

Bas E Dutilh

List of Publications by Year in descending order

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Version: 2024-02-01

147
papers

16,982
citations

28274

55
h-index

18130

120
g-index

181
all docs

181
docs citations

181
times ranked

20920
citing authors

#	ARTICLE	IF	CITATIONS
1	Nitrite-driven anaerobic methane oxidation by oxygenic bacteria. <i>Nature</i> , 2010, 464, 543-548.	27.8	1,521
2	Deciphering the evolution and metabolism of an anammox bacterium from a community genome. <i>Nature</i> , 2006, 440, 790-794.	27.8	1,075
3	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020, 21, 31.	8.8	742
4	A bacterial driverâ€“passenger model for colorectal cancer: beyond the usual suspects. <i>Nature Reviews Microbiology</i> , 2012, 10, 575-582.	28.6	672
5	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016, 537, 689-693.	27.8	629
6	A highly abundant bacteriophage discovered in the unknown sequences of human faecal metagenomes. <i>Nature Communications</i> , 2014, 5, 4498.	12.8	617
7	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2018). <i>Archives of Virology</i> , 2018, 163, 2601-2631.	2.1	567
8	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	28.9	541
9	Metagenomics and future perspectives in virus discovery. <i>Current Opinion in Virology</i> , 2012, 2, 63-77.	5.4	493
10	Towards the Human Colorectal Cancer Microbiome. <i>PLoS ONE</i> , 2011, 6, e20447.	2.5	470
11	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
12	Computational approaches to predict bacteriophageâ€“host relationships. <i>FEMS Microbiology Reviews</i> , 2016, 40, 258-272.	8.6	394
13	Genome-based microbial ecology of anammox granules in a full-scale wastewater treatment system. <i>Nature Communications</i> , 2016, 7, 11172.	12.8	373
14	Targeting mechanisms of tailed bacteriophages. <i>Nature Reviews Microbiology</i> , 2018, 16, 760-773.	28.6	310
15	Molecular and Evolutionary Determinants of Bacteriophage Host Range. <i>Trends in Microbiology</i> , 2019, 27, 51-63.	7.7	277
16	Robust taxonomic classification of uncharted microbial sequences and bins with CAT and BAT. <i>Genome Biology</i> , 2019, 20, 217.	8.8	269
17	Changes to virus taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2019). <i>Archives of Virology</i> , 2019, 164, 2417-2429.	2.1	257
18	The metagenome of the marine anammox bacterium <i>Candidatus</i> <i>Scalindua profunda</i> ™ illustrates the versatility of this globally important nitrogen cycle bacterium. <i>Environmental Microbiology</i> , 2013, 15, 1275-1289.	3.8	246

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19	Marine viruses discovered via metagenomics shed light on viral strategies throughout the oceans. <i>Nature Communications</i> , 2017, 8, 15955.	12.8	231
20	Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). <i>Archives of Virology</i> , 2021, 166, 2633-2648.	2.1	219
21	Computational pan-genomics: status, promises and challenges. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw089.	6.5	207
22	Changes to virus taxonomy and the Statutes ratified by the International Committee on Taxonomy of Viruses (2020). <i>Archives of Virology</i> , 2020, 165, 2737-2748.	2.1	202
23	The new scope of virus taxonomy: partitioning the virosphere into 15 hierarchical ranks. <i>Nature Microbiology</i> , 2020, 5, 668-674.	13.3	198
24	Pyrosequencing of 16S rRNA gene amplicons to study the microbiota in the gastrointestinal tract of carp (<i>Cyprinus carpio</i> L.). <i>AMB Express</i> , 2011, 1, 41.	3.0	186
25	GENOME TREES AND THE NATURE OF GENOME EVOLUTION. <i>Annual Review of Microbiology</i> , 2005, 59, 191-209.	7.3	184
26	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	13.3	184
27	Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2018, 163, 1125-1129.	2.1	172
28	Genome-Wide Profiling of p63 DNA-Binding Sites Identifies an Element that Regulates Gene Expression during Limb Development in the 7q21 SHFM1 Locus. <i>PLoS Genetics</i> , 2010, 6, e1001065.	3.5	169
29	Discovery of a hapE Mutation That Causes Azole Resistance in <i>Aspergillus fumigatus</i> through Whole Genome Sequencing and Sexual Crossing. <i>PLoS ONE</i> , 2012, 7, e50034.	2.5	168
30	SUPER-FOCUS: a tool for agile functional analysis of shotgun metagenomic data. <i>Bioinformatics</i> , 2016, 32, 354-361.	4.1	161
31	The bacterial sulfur cycle in expanding dysoxic and euxinic marine waters. <i>Environmental Microbiology</i> , 2021, 23, 2834-2857.	3.8	145
32	Microbial taxonomy in the post-genomic era: Rebuilding from scratch?. <i>Archives of Microbiology</i> , 2015, 197, 359-370.	2.2	144
33	Taxonomy of prokaryotic viruses: 2018-2019 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2020, 165, 1253-1260.	2.1	144
34	Horizontal gene transfer from Bacteria to rumen Ciliates indicates adaptation to their anaerobic, carbohydrates-rich environment. <i>BMC Genomics</i> , 2006, 7, 22.	2.8	138
35	Pharmacomicrobiomics: The Impact of Human Microbiome Variations on Systems Pharmacology and Personalized Therapeutics. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 402-414.	2.0	122
36	From cultured to uncultured genome sequences: metagenomics and modeling microbial ecosystems. <i>Cellular and Molecular Life Sciences</i> , 2015, 72, 4287-4308.	5.4	114

