

# Robert A Edwards

## List of Publications by Citations

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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	The RAST Server: rapid annotations using subsystems technology. <i>BMC Genomics</i> , <b>2008</b> , 9, 75	4.5	7153
219	Quality control and preprocessing of metagenomic datasets. <i>Bioinformatics</i> , <b>2011</b> , 27, 863-4	7.2	2975
218	The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D206-14	20.1	2534
217	The metagenomics RAST server - a public resource for the automatic phylogenetic and functional analysis of metagenomes. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 386	3.6	2527
216	The subsystems approach to genome annotation and its use in the project to annotate 1000 genomes. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 5691-702	20.1	1485
215	RASTtk: a modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. <i>Scientific Reports</i> , <b>2015</b> , 5, 8365	4.9	1061
214	Community genomics among stratified microbial assemblages in the ocean's interior. <i>Science</i> , <b>2006</b> , 311, 496-503	33.3	1055
213	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 541-7	44.5	964
212	Functional metagenomic profiling of nine biomes. <i>Nature</i> , <b>2008</b> , 452, 629-32	50.4	726
211	The marine viromes of four oceanic regions. <i>PLoS Biology</i> , <b>2006</b> , 4, e368	9.7	726
210	Viral metagenomics. <i>Nature Reviews Microbiology</i> , <b>2005</b> , 3, 504-10	22.2	639
209	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> , <b>2009</b> , 106, 1948-53	11.5	495
208	Fast identification and removal of sequence contamination from genomic and metagenomic datasets. <i>PLoS ONE</i> , <b>2011</b> , 6, e17288	3.7	471
207	The Phage Proteomic Tree: a genome-based taxonomy for phage. <i>Journal of Bacteriology</i> , <b>2002</b> , 184, 4529-35	3.5	431
206	Improved allelic exchange vectors and their use to analyze 987P fimbria gene expression. <i>Gene</i> , <b>1998</b> , 207, 149-57	3.8	430
205	A highly abundant bacteriophage discovered in the unknown sequences of human faecal metagenomes. <i>Nature Communications</i> , <b>2014</b> , 5, 4498	17.4	420
204	Critical Assessment of Metagenome Interpretation-a benchmark of metagenomics software. <i>Nature Methods</i> , <b>2017</b> , 14, 1063-1071	21.6	412

203	Metagenomic analysis of stressed coral holobionts. <i>Environmental Microbiology</i> , <b>2009</b> , 11, 2148-63	5.2	410
202	Metagenomic and small-subunit rRNA analyses reveal the genetic diversity of bacteria, archaea, fungi, and viruses in soil. <i>Applied and Environmental Microbiology</i> , <b>2007</b> , 73, 7059-66	4.8	406
201	Metagenomic analysis of the microbial community associated with the coral <i>Porites astreoides</i> . <i>Environmental Microbiology</i> , <b>2007</b> , 9, 2707-19	5.2	395
200	Using pyrosequencing to shed light on deep mine microbial ecology. <i>BMC Genomics</i> , <b>2006</b> , 7, 57	4.5	352
199	Indirect effects of algae on coral: algae-mediated, microbe-induced coral mortality. <i>Ecology Letters</i> , <b>2006</b> , 9, 835-45	10	349
198	Viral and microbial community dynamics in four aquatic environments. <i>ISME Journal</i> , <b>2010</b> , 4, 739-51	11.9	305
197	Microbial ecology of four coral atolls in the Northern Line Islands. <i>PLoS ONE</i> , <b>2008</b> , 3, e1584	3.7	292
196	Detection of large numbers of novel sequences in the metatranscriptomes of complex marine microbial communities. <i>PLoS ONE</i> , <b>2008</b> , 3, e3042	3.7	289
195	Probiotic bacteria reduce salmonella typhimurium intestinal colonization by competing for iron. <i>Cell Host and Microbe</i> , <b>2013</b> , 14, 26-37	23.4	287
194	Lytic to temperate switching of viral communities. <i>Nature</i> , <b>2016</b> , 531, 466-70	50.4	278
193	Wnt signaling directs a metabolic program of glycolysis and angiogenesis in colon cancer. <i>EMBO Journal</i> , <b>2014</b> , 33, 1454-73	13	256
192	Zinc sequestration by the neutrophil protein calprotectin enhances Salmonella growth in the inflamed gut. <i>Cell Host and Microbe</i> , <b>2012</b> , 11, 227-39	23.4	243
191	PhiSpy: a novel algorithm for finding prophages in bacterial genomes that combines similarity- and composition-based strategies. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, e126	20.1	242
190	Computational approaches to predict bacteriophage-host relationships. <i>FEMS Microbiology Reviews</i> , <b>2016</b> , 40, 258-72	15.1	235
189	Bacterial carbon processing by generalist species in the coastal ocean. <i>Nature</i> , <b>2008</b> , 451, 708-11	50.4	235
188	Viral diversity and dynamics in an infant gut. <i>Research in Microbiology</i> , <b>2008</b> , 159, 367-73	4	234
187	Phylogenetic classification of short environmental DNA fragments. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, 2230-9	10.1	222
186	Biodiversity and biogeography of phages in modern stromatolites and thrombolites. <i>Nature</i> , <b>2008</b> , 452, 340-3	50.4	212

