

Robert A Edwards

List of Publications by Year in descending order

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209
papers

52,012
citations

5876

81
h-index

2375

198
g-index

241
all docs

241
docs citations

241
times ranked

48249
citing authors

#	ARTICLE	IF	CITATIONS
1	The RAST Server: Rapid Annotations using Subsystems Technology. BMC Genomics, 2008, 9, 75.	1.2	9,977
2	Quality control and preprocessing of metagenomic datasets. Bioinformatics, 2011, 27, 863-864.	1.8	4,402
3	The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). Nucleic Acids Research, 2014, 42, D206-D214.	6.5	3,832
4	The metagenomics RAST server – a public resource for the automatic phylogenetic and functional analysis of metagenomes. BMC Bioinformatics, 2008, 9, 386.	1.2	3,200
5	RASTtk: A modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. Scientific Reports, 2015, 5, 8365.	1.6	2,080
6	The Subsystems Approach to Genome Annotation and its Use in the Project to Annotate 1000 Genomes. Nucleic Acids Research, 2005, 33, 5691-5702.	6.5	1,806
7	Community Genomics Among Stratified Microbial Assemblages in the Ocean's Interior. Science, 2006, 311, 496-503.	6.0	1,261
8	The minimum information about a genome sequence (MIGS) specification. Nature Biotechnology, 2008, 26, 541-547.	9.4	1,069
9	The Marine Viromes of Four Oceanic Regions. PLoS Biology, 2006, 4, e368.	2.6	867
10	Functional metagenomic profiling of nine biomes. Nature, 2008, 452, 629-632.	13.7	842
11	Viral metagenomics. Nature Reviews Microbiology, 2005, 3, 504-510.	13.6	783
12	Gene-centric metagenomics of the fiber-adherent bovine rumen microbiome reveals forage specific glycoside hydrolases. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1948-1953.	3.3	669
13	Critical Assessment of Metagenome Interpretation – a benchmark of metagenomics software. Nature Methods, 2017, 14, 1063-1071.	9.0	635
14	Fast Identification and Removal of Sequence Contamination from Genomic and Metagenomic Datasets. PLoS ONE, 2011, 6, e17288.	1.1	630
15	A highly abundant bacteriophage discovered in the unknown sequences of human faecal metagenomes. Nature Communications, 2014, 5, 4498.	5.8	617
16	Metagenomic analysis of stressed coral holobionts. Environmental Microbiology, 2009, 11, 2148-2163.	1.8	551
17	The Phage Proteomic Tree: a Genome-Based Taxonomy for Phage. Journal of Bacteriology, 2002, 184, 4529-4535.	1.0	529
18	Metagenomic analysis of the microbial community associated with the coral <i>Porites astreoides</i> . Environmental Microbiology, 2007, 9, 2707-2719.	1.8	520

