

Shawn W Polson

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

3,524
citations

201575

27
h-index

149623

56
g-index

78
all docs

78
docs citations

78
times ranked

5670
citing authors

#	ARTICLE	IF	CITATIONS
1	Towards an integrative view of virus phenotypes. <i>Nature Reviews Microbiology</i> , 2022, 20, 83-94.	13.6	15
2	Unraveling Fe(II)-Oxidizing Mechanisms in a Facultative Fe(II) Oxidizer, <i>Sideroxydans lithotrophicus</i> Strain ES-1, via Culturing, Transcriptomics, and Reverse Transcription-Quantitative PCR. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0159521.	1.4	14
3	Novel Viral DNA Polymerases From Metagenomes Suggest Genomic Sources of Strand-Displacing Biochemical Phenotypes. <i>Frontiers in Microbiology</i> , 2022, 13, 858366.	1.5	2
4	Investigation of allele specific expression in various tissues of broiler chickens using the detection tool VADT. <i>Scientific Reports</i> , 2021, 11, 3968.	1.6	5
5	Bacteriophages against <i>Vibrio coralliilyticus</i> and <i>Vibrio tubiashii</i> : Isolation, Characterization, and Remediation of Larval Oyster Mortalities. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	13
6	<i>k</i>-mer-Based Metagenomics Tools Provide a Fast and Sensitive Approach for the Detection of Viral Contaminants in Biopharmaceutical and Vaccine Manufacturing Applications Using Next-Generation Sequencing. <i>MSphere</i> , 2021, 6, .	1.3	5
7	Urbanization pressures alter tree rhizosphere microbiomes. <i>Scientific Reports</i> , 2021, 11, 9447.	1.6	14
8	Deletion of <i>Fibroblast growth factor 9</i> globally and in skeletal muscle results in enlarged tuberousities at sites of deltoid tendon attachments. <i>Developmental Dynamics</i> , 2021, 250, 1778-1795.	0.8	7
9	Enhanced copper-resistance gene repertoire in <i>Alteromonas macleodii</i> strains isolated from copper-treated marine coatings. <i>PLoS ONE</i> , 2021, 16, e0257800.	1.1	5
10	Aerobic and anaerobic iron oxidizers together drive denitrification and carbon cycling at marine iron-rich hydrothermal vents. <i>ISME Journal</i> , 2021, 15, 1271-1286.	4.4	46
11	Unravelling <i>Sideroxydans lithotrophicus</i> ES-1 Fe(II)-oxidizing pathway using transcriptomics and RT-qPCR. , 2021, , .		0
12	Multiple Megaplastids Confer Extremely High Levels of Metal Tolerance in <i>Alteromonas</i> Strains. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	11
13	The Tudor-domain protein TDRD7, mutated in congenital cataract, controls the heat shock protein HSPB1 (HSP27) and lens fiber cell morphology. <i>Human Molecular Genetics</i> , 2020, 29, 2076-2097.	1.4	27
14	Validating the Cyc2 Neutrophilic Iron Oxidation Pathway Using Meta-omics of <i>Zetaproteobacteria</i> Iron Mats at Marine Hydrothermal Vents. <i>MSystems</i> , 2020, 5, .	1.7	65
15	Understanding ER+ Breast Cancer Dormancy Using Bioinspired Synthetic Matrices for Long-Term 3D Culture and Insights into Late Recurrence. <i>Advanced Biology</i> , 2020, 4, e2000119.	3.0	17
16	Whole-Genome Sequence of the Cyanobacterium <i>Synechococcus</i> sp. Strain WH 8101. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
17	Oyster calcifying fluid harbors persistent and dynamic autochthonous bacterial populations that may aid in shell formation. <i>Marine Ecology - Progress Series</i> , 2020, 653, 57-75.	0.9	6
18	Iroki: automatic customization and visualization of phylogenetic trees. <i>PeerJ</i> , 2020, 8, e8584.	0.9	78

