Rex R Malmstrom

List of Publications by Year
in descending order

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53

papers

8,032

citations

94381

37

h-index

168321

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63

docs citations

63

times ranked

9226

citing authors

#	Article	IF	Citations
1	Activity-based, genome-resolved metagenomics uncovers key populations and pathways involved in subsurface conversions of coal to methane. ISME Journal, 2022, 16, 915-926.	4.4	17
2	Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. PLoS Biology, 2022, 20, e3001508.	2.6	62
3	Subsurface hydrocarbon degradation strategies in low- and high-sulfate coal seam communities identified with activity-based metagenomics. Npj Biofilms and Microbiomes, 2022, 8, 7.	2.9	12
4	Dissecting the dominant hot spring microbial populations based on community-wide sampling at single-cell genomic resolution. ISME Journal, 2022, 16, 1337-1347.	4.4	15
5	Community Structure and Microbial Associations in Sediment-Free Methanotrophic Enrichment Cultures from a Marine Methane Seep. Applied and Environmental Microbiology, 2022, 88, .	1.4	8
6	A centimeter-long bacterium with DNA contained in metabolically active, membrane-bound organelles. Science, 2022, 376, 1453-1458.	6.0	45
7	Host population diversity as a driver of viral infection cycle in wild populations of green sulfur bacteria with long standing virus-host interactions. ISME Journal, 2021, 15, 1569-1584.	4.4	16
8	Metapangenomics reveals depth-dependent shifts in metabolic potential for the ubiquitous marine bacterial SAR324 lineage. Microbiome, 2021, 9, 172.	4.9	25
9	Novel copper-containing membrane monooxygenases (CuMMOs) encoded by alkane-utilizing <i>Betaproteobacteria</i>. ISME Journal, 2020, 14, 714-726.	4.4	16
10	Ecological and genomic analyses of candidate phylum <scp>WPS</scp>â€•2 bacteria in an unvegetated soil. Environmental Microbiology, 2020, 22, 3143-3157.	1.8	42
11	A pipeline for targeted metagenomics of environmental bacteria. Microbiome, 2020, 8, 21.	4.9	39
12	Niche differentiation is spatially and temporally regulated in the rhizosphere. ISME Journal, 2020, 14, 999-1014.	4.4	135
13	Probing the active fraction of soil microbiomes using BONCAT-FACS. Nature Communications, 2019, 10, 2770.	5.8	93
14	Advancing Genome-Resolved Metagenomics beyond the Shotgun. MSystems, 2019, 4, .	1.7	14
15	Minimum Information about an Uncultivated Virus Genome (MIUViG). Nature Biotechnology, 2019, 37, 29-37.	9.4	414
16	Optimizing <i>de novo</i> genome assembly from PCR-amplified metagenomes. PeerJ, 2019, 7, e6902.	0.9	28
17	Differential depth distribution of microbial function and putative symbionts through sediment-hosted aquifers in the deep terrestrial subsurface. Nature Microbiology, 2018, 3, 328-336.	5.9	227
18	Contrasting patterns of genome-level diversity across distinct co-occurring bacterial populations. ISME Journal, 2018, 12, 742-755.	4.4	76

#	ARTICLE	IF	CITATIONS
19	Freshwater carbon and nutrient cycles revealed through reconstructed population genomes. PeerJ, 2018, 6, e6075.	0.9	64
20	Hidden diversity of soil giant viruses. Nature Communications, 2018, 9, 4881.	5.8	112
21	Single cell genomic and transcriptomic evidence for the use of alternative nitrogen substrates by anammox bacteria. ISME Journal, 2018, 12, 2706-2722.	4.4	45
22	Single-cell genomics of co-sorted Nanoarchaeota suggests novel putative host associations and diversification of proteins involved in symbiosis. Microbiome, 2018, 6, 161.	4.9	44
23	Ecophysiology of Freshwater Verrucomicrobia Inferred from Metagenome-Assembled Genomes. MSphere, 2017, 2, .	1.3	87
24	Ecogenomics of virophages and their giant virus hosts assessed through time series metagenomics. Nature Communications, 2017, 8, 858.	5.8	107
25	Metabolic Network Analysis and Metatranscriptomics Reveal Auxotrophies and Nutrient Sources of the Cosmopolitan Freshwater Microbial Lineage acI. MSystems, 2017, 2, .	1.7	21
26	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. Nature Biotechnology, 2017, 35, 725-731.	9.4	1,512
27	Largeâ€scale maps of variable infection efficiencies in aquatic <i>Bacteroidetes</i> phageâ€host model systems. Environmental Microbiology, 2016, 18, 3949-3961.	1.8	22
28	Visualizing in situ translational activity for identifying and sorting slow-growing archaealâˆ'bacterial consortia. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4069-78.	3.3	180
29	SAR11 bacteria linked to ocean anoxia and nitrogen loss. Nature, 2016, 536, 179-183.	13.7	160
30	Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. ISME Journal, 2016, 10, 1589-1601.	4.4	226
31	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. Nature Communications, 2016, 7, 10476.	5.8	189
32	The Epigenomic Landscape of Prokaryotes. PLoS Genetics, 2016, 12, e1005854.	1.5	348
33	Comparative single-cell genomics reveals potential ecological niches for the freshwater acI Actinobacteria lineage. ISME Journal, 2014, 8, 2503-2516.	4.4	137
34	Single-Cell Genomics Reveals Hundreds of Coexisting Subpopulations in Wild <i>Prochlorococcus</i>. Science, 2014, 344, 416-420.	6.0	506
35	Obtaining genomes from uncultivated environmental microorganisms using FACSâ€"based single-cell genomics. Nature Protocols, 2014, 9, 1038-1048.	5.5	243
36	Gill bacteria enable a novel digestive strategy in a wood-feeding mollusk. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5096-104.	3.3	98

