

Robert A Edwards

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/1621144/robert-a-edwards-publications-by-year.pdf>

Version: 2024-04-25

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

220
papers

37,707
citations

74
h-index

194
g-index

241
ext. papers

47,389
ext. citations

8.3
avg, IF

7.14
L-index

#	Paper	IF	Citations
220	Predicting the capsid architecture of phages from metagenomic data.. <i>Computational and Structural Biotechnology Journal</i> , 2022 , 20, 721-732	6.8	1
219	The StkSR Two-Component System Influences Colistin Resistance in <i>Acinetobacter baumannii</i> . <i>Microorganisms</i> , 2022 , 10, 985	4.9	0
218	Patient-derived xenograft culture-transplant system for investigation of human breast cancer metastasis. <i>Communications Biology</i> , 2021 , 4, 1268	6.7	1
217	Microglia do not restrict SARS-CoV-2 replication following infection of the central nervous system of K18-hACE2 transgenic mice 2021 ,		2
216	Perspective on taxonomic classification of uncultivated viruses. <i>Current Opinion in Virology</i> , 2021 , 51, 207-215	7.5	5
215	MultiPhATE2: code for functional annotation and comparison of phage genomes. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	3
214	Gut Microbiota Represent a Major Thermogenic Biomass. <i>Function</i> , 2021 , 2, zqab019	6.1	4
213	No Evidence Known Viruses Play a Role in the Pathogenesis of Onchocerciasis-Associated Epilepsy. An Explorative Metagenomic Case-Control Study. <i>Pathogens</i> , 2021 , 10,	4.5	2
212	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	9.2	5
211	RaFAH: Host prediction for viruses of Bacteria and Archaea based on protein content. <i>Patterns</i> , 2021 , 2, 100274	5.1	7
210	A Novel Group of Promiscuous Podophages Infecting Diverse Gammaproteobacteria from River Communities Exhibits Dynamic Intergenous Host Adaptation. <i>MSystems</i> , 2021 , 6,	7.6	7
209	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	2.6	5
208	Utilizing Amino Acid Composition and Entropy of Potential Open Reading Frames to Identify Protein-Coding Genes. <i>Microorganisms</i> , 2021 , 9,	4.9	3
207	Microglia do not restrict SARS-CoV-2 replication following infection of the central nervous system of K18-hACE2 transgenic mice.. <i>Journal of Virology</i> , 2021 , jvi0196921	6.6	5
206	NCBI Virus Discovery Codeathon: Building "FIVE" -The Federated Index of Viral Experiments API Index. <i>Viruses</i> , 2020 , 12,	6.2	1
205	The skin microbiome of elasmobranchs follows phyllosymbiosis, but in teleost fishes, the microbiomes converge. <i>Microbiome</i> , 2020 , 8, 93	16.6	15
204	Taxonomy of prokaryotic viruses: 2018-2019 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2020 , 165, 1253-1260	2.6	66