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19	Improved allelic exchange vectors and their use to analyze 987P fimbria gene expression. <i>Gene</i> , 1998, 207, 149-157.	1.0	509
20	Metagenomic and Small-Subunit rRNA Analyses Reveal the Genetic Diversity of Bacteria, Archaea, Fungi, and Viruses in Soil. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7059-7066.	1.4	480
21	Indirect effects of algae on coral: algae-mediated, microbe-induced coral mortality. <i>Ecology Letters</i> , 2006, 9, 835-845.	3.0	444
22	Lytic to temperate switching of viral communities. <i>Nature</i> , 2016, 531, 466-470.	13.7	440
23	Probiotic Bacteria Reduce <i>Salmonella Typhimurium</i> Intestinal Colonization by Competing for Iron. <i>Cell Host and Microbe</i> , 2013, 14, 26-37.	5.1	413
24	PhiSpy: a novel algorithm for finding prophages in bacterial genomes that combines similarity- and composition-based strategies. <i>Nucleic Acids Research</i> , 2012, 40, e126-e126.	6.5	406
25	Using pyrosequencing to shed light on deep mine microbial ecology. <i>BMC Genomics</i> , 2006, 7, 57.	1.2	405
26	Computational approaches to predict bacteriophage-host relationships. <i>FEMS Microbiology Reviews</i> , 2016, 40, 258-272.	3.9	394
27	Viral and microbial community dynamics in four aquatic environments. <i>ISME Journal</i> , 2010, 4, 739-751.	4.4	387
28	Microbial Ecology of Four Coral Atolls in the Northern Line Islands. <i>PLoS ONE</i> , 2008, 3, e1584.	1.1	383
29	Wnt signaling directs a metabolic program of glycolysis and angiogenesis in colon cancer. <i>EMBO Journal</i> , 2014, 33, 1454-1473.	3.5	348
30	Detection of Large Numbers of Novel Sequences in the Metatranscriptomes of Complex Marine Microbial Communities. <i>PLoS ONE</i> , 2008, 3, e3042.	1.1	321
31	Microbial genomic taxonomy. <i>BMC Genomics</i> , 2013, 14, 913.	1.2	316
32	Viral diversity and dynamics in an infant gut. <i>Research in Microbiology</i> , 2008, 159, 367-373.	1.0	288
33	Zinc Sequestration by the Neutrophil Protein Calprotectin Enhances <i>Salmonella</i> Growth in the Inflamed Gut. <i>Cell Host and Microbe</i> , 2012, 11, 227-239.	5.1	286
34	Bacterial carbon processing by generalist species in the coastal ocean. <i>Nature</i> , 2008, 451, 708-711.	13.7	284
35	Transposases are the most abundant, most ubiquitous genes in nature. <i>Nucleic Acids Research</i> , 2010, 38, 4207-4217.	6.5	270
36	The Cytokine IL-22 Promotes Pathogen Colonization by Suppressing Related Commensal Bacteria. <i>Immunity</i> , 2014, 40, 262-273.	6.6	252

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37	Biodiversity and biogeography of phages in modern stromatolites and thrombolites. <i>Nature</i> , 2008, 452, 340-343.	13.7	251
38	Insights into antibiotic resistance through metagenomic approaches. <i>Future Microbiology</i> , 2012, 7, 73-89.	1.0	251
39	Comparative Metagenomics Reveals Host Specific Metavirulomes and Horizontal Gene Transfer Elements in the Chicken Cecum Microbiome. <i>PLoS ONE</i> , 2008, 3, e2945.	1.1	247
40	Phylogenetic classification of short environmental DNA fragments. <i>Nucleic Acids Research</i> , 2008, 36, 2230-2239.	6.5	246
41	Discovery of an expansive bacteriophage family that includes the most abundant viruses from the human gut. <i>Nature Microbiology</i> , 2018, 3, 38-46.	5.9	245
42	Experimental and Computational Assessment of Conditionally Essential Genes in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2006, 188, 8259-8271.	1.0	237
43	Marine viruses discovered via metagenomics shed light on viral strategies throughout the oceans. <i>Nature Communications</i> , 2017, 8, 15955.	5.8	231
44	Local genomic adaptation of coral reef-associated microbiomes to gradients of natural variability and anthropogenic stressors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10227-10232.	3.3	220
45	Global microbialization of coral reefs. <i>Nature Microbiology</i> , 2016, 1, 16042.	5.9	214
46	Identification and removal of ribosomal RNA sequences from metatranscriptomes. <i>Bioinformatics</i> , 2012, 28, 433-435.	1.8	212
47	PHACTS, a computational approach to classifying the lifestyle of phages. <i>Bioinformatics</i> , 2012, 28, 614-618.	1.8	210
48	TagCleaner: Identification and removal of tag sequences from genomic and metagenomic datasets. <i>BMC Bioinformatics</i> , 2010, 11, 341.	1.2	207
49	Metagenomic analysis indicates that stressors induce production of herpes-like viruses in the coral <i>Porites compressa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18413-18418.	3.3	205
50	Metagenomic and stable isotopic analyses of modern freshwater microbialites in Cuatro Ci�negas, Mexico. <i>Environmental Microbiology</i> , 2009, 11, 16-34.	1.8	204
51	Taxonomic composition and gene content of a methane-producing microbial community isolated from a biogas reactor. <i>Journal of Biotechnology</i> , 2008, 136, 91-101.	1.9	202
52	Genome of Staphylococcal Phage K: a New Lineage of Myoviridae Infecting Gram-Positive Bacteria with a Low G+C Content. <i>Journal of Bacteriology</i> , 2004, 186, 2862-2871.	1.0	199
53	Comparative genomics of closely related salmonellae. <i>Trends in Microbiology</i> , 2002, 10, 94-99.	3.5	193
54	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	5.9	184

