

Karla B Heidelberg

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

5,411
citations

172457

29
h-index

289244

40
g-index

40
all docs

40
docs citations

40
times ranked

6330
citing authors

#	ARTICLE	IF	CITATIONS
1	The Sorcerer II Global Ocean Sampling Expedition: Northwest Atlantic through Eastern Tropical Pacific. <i>PLoS Biology</i> , 2007, 5, e77.	5.6	1,757
2	The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. <i>PLoS Biology</i> , 2007, 5, e16.	5.6	736
3	<i>De novo</i> metagenomic assembly reveals abundant novel major lineage of Archaea in hypersaline microbial communities. <i>ISME Journal</i> , 2012, 6, 81-93.	9.8	347
4	Functional genomic signatures of sponge bacteria reveal unique and shared features of symbiosis. <i>ISME Journal</i> , 2010, 4, 1557-1567.	9.8	278
5	The Sorcerer II Global Ocean Sampling Expedition: Metagenomic Characterization of Viruses within Aquatic Microbial Samples. <i>PLoS ONE</i> , 2008, 3, e1456.	2.5	276
6	Probing the evolution, ecology and physiology of marine protists using transcriptomics. <i>Nature Reviews Microbiology</i> , 2017, 15, 6-20.	28.6	176
7	Protists are microbes too: a perspective. <i>ISME Journal</i> , 2009, 3, 4-12.	9.8	168
8	Bacteria of the β -Subclass <i>Proteobacteria</i> Associated with Zooplankton in Chesapeake Bay. <i>Applied and Environmental Microbiology</i> , 2002, 68, 5498-5507.	3.1	163
9	Seasonality of Chesapeake Bay Bacterioplankton Species. <i>Applied and Environmental Microbiology</i> , 2002, 68, 5488-5497.	3.1	147
10	Assembly-Driven Community Genomics of a Hypersaline Microbial Ecosystem. <i>PLoS ONE</i> , 2013, 8, e61692.	2.5	101
11	Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. <i>ISME Journal</i> , 2014, 8, 979-990.	9.8	91
12	Composition and sources of near reef zooplankton on a Jamaican forereef along with implications for coral feeding. <i>Coral Reefs</i> , 2004, 23, 263.	2.2	83
13	Dynamic Viral Populations in Hypersaline Systems as Revealed by Metagenomic Assembly. <i>Applied and Environmental Microbiology</i> , 2012, 78, 6309-6320.	3.1	83
14	Virus-Host and CRISPR Dynamics in Archaea-Dominated Hypersaline Lake Tyrrell, Victoria, Australia. <i>Archaea</i> , 2013, 2013, 1-12.	2.3	82
15	Autotrophic and heterotrophic acquisition of carbon and nitrogen by a mixotrophic chrysophyte established through stable isotope analysis. <i>ISME Journal</i> , 2017, 11, 2022-2034.	9.8	74
16	Swimming and feeding by the scyphomedusa <i>Chrysaora quinquecirrha</i> . <i>Marine Biology</i> , 1997, 129, 355-362.	1.5	61
17	Characterization of eukaryotic microbial diversity in hypersaline Lake Tyrrell, Australia. <i>Frontiers in Microbiology</i> , 2013, 4, 115.	3.5	53
18	Marine genomics: at the interface of marine microbial ecology and biodiscovery. <i>Microbial Biotechnology</i> , 2010, 3, 531-543.	4.2	51

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19	A tale of two mixotrophic chrysophytes: Insights into the metabolisms of two <i>Ochromonas</i> species (Chrysophyceae) through a comparison of gene expression. <i>PLoS ONE</i> , 2018, 13, e0192439.	2.5	51
20	Microbial secondary succession in soil microcosms of a desert oasis in the Cuatro Ciénegas Basin, Mexico. <i>PeerJ</i> , 2013, 1, e47.	2.0	50
21	Changes in gene expression of <i>Prymnesium parvum</i> induced by nitrogen and phosphorus limitation. <i>Frontiers in Microbiology</i> , 2015, 6, 631.	3.5	46
22	Gene expression characterizes different nutritional strategies among three mixotrophic protists. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw106.	2.7	45
23	Escape of the ctenophore <i>Mnemiopsis leidyi</i> from the scyphomedusa predator <i>Chrysaora quinquecirrha</i> . <i>Marine Biology</i> , 1997, 128, 441-446.	1.5	42
24	Comparative Analysis of Eukaryotic Marine Microbial Assemblages from 18S rRNA Gene and Gene Transcript Clone Libraries by Using Different Methods of Extraction. <i>Applied and Environmental Microbiology</i> , 2012, 78, 3958-3965.	3.1	39
25	New Approaches Indicate Constant Viral Diversity despite Shifts in Assemblage Structure in an Australian Hypersaline Lake. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6755-6764.	3.1	37
26	Gene expression in the mixotrophic prymnesiophyte, <i>Prymnesium parvum</i> , responds to prey availability. <i>Frontiers in Microbiology</i> , 2015, 6, 319.	3.5	37
27	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. <i>ISME Journal</i> , 2015, 9, 2697-2711.	9.8	35
28	Comparative Transcriptome Analysis of Four Prymnesiophyte Algae. <i>PLoS ONE</i> , 2014, 9, e97801.	2.5	34
29	Microbiomes of <i>Muricea californica</i> and <i>M. fruticosa</i> : Comparative Analyses of Two Co-occurring Eastern Pacific Octocorals. <i>Frontiers in Microbiology</i> , 2016, 7, 917.	3.5	33
30	Vertical distribution and diel patterns of zooplankton abundance and biomass at Conch Reef, Florida Keys (USA). <i>Journal of Plankton Research</i> , 2010, 32, 75-91.	1.8	32
31	Shifting metabolic priorities among key protistan taxa within and below the euphotic zone. <i>Environmental Microbiology</i> , 2018, 20, 2865-2879.	3.8	32
32	Comparative genomics of planktonic Flavobacteriaceae from the Gulf of Maine using metagenomic data. <i>Microbiome</i> , 2014, 2, 34.	11.1	28
33	Effect of light and prey availability on gene expression of the mixotrophic chrysophyte, <i>Ochromonas</i> sp.. <i>BMC Genomics</i> , 2017, 18, 163.	2.8	28
34	<sc>SSU</sc>â€<sc>rRNA</sc> Gene Sequencing Survey of Benthic Microbial Eukaryotes from Guaymas Basin Hydrothermal Vent. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 637-653.	1.7	27
35	<i>De Novo</i> Sequences of <i>Haloquadratum walsbyi</i> from Lake Tyrrell, Australia, Reveal a Variable Genomic Landscape. <i>Archaea</i> , 2015, 2015, 1-12.	2.3	26
36	Single-cell transcriptomics of small microbial eukaryotes: limitations and potential. <i>ISME Journal</i> , 2017, 11, 1282-1285.	9.8	23

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37	Single-Cell View of Carbon and Nitrogen Acquisition in the Mixotrophic Alga <i>Prymnesium parvum</i> (Haptophyta) Inferred From Stable Isotope Tracers and NanoSIMS. <i>Frontiers in Marine Science</i> , 2018, 5, .	2.5	17
38	Marine Environmental Genomics: New Secrets from a Mysterious Ocean. <i>Marine Technology Society Journal</i> , 2005, 39, 94-98.	0.4	8
39	Taking metagenomic studies in context. <i>Trends in Microbiology</i> , 2005, 13, 404.	7.7	8
40	Primer selection influences abundance estimates of ammonia oxidizing archaea in coastal marine sediments. <i>Marine Environmental Research</i> , 2018, 140, 90-95.	2.5	6