

Robertson Papke

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

4,780
citations

147566

31
h-index

118652

62
g-index

69
all docs

69
docs citations

69
times ranked

5040
citing authors

#	ARTICLE	IF	CITATIONS
1	Adaptation reduces competitive dominance and alters community assembly. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20203133.	1.2	12
2	Nutrient supplementation experiments with saltern microbial communities implicate utilization of DNA as a source of phosphorus. <i>ISME Journal</i> , 2021, 15, 2853-2864.	4.4	12
3	The Evolutionary Origins of Extreme Halophilic Archaeal Lineages. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	20
4	Interaction of two strongly divergent archaeellins stabilizes the structure of the <i>Halorubrum</i> archaeellum. <i>MicrobiologyOpen</i> , 2020, 9, e1047.	1.2	10
5	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	5.9	115
6	Insights into gene expression changes under conditions that facilitate horizontal gene transfer (mating) of a model archaeon. <i>Scientific Reports</i> , 2020, 10, 22297.	1.6	8
7	The Patchy Distribution of Restriction Modification System Genes and the Conservation of Orphan Methyltransferases in Halobacteria. <i>Genes</i> , 2019, 10, 233.	1.0	27
8	Complete Genome Sequence of <i>Halorubrum ezzemoulense</i> Strain Fb21. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
9	Characterizing the DNA Methyltransferases of <i>Haloferax volcanii</i> via Bioinformatics, Gene Deletion, and SMRT Sequencing. <i>Genes</i> , 2018, 9, 129.	1.0	18
10	Genotypic and Lipid Analyses of Strains From the Archaeal Genus <i>Halorubrum</i> Reveal Insights Into Their Taxonomy, Divergence, and Population Structure. <i>Frontiers in Microbiology</i> , 2018, 9, 512.	1.5	19
11	Comparative Analysis of Surface Layer Glycoproteins and Genes Involved in Protein Glycosylation in the Genus <i>Haloferax</i> . <i>Genes</i> , 2018, 9, 172.	1.0	20
12	Hundreds of novel composite genes and chimeric genes with bacterial origins contributed to haloarchaeal evolution. <i>Genome Biology</i> , 2018, 19, 75.	3.8	36
13	<i>Halorubrum chaoviator</i> Mancinelli et al. 2009 is a later, heterotypic synonym of <i>Halorubrum ezzemoulense</i> Kharroub et al. 2006. Emended description of <i>Halorubrum ezzemoulense</i> Kharroub et al. 2006. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3657-3665.	0.8	11
14	Assessment of MultiLocus Sequence Analysis As a Valuable Tool for the Classification of the Genus <i>Salinivibrio</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1107.	1.5	19
15	Deciphering the Translation Initiation Factor 5A Modification Pathway in Halophilic Archaea. <i>Archaea</i> , 2016, 2016, 1-14.	2.3	24
16	Analysis of the bacteriorhodopsin-producing haloarchaea reveals a core community that is stable over time in the salt crystallizers of Eilat, Israel. <i>Extremophiles</i> , 2016, 20, 747-757.	0.9	8
17	<i>Halorubrum halodurans</i> sp. nov., an extremely halophilic archaeon isolated from a hypersaline lake. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 435-444.	0.8	16
18	Horizontal Gene Transfer, Dispersal and Haloarchaeal Speciation. <i>Life</i> , 2015, 5, 1405-1426.	1.1	28

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19	Genome-wide DNA methylation analysis of <i>Haloferax volcanii</i> H26 and identification of DNA methyltransferase related PD-(D/E)XK nuclease family protein HVO_A0006. <i>Frontiers in Microbiology</i> , 2015, 6, 251.	1.5	28
20	Preface to the proceedings of Halophiles 2013. <i>Frontiers in Microbiology</i> , 2015, 6, 341.	1.5	3
21	Getting a hold on archaeal type IV pili: an expanding repertoire of cellular appendages implicates complex regulation and diverse functions. <i>Frontiers in Microbiology</i> , 2015, 6, 362.	1.5	4
22	Microbial diversity of hypersaline environments: a metagenomic approach. <i>Current Opinion in Microbiology</i> , 2015, 25, 80-87.	2.3	157
23	<i>Halorubrum persicum</i> sp. nov., an extremely halophilic archaeon isolated from sediment of a hypersaline lake. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 1770-1778.	0.8	23
24	DNA as a Phosphate Storage Polymer and the Alternative Advantages of Polyploidy for Growth or Survival. <i>PLoS ONE</i> , 2014, 9, e94819.	1.1	78
25	Extracellular DNA metabolism in <i>Haloferax volcanii</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 57.	1.5	37
26	Population and genomic analysis of the genus <i>Halorubrum</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 140.	1.5	46
27	Evidence from phylogenetic and genome fingerprinting analyses suggests rapidly changing variation in <i>Halorubrum</i> and <i>Haloarcula</i> populations. <i>Frontiers in Microbiology</i> , 2014, 5, 143.	1.5	25
28	Comparison of prokaryotic community structure from Mediterranean and Atlantic saltern concentrator ponds by a metagenomic approach. <i>Frontiers in Microbiology</i> , 2014, 5, 196.	1.5	80
29	Viruses of Haloarchaea. <i>Life</i> , 2014, 4, 681-715.	1.1	51
30	Inteins as indicators of gene flow in the halobacteria. <i>Frontiers in Microbiology</i> , 2014, 5, 299.	1.5	24
31	Biofilms formed by the archaeon <i>Haloferax volcanii</i> exhibit cellular differentiation and social motility, and facilitate horizontal gene transfer. <i>BMC Biology</i> , 2014, 12, 65.	1.7	81
32	Cell sorting analysis of geographically separated hypersaline environments. <i>Extremophiles</i> , 2013, 17, 265-275.	0.9	46
33	Draft Genome Sequence of the Moderately Halophilic Bacterium <i>Marinobacter lipolyticus</i> Strain SM19. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
34	Draft Genome Sequence of the Moderately Halophilic Bacterium <i>Pseudoalteromonas ruthenica</i> Strain CP76. <i>Genome Announcements</i> , 2013, 1, .	0.8	2
35	Dihydroxyacetone metabolism in <i>Haloferax volcanii</i> . <i>Frontiers in Microbiology</i> , 2013, 4, 376.	1.5	13
36	Quantifying Homologous Replacement of Loci between Haloarchaeal Species. <i>Genome Biology and Evolution</i> , 2012, 4, 1223-1244.	1.1	55