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55	The GAAS Metagenomic Tool and Its Estimations of Viral and Microbial Average Genome Size in Four Major Biomes. <i>PLoS Computational Biology</i> , 2009, 5, e1000593.	1.5	177
56	Whole proteome analysis of post-translational modifications: Applications of mass-spectrometry for proteogenomic annotation. <i>Genome Research</i> , 2007, 17, 1362-1377.	2.4	175
57	Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2018, 163, 1125-1129.	0.9	172
58	SEED Servers: High-Performance Access to the SEED Genomes, Annotations, and Metabolic Models. <i>PLoS ONE</i> , 2012, 7, e48053.	1.1	169
59	<i>Salmonella enterica</i> Serovar Typhi Possesses a Unique Repertoire of Fimbrial Gene Sequences. <i>Infection and Immunity</i> , 2001, 69, 2894-2901.	1.0	166
60	SUPER-FOCUS: a tool for agile functional analysis of shotgun metagenomic data. <i>Bioinformatics</i> , 2016, 32, 354-361.	1.8	161
61	PHANOTATE: a novel approach to gene identification in phage genomes. <i>Bioinformatics</i> , 2019, 35, 4537-4542.	1.8	147
62	Microbial taxonomy in the post-genomic era: Rebuilding from scratch?. <i>Archives of Microbiology</i> , 2015, 197, 359-370.	1.0	144
63	Taxonomy of prokaryotic viruses: 2018-2019 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2020, 165, 1253-1260.	0.9	144
64	Metagenomics and metatranscriptomics: Windows on CF-associated viral and microbial communities. <i>Journal of Cystic Fibrosis</i> , 2013, 12, 154-164.	0.3	142
65	An application of statistics to comparative metagenomics. <i>BMC Bioinformatics</i> , 2006, 7, 162.	1.2	135
66	Phage-bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. <i>Environmental Microbiology</i> , 2012, 14, 207-227.	1.8	128
67	Viral communities associated with healthy and bleaching corals. <i>Environmental Microbiology</i> , 2008, 10, 2277-2286.	1.8	125
68	Abrolhos Bank Reef Health Evaluated by Means of Water Quality, Microbial Diversity, Benthic Cover, and Fish Biomass Data. <i>PLoS ONE</i> , 2012, 7, e36687.	1.1	125
69	A bioinformatic analysis of ribonucleotide reductase genes in phage genomes and metagenomes. <i>BMC Evolutionary Biology</i> , 2013, 13, 33.	3.2	123
70	Accessing the SEED Genome Databases via Web Services API: Tools for Programmers. <i>BMC Bioinformatics</i> , 2010, 11, 319.	1.2	122
71	Clinical Insights from Metagenomic Analysis of Sputum Samples from Patients with Cystic Fibrosis. <i>Journal of Clinical Microbiology</i> , 2014, 52, 425-437.	1.8	120
72	Mosaic Prophages with Horizontally Acquired Genes Account for the Emergence and Diversification of the Globally Disseminated MIT1 Clone of <i>Streptococcus pyogenes</i> . <i>Journal of Bacteriology</i> , 2005, 187, 3311-3318.	1.0	109