203	β-Ketoglutarate attenuates Wnt signaling and drives differentiation in colorectal cancer. <i>Nature Cancer</i> , 2020 , 1, 345-358	15.4	27
202	Latitude and chlorophyll a density drive the distribution of carbohydrate-active enzymes in the planktonic microbial fraction of the epipelagic zone. <i>Environmental Microbiology Reports</i> , 2020 , 12, 473-485	3.7	2
201	Genomic and ecological attributes of marine bacteriophages encoding bacterial virulence genes. <i>BMC Genomics</i> , 2020 , 21, 126	4.5	15
200	Mitochondrial genome to aid species delimitation and effective conservation of the Sharpnose Guitarfish (<i>Glaucostegus granulatus</i>). <i>Meta Gene</i> , 2020 , 24, 100648	0.7	7
199	Modeling of the Coral Microbiome: the Influence of Temperature and Microbial Network. <i>MBio</i> , 2020 , 11,	7.8	10
198	Decoding diversity in a coral reef fish species complex with restricted range using metagenomic sequencing of gut contents. <i>Ecology and Evolution</i> , 2020 , 10, 3413-3423	2.8	1
197	PhANNs, a fast and accurate tool and web server to classify phage structural proteins. <i>PLoS Computational Biology</i> , 2020 , 16, e1007845	5	19
196	Standardized bacteriophage purification for personalized phage therapy. <i>Nature Protocols</i> , 2020 , 15, 2867-2890	18.8	40
195	A Distinct Contractile Injection System Gene Cluster Found in a Majority of Healthy Adult Human Microbiomes. <i>MSystems</i> , 2020 , 5,	7.6	4
194	Transcriptome Analysis of Ovarian and Uterine Clear Cell Malignancies. <i>Frontiers in Oncology</i> , 2020 , 10, 598579	5.3	3
193	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. <i>Systematic Biology</i> , 2020 , 69, 110-123	8.4	56
192	Towards Predicting Gut Microbial Metabolism: Integration of Flux Balance Analysis and Untargeted Metabolomics. <i>Metabolites</i> , 2020 , 10,	5.6	6
191	PhANNs, a fast and accurate tool and web server to classify phage structural proteins 2020 , 16, e1007845		
190	PhANNs, a fast and accurate tool and web server to classify phage structural proteins 2020 , 16, e1007845		
189	PhANNs, a fast and accurate tool and web server to classify phage structural proteins 2020 , 16, e1007845		
188	NCBI® Virus Discovery Hackathon: Engaging Research Communities to Identify Cloud Infrastructure Requirements. <i>Genes</i> , 2019 , 10,	4.2	8
187	CRTAM Shapes the Gut Microbiota and Enhances the Severity of Infection. <i>Journal of Immunology</i> , 2019 , 203, 532-543	5.3	3
186	multiPhATE: bioinformatics pipeline for functional annotation of phage isolates. <i>Bioinformatics</i> , 2019 , 35, 4402-4404	7.2	26

185	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	3	6
184	Cystic Fibrosis Rapid Response: Translating Multi-omics Data into Clinically Relevant Information. <i>MBio</i> , 2019 , 10,	7.8	16
183	PHANOTATE: a novel approach to gene identification in phage genomes. <i>Bioinformatics</i> , 2019 , 35, 4537-4542	4.4	65
182	Prodigious Prevotella phages. <i>Nature Microbiology</i> , 2019 , 4, 550-551	26.6	1
181	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	4.9	28
180	Diel population and functional synchrony of microbial communities on coral reefs. <i>Nature Communications</i> , 2019 , 10, 1691	17.4	13
179	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	5.7	30
178	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019 , 4, 1727-1736	26.6	100
177	Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2018 , 163, 1125-1129	2.6	62
176	Aging and Intermittent Fasting Impact on Transcriptional Regulation and Physiological Responses of Adult Drosophila Neuronal and Muscle Tissues. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	11
175	Functional characterization of ligninolytic Klebsiella spp. strains associated with soil and freshwater. <i>Archives of Microbiology</i> , 2018 , 200, 1267-1278	3	8
174	Phage Genome Annotation Using the RAST Pipeline. <i>Methods in Molecular Biology</i> , 2018 , 1681, 231-238	1.4	38
173	Discovery of an expansive bacteriophage family that includes the most abundant viruses from the human gut. <i>Nature Microbiology</i> , 2018 , 3, 38-46	26.6	148
172	Searching the Sequence Read Archive using Jetstream and Wrangler 2018 ,		11
171	A diversity-generating retroelement encoded by a globally ubiquitous Bacteroides phage. <i>Microbiome</i> , 2018 , 6, 191	16.6	28
170	Bariatric surgery attenuates colitis in an obese murine model. <i>Surgery for Obesity and Related Diseases</i> , 2017 , 13, 661-668	3	4
169	An Agile Functional Analysis of Metagenomic Data Using SUPER-FOCUS. <i>Methods in Molecular Biology</i> , 2017 , 1611, 35-44	1.4	1
168	Variability and host density independence in inductions-based estimates of environmental lysogeny. <i>Nature Microbiology</i> , 2017 , 2, 17064	26.6	40