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37	Additional changes to taxonomy ratified in a special vote by the International Committee on Taxonomy of Viruses (October 2018). <i>Archives of Virology</i> , 2019, 164, 943-946.	2.1	102
38	Ecogenomics and Taxonomy of Cyanobacteria Phylum. <i>Frontiers in Microbiology</i> , 2017, 8, 2132.	3.5	99
39	Practical and theoretical advances in predicting the function of a protein by its phylogenetic distribution. <i>Journal of the Royal Society Interface</i> , 2008, 5, 151-170.	3.4	97
40	A Phage Protein Aids Bacterial Symbionts in Eukaryote Immune Evasion. <i>Cell Host and Microbe</i> , 2019, 26, 542-550.e5.	11.0	94
41	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. <i>Systematic Biology</i> , 2020, 69, 110-123.	5.6	89
42	FOCUS: an alignment-free model to identify organisms in metagenomes using non-negative least squares. <i>PeerJ</i> , 2014, 2, e425.	2.0	89
43	The Consistent Phylogenetic Signal in Genome Trees Revealed by Reducing the Impact of Noise. <i>Journal of Molecular Evolution</i> , 2004, 58, 527-539.	1.8	88
44	Assessment of phylogenomic and orthology approaches for phylogenetic inference. <i>Bioinformatics</i> , 2007, 23, 815-824.	4.1	87
45	Reference-independent comparative metagenomics using cross-assembly: crAss. <i>Bioinformatics</i> , 2012, 28, 3225-3231.	4.1	87
46	Taxonomy of prokaryotic viruses: update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2016, 161, 1095-1099.	2.1	83
47	The Organellar Genome and Metabolic Potential of the Hydrogen-Producing Mitochondrion of <i>Nyctotherus ovalis</i> . <i>Molecular Biology and Evolution</i> , 2011, 28, 2379-2391.	8.9	82
48	The human gut microbiome and health inequities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	82
49	Towards predicting the environmental metabolome from metagenomics with a mechanistic model. <i>Nature Microbiology</i> , 2018, 3, 456-460.	13.3	79
50	Draft Genome of <i>Scalindua rubra</i> , Obtained from the Interface Above the Discovery Deep Brine in the Red Sea, Sheds Light on Potential Salt Adaptation Strategies in Anammox Bacteria. <i>Microbial Ecology</i> , 2017, 74, 1-5.	2.8	73
51	Signature Genes as a Phylogenomic Tool. <i>Molecular Biology and Evolution</i> , 2008, 25, 1659-1667.	8.9	72
52	Dispersion of the HIV-1 Epidemic in Men Who Have Sex with Men in the Netherlands: A Combined Mathematical Model and Phylogenetic Analysis. <i>PLoS Medicine</i> , 2015, 12, e1001898.	8.4	69
53	Oxygen minimum zones harbour novel viral communities with low diversity. <i>Environmental Microbiology</i> , 2012, 14, 3043-3065.	3.8	68
54	Phage Genome Annotation Using the RAST Pipeline. <i>Methods in Molecular Biology</i> , 2018, 1681, 231-238.	0.9	64