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73	Salmonella Mitigates Oxidative Stress and Thrives in the Inflamed Gut by Evading Calprotectin-Mediated Manganese Sequestration. <i>Cell Host and Microbe</i> , 2016, 19, 814-825.	5.1	109
74	Standardized bacteriophage purification for personalized phage therapy. <i>Nature Protocols</i> , 2020, 15, 2867-2890.	5.5	109
75	Essential genes on metabolic maps. <i>Current Opinion in Biotechnology</i> , 2006, 17, 448-456.	3.3	106
76	Metagenomic Analysis of Healthy and White Plague-Affected <i>Mussismilia braziliensis</i> Corals. <i>Microbial Ecology</i> , 2013, 65, 1076-1086.	1.4	103
77	Excessive folate synthesis limits lifespan in the <i>C. elegans</i> : <i>E. coli</i> aging model. <i>BMC Biology</i> , 2012, 10, 67.	1.7	102
78	Allelic variation contributes to bacterial host specificity. <i>Nature Communications</i> , 2015, 6, 8754.	5.8	100
79	Diversification of the Salmonella Fimbriae: A Model of Macro- and Microevolution. <i>PLoS ONE</i> , 2012, 7, e38596.	1.1	96
80	A role for Salmonella fimbriae in intraperitoneal infections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 1258-1262.	3.3	95
81	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. <i>Systematic Biology</i> , 2020, 69, 110-123.	2.7	89
82	FOCUS: an alignment-free model to identify organisms in metagenomes using non-negative least squares. <i>PeerJ</i> , 2014, 2, e425.	0.9	89
83	The National Microbial Pathogen Database Resource (NMPDR): a genomics platform based on subsystem annotation. <i>Nucleic Acids Research</i> , 2007, 35, D347-D353.	6.5	87
84	Reference-independent comparative metagenomics using cross-assembly: crAss. <i>Bioinformatics</i> , 2012, 28, 3225-3231.	1.8	87
85	Î±-Ketoglutarate attenuates Wnt signaling and drives differentiation in colorectal cancer. <i>Nature Cancer</i> , 2020, 1, 345-358.	5.7	85
86	Taxonomy of prokaryotic viruses: update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2016, 161, 1095-1099.	0.9	83
87	Baseline Assessment of Mesophotic Reefs of the Vitória-Trindade Seamount Chain Based on Water Quality, Microbial Diversity, Benthic Cover and Fish Biomass Data. <i>PLoS ONE</i> , 2015, 10, e0130084.	1.1	81
88	Fimbrial expression in enteric bacteria: a critical step in intestinal pathogenesis. <i>Trends in Microbiology</i> , 1998, 6, 282-287.	3.5	75
89	Draft Sequencing and Comparative Genomics of <i>Xylella fastidiosa</i> Strains Reveal Novel Biological Insights. <i>Genome Research</i> , 2002, 12, 1556-1563.	2.4	70
90	Finding novel genes in bacterial communities isolated from the environment. <i>Bioinformatics</i> , 2006, 22, e281-e289.	1.8	68