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19	Bioinformatics Core Survey Highlights the Challenges Facing Data Analysis Facilities. <i>Journal of Biomolecular Techniques</i> , 2020, 31, jbt.20-3102-005.	0.8	2
20	Light Modulates the Physiology of Nonphototrophic Actinobacteria. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	22
21	Whole-Genome Sequences of Two <i>Pseudoalteromonas piscicida</i> Strains, DE1-A and DE2-A, with Strong Antibacterial Activity against <i>Vibrio vulnificus</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
22	Genome sequencing and transcript analysis of <i>Hemileia vastatrix</i> reveal expression dynamics of candidate effectors dependent on host compatibility. <i>PLoS ONE</i> , 2019, 14, e0215598.	1.1	30
23	CRISPR Spacers Indicate Preferential Matching of Specific Virioplankton Genes. <i>MBio</i> , 2019, 10, .	1.8	26
24	Complete Genome Sequence of <i>Microbacterium</i> sp. Strain 10M-3C3, Isolated from an Extremely Phosphorus-Poor Lake. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
25	Reannotation of the Ribonucleotide Reductase in a Cyanophage Reveals Life History Strategies Within the Virioplankton. <i>Frontiers in Microbiology</i> , 2019, 10, 134.	1.5	19
26	590. Reduction of Endotracheal Colonization by Gram-Negative Bacilli in a Neonatal Intensive Care Unit Through Use of a Novel Drain Cover. <i>Open Forum Infectious Diseases</i> , 2019, 6, S279-S279.	0.4	0
27	Identification of Chondrocyte Genes and Signaling Pathways in Response to Acute Joint Inflammation. <i>Scientific Reports</i> , 2019, 9, 93.	1.6	43
28	A reference genome of the Chinese hamster based on a hybrid assembly strategy. <i>Biotechnology and Bioengineering</i> , 2018, 115, 2087-2100.	1.7	95
29	Family A DNA Polymerase Phylogeny Uncovers Diversity and Replication Gene Organization in the Virioplankton. <i>Frontiers in Microbiology</i> , 2018, 9, 3053.	1.5	18
30	Phased Genotyping-by-Sequencing Enhances Analysis of Genetic Diversity and Reveals Divergent Copy Number Variants in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2161-2170.	0.8	29
31	Novel chaperonins are prevalent in the virioplankton and demonstrate links to viral biology and ecology. <i>ISME Journal</i> , 2017, 11, 2479-2491.	4.4	31
32	Genotyping-by-Sequencing to Predict Resistance to Lima Bean Downy Mildew in a Diversity Panel. <i>Phytopathology</i> , 2016, 106, 1152-1158.	1.1	4
33	Computational clustering for viral reference proteomes: Table 1.. <i>Bioinformatics</i> , 2016, 32, 2041-2043.	1.8	3
34	Polygenic inheritance of cryptorchidism susceptibility in the LE/orl rat. <i>Molecular Human Reproduction</i> , 2016, 22, 18-34.	1.3	9
35	Pressing needs of biomedical text mining in biocuration and beyond: opportunities and challenges. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw161.	1.4	30
36	An Integrated Approach for Analyzing Clinical Genomic Variant Data from Next-Generation Sequencing. <i>Journal of Biomolecular Techniques</i> , 2015, 26, 19-28.	0.8	9

