

Rex R Malmstrom

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

8,032
citations

94381

37
h-index

168321

53
g-index

63
all docs

63
docs citations

63
times ranked

9226
citing authors

#	ARTICLE	IF	CITATIONS
1	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	9.4	1,512
2	Single-Cell Genomics Reveals Hundreds of Coexisting Subpopulations in Wild <i>Prochlorococcus</i> . <i>Science</i> , 2014, 344, 416-420.	6.0	506
3	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
4	Microbial community transcriptomes reveal microbes and metabolic pathways associated with dissolved organic matter turnover in the sea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16420-16427.	3.3	384
5	The Epigenomic Landscape of Prokaryotes. <i>PLoS Genetics</i> , 2016, 12, e1005854.	1.5	348
6	Obtaining genomes from uncultivated environmental microorganisms using FACS-based single-cell genomics. <i>Nature Protocols</i> , 2014, 9, 1038-1048.	5.5	243
7	Differential depth distribution of microbial function and putative symbionts through sediment-hosted aquifers in the deep terrestrial subsurface. <i>Nature Microbiology</i> , 2018, 3, 328-336.	5.9	227
8	Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. <i>ISME Journal</i> , 2016, 10, 1589-1601.	4.4	226
9	Whole Genome Amplification and De novo Assembly of Single Bacterial Cells. <i>PLoS ONE</i> , 2009, 4, e6864.	1.1	225
10	Temporal dynamics of <i>Prochlorococcus</i> ecotypes in the Atlantic and Pacific oceans. <i>ISME Journal</i> , 2010, 4, 1252-1264.	4.4	221
11	Biogeography of major bacterial groups in the Delaware Estuary. <i>Limnology and Oceanography</i> , 2005, 50, 1697-1706.	1.6	204
12	Contribution of SAR11 Bacteria to Dissolved Dimethylsulfoniopropionate and Amino Acid Uptake in the North Atlantic Ocean. <i>Applied and Environmental Microbiology</i> , 2004, 70, 4129-4135.	1.4	200
13	Standing stocks and activity of Archaea and Bacteria in the western Arctic Ocean. <i>Limnology and Oceanography</i> , 2007, 52, 495-507.	1.6	190
14	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016, 7, 10476.	5.8	189
15	Visualizing in situ translational activity for identifying and sorting slow-growing archaeal bacterial consortia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4069-78.	3.3	180
16	Decontamination of MDA Reagents for Single Cell Whole Genome Amplification. <i>PLoS ONE</i> , 2011, 6, e26161.	1.1	163
17	SAR11 bacteria linked to ocean anoxia and nitrogen loss. <i>Nature</i> , 2016, 536, 179-183.	13.7	160
18	Unlocking Short Read Sequencing for Metagenomics. <i>PLoS ONE</i> , 2010, 5, e11840.	1.1	157

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19	Biomass Production and Assimilation of Dissolved Organic Matter by SAR11 Bacteria in the Northwest Atlantic Ocean. <i>Applied and Environmental Microbiology</i> , 2005, 71, 2979-2986.	1.4	150
20	Comparative single-cell genomics reveals potential ecological niches for the freshwater actinobacteria lineage. <i>ISME Journal</i> , 2014, 8, 2503-2516.	4.4	137
21	Niche differentiation is spatially and temporally regulated in the rhizosphere. <i>ISME Journal</i> , 2020, 14, 999-1014.	4.4	135
22	Assimilation of Polysaccharides and Glucose by Major Bacterial Groups in the Delaware Estuary. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7799-7805.	1.4	123
23	Identification and enumeration of bacteria assimilating dimethylsulfoniopropionate (DMSP) in the North Atlantic and Gulf of Mexico. <i>Limnology and Oceanography</i> , 2004, 49, 597-606.	1.6	117
24	Control of bacterial growth by temperature and organic matter in the Western Arctic. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2005, 52, 3386-3395.	0.6	117
25	Standing stocks, production, and respiration of phytoplankton and heterotrophic bacteria in the western Arctic Ocean. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2009, 56, 1237-1248.	0.6	117
26	Hidden diversity of soil giant viruses. <i>Nature Communications</i> , 2018, 9, 4881.	5.8	112
27	Ecogenomics of virophages and their giant virus hosts assessed through time series metagenomics. <i>Nature Communications</i> , 2017, 8, 858.	5.8	107
28	Ecology of uncultured <i>Prochlorococcus</i> clades revealed through single-cell genomics and biogeographic analysis. <i>ISME Journal</i> , 2013, 7, 184-198.	4.4	105
29	Gill bacteria enable a novel digestive strategy in a wood-feeding mollusk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5096-104.	3.3	98
30	Probing the active fraction of soil microbiomes using BONCAT-FACS. <i>Nature Communications</i> , 2019, 10, 2770.	5.8	93
31	Ecophysiology of Freshwater Verrucomicrobia Inferred from Metagenome-Assembled Genomes. <i>MSphere</i> , 2017, 2, .	1.3	87
32	Contrasting patterns of genome-level diversity across distinct co-occurring bacterial populations. <i>ISME Journal</i> , 2018, 12, 742-755.	4.4	76
33	Freshwater carbon and nutrient cycles revealed through reconstructed population genomes. <i>PeerJ</i> , 2018, 6, e6075.	0.9	64
34	Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. <i>PLoS Biology</i> , 2022, 20, e3001508.	2.6	62
35	Dimethylsulfoniopropionate (DMSP) assimilation by <i>Synechococcus</i> in the Gulf of Mexico and northwest Atlantic Ocean. <i>Limnology and Oceanography</i> , 2005, 50, 1924-1931.	1.6	56
36	Single cell genomic and transcriptomic evidence for the use of alternative nitrogen substrates by anammox bacteria. <i>ISME Journal</i> , 2018, 12, 2706-2722.	4.4	45