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91	Phage Genome Annotation Using the RAST Pipeline. <i>Methods in Molecular Biology</i> , 2018, 1681, 231-238.	0.4	64
92	Lactate/pyruvate transporter MCT-1 is a direct Wnt target that confers sensitivity to 3-bromopyruvate in colon cancer. <i>Cancer & Metabolism</i> , 2016, 4, 20.	2.4	63
93	Acidobacteria Subgroups and Their Metabolic Potential for Carbon Degradation in Sugarcane Soil Amended With Vinasse and Nitrogen Fertilizers. <i>Frontiers in Microbiology</i> , 2019, 10, 1680.	1.5	61
94	Combining de novo and reference-guided assembly with scaffold_builder. <i>Source Code for Biology and Medicine</i> , 2013, 8, 23.	1.7	59
95	Optimizing and evaluating the reconstruction of Metagenome-assembled microbial genomes. <i>BMC Genomics</i> , 2017, 18, 915.	1.2	59
96	Transcriptional Profiling of <i>Mycoplasma hyopneumoniae</i> during Heat Shock Using Microarrays. <i>Infection and Immunity</i> , 2006, 74, 160-166.	1.0	57
97	Explaining microbial phenotypes on a genomic scale: GWAS for microbes. <i>Briefings in Functional Genomics</i> , 2013, 12, 366-380.	1.3	57
98	Variability and host density independence in inductions-based estimates of environmental lysogeny. <i>Nature Microbiology</i> , 2017, 2, 17064.	5.9	57
99	Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2017, 162, 1153-1157.	0.9	57
100	Taxonomic and Functional Microbial Signatures of the Endemic Marine Sponge <i>Arenosclera brasiliensis</i> . <i>PLoS ONE</i> , 2012, 7, e39905.	1.1	56
101	Siderophore-based immunization strategy to inhibit growth of enteric pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13462-13467.	3.3	56
102	A Glimpse into the Expanded Genome Content of <i>Vibrio cholerae</i> through Identification of Genes Present in Environmental Strains. <i>Journal of Bacteriology</i> , 2005, 187, 2992-3001.	1.0	54
103	RaFAH: Host prediction for viruses of Bacteria and Archaea based on protein content. <i>Patterns</i> , 2021, 2, 100274.	3.1	53
104	Multi-Analytical Approach Reveals Potential Microbial Indicators in Soil for Sugarcane Model Systems. <i>PLoS ONE</i> , 2015, 10, e0129765.	1.1	52
105	Integration of genomic and proteomic analyses in the classification of the Siphoviridae family. <i>Virology</i> , 2015, 477, 144-154.	1.1	52
106	Low-Molecular-Weight Protein Tyrosine Phosphatases of <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2005, 187, 4945-4956.	1.0	51
107	Mechanistic Model of <i>Rothia mucilaginosa</i> Adaptation toward Persistence in the CF Lung, Based on a Genome Reconstructed from Metagenomic Data. <i>PLoS ONE</i> , 2013, 8, e64285.	1.1	51
108	PhANNs, a fast and accurate tool and web server to classify phage structural proteins. <i>PLoS Computational Biology</i> , 2020, 16, e1007845.	1.5	50