185	The cytokine IL-22 promotes pathogen colonization by suppressing related commensal bacteria. <i>Immunity</i> , <b>2014</b> , 40, 262-73	32.3	205
184	Experimental and computational assessment of conditionally essential genes in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 8259-71	3.5	205
183	Comparative metagenomics reveals host specific metavirulomes and horizontal gene transfer elements in the chicken cecum microbiome. <i>PLoS ONE</i> , <b>2008</b> , 3, e2945	3.7	202
182	Insights into antibiotic resistance through metagenomic approaches. <i>Future Microbiology</i> , <b>2012</b> , 7, 73-89	2.9	199
181	Transposases are the most abundant, most ubiquitous genes in nature. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 4207-17	20.1	196
180	Taxonomic composition and gene content of a methane-producing microbial community isolated from a biogas reactor. <i>Journal of Biotechnology</i> , <b>2008</b> , 136, 91-101	3.7	177
179	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> , <b>2004</b> , 186, 2862-71	3.5	171
178	Comparative genomics of closely related salmonellae. <i>Trends in Microbiology</i> , <b>2002</b> , 10, 94-9	12.4	170
177	The GAAS metagenomic tool and its estimations of viral and microbial average genome size in four major biomes. <i>PLoS Computational Biology</i> , <b>2009</b> , 5, e1000593	5	162
176	Metagenomic and stable isotopic analyses of modern freshwater microbialites in Cuatro Ciénegas, Mexico. <i>Environmental Microbiology</i> , <b>2009</b> , 11, 16-34	5.2	158
175	TagCleaner: Identification and removal of tag sequences from genomic and metagenomic datasets. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 341	3.6	157
174	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> , <b>2008</b> , 105, 18413-8	11.5	155
173	Whole proteome analysis of post-translational modifications: applications of mass-spectrometry for proteogenomic annotation. <i>Genome Research</i> , <b>2007</b> , 17, 1362-77	9.7	155
172	Identification and removal of ribosomal RNA sequences from metatranscriptomes. <i>Bioinformatics</i> , <b>2012</b> , 28, 433-5	7.2	148
171	Discovery of an expansive bacteriophage family that includes the most abundant viruses from the human gut. <i>Nature Microbiology</i> , <b>2018</b> , 3, 38-46	26.6	148
170	PHACTS, a computational approach to classifying the lifestyle of phages. <i>Bioinformatics</i> , <b>2012</b> , 28, 614-8	7.2	144
169	<i>Salmonella enterica</i> serovar Typhi possesses a unique repertoire of fimbrial gene sequences. <i>Infection and Immunity</i> , <b>2001</b> , 69, 2894-901	3.7	142
168	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> , <b>2014</b> , 111, 10227-32	11.5	139