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55	Bridging the membrane lipid divide: bacteria of the FCB group superphylum have the potential to synthesize archaeal ether lipids. <i>ISME Journal</i> , 2021, 15, 168-182.	9.8	62
56	Combining de novo and reference-guided assembly with scaffold_builder. <i>Source Code for Biology and Medicine</i> , 2013, 8, 23.	1.7	59
57	Characterization and Temperature Dependence of Arctic <i>Micromonas polaris</i> Viruses. <i>Viruses</i> , 2017, 9, 134.	3.3	59
58	Ultra-deep pyrosequencing of pmoA amplicons confirms the prevalence of <i>Methylomonas</i> and <i>Methylocystis</i> in <i>Sphagnum</i> mosses from a Dutch peat bog. <i>Environmental Microbiology Reports</i> , 2011, 3, 667-673.	2.4	58
59	Identification of a Novel Human Papillomavirus by Metagenomic Analysis of Samples from Patients with Febrile Respiratory Illness. <i>PLoS ONE</i> , 2013, 8, e58404.	2.5	58
60	Explaining microbial phenotypes on a genomic scale: GWAS for microbes. <i>Briefings in Functional Genomics</i> , 2013, 12, 366-380.	2.7	57
61	Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2017, 162, 1153-1157.	2.1	57
62	Taxonomic and Functional Microbial Signatures of the Endemic Marine Sponge <i>Arenosclera brasiliensis</i> . <i>PLoS ONE</i> , 2012, 7, e39905.	2.5	56
63	Microbial Metabolism Shifts Towards an Adverse Profile with Supplementary Iron in the TIM-2 In vitro Model of the Human Colon. <i>Frontiers in Microbiology</i> , 2015, 6, 1481.	3.5	55
64	RaFAH: Host prediction for viruses of Bacteria and Archaea based on protein content. <i>Patterns</i> , 2021, 2, 100274.	5.9	53
65	Metagenomic and metaproteomic analyses of <i>Accumulibacter phosphatis</i> -enriched floccular and granular biofilm. <i>Environmental Microbiology</i> , 2016, 18, 273-287.	3.8	51
66	Binomial nomenclature for virus species: a consultation. <i>Archives of Virology</i> , 2020, 165, 519-525.	2.1	51
67	Conservation of divergent transcription in fungi. <i>Trends in Genetics</i> , 2008, 24, 207-211.	6.7	48
68	Metagenomic Characterization of the Human Intestinal Microbiota in Fecal Samples from STEC-Infected Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 25.	3.9	47
69	Decline in excision circles requires homeostatic renewal or homeostatic death of naive T cells. <i>Journal of Theoretical Biology</i> , 2003, 224, 351-358.	1.7	46
70	Draft Genome Sequence of Anammox Bacterium <i>Candidatus Scalindua brodae</i> , Obtained Using Differential Coverage Binning of Sequencing Data from Two Reactor Enrichments. <i>Genome Announcements</i> , 2015, 3, .	0.8	46
71	Microbial diversity, ecological networks and functional traits associated to materials used in drinking water distribution systems. <i>Water Research</i> , 2020, 173, 115586.	11.3	45
72	Temporal dynamics of uncultured viruses: a new dimension in viral diversity. <i>ISME Journal</i> , 2018, 12, 199-211.	9.8	44