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109	In Vitro Characterization of the <i>Bacillus subtilis</i> Protein Tyrosine Phosphatase YwqE. <i>Journal of Bacteriology</i> , 2005, 187, 3384-3390.	1.0	49
110	A diversity-generating retroelement encoded by a globally ubiquitous <i>Bacteroides</i> phage. <i>Microbiome</i> , 2018, 6, 191.	4.9	48
111	Differential regulation of <i>fasA</i> and <i>fasH</i> expression of <i>Escherichia coli</i> 987P fimbriae by environmental cues. <i>Molecular Microbiology</i> , 1997, 25, 797-809.	1.2	47
112	Multivariate analysis of functional metagenomes. <i>Frontiers in Genetics</i> , 2013, 4, 41.	1.1	47
113	Genome skimming™ with the MinION hand-held sequencer identifies CITES-listed shark species in India's exports market. <i>Scientific Reports</i> , 2019, 9, 4476.	1.6	45
114	Genomic Taxonomy of the Genus <i>Prochlorococcus</i> . <i>Microbial Ecology</i> , 2013, 66, 752-762.	1.4	44
115	multiPhATE: bioinformatics pipeline for functional annotation of phage isolates. <i>Bioinformatics</i> , 2019, 35, 4402-4404.	1.8	44
116	Increasing DNA Transfer Efficiency by Temporary Inactivation of Host Restriction. <i>BioTechniques</i> , 1999, 26, 892-900.	0.8	42
117	Sequencing of Seven Haloarchaeal Genomes Reveals Patterns of Genomic Flux. <i>PLoS ONE</i> , 2012, 7, e41389.	1.1	42
118	MetaBase--the wiki-database of biological databases. <i>Nucleic Acids Research</i> , 2012, 40, D1250-D1254.	6.5	40
119	From DNA to FBA: How to Build Your Own Genome-Scale Metabolic Model. <i>Frontiers in Microbiology</i> , 2016, 7, 907.	1.5	40
120	Genomic Comparison of the Closely-Related <i>Salmonella enterica</i> Serovars Enteritidis, Dublin and Gallinarum. <i>PLoS ONE</i> , 2015, 10, e0126883.	1.1	39
121	The skin microbiome of elasmobranchs follows phylosymbiosis, but in teleost fishes, the microbiomes converge. <i>Microbiome</i> , 2020, 8, 93.	4.9	37
122	The role of uridylyltransferase in the control of <i>Klebsiella pneumoniae</i> <i>nif</i> gene regulation. <i>Molecular Genetics and Genomics</i> , 1995, 247, 189-198.	2.4	36
123	Real Time Metagenomics: Using k-mers to annotate metagenomes. <i>Bioinformatics</i> , 2012, 28, 3316-3317.	1.8	35
124	Structure and function of a cyanophage-encoded peptide deformylase. <i>ISME Journal</i> , 2013, 7, 1150-1160.	4.4	32
125	Identification of major and minor chaperone proteins involved in the export of 987P fimbriae. <i>Journal of Bacteriology</i> , 1996, 178, 3426-3433.	1.0	31
126	Perspective on taxonomic classification of uncultivated viruses. <i>Current Opinion in Virology</i> , 2021, 51, 207-215.	2.6	31

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127	Bacterial Community Associated with the Reef Coral <i>Mussismilia braziliensis</i> 's Momentum Boundary Layer over a Diel Cycle. <i>Frontiers in Microbiology</i> , 2017, 8, 784.	1.5	30
128	Modeling of the Coral Microbiome: the Influence of Temperature and Microbial Network. <i>MBio</i> , 2020, 11, .	1.8	30
129	Coastal bacterioplankton community diversity along a latitudinal gradient in Latin America by means of V6 tag pyrosequencing. <i>Archives of Microbiology</i> , 2011, 193, 105-114.	1.0	29
130	Connecting genotype to phenotype in the era of high-throughput sequencing. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2011, 1810, 967-977.	1.1	28
131	Applying Shannon's information theory to bacterial and phage genomes and metagenomes. <i>Scientific Reports</i> , 2013, 3, 1033.	1.6	28
132	Multidimensional metrics for estimating phage abundance, distribution, gene density, and sequence coverage in metagenomes. <i>Frontiers in Microbiology</i> , 2015, 6, 381.	1.5	28
133	Diel population and functional synchrony of microbial communities on coral reefs. <i>Nature Communications</i> , 2019, 10, 1691.	5.8	28
134	Microbes, metagenomes and marine mammals: enabling the next generation of scientist to enter the genomic era. <i>BMC Genomics</i> , 2013, 14, 600.	1.2	27
135	Genomic and ecological attributes of marine bacteriophages encoding bacterial virulence genes. <i>BMC Genomics</i> , 2020, 21, 126.	1.2	26
136	Genome analysis of the obligately lytic bacteriophage 4268 of <i>Lactococcus lactis</i> provides insight into its adaptable nature. <i>Gene</i> , 2006, 366, 189-199.	1.0	25
137	PARTIE: a partition engine to separate metagenomic and amplicon projects in the Sequence Read Archive. <i>Bioinformatics</i> , 2017, 33, 2389-2391.	1.8	25
138	Comparative genomics of 274 <i>Vibrio cholerae</i> genomes reveals mobile functions structuring three niche dimensions. <i>BMC Genomics</i> , 2014, 15, 654.	1.2	24
139	Bacterial Viruses Subcommittee and Archaeal Viruses Subcommittee of the ICTV: update of taxonomy changes in 2021. <i>Archives of Virology</i> , 2021, 166, 3239-3244.	0.9	24
140	Characterization of the ELPhiS Prophage from <i>Salmonella enterica</i> Serovar Enteritidis Strain LK5. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1785-1793.	1.4	23
141	PhiSiGns: an online tool to identify signature genes in phages and design PCR primers for examining phage diversity. <i>BMC Bioinformatics</i> , 2012, 13, 37.	1.2	21
142	Genomic analysis and growth-phase-dependent regulation of the SEF14 fimbriae of <i>Salmonella enterica</i> serovar Enteritidis The GenBank accession number for the sequence reported in this paper is AF239978.. <i>Microbiology (United Kingdom)</i> , 2001, 147, 2705-2715.	0.7	21
143	Aging and Intermittent Fasting Impact on Transcriptional Regulation and Physiological Responses of Adult <i>Drosophila</i> Neuronal and Muscle Tissues. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1140.	1.8	20
144	Cystic Fibrosis Rapid Response: Translating Multi-omics Data into Clinically Relevant Information. <i>MBio</i> , 2019, 10, .	1.8	20