167	Marine viruses discovered via metagenomics shed light on viral strategies throughout the oceans. <i>Nature Communications</i> , <b>2017</b> , 8, 15955	17.4	129
166	An application of statistics to comparative metagenomics. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 162	3.6	126
165	Global microbialization of coral reefs. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16042	26.6	121
164	SEED servers: high-performance access to the SEED genomes, annotations, and metabolic models. <i>PLoS ONE</i> , <b>2012</b> , 7, e48053	3.7	121
163	Metagenomics and metatranscriptomics: windows on CF-associated viral and microbial communities. <i>Journal of Cystic Fibrosis</i> , <b>2013</b> , 12, 154-64	4.1	118
162	Viral communities associated with healthy and bleaching corals. <i>Environmental Microbiology</i> , <b>2008</b> , 10, 2277-86	5.2	107
161	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , <b>2019</b> , 4, 1727-1736	26.6	100
160	Accessing the SEED genome databases via Web services API: tools for programmers. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 319	3.6	99
159	Clinical insights from metagenomic analysis of sputum samples from patients with cystic fibrosis. <i>Journal of Clinical Microbiology</i> , <b>2014</b> , 52, 425-37	9.7	96
158	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> , <b>2005</b> , 187, 3311-8	3.5	96
157	Abrolhos bank reef health evaluated by means of water quality, microbial diversity, benthic cover, and fish biomass data. <i>PLoS ONE</i> , <b>2012</b> , 7, e36687	3.7	93
156	Essential genes on metabolic maps. <i>Current Opinion in Biotechnology</i> , <b>2006</b> , 17, 448-56	11.4	92
155	SUPER-FOCUS: a tool for agile functional analysis of shotgun metagenomic data. <i>Bioinformatics</i> , <b>2016</b> , 32, 354-61	7.2	82
154	Phage-bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 207-27	5.2	82
153	Excessive folate synthesis limits lifespan in the <i>C. elegans</i> : <i>E. coli</i> aging model. <i>BMC Biology</i> , <b>2012</b> , 10, 67	7.3	81
152	A bioinformatic analysis of ribonucleotide reductase genes in phage genomes and metagenomes. <i>BMC Evolutionary Biology</i> , <b>2013</b> , 13, 33	3	79
151	Microbial taxonomy in the post-genomic era: rebuilding from scratch?. <i>Archives of Microbiology</i> , <b>2015</b> , 197, 359-70	3	78
150	The National Microbial Pathogen Database Resource (NMPDR): a genomics platform based on subsystem annotation. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D347-53	20.1	77

149	A role for Salmonella fimbriae in intraperitoneal infections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2000</b> , 97, 1258-62	11.5	76
148	Salmonella Mitigates Oxidative Stress and Thrives in the Inflamed Gut by Evading Calprotectin-Mediated Manganese Sequestration. <i>Cell Host and Microbe</i> , <b>2016</b> , 19, 814-25	23.4	74
147	Diversification of the Salmonella fimbriae: a model of macro- and microevolution. <i>PLoS ONE</i> , <b>2012</b> , 7, e38596	3.7	68
146	Taxonomy of prokaryotic viruses: update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , <b>2016</b> , 161, 1095-9	2.6	67
145	Taxonomy of prokaryotic viruses: 2018-2019 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , <b>2020</b> , 165, 1253-1260	2.6	66
144	PHANOTATE: a novel approach to gene identification in phage genomes. <i>Bioinformatics</i> , <b>2019</b> , 35, 4537-4542	4.4	65
143	Fimbrial expression in enteric bacteria: a critical step in intestinal pathogenesis. <i>Trends in Microbiology</i> , <b>1998</b> , 6, 282-7	12.4	65
142	Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , <b>2018</b> , 163, 1125-1129	2.6	62
141	Metagenomic analysis of healthy and white plague-affected <i>Mussismilia braziliensis</i> corals. <i>Microbial Ecology</i> , <b>2013</b> , 65, 1076-86	4.4	62
140	Finding novel genes in bacterial communities isolated from the environment. <i>Bioinformatics</i> , <b>2006</b> , 22, e281-9	7.2	61
139	Draft sequencing and comparative genomics of <i>Xylella fastidiosa</i> strains reveal novel biological insights. <i>Genome Research</i> , <b>2002</b> , 12, 1556-63	9.7	59
138	FOCUS: an alignment-free model to identify organisms in metagenomes using non-negative least squares. <i>PeerJ</i> , <b>2014</b> , 2, e425	3.1	59
137	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. <i>Systematic Biology</i> , <b>2020</b> , 69, 110-123	8.4	56
136	Allelic variation contributes to bacterial host specificity. <i>Nature Communications</i> , <b>2015</b> , 6, 8754	17.4	54
135	Reference-independent comparative metagenomics using cross-assembly: crAss. <i>Bioinformatics</i> , <b>2012</b> , 28, 3225-31	7.2	52
134	Transcriptional profiling of <i>Mycoplasma hyopneumoniae</i> during heat shock using microarrays. <i>Infection and Immunity</i> , <b>2006</b> , 74, 160-6	3.7	52
133	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> , <b>2005</b> , 187, 2992-3001	3.5	49
132	Taxonomic and functional microbial signatures of the endemic marine sponge <i>Arenosclera brasiliensis</i> . <i>PLoS ONE</i> , <b>2012</b> , 7, e39905	3.7	46