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73	Bacterial Responses to a Simulated Colon Tumor Microenvironment. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 851-862.	3.8	43
74	FACIL: Fast and Accurate Genetic Code Inference and Logo. <i>Bioinformatics</i> , 2011, 27, 1929-1933.	4.1	42
75	Asymmetric relationships between proteins shape genome evolution. <i>Genome Biology</i> , 2009, 10, R19.	9.6	39
76	Genomic Comparison of the Closely-Related <i>Salmonella enterica</i> Serovars Enteritidis, Dublin and Gallinarum. <i>PLoS ONE</i> , 2015, 10, e0126883.	2.5	39
77	The mitochondrial genomes of the ciliates <i>Euplotes minuta</i> and <i>Euplotes crassus</i> . <i>BMC Genomics</i> , 2009, 10, 514.	2.8	36
78	Screening metatranscriptomes for toxin genes as functional drivers of human colorectal cancer. <i>Bailliere's Best Practice and Research in Clinical Gastroenterology</i> , 2013, 27, 85-99.	2.4	36
79	Niche distribution and influence of environmental parameters in marine microbial communities: a systematic review. <i>PeerJ</i> , 2015, 3, e1008.	2.0	36
80	Using the structure of genome data in the design of deep neural networks for predicting amyotrophic lateral sclerosis from genotype. <i>Bioinformatics</i> , 2019, 35, i538-i547.	4.1	35
81	Prophages are associated with extensive CRISPR-Cas auto-immunity. <i>Nucleic Acids Research</i> , 2020, 48, 12074-12084.	14.5	35
82	Microbial community diversity and physical-chemical features of the Southwestern Atlantic Ocean. <i>Archives of Microbiology</i> , 2015, 197, 165-179.	2.2	34
83	Stability of the human gut virome and effect of gluten-free diet. <i>Cell Reports</i> , 2021, 35, 109132.	6.4	34
84	Macronuclear genome structure of the ciliate <i>Nyctotherus ovalis</i> : Single-gene chromosomes and tiny introns. <i>BMC Genomics</i> , 2008, 9, 587.	2.8	33
85	Differentiating between viruses and virus species by writing their names correctly. <i>Archives of Virology</i> , 2022, 167, 1231-1234.	2.1	33
86	Editorial: Virus Discovery by Metagenomics: The (Im)possibilities. <i>Frontiers in Microbiology</i> , 2017, 8, 1710.	3.5	32
87	Gut virome profiling identifies a widespread bacteriophage family associated with metabolic syndrome. <i>Nature Communications</i> , 2022, 13, .	12.8	32
88	Perspective on taxonomic classification of uncultivated viruses. <i>Current Opinion in Virology</i> , 2021, 51, 207-215.	5.4	31
89	Increasing the coverage of a metapopulation consensus genome by iterative read mapping and assembly. <i>Bioinformatics</i> , 2009, 25, 2878-2881.	4.1	29
90	A global definition of expression context is conserved between orthologs, but does not correlate with sequence conservation. <i>BMC Genomics</i> , 2006, 7, 10.	2.8	28

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91	Insights of Phage-Host Interaction in Hypersaline Ecosystem through Metagenomics Analyses. <i>Frontiers in Microbiology</i> , 2017, 8, 352.	3.5	28
92	Metabolic models predict bacterial passengers in colorectal cancer. <i>Cancer & Metabolism</i> , 2020, 8, 3.	5.0	28
93	Metagenomic ventures into outer sequence space. <i>Bacteriophage</i> , 2014, 4, e979664.	1.9	27
94	Growth rate alterations of human colorectal cancer cells by 157 gut bacteria. <i>Gut Microbes</i> , 2020, 12, 1799733.	9.8	26
95	Mass Spectrometry Analysis of Hepcidin Peptides in Experimental Mouse Models. <i>PLoS ONE</i> , 2011, 6, e16762.	2.5	25
96	Comparative genomics of 274 <i>Vibrio cholerae</i> genomes reveals mobile functions structuring three niche dimensions. <i>BMC Genomics</i> , 2014, 15, 654.	2.8	24
97	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.	2.1	24
98	Adsorption Sequencing as a Rapid Method to Link Environmental Bacteriophages to Hosts. <i>IScience</i> , 2020, 23, 101439.	4.1	23
99	Metagenomics in <i>Virology</i> . , 2021, , 133-140.		23
100	Identical sequences found in distant genomes reveal frequent horizontal transfer across the bacterial domain. <i>ELife</i> , 2021, 10, .	6.0	23
101	Cell Wall Modifications during Conidial Maturation of the Human Pathogenic Fungus <i>Pseudallescheria boydii</i> . <i>PLoS ONE</i> , 2014, 9, e100290.	2.5	23
102	High viral abundance and low diversity are associated with increased CRISPR-Cas prevalence across microbial ecosystems. <i>Current Biology</i> , 2022, 32, 220-227.e5.	3.9	23
103	Development of the first marmoset-specific DNA microarray (EUMAMA): a new genetic tool for large-scale expression profiling in a non-human primate. <i>BMC Genomics</i> , 2007, 8, 190.	2.8	22
104	Microsatellite instability screening in colorectal adenomas to detect Lynch syndrome patients? A systematic review and meta-analysis. <i>European Journal of Human Genetics</i> , 2020, 28, 277-286.	2.8	22
105	Beyond research: a primer for considerations on using viral metagenomics in the field and clinic. <i>Frontiers in Microbiology</i> , 2015, 6, 224.	3.5	21
106	Modelling the influence of environmental parameters over marine planktonic microbial communities using artificial neural networks. <i>Science of the Total Environment</i> , 2019, 677, 205-214.	8.0	21
107	Optimized bacterial DNA isolation method for microbiome analysis of human tissues. <i>MicrobiologyOpen</i> , 2021, 10, e1191.	3.0	21
108	Establishing normal metabolism and differentiation in hepatocellular carcinoma cells by culturing in adult human serum. <i>Scientific Reports</i> , 2018, 8, 11685.	3.3	20