167	PARTIE: a partition engine to separate metagenomic and amplicon projects in the Sequence Read Archive. <i>Bioinformatics</i> , 2017 , 33, 2389-2391	7.2	13
166	Critical Assessment of Metagenome Interpretation-a benchmark of metagenomics software. <i>Nature Methods</i> , 2017 , 14, 1063-1071	21.6	412
165	PMAnalyzer: a new web interface for bacterial growth curve analysis. <i>Bioinformatics</i> , 2017 , 33, 1905-1906	6.2	9
164	Optimizing and evaluating the reconstruction of Metagenome-assembled microbial genomes. <i>BMC Genomics</i> , 2017 , 18, 915	4.5	25
163	Biological chlorine cycling in the Arctic Coastal Plain. <i>Biogeochemistry</i> , 2017 , 134, 243-260	3.8	9
162	Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2017 , 162, 1153-1157	2.6	38
161	Marine viruses discovered via metagenomics shed light on viral strategies throughout the oceans. <i>Nature Communications</i> , 2017 , 8, 15955	17.4	129
160	Bacterial Community Associated with the Reef Coral Momentum Boundary Layer over a Diel Cycle. <i>Frontiers in Microbiology</i> , 2017 , 8, 784	5.7	17
159	Kullback Leibler divergence in complete bacterial and phage genomes. <i>PeerJ</i> , 2017 , 5, e4026	3.1	1
158	SUPER-FOCUS: a tool for agile functional analysis of shotgun metagenomic data. <i>Bioinformatics</i> , 2016 , 32, 354-61	7.2	82
157	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	11.5	42
156	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	5.4	45
155	Global microbialization of coral reefs. <i>Nature Microbiology</i> , 2016 , 1, 16042	26.6	121
154	Salmonella Mitigates Oxidative Stress and Thrives in the Inflamed Gut by Evading Calprotectin-Mediated Manganese Sequestration. <i>Cell Host and Microbe</i> , 2016 , 19, 814-25	23.4	74
153	Computational approaches to predict bacteriophage-host relationships. <i>FEMS Microbiology Reviews</i> , 2016 , 40, 258-72	15.1	235
152	Lytic to temperate switching of viral communities. <i>Nature</i> , 2016 , 531, 466-70	50.4	278
151	Taxonomy of prokaryotic viruses: update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2016 , 161, 1095-9	2.6	67
150	Microbial Community Profile and Water Quality in a Protected Area of the Caatinga Biome. <i>PLoS ONE</i> , 2016 , 11, e0148296	3.7	17