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37	Draft Genome Sequence of a Natural Root Isolate, <i>Bacillus subtilis</i> UD1022, a Potential Plant Growth-Promoting Biocontrol Agent. <i>Genome Announcements</i> , 2015, 3, .	0.8	12
38	Complete Genome Sequence of <i>Vibrio parahaemolyticus</i> Environmental Strain UCM-V493. <i>Genome Announcements</i> , 2014, 2, .	0.8	24
39	Genome Sequence and Methylome of Soil Bacterium <i>Gemmatirosa kalamazonensis</i> KBS708 T , a Member of the Rarely Cultivated Gemmatimonadetes Phylum. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
40	Development of novel filtering criteria to analyze RNA-sequencing data obtained from the murine ocular lens during embryogenesis. <i>Genomics Data</i> , 2014, 2, 369-374.	1.3	20
41	Shotgun metagenomics indicates novel family A DNA polymerases predominate within marine viroplankton. <i>ISME Journal</i> , 2014, 8, 103-114.	4.4	51
42	Ribonucleotide reductases reveal novel viral diversity and predict biological and ecological features of unknown marine viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15786-15791.	3.3	56
43	High-fat-diet-mediated dysbiosis promotes intestinal carcinogenesis independently of obesity. <i>Nature</i> , 2014, 514, 508-512.	13.7	366
44	Caught in the middle with multiple displacement amplification: the myth of pooling for avoiding multiple displacement amplification bias in a metagenome. <i>Microbiome</i> , 2014, 2, 3.	4.9	105
45	SkateBase, an elasmobranch genome project and collection of molecular resources for chondrichthyan fishes. <i>F1000Research</i> , 2014, 3, 191.	0.8	61
46	No-boundary thinking in bioinformatics research. <i>BioData Mining</i> , 2013, 6, 19.	2.2	10
47	Direct Assessment of Viral Diversity in Soils by Random PCR Amplification of Polymorphic DNA. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5450-5457.	1.4	28
48	Diffuse flow environments within basalt- and sediment-based hydrothermal vent ecosystems harbor specialized microbial communities. <i>Frontiers in Microbiology</i> , 2013, 4, 182.	1.5	44
49	DNA polymerase phylogeny recapitulates viroplankton biology. <i>FASEB Journal</i> , 2013, 27, 540.2.	0.2	0
50	Evaluation of Two Approaches for Assessing the Genetic Similarity of Viroplankton Populations as Defined by Genome Size. <i>Applied and Environmental Microbiology</i> , 2012, 78, 8773-8783.	1.4	15
51	VIROME: a standard operating procedure for analysis of viral metagenome sequences. <i>Standards in Genomic Sciences</i> , 2012, 6, 427-439.	1.5	169
52	Groundtruthing Next-Gen Sequencing for Microbial Ecology—Biases and Errors in Community Structure Estimates from PCR Amplicon Pyrosequencing. <i>PLoS ONE</i> , 2012, 7, e44224.	1.1	145
53	Profiling conserved microRNA expression in recombinant CHO cell lines using illumina sequencing. <i>Biotechnology and Bioengineering</i> , 2012, 109, 1371-1375.	1.7	37
54	Impacts of Poultry House Environment on Poultry Litter Bacterial Community Composition. <i>PLoS ONE</i> , 2011, 6, e24785.	1.1	79

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55	Unraveling the viral tapestry (from inside the capsid out). <i>ISME Journal</i> , 2011, 5, 165-168.	4.4	27
56	Optimizing the indirect extraction of prokaryotic DNA from soils. <i>Soil Biology and Biochemistry</i> , 2011, 43, 736-748.	4.2	44
57	Evaluation of a Transposase Protocol for Rapid Generation of Shotgun High-Throughput Sequencing Libraries from Nanogram Quantities of DNA. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8071-8079.	1.4	89
58	The effect of nutrient deposition on bacterial communities in Arctic tundra soil. <i>Environmental Microbiology</i> , 2010, 12, 1842-1854.	1.8	323
59	Functional viral metagenomics and the next generation of molecular tools. <i>Trends in Microbiology</i> , 2010, 18, 20-29.	3.5	78
60	Observation of Virus-Like Particles in Vascular and Coelomic Hemolymph of <i>Riftia pachyptil</i> . <i>Microscopy and Microanalysis</i> , 2009, 15, 100-101.	0.2	0
61	Identification of bacteria associated with a disease affecting the marine sponge <i>Ianthella basta</i> in New Britain, Papua New Guinea. <i>Marine Ecology - Progress Series</i> , 2006, 324, 139-150.	0.9	56
62	Relationship of <i>Vibrio</i> Species Infection and Elevated Temperatures to Yellow Blotch/Band Disease in Caribbean Corals. <i>Applied and Environmental Microbiology</i> , 2004, 70, 6855-6864.	1.4	156
63	<i>Aurantimonas corallicida</i> gen. nov., sp. nov., the causative agent of white plague type II on Caribbean scleractinian corals. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 1115-1122.	0.8	210
64	The etiology of white pox, a lethal disease of the Caribbean elkhorn coral, <i>Acropora palmata</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 8725-8730.	3.3	376
65	Molecular diversity of diazotrophs in oligotrophic tropical seagrass bed communities. <i>FEMS Microbiology Ecology</i> , 2002, 39, 113-119.	1.3	97
66	Microbial disease causation in marine invertebrates: problems, practices, and future prospects. <i>Hydrobiologia</i> , 2001, 460, 131-139.	1.0	24