology in the Sargasso Sea. <i>Limnology and Oceanography</i> , 2002, 47, 976-988.	3.1	195
6	Co-occurring <i>Synechococcus</i> ecotypes occupy four major oceanic regimes defined by temperature, macronutrients and iron. <i>ISME Journal</i> , 2016, 10, 333-345.	9.8	169
7	Culture Isolation and Culture-Independent Clone Libraries Reveal New Marine <i>Synechococcus</i> Ecotypes with Distinctive Light and N Physiologies. <i>Applied and Environmental Microbiology</i> , 2006, 72, 7193-7204.	3.1	142
8	Diversity and Distribution of Marine <i>Synechococcus</i> : Multiple Gene Phylogenies for Consensus Classification and Development of qPCR Assays for Sensitive Measurement of Clades in the Ocean. <i>Frontiers in Microbiology</i> , 2012, 3, 213.	3.5	128
9	Aryl-homoserine lactone quorum sensing in stem-nodulating photosynthetic bradyrhizobia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7183-7188.	7.1	111
10	Discovery of several novel, widespread, and ecologically distinct marine <i>Thaumarchaeota</i> viruses that encode <i>amoC</i> nitrification genes. <i>ISME Journal</i> , 2019, 13, 618-631.	9.8	103
11	Measurement of <i>Prochlorococcus</i> ecotypes using real-time polymerase chain reaction reveals different abundances of genotypes with similar light physiologies. <i>Environmental Microbiology</i> , 2006, 8, 441-454.	3.8	101
12	Genome and epigenome of a novel marine <i>Thaumarchaeota</i> strain suggest viral infection, phosphorothioation DNA modification and multiple restriction systems. <i>Environmental Microbiology</i> , 2017, 19, 2434-2452.	3.8	71
13	A network-based integrated framework for predicting virus-prokaryote interactions. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa044.	3.2	69
14	Long-term stability and Red Queen-like strain dynamics in marine viruses. <i>Nature Microbiology</i> , 2020, 5, 265-271.	13.3	62
15	The unique trace metal and mixed layer conditions of the Costa Rica upwelling dome support a distinct and dense community of <i>Synechococcus</i> . <i>Limnology and Oceanography</i> , 2014, 59, 2166-2184.	3.1	51
16	Multi-year dynamics of fine-scale marine cyanobacterial populations are more strongly explained by phage interactions than abiotic, bottom-up factors. <i>Environmental Microbiology</i> , 2019, 21, 2948-2963.	3.8	45
17	Prediction of virus-host infectious association by supervised learning methods. <i>BMC Bioinformatics</i> , 2017, 18, 60.	2.6	38
18	Genomic mosaicism underlies the adaptation of marine <i>Synechococcus</i> ecotypes to distinct oceanic iron niches. <i>Environmental Microbiology</i> , 2020, 22, 1801-1815.	3.8	32

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19	Marine <i>Synechococcus</i> isolates representing globally abundant genomic lineages demonstrate a unique evolutionary path of genome reduction without a decrease in GC content. <i>Environmental Microbiology</i> , 2019, 21, 1677-1686.	3.8	28
20	Optimizing <i>de novo</i> genome assembly from PCR-amplified metagenomes. <i>PeerJ</i> , 2019, 7, e6902.	2.0	28
21	Dynamics of <i>Prochlorococcus</i> Diversity and Photoacclimation During Short-Term Shifts in Water Column Stratification at Station ALOHA. <i>Frontiers in Marine Science</i> , 2018, 5, .	2.5	17
22	Characterization of IS 1676 from <i>Rhodococcus erythropolis</i> SQ1. <i>Applied Microbiology and Biotechnology</i> , 1999, 52, 811-819.	3.6	15
23	Niche partitioning of low-light adapted <i>Prochlorococcus</i> subecotypes across oceanographic gradients of the North Pacific Subtropical Front. <i>Limnology and Oceanography</i> , 2021, 66, 1548-1562.	3.1	14
24	Genome Sequences of <i>Synechococcus</i> sp. Strain MIT S9220 and Cocultured Cyanophage SynMITS9220M01. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	3
25	Genome Sequence of the Estuarine <i>Synechococcus</i> sp. Strain NB0720_010. <i>Microbiology Resource Announcements</i> , 0, , .	0.6	0