149	From DNA to FBA: How to Build Your Own Genome-Scale Metabolic Model. <i>Frontiers in Microbiology</i> , 2016 , 7, 907	5.7	28
148	Using viromes to predict novel immune proteins in non-model organisms. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016 , 283,	4.4	4
147	Some of the most interesting CASP11 targets through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84 Suppl 1, 34-50	4.2	12
146	Draft Genome Sequence of <i>Cylindrospermopsis raciborskii</i> (Cyanobacteria) Strain ITEP-A1 Isolated from a Brazilian Semiarid Freshwater Body: Evidence of Saxitoxin and Cylindrospermopsin Synthetase Genes. <i>Genome Announcements</i> , 2016 , 4,		4
145	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,		11
144	Microbial taxonomy in the post-genomic era: rebuilding from scratch?. <i>Archives of Microbiology</i> , 2015 , 197, 359-70	3	78
143	Integration of genomic and proteomic analyses in the classification of the Siphoviridae family. <i>Virology</i> , 2015 , 477, 144-154	3.6	39
142	Allelic variation contributes to bacterial host specificity. <i>Nature Communications</i> , 2015 , 6, 8754	17.4	54
141	RASTtk: a modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. <i>Scientific Reports</i> , 2015 , 5, 8365	4.9	1061
140	Phage Phenomics: Physiological Approaches to Characterize Novel Viral Proteins. <i>Journal of Visualized Experiments</i> , 2015 , e52854	1.6	8
139	Genomic Comparison of the Closely-Related <i>Salmonella enterica</i> Serovars Enteritidis, Dublin and Gallinarum. <i>PLoS ONE</i> , 2015 , 10, e0126883	3.7	27
138	Multi-Analytical Approach Reveals Potential Microbial Indicators in Soil for Sugarcane Model Systems. <i>PLoS ONE</i> , 2015 , 10, e0129765	3.7	34
137	Multidimensional metrics for estimating phage abundance, distribution, gene density, and sequence coverage in metagenomes. <i>Frontiers in Microbiology</i> , 2015 , 6, 381	5.7	21
136	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	3.7	41
135	GenomePeek-an online tool for prokaryotic genome and metagenome analysis. <i>PeerJ</i> , 2015 , 3, e1025	3.1	10
134	The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). <i>Nucleic Acids Research</i> , 2014 , 42, D206-14	20.1	2534
133	A highly abundant bacteriophage discovered in the unknown sequences of human faecal metagenomes. <i>Nature Communications</i> , 2014 , 5, 4498	17.4	420
132	Comparative genomics of 274 <i>Vibrio cholerae</i> genomes reveals mobile functions structuring three niche dimensions. <i>BMC Genomics</i> , 2014 , 15, 654	4.5	21

131	The cytokine IL-22 promotes pathogen colonization by suppressing related commensal bacteria. <i>Immunity</i> , 2014 , 40, 262-73	32.3	205
130	Wnt signaling directs a metabolic program of glycolysis and angiogenesis in colon cancer. <i>EMBO Journal</i> , 2014 , 33, 1454-73	13	256
129	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, 10227-32	11.5	139
128	Clinical insights from metagenomic analysis of sputum samples from patients with cystic fibrosis. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 425-37	9.7	96
127	FOCUS: an alignment-free model to identify organisms in metagenomes using non-negative least squares. <i>PeerJ</i> , 2014 , 2, e425	3.1	59
126	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	3.1	15
125	A bioinformatic analysis of ribonucleotide reductase genes in phage genomes and metagenomes. <i>BMC Evolutionary Biology</i> , 2013 , 13, 33	3	79
124	Genomic taxonomy of the genus prochlorococcus. <i>Microbial Ecology</i> , 2013 , 66, 752-62	4.4	27
123	Probiotic bacteria reduce salmonella typhimurium intestinal colonization by competing for iron. <i>Cell Host and Microbe</i> , 2013 , 14, 26-37	23.4	287
122	Microbes, metagenomes and marine mammals: enabling the next generation of scientist to enter the genomic era. <i>BMC Genomics</i> , 2013 , 14, 600	4.5	18
121	Metagenomics and metatranscriptomics: windows on CF-associated viral and microbial communities. <i>Journal of Cystic Fibrosis</i> , 2013 , 12, 154-64	4.1	118
120	Structure and function of a cyanophage-encoded peptide deformylase. <i>ISME Journal</i> , 2013 , 7, 1150-60	11.9	30
119	Metagenomic analysis of healthy and white plague-affected <i>Mussismilia braziliensis</i> corals. <i>Microbial Ecology</i> , 2013 , 65, 1076-86	4.4	62
118	Combining de novo and reference-guided assembly with scaffold_builder. <i>Source Code for Biology and Medicine</i> , 2013 , 8, 23	1.9	39
117	Explaining microbial phenotypes on a genomic scale: GWAS for microbes. <i>Briefings in Functional Genomics</i> , 2013 , 12, 366-80	4.9	38
116	Draft Genome Sequence of the Fish Pathogen <i>Piscirickettsia salmonis</i> . <i>Genome Announcements</i> , 2013 , 1,		15
115	Applying Shannon's information theory to bacterial and phage genomes and metagenomes. <i>Scientific Reports</i> , 2013 , 3, 1033	4.9	22
114	Multivariate analysis of functional metagenomes. <i>Frontiers in Genetics</i> , 2013 , 4, 41	4.5	38