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145	Growth faltering regardless of chronic diarrhea is associated with mucosal immune dysfunction and microbial dysbiosis in the gut lumen. <i>Mucosal Immunology</i> , 2021, 14, 1113-1126.	2.7	20
146	Microbial Community Profile and Water Quality in a Protected Area of the Caatinga Biome. <i>PLoS ONE</i> , 2016, 11, e0148296.	1.1	20
147	Gut Microbiota Represent a Major Thermogenic Biomass. <i>Function</i> , 2021, 2, zqab019.	1.1	19
148	Sequencing at sea: challenges and experiences in Ion Torrent PGM sequencing during the 2013 Southern Line Islands Research Expedition. <i>PeerJ</i> , 2014, 2, e520.	0.9	19
149	Functional characterization of ligninolytic <i>Klebsiella</i> spp. strains associated with soil and freshwater. <i>Archives of Microbiology</i> , 2018, 200, 1267-1278.	1.0	18
150	Microglia Do Not Restrict SARS-CoV-2 Replication following Infection of the Central Nervous System of K18-Human ACE2 Transgenic Mice. <i>Journal of Virology</i> , 2022, 96, jvi0196921.	1.5	18
151	Draft Genome Sequence of the Fish Pathogen <i>Piscirickettsia salmonis</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	17
152	Searching the Sequence Read Archive using Jetstream and Wrangler. , 2018, , .		17
153	A Novel Group of Promiscuous Podophages Infecting Diverse Gammaproteobacteria from River Communities Exhibits Dynamic Intergenous Host Adaptation. <i>MSystems</i> , 2021, 6, .	1.7	17
154	Some of the most interesting <scp>CASP</scp>11 targets through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 34-50.	1.5	16
155	Biological chlorine cycling in the Arctic Coastal Plain. <i>Biogeochemistry</i> , 2017, 134, 243-260.	1.7	16
156	PMAnalyzer: a new web interface for bacterial growth curve analysis. <i>Bioinformatics</i> , 2017, 33, 1905-1906.	1.8	15
157	Microfluidic PCR Combined with Pyrosequencing for Identification of Allelic Variants with Phenotypic Associations among Targeted <i>Salmonella</i> Genes. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7480-7482.	1.4	14
158	Complete Genome Sequencing of a Multidrug-Resistant and Human-Invasive <i>Salmonella enterica</i> Serovar Typhimurium Strain of the Emerging Sequence Type 213 Genotype. <i>Genome Announcements</i> , 2015, 3, .	0.8	14
159	Cyanobacterial biodiversity of semiarid public drinking water supply reservoirs assessed via next-generation DNA sequencing technology. <i>Journal of Microbiology</i> , 2019, 57, 450-460.	1.3	14
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