

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 | Geographical isolation in hot spring cyanobacteria. <i>Environmental Microbiology</i> , 2003, 5, 650-659. | 1.8 | 446 |
| 2 | Lateral Gene Transfer and the Origins of Prokaryotic Groups. <i>Annual Review of Genetics</i> , 2003, 37, 283-328. | 3.2 | 357 |
| 3 | 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 |
| 4 | New Abundant Microbial Groups in Aquatic Hypersaline Environments. <i>Scientific Reports</i> , 2011, 1, 135. | 1.6 | 288 |
| 5 | Phylogenetic analyses of cyanobacterial genomes: Quantification of horizontal gene transfer events. <i>Genome Research</i> , 2006, 16, 1099-1108. | 2.4 | 278 |
| 6 | Ancient origins determine global biogeography of hot and cold desert cyanobacteria. <i>Nature Communications</i> , 2011, 2, 163. | 5.8 | 203 |
| 7 | Genomics and the bacterial species problem. <i>Genome Biology</i> , 2006, 7, 116. | 13.9 | 200 |
| 8 | Transmission of Creutzfeldt-Jakob disease from man to the guinea pig. <i>Science</i> , 1975, 190, 571-572. | 6.0 | 193 |
| 9 | The importance of physical isolation to microbial diversification. <i>FEMS Microbiology Ecology</i> , 2004, 48, 293-303. | 1.3 | 170 |
| 10 | Microbial diversity of hypersaline environments: a metagenomic approach. <i>Current Opinion in Microbiology</i> , 2015, 25, 80-87. | 2.3 | 157 |
| 11 | Actinorhodopsins: proteorhodopsin-like gene sequences found predominantly in non-marine environments. <i>Environmental Microbiology</i> , 2008, 10, 1039-1056. | 1.8 | 136 |
| 12 | Archaeal diversity along a soil salinity gradient prone to disturbance. <i>Environmental Microbiology</i> , 2005, 7, 1655-1666. | 1.8 | 135 |
| 13 | Environmental genomics of " <i>Haloquadratum walsbyi</i> " 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 |
| 14 | 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 |
| 15 | Low Species Barriers in Halophilic Archaea and the Formation of Recombinant Hybrids. <i>Current Biology</i> , 2012, 22, 1444-1448. | 1.8 | 123 |
| 16 | Genomic plasticity in prokaryotes: the case of the square haloarchaeon. <i>ISME Journal</i> , 2007, 1, 235-245. | 4.4 | 116 |
| 17 | Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994. | 5.9 | 115 |
| 18 | Multilocus sequence analysis of the family Halomonadaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 520-538. | 0.8 | 86 |

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|----|--|-----|-----------|
| 19 | 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 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | Quantifying Homologous Replacement of Loci between Haloarchaeal Species. <i>Genome Biology and Evolution</i> , 2012, 4, 1223-1244. | 1.1 | 55 |
| 24 | Evolution of rhodopsin ion pumps in haloarchaea. <i>BMC Evolutionary Biology</i> , 2007, 7, 79. | 3.2 | 54 |
| 25 | 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 |
| 26 | Viruses of Haloarchaea. <i>Life</i> , 2014, 4, 681-715. | 1.1 | 51 |
| 27 | Cell sorting analysis of geographically separated hypersaline environments. <i>Extremophiles</i> , 2013, 17, 265-275. | 0.9 | 46 |
| 28 | Population and genomic analysis of the genus <i>Halorubrum</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 140. | 1.5 | 46 |
| 29 | How Bacterial Lineages Emerge. <i>Science</i> , 2012, 336, 45-46. | 6.0 | 37 |
| 30 | Extracellular DNA metabolism in <i>Haloferax volcanii</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 57. | 1.5 | 37 |
| 31 | 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 |
| 32 | Diversity of bacteriorhodopsins in different hypersaline waters from a single Spanish saltern. <i>Environmental Microbiology</i> , 2003, 5, 1039-1045. | 1.8 | 29 |
| 33 | Horizontal Gene Transfer, Dispersal and Haloarchaeal Speciation. <i>Life</i> , 2015, 5, 1405-1426. | 1.1 | 28 |
| 34 | 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 |
| 35 | 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 |
| 36 | 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 |

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|----|---|-----|-----------|
| 37 | Inteins as indicators of gene flow in the halobacteria. <i>Frontiers in Microbiology</i> , 2014, 5, 299. | 1.5 | 24 |
| 38 | Deciphering the Translation Initiation Factor 5A Modification Pathway in Halophilic Archaea. <i>Archaea</i> , 2016, 2016, 1-14. | 2.3 | 24 |
| 39 | <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 |
| 40 | A Critique of Prokaryotic Species Concepts. <i>Methods in Molecular Biology</i> , 2009, 532, 379-395. | 0.4 | 21 |
| 41 | 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 |
| 42 | The Evolutionary Origins of Extreme Halophilic Archaeal Lineages. <i>Genome Biology and Evolution</i> , 2021, 13, . | 1.1 | 20 |
| 43 | 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 |
| 44 | 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 |
| 45 | In Vivo Characterization of the Homing Endonuclease within the <i>polB</i> Gene in the Halophilic Archaeon <i>Haloferax volcanii</i> . <i>PLoS ONE</i> , 2011, 6, e15833. | 1.1 | 18 |
| 46 | 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 |
| 47 | <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 |
| 48 | Ancient origin of the divergent forms of leucyl-tRNA synthetases in the Halobacteriales. <i>BMC Evolutionary Biology</i> , 2012, 12, 85. | 3.2 | 15 |
| 49 | Dihydroxyacetone metabolism in <i>Haloferax volcanii</i> . <i>Frontiers in Microbiology</i> , 2013, 4, 376. | 1.5 | 13 |
| 50 | Adaptation reduces competitive dominance and alters community assembly. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20203133. | 1.2 | 12 |
| 51 | 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 |
| 52 | <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 |
| 53 | Interaction of two strongly divergent archaeellins stabilizes the structure of the <i>Halorubrum</i> archaeellum. <i>MicrobiologyOpen</i> , 2020, 9, e1047. | 1.2 | 10 |
| 54 | Draft Genome Sequence of the Moderately Halophilic Bacterium <i>Marinobacter lipolyticus</i> Strain SM19. <i>Genome Announcements</i> , 2013, 1, . | 0.8 | 8 |

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|----|---|-----|-----------|
| 55 | 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 |
| 56 | 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 |
| 57 | Phage evolution: New worlds of genomic diversity. <i>Current Biology</i> , 2003, 13, R606-R607. | 1.8 | 7 |
| 58 | 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 |
| 59 | Preface to the proceedings of Halophiles 2013. <i>Frontiers in Microbiology</i> , 2015, 6, 341. | 1.5 | 3 |
| 60 | Draft Genome Sequence of the Moderately Halophilic Bacterium <i>Pseudoalteromonas ruthenica</i> Strain CP76. <i>Genome Announcements</i> , 2013, 1, . | 0.8 | 2 |
| 61 | Complete Genome Sequence of <i>Halorubrum ezzemoulense</i> Strain Fb21. <i>Microbiology Resource Announcements</i> , 2019, 8, . | 0.3 | 2 |
| 62 | Gene Transfer Mechanisms, Population Genetics/Genomics and the Evolution of Haloarchaea. , 2012, , 199-216. | | 0 |