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37	A centimeter-long bacterium with DNA contained in metabolically active, membrane-bound organelles. <i>Science</i> , 2022, 376, 1453-1458.	6.0	45
38	Single-cell genomics of co-sorted Nanoarchaeota suggests novel putative host associations and diversification of proteins involved in symbiosis. <i>Microbiome</i> , 2018, 6, 161.	4.9	44
39	The metabolic balance between autotrophy and heterotrophy in the western Arctic Ocean. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2006, 53, 1831-1844.	0.6	43
40	Exploring the Roles of DNA Methylation in the Metal-Reducing Bacterium <i>Shewanella oneidensis</i> MR-1. <i>Journal of Bacteriology</i> , 2013, 195, 4966-4974.	1.0	43
41	Ecological and genomic analyses of candidate phylum <i>WPS</i> bacteria in an unvegetated soil. <i>Environmental Microbiology</i> , 2020, 22, 3143-3157.	1.8	42
42	A pipeline for targeted metagenomics of environmental bacteria. <i>Microbiome</i> , 2020, 8, 21.	4.9	39
43	Optimizing <i>de novo</i> genome assembly from PCR-amplified metagenomes. <i>PeerJ</i> , 2019, 7, e6902.	0.9	28
44	Metapangenomics reveals depth-dependent shifts in metabolic potential for the ubiquitous marine bacterial SAR324 lineage. <i>Microbiome</i> , 2021, 9, 172.	4.9	25
45	Large-scale maps of variable infection efficiencies in aquatic <i>Bacteroidetes</i> phage-host model systems. <i>Environmental Microbiology</i> , 2016, 18, 3949-3961.	1.8	22
46	Metabolic Network Analysis and Metatranscriptomics Reveal Auxotrophies and Nutrient Sources of the Cosmopolitan Freshwater Microbial Lineage <i>acl</i> . <i>MSystems</i> , 2017, 2, .	1.7	21
47	Activity-based, genome-resolved metagenomics uncovers key populations and pathways involved in subsurface conversions of coal to methane. <i>ISME Journal</i> , 2022, 16, 915-926.	4.4	17
48	Novel copper-containing membrane monooxygenases (CuMMOs) encoded by alkane-utilizing <i>Betaproteobacteria</i> . <i>ISME Journal</i> , 2020, 14, 714-726.	4.4	16
49	Host population diversity as a driver of viral infection cycle in wild populations of green sulfur bacteria with long standing virus-host interactions. <i>ISME Journal</i> , 2021, 15, 1569-1584.	4.4	16
50	Dissecting the dominant hot spring microbial populations based on community-wide sampling at single-cell genomic resolution. <i>ISME Journal</i> , 2022, 16, 1337-1347.	4.4	15
51	Advancing Genome-Resolved Metagenomics beyond the Shotgun. <i>MSystems</i> , 2019, 4, .	1.7	14
52	Subsurface hydrocarbon degradation strategies in low- and high-sulfate coal seam communities identified with activity-based metagenomics. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 7.	2.9	12
53	Community Structure and Microbial Associations in Sediment-Free Methanotrophic Enrichment Cultures from a Marine Methane Seep. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	8