131	Lactate/pyruvate transporter MCT-1 is a direct Wnt target that confers sensitivity to 3-bromopyruvate in colon cancer. <i>Cancer &amp; Metabolism</i> , <b>2016</b> , 4, 20	5.4	45
130	Differential regulation of fasA and fasH expression of Escherichia coli 987P fimbriae by environmental cues. <i>Molecular Microbiology</i> , <b>1997</b> , 25, 797-809	4.1	43
129	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> , <b>2016</b> , 113, 13462-13467	11.5	42
128	Low-molecular-weight protein tyrosine phosphatases of Bacillus subtilis. <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 4945-56	3.5	42
127	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> , <b>2015</b> , 10, e0130084	3.7	41
126	Variability and host density independence in inductions-based estimates of environmental lysogeny. <i>Nature Microbiology</i> , <b>2017</b> , 2, 17064	26.6	40
125	Standardized bacteriophage purification for personalized phage therapy. <i>Nature Protocols</i> , <b>2020</b> , 15, 2867-2890	18.8	40
124	Integration of genomic and proteomic analyses in the classification of the Siphoviridae family. <i>Virology</i> , <b>2015</b> , 477, 144-154	3.6	39
123	Combining de novo and reference-guided assembly with scaffold_builder. <i>Source Code for Biology and Medicine</i> , <b>2013</b> , 8, 23	1.9	39
122	In vitro characterization of the Bacillus subtilis protein tyrosine phosphatase YwqE. <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 3384-90	3.5	39
121	Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , <b>2017</b> , 162, 1153-1157	2.6	38
120	Explaining microbial phenotypes on a genomic scale: GWAS for microbes. <i>Briefings in Functional Genomics</i> , <b>2013</b> , 12, 366-80	4.9	38
119	Multivariate analysis of functional metagenomes. <i>Frontiers in Genetics</i> , <b>2013</b> , 4, 41	4.5	38
118	Mechanistic model of Rothia mucilaginosa adaptation toward persistence in the CF lung, based on a genome reconstructed from metagenomic data. <i>PLoS ONE</i> , <b>2013</b> , 8, e64285	3.7	38
117	Phage Genome Annotation Using the RAST Pipeline. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1681, 231-238	1.4	38
116	Increasing DNA transfer efficiency by temporary inactivation of host restriction. <i>BioTechniques</i> , <b>1999</b> , 26, 892-4, 896, 898 passim	2.5	37
115	Sequencing of seven haloarchaeal genomes reveals patterns of genomic flux. <i>PLoS ONE</i> , <b>2012</b> , 7, e41389	3.7	37
114	Multi-Analytical Approach Reveals Potential Microbial Indicators in Soil for Sugarcane Model Systems. <i>PLoS ONE</i> , <b>2015</b> , 10, e0129765	3.7	34

113	MetaBase--the wiki-database of biological databases. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D1250-4	20.1	31
112	Acidobacteria Subgroups and Their Metabolic Potential for Carbon Degradation in Sugarcane Soil Amended With Vinasse and Nitrogen Fertilizers. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 1680	5.7	30
111	Structure and function of a cyanophage-encoded peptide deformylase. <i>ISME Journal</i> , <b>2013</b> , 7, 1150-60	11.9	30
110	Real time metagenomics: using k-mers to annotate metagenomes. <i>Bioinformatics</i> , <b>2012</b> , 28, 3316-7	7.2	29
109	The role of uridylyltransferase in the control of <i>Klebsiella pneumoniae</i> nif gene regulation. <i>Molecular Genetics and Genomics</i> , <b>1995</b> , 247, 189-98		29
108	Genome skimming with the MinION hand-held sequencer identifies CITES-listed shark species in India's exports market. <i>Scientific Reports</i> , <b>2019</b> , 9, 4476	4.9	28
107	From DNA to FBA: How to Build Your Own Genome-Scale Metabolic Model. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 907	5.7	28
106	A diversity-generating retroelement encoded by a globally ubiquitous <i>Bacteroides</i> phage. <i>Microbiome</i> , <b>2018</b> , 6, 191	16.6	28
105	β-Ketoglutarate attenuates Wnt signaling and drives differentiation in colorectal cancer. <i>Nature Cancer</i> , <b>2020</b> , 1, 345-358	15.4	27
104	Genomic taxonomy of the genus <i>prochlorococcus</i> . <i>Microbial Ecology</i> , <b>2013</b> , 66, 752-62	4.4	27
103	Genomic Comparison of the Closely-Related <i>Salmonella enterica</i> Serovars Enteritidis, Dublin and Gallinarum. <i>PLoS ONE</i> , <b>2015</b> , 10, e0126883	3.7	27
102	Coastal bacterioplankton community diversity along a latitudinal gradient in Latin America by means of V6 tag pyrosequencing. <i>Archives of Microbiology</i> , <b>2011</b> , 193, 105-14	3	27
101	Identification of major and minor chaperone proteins involved in the export of 987P fimbriae. <i>Journal of Bacteriology</i> , <b>1996</b> , 178, 3426-33	3.5	27
100	multiPhATE: bioinformatics pipeline for functional annotation of phage isolates. <i>Bioinformatics</i> , <b>2019</b> , 35, 4402-4404	7.2	26
99	Optimizing and evaluating the reconstruction of Metagenome-assembled microbial genomes. <i>BMC Genomics</i> , <b>2017</b> , 18, 915	4.5	25
98	Connecting genotype to phenotype in the era of high-throughput sequencing. <i>Biochimica Et Biophysica Acta - General Subjects</i> , <b>2011</b> , 1810, 967-77	4	24
97	Genome analysis of the obligately lytic bacteriophage 4268 of <i>Lactococcus lactis</i> provides insight into its adaptable nature. <i>Gene</i> , <b>2006</b> , 366, 189-99	3.8	23
96	Applying Shannon's information theory to bacterial and phage genomes and metagenomes. <i>Scientific Reports</i> , <b>2013</b> , 3, 1033	4.9	22