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37	Ecology of uncultured <i>Prochlorococcus</i> clades revealed through single-cell genomics and biogeographic analysis. ISME Journal, 2013, 7, 184-198.	4.4	105
38	Exploring the Roles of DNA Methylation in the Metal-Reducing Bacterium Shewanella oneidensis MR-1. Journal of Bacteriology, 2013, 195, 4966-4974.	1.0	43
39	Decontamination of MDA Reagents for Single Cell Whole Genome Amplification. PLoS ONE, 2011, 6, e26161.	1.1	163
40	Temporal dynamics of <i>Prochlorococcus</i> ecotypes in the Atlantic and Pacific oceans. ISME Journal, 2010, 4, 1252-1264.	4.4	221
41	Unlocking Short Read Sequencing for Metagenomics. PLoS ONE, 2010, 5, e11840.	1.1	157
42	Microbial community transcriptomes reveal microbes and metabolic pathways associated with dissolved organic matter turnover in the sea. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16420-16427.	3.3	384
43	Standing stocks, production, and respiration of phytoplankton and heterotrophic bacteria in the western Arctic Ocean. Deep-Sea Research Part II: Topical Studies in Oceanography, 2009, 56, 1237-1248.	0.6	117
44	Whole Genome Amplification and De novo Assembly of Single Bacterial Cells. PLoS ONE, 2009, 4, e6864.	1.1	225
45	Standing stocks and activity of Archaea and Bacteria in the western Arctic Ocean. Limnology and Oceanography, 2007, 52, 495-507.	1.6	190
46	The metabolic balance between autotrophy and heterotrophy in the western Arctic Ocean. Deep-Sea Research Part I: Oceanographic Research Papers, 2006, 53, 1831-1844.	0.6	43
47	Biogeography of major bacterial groups in the Delaware Estuary. Limnology and Oceanography, 2005, 50, 1697-1706.	1.6	204
48	Dimethylsulfoniopropionate (DMSP) assimilation by <i>Synechococcus</i> in the Gulf of Mexico and northwest Atlantic Ocean. Limnology and Oceanography, 2005, 50, 1924-1931.	1.6	56
49	Assimilation of Polysaccharides and Glucose by Major Bacterial Groups in the Delaware Estuary. Applied and Environmental Microbiology, 2005, 71, 7799-7805.	1.4	123
50	Biomass Production and Assimilation of Dissolved Organic Matter by SAR11 Bacteria in the Northwest Atlantic Ocean. Applied and Environmental Microbiology, 2005, 71, 2979-2986.	1.4	150
51	Control of bacterial growth by temperature and organic matter in the Western Arctic. Deep-Sea Research Part II: Topical Studies in Oceanography, 2005, 52, 3386-3395.	0.6	117
52	Contribution of SAR11 Bacteria to Dissolved Dimethylsulfoniopropionate and Amino Acid Uptake in the North Atlantic Ocean. Applied and Environmental Microbiology, 2004, 70, 4129-4135.	1.4	200
53	Identification and enumeration of bacteria assimilating dimethylsulfoniopropionate (DMSP) in the North Atlantic and Gulf of Mexico. Limnology and Oceanography, 2004, 49, 597-606.	1.6	117