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37	Multilocus sequence analysis of the family Halomonadaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 520-538.	0.8	86
38	Ancient origin of the divergent forms of leucyl-tRNA synthetases in the Halobacteriales. <i>BMC Evolutionary Biology</i> , 2012, 12, 85.	3.2	15
39	Gene Transfer Mechanisms, Population Genetics/Genomics and the Evolution of Haloarchaea. , 2012, , 199-216.		0
40	Low Species Barriers in Halophilic Archaea and the Formation of Recombinant Hybrids. <i>Current Biology</i> , 2012, 22, 1444-1448.	1.8	123
41	How Bacterial Lineages Emerge. <i>Science</i> , 2012, 336, 45-46.	6.0	37
42	New Abundant Microbial Groups in Aquatic Hypersaline Environments. <i>Scientific Reports</i> , 2011, 1, 135.	1.6	288
43	Ancient origins determine global biogeography of hot and cold desert cyanobacteria. <i>Nature Communications</i> , 2011, 2, 163.	5.8	203
44	A multilocus sequence analysis approach to the phylogeny and taxonomy of the Halobacteriales. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 2984-2995.	0.8	54
45	In Vivo Characterization of the Homing Endonuclease within the polB Gene in the Halophilic Archaeon <i>Haloferax volcanii</i> . <i>PLoS ONE</i> , 2011, 6, e15833.	1.1	18
46	Intertwined Evolutionary Histories of Marine <i>Synechococcus</i> and <i>Prochlorococcus marinus</i> . <i>Genome Biology and Evolution</i> , 2009, 1, 325-339.	1.1	80
47	A Critique of Prokaryotic Species Concepts. <i>Methods in Molecular Biology</i> , 2009, 532, 379-395.	0.4	21
48	Actinorhodopsins: proteorhodopsin-like gene sequences found predominantly in non-marine environments. <i>Environmental Microbiology</i> , 2008, 10, 1039-1056.	1.8	136
49	Searching for species in haloarchaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14092-14097.	3.3	128
50	Genomic plasticity in prokaryotes: the case of the square haloarchaeon. <i>ISME Journal</i> , 2007, 1, 235-245.	4.4	116
51	Evolution of rhodopsin ion pumps in haloarchaea. <i>BMC Evolutionary Biology</i> , 2007, 7, 79.	3.2	54
52	Genomics and the bacterial species problem. <i>Genome Biology</i> , 2006, 7, 116.	13.9	200
53	Environmental genomics of "Haloquadratum walsbyi" in a saltern crystallizer indicates a large pool of accessory genes in an otherwise coherent species. <i>BMC Genomics</i> , 2006, 7, 171.	1.2	128
54	Phylogenetic analyses of cyanobacterial genomes: Quantification of horizontal gene transfer events. <i>Genome Research</i> , 2006, 16, 1099-1108.	2.4	278

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55	Archaeal diversity along a soil salinity gradient prone to disturbance. <i>Environmental Microbiology</i> , 2005, 7, 1655-1666.	1.8	135
56	The genome of <i>Salinibacter ruber</i> : Convergence and gene exchange among hyperhalophilic bacteria and archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18147-18152.	3.3	299
57	The importance of physical isolation to microbial diversification. <i>FEMS Microbiology Ecology</i> , 2004, 48, 293-303.	1.3	170
58	Phage evolution: New worlds of genomic diversity. <i>Current Biology</i> , 2003, 13, R606-R607.	1.8	7
59	Geographical isolation in hot spring cyanobacteria. <i>Environmental Microbiology</i> , 2003, 5, 650-659.	1.8	446
60	Diversity of bacteriorhodopsins in different hypersaline waters from a single Spanish saltern. <i>Environmental Microbiology</i> , 2003, 5, 1039-1045.	1.8	29
61	Lateral Gene Transfer and the Origins of Prokaryotic Groups. <i>Annual Review of Genetics</i> , 2003, 37, 283-328.	3.2	357
62	Transmission of Creutzfeldt-Jakob disease from man to the guinea pig. <i>Science</i> , 1975, 190, 571-572.	6.0	193