113	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	3.7	38
112	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	3.6	19
111	Zinc sequestration by the neutrophil protein calprotectin enhances <i>Salmonella</i> growth in the inflamed gut. <i>Cell Host and Microbe</i> , 2012 , 11, 227-39	23.4	243
110	Genome sequences of the ethanol-tolerant <i>Lactobacillus vini</i> strains LMG 23202T and JP7.8.9. <i>Journal of Bacteriology</i> , 2012 , 194, 3018	3.5	9
109	Excessive folate synthesis limits lifespan in the <i>C. elegans</i> : <i>E. coli</i> aging model. <i>BMC Biology</i> , 2012 , 10, 67	7.3	81
108	Insights into antibiotic resistance through metagenomic approaches. <i>Future Microbiology</i> , 2012 , 7, 73-89	2.9	199
107	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	3.7	93
106	Genome-wide study of the defective sucrose fermenter strain of <i>Vibrio cholerae</i> from the Latin American cholera epidemic. <i>PLoS ONE</i> , 2012 , 7, e37283	3.7	12
105	Taxonomic and functional microbial signatures of the endemic marine sponge <i>Arenosclera brasiliensis</i> . <i>PLoS ONE</i> , 2012 , 7, e39905	3.7	46
104	Diversification of the <i>Salmonella</i> fimbriae: a model of macro- and microevolution. <i>PLoS ONE</i> , 2012 , 7, e38596	3.7	68
103	SEED servers: high-performance access to the SEED genomes, annotations, and metabolic models. <i>PLoS ONE</i> , 2012 , 7, e48053	3.7	121
102	Phage-bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. <i>Environmental Microbiology</i> , 2012 , 14, 207-27	5.2	82
101	Identification and removal of ribosomal RNA sequences from metatranscriptomes. <i>Bioinformatics</i> , 2012 , 28, 433-5	7.2	148
100	PHACTS, a computational approach to classifying the lifestyle of phages. <i>Bioinformatics</i> , 2012 , 28, 614-8	7.2	144
99	Characterization of the ELPhiS prophage from <i>Salmonella enterica</i> serovar Enteritidis strain LK5. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 1785-93	4.8	20
98	MetaBase--the wiki-database of biological databases. <i>Nucleic Acids Research</i> , 2012 , 40, D1250-4	20.1	31
97	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, 7480-2	4.8	11
96	Genome sequence of the bacterioplanktonic, mixotrophic <i>Vibrio campbellii</i> strain PEL22A, isolated in the Abrolhos Bank. <i>Journal of Bacteriology</i> , 2012 , 194, 2759-60	3.5	10