95	Comparative genomics of 274 <i>Vibrio cholerae</i> genomes reveals mobile functions structuring three niche dimensions. <i>BMC Genomics</i> , <b>2014</b> , 15, 654	4.5	21
94	Multidimensional metrics for estimating phage abundance, distribution, gene density, and sequence coverage in metagenomes. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 381	5.7	21
93	Characterization of the ELPhiS prophage from <i>Salmonella enterica</i> serovar Enteritidis strain LK5. <i>Applied and Environmental Microbiology</i> , <b>2012</b> , 78, 1785-93	4.8	20
92	PhiSiGns: an online tool to identify signature genes in phages and design PCR primers for examining phage diversity. <i>BMC Bioinformatics</i> , <b>2012</b> , 13, 37	3.6	19
91	PhANNs, a fast and accurate tool and web server to classify phage structural proteins. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1007845	5	19
90	Microbes, metagenomes and marine mammals: enabling the next generation of scientist to enter the genomic era. <i>BMC Genomics</i> , <b>2013</b> , 14, 600	4.5	18
89	Genomic analysis and growth-phase-dependent regulation of the SEF14 fimbriae of <i>Salmonella enterica</i> serovar Enteritidis. <i>Microbiology (United Kingdom)</i> , <b>2001</b> , 147, 2705-2715	2.9	18
88	Bacterial Community Associated with the Reef Coral Momentum Boundary Layer over a Diel Cycle. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 784	5.7	17
87	Microbial Community Profile and Water Quality in a Protected Area of the Caatinga Biome. <i>PLoS ONE</i> , <b>2016</b> , 11, e0148296	3.7	17
86	Critical Assessment of Metagenome Interpretation $\alpha$ benchmark of computational metagenomics software		17
85	Prophage genomics reveals patterns in phage genome organization and replication		17
84	Cystic Fibrosis Rapid Response: Translating Multi-omics Data into Clinically Relevant Information. <i>MBio</i> , <b>2019</b> , 10,	7.8	16
83	Fastq-pair: efficient synchronization of paired-end fastq files		16
82	The skin microbiome of elasmobranchs follows phylosymbiosis, but in teleost fishes, the microbiomes converge. <i>Microbiome</i> , <b>2020</b> , 8, 93	16.6	15
81	Genomic and ecological attributes of marine bacteriophages encoding bacterial virulence genes. <i>BMC Genomics</i> , <b>2020</b> , 21, 126	4.5	15
80	Draft Genome Sequence of the Fish Pathogen <i>Piscirickettsia salmonis</i> . <i>Genome Announcements</i> , <b>2013</b> , 1,		15
79	Sequencing at sea: challenges and experiences in Ion Torrent PGM sequencing during the 2013 Southern Line Islands Research Expedition. <i>PeerJ</i> , <b>2014</b> , 2, e520	3.1	15
78	PARTIE: a partition engine to separate metagenomic and amplicon projects in the Sequence Read Archive. <i>Bioinformatics</i> , <b>2017</b> , 33, 2389-2391	7.2	13

77	Diel population and functional synchrony of microbial communities on coral reefs. <i>Nature Communications</i> , <b>2019</b> , 10, 1691	17.4	13
76	Genome-wide study of the defective sucrose fermenter strain of <i>Vibrio cholerae</i> from the Latin American cholera epidemic. <i>PLoS ONE</i> , <b>2012</b> , 7, e37283	3.7	12
75	Some of the most interesting CASP11 targets through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2016</b> , 84 Suppl 1, 34-50	4.2	12
74	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> , <b>2015</b> , 3,		11
73	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> , <b>2018</b> , 19,	6.3	11
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