95	Real time metagenomics: using k-mers to annotate metagenomes. <i>Bioinformatics</i> , 2012 , 28, 3316-7	7.2	29
94	Reference-independent comparative metagenomics using cross-assembly: crAss. <i>Bioinformatics</i> , 2012 , 28, 3225-31	7.2	52
93	Draft genome sequence of the shrimp pathogen <i>Vibrio harveyi</i> CAIM 1792. <i>Journal of Bacteriology</i> , 2012 , 194, 2104	3.5	8
92	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	20.1	242
91	Sequencing of seven haloarchaeal genomes reveals patterns of genomic flux. <i>PLoS ONE</i> , 2012 , 7, e41389	3.7	37
90	Biodiversity and Biogeography of Phages in Modern Stromatolites and Thrombolites 2011 , 37-44		
89	Detection of Large Numbers of Novel Sequences in the Metatranscriptomes of Complex Marine Microbial Communities 2011 , 277-286		3
88	Connecting genotype to phenotype in the era of high-throughput sequencing. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2011 , 1810, 967-77	4	24
87	Fast identification and removal of sequence contamination from genomic and metagenomic datasets. <i>PLoS ONE</i> , 2011 , 6, e17288	3.7	471
86	Coastal bacterioplankton community diversity along a latitudinal gradient in Latin America by means of V6 tag pyrosequencing. <i>Archives of Microbiology</i> , 2011 , 193, 105-14	3	27
85	Phage Eco-Locator: a web tool for visualization and analysis of phage genomes in metagenomic data sets. <i>BMC Bioinformatics</i> , 2011 , 12,	3.6	3
84	Genome sequence of the human pathogen <i>Vibrio cholerae</i> Amazonia. <i>Journal of Bacteriology</i> , 2011 , 193, 5877-8	3.5	5
83	Quality control and preprocessing of metagenomic datasets. <i>Bioinformatics</i> , 2011 , 27, 863-4	7.2	2975
82	Viral and microbial community dynamics in four aquatic environments. <i>ISME Journal</i> , 2010 , 4, 739-51	11.9	305
81	Chromosomal rearrangements formed by <i>rrn</i> recombination do not improve replicore balance in host-specific <i>Salmonella enterica</i> serovars. <i>PLoS ONE</i> , 2010 , 5, e13503	3.7	10
80	Transposases are the most abundant, most ubiquitous genes in nature. <i>Nucleic Acids Research</i> , 2010 , 38, 4207-17	20.1	196
79	Lysogeny and sporulation in <i>Bacillus</i> isolates from the Gulf of Mexico. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 829-42	4.8	5
78	Accessing the SEED genome databases via Web services API: tools for programmers. <i>BMC Bioinformatics</i> , 2010 , 11, 319	3.6	99

77	TagCleaner: Identification and removal of tag sequences from genomic and metagenomic datasets. <i>BMC Bioinformatics</i> , 2010 , 11, 341	3.6	157
76	Deviations from Ultrametricity in Phage Protein Distances. <i>Open Systems and Information Dynamics</i> , 2009 , 16, 75-84	0.4	
75	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	5	162
74	Metagenomic and stable isotopic analyses of modern freshwater microbialites in Cuatro Ciénegas, Mexico. <i>Environmental Microbiology</i> , 2009 , 11, 16-34	5.2	158
73	Metagenomic analysis of stressed coral holobionts. <i>Environmental Microbiology</i> , 2009 , 11, 2148-63	5.2	410
72	Gene-centric metagenomics of the fiber-adherent bovine rumen microbiome reveals forage specific glycoside hydrolases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 1948-53	11.5	495
71	Bacterial carbon processing by generalist species in the coastal ocean. <i>Nature</i> , 2008 , 451, 708-11	50.4	235
70	Biodiversity and biogeography of phages in modern stromatolites and thrombolites. <i>Nature</i> , 2008 , 452, 340-3	50.4	212
69	Functional metagenomic profiling of nine biomes. <i>Nature</i> , 2008 , 452, 629-32	50.4	726
68	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008 , 26, 541-7	44.5	964
67	Viral communities associated with healthy and bleaching corals. <i>Environmental Microbiology</i> , 2008 , 10, 2277-86	5.2	107
66	The metagenomics RAST server - a public resource for the automatic phylogenetic and functional analysis of metagenomes. <i>BMC Bioinformatics</i> , 2008 , 9, 386	3.6	2527
65	The RAST Server: rapid annotations using subsystems technology. <i>BMC Genomics</i> , 2008 , 9, 75	4.5	7153
64	Viral diversity and dynamics in an infant gut. <i>Research in Microbiology</i> , 2008 , 159, 367-73	4	234
63	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, 18413-8	11.5	155
62	Phylogenetic classification of short environmental DNA fragments. <i>Nucleic Acids Research</i> , 2008 , 36, 2230-9	4.1	222
61	The smallest cells pose the biggest problems: high-performance computing and the analysis of metagenome sequence data. <i>Journal of Physics: Conference Series</i> , 2008 , 125, 012050	0.3	
60	Microbial ecology of four coral atolls in the Northern Line Islands. <i>PLoS ONE</i> , 2008 , 3, e1584	3.7	292

59	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	3.7	177
58	Comparative metagenomics reveals host specific metavirulomes and horizontal gene transfer elements in the chicken cecum microbiome. <i>PLoS ONE</i> , 2008 , 3, e2945	3.7	202
57	Detection of large numbers of novel sequences in the metatranscriptomes of complex marine microbial communities. <i>PLoS ONE</i> , 2008 , 3, e3042	3.7	289
56	Whole proteome analysis of post-translational modifications: applications of mass-spectrometry for proteogenomic annotation. <i>Genome Research</i> , 2007 , 17, 1362-77	9.7	155
55	Marine Environmental Genomics: Unlocking the Ocean's Secrets. <i>Oceanography</i> , 2007 , 20, 56-61	2.3	6
54	Metagenomic analysis of the microbial community associated with the coral <i>Porites astreoides</i> . <i>Environmental Microbiology</i> , 2007 , 9, 2707-19	5.2	395
53	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, 7059-66	4.8	406
52	The National Microbial Pathogen Database Resource (NMPDR): a genomics platform based on subsystem annotation. <i>Nucleic Acids Research</i> , 2007 , 35, D347-53	20.1	77
51	An application of statistics to comparative metagenomics. <i>BMC Bioinformatics</i> , 2006 , 7, 162	3.6	126
50	Using pyrosequencing to shed light on deep mine microbial ecology. <i>BMC Genomics</i> , 2006 , 7, 57	4.5	352
49	Finding novel genes in bacterial communities isolated from the environment. <i>Bioinformatics</i> , 2006 , 22, e281-9	7.2	61
48	The marine viromes of four oceanic regions. <i>PLoS Biology</i> , 2006 , 4, e368	9.7	726
47	Experimental and computational assessment of conditionally essential genes in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2006 , 188, 8259-71	3.5	205
46	Transcriptional profiling of <i>Mycoplasma hyopneumoniae</i> during heat shock using microarrays. <i>Infection and Immunity</i> , 2006 , 74, 160-6	3.7	52
45	Community genomics among stratified microbial assemblages in the ocean's interior. <i>Science</i> , 2006 , 311, 496-503	33.3	1055
44	Genome analysis of the obligately lytic bacteriophage 4268 of <i>Lactococcus lactis</i> provides insight into its adaptable nature. <i>Gene</i> , 2006 , 366, 189-99	3.8	23
43	Indirect effects of algae on coral: algae-mediated, microbe-induced coral mortality. <i>Ecology Letters</i> , 2006 , 9, 835-45	10	349
42	Essential genes on metabolic maps. <i>Current Opinion in Biotechnology</i> , 2006 , 17, 448-56	11.4	92

41	The subsystems approach to genome annotation and its use in the project to annotate 1000 genomes. <i>Nucleic Acids Research</i> , 2005 , 33, 5691-702	20.1	1485
40	Viral metagenomics. <i>Nature Reviews Microbiology</i> , 2005 , 3, 504-10	22.2	639
39	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	3.5	49
38	Mosaic prophages with horizontally acquired genes account for the emergence and diversification of the globally disseminated M1T1 clone of <i>Streptococcus pyogenes</i> . <i>Journal of Bacteriology</i> , 2005 , 187, 3311-8	3.5	96
37	In vitro characterization of the <i>Bacillus subtilis</i> protein tyrosine phosphatase YwqE. <i>Journal of Bacteriology</i> , 2005 , 187, 3384-90	3.5	39
36	Low-molecular-weight protein tyrosine phosphatases of <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2005 , 187, 4945-56	3.5	42
35	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, 2862-71	3.5	171
34	Draft sequencing and comparative genomics of <i>Xylella fastidiosa</i> strains reveal novel biological insights. <i>Genome Research</i> , 2002 , 12, 1556-63	9.7	59
33	The Phage Proteomic Tree: a genome-based taxonomy for phage. <i>Journal of Bacteriology</i> , 2002 , 184, 4529-35	3.5	431
32	Comparative genomics of closely related salmonellae. <i>Trends in Microbiology</i> , 2002 , 10, 94-9	12.4	170
31	The importance of complete genome sequences. <i>Trends in Microbiology</i> , 2002 , 10, 219-20; author reply 220	12.4	8
30	The importance of complete genome sequences. <i>Trends in Microbiology</i> , 2002 , 10, 220	12.4	
29	<i>Salmonella enterica</i> serovar Typhi possesses a unique repertoire of fimbrial gene sequences. <i>Infection and Immunity</i> , 2001 , 69, 2894-901	3.7	142
28	Inside or outside: detecting the cellular location of bacterial pathogens. <i>BioTechniques</i> , 2001 , 30, 304-6, 308-11	2.5	4
27	Genomic analysis and growth-phase-dependent regulation of the SEF14 fimbriae of <i>Salmonella enterica</i> serovar Enteritidis. <i>Microbiology (United Kingdom)</i> , 2001 , 147, 2705-2715	2.9	18
26	A role for <i>Salmonella</i> fimbriae in intraperitoneal infections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 1258-62	11.5	76
25	Increasing DNA transfer efficiency by temporary inactivation of host restriction. <i>BioTechniques</i> , 1999 , 26, 892-4, 896, 898 passim	2.5	37
24	Improved allelic exchange vectors and their use to analyze 987P fimbria gene expression. <i>Gene</i> , 1998 , 207, 149-57	3.8	430

23	Fimbrial expression in enteric bacteria: a critical step in intestinal pathogenesis. <i>Trends in Microbiology</i> , 1998 , 6, 282-7	12.4	65
22	Differential regulation of fasA and fasH expression of Escherichia coli 987P fimbriae by environmental cues. <i>Molecular Microbiology</i> , 1997 , 25, 797-809	4.1	43
21	Identification of major and minor chaperone proteins involved in the export of 987P fimbriae. <i>Journal of Bacteriology</i> , 1996 , 178, 3426-33	3.5	27
20	The role of uridylyltransferase in the control of Klebsiella pneumoniae nif gene regulation. <i>Molecular Genetics and Genomics</i> , 1995 , 247, 189-98		29
19	Elucidating genomic gaps using phenotypic profiles. <i>F1000Research</i> , 3, 210	3.6	2
18	Elucidating genomic gaps using phenotypic profiles. <i>F1000Research</i> , 3, 210	3.6	5
17	PRINSEQ++, a multi-threaded tool for fast and efficient quality control and preprocessing of sequencing datasets		2
16	PRINSEQ++, a multi-threaded tool for fast and efficient quality control and preprocessing of sequencing datasets		3
15	A Distinct Contractile Injection System Found in a Majority of Adult Human Microbiomes		1
14	Differential dynamics of peripheral immune responses to acute SARS-CoV-2 infection in older adults. <i>Nature Aging</i> ,		1
13	Critical Assessment of Metagenome Interpretation a benchmark of computational metagenomics software		17
12	Prophage genomics reveals patterns in phage genome organization and replication		17
11	PhANNs, a fast and accurate tool and web server to classify phage structural proteins		1
10	Phage and bacteria diversification through a prophage acquisition ratchet		4
9	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Bacteriophages		8
8	THEA: A novel approach to gene identification in phage genomes		2
7	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage		5
6	Fastq-pair: efficient synchronization of paired-end fastq files		16

5	FOCUS2: agile and sensitive classification of metagenomics data using a reduced database	1
4	Philympics 2021: Prophage Predictions Perplex Programs	1
3	hafeZ: Active prophage identification through read mapping	4
2	Philympics 2021: Prophage Predictions Perplex Programs. <i>F1000Research</i> ,10, 758	3.6 0
1	Philympics 2021: Prophage Predictions Perplex Programs. <i>F1000Research</i> ,10, 758	3.6 0