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109	Evolution of BACON Domain Tandem Repeats in crAssphage and Novel Gut Bacteriophage Lineages. <i>Viruses</i> , 2019, 11, 1085.	3.3	20
110	Impact of phosphate dosing on the microbial ecology of drinking water distribution systems: Fieldwork studies in chlorinated networks. <i>Water Research</i> , 2020, 187, 116416.	11.3	19
111	Lifestyle of sponge symbiont phages by host prediction and correlative microscopy. <i>ISME Journal</i> , 2021, 15, 2001-2011.	9.8	19
112	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.	2.0	19
113	Sequence specificity between interacting and non-interacting homologs identifies interface residues in a homodimer and monomer use case. <i>BMC Bioinformatics</i> , 2015, 16, 325.	2.6	18
114	The gill-associated microbiome is the main source of wood plant polysaccharide hydrolases and secondary metabolite gene clusters in the mangrove shipworm <i>Neoteredo reynei</i> . <i>PLoS ONE</i> , 2018, 13, e0200437.	2.5	18
115	Large-scale genomic analysis shows association between homoplastic genetic variation in <i>Mycobacterium tuberculosis</i> genes and meningeal or pulmonary tuberculosis. <i>BMC Genomics</i> , 2018, 19, 122.	2.8	18
116	Ecogenomics and metabolic potential of the South Atlantic Ocean microbiome. <i>Science of the Total Environment</i> , 2021, 765, 142758.	8.0	16
117	A Prioritized and Validated Resource of Mitochondrial Proteins in <i>Plasmodium</i> Identifies Unique Biology. <i>MSphere</i> , 2021, 6, e0061421.	2.9	16
118	Signature, a web server for taxonomic characterization of sequence samples using signature genes. <i>Nucleic Acids Research</i> , 2008, 36, W470-W474.	14.5	14
119	Genome reconstruction of the non-culturable spinach downy mildew <i>Peronospora effusa</i> by metagenome filtering. <i>PLoS ONE</i> , 2020, 15, e0225808.	2.5	14
120	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.	2.5	13
121	Ultrastructure and Viral Metagenome of Bacteriophages from an Anaerobic Methane Oxidizing <i>Methyloirabilis</i> Bioreactor Enrichment Culture. <i>Frontiers in Microbiology</i> , 2016, 7, 1740.	3.5	13
122	Use of whole-genome sequencing to predict <i>Mycobacterium tuberculosis</i> drug resistance in Indonesia. <i>Journal of Global Antimicrobial Resistance</i> , 2019, 16, 170-177.	2.2	13
123	<i>Virus Bioinformatics</i> . , 2021, , 124-132.		12
124	Production of inactivated gram-positive and gram-negative species with preserved cellular morphology and integrity. <i>Journal of Microbiological Methods</i> , 2021, 184, 106208.	1.6	12
125	Quantifying the Impact of Human Leukocyte Antigen on the Human Gut Microbiota. <i>MSphere</i> , 2021, 6, e0047621.	2.9	12
126	Genome-wide association studies of <i>Shigella</i> spp. and Enteroinvasive <i>Escherichia coli</i> isolates demonstrate an absence of genetic markers for prediction of disease severity. <i>BMC Genomics</i> , 2020, 21, 138.	2.8	11

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127	Novel high-resolution targeted sequencing of the cervicovaginal microbiome. BMC Biology, 2021, 19, 267.	3.8	11
128	A metagenomic portrait of the microbial community responsible for two decades of bioremediation of poly-contaminated groundwater. Water Research, 2022, 221, 118767.	11.3	11
129	Proposal of fifteen new species of <i>Parasynecococcus</i> based on genomic, physiological and ecological features. Archives of Microbiology, 2016, 198, 973-986.	2.2	10
130	Drug Discovery and Repurposing Inhibits a Major Gut Pathogen-Derived Oncogenic Toxin. Frontiers in Cellular and Infection Microbiology, 2019, 9, 364.	3.9	10
131	Genome Sequences of the Ethanol-Tolerant <i>Lactobacillus vini</i> Strains LMG 23202 T and JP7.8.9. Journal of Bacteriology, 2012, 194, 3018-3018.	2.2	9
132	Genome Sequence of the Human Pathogen <i>Vibrio cholerae</i> Amazonia. Journal of Bacteriology, 2011, 193, 5877-5878.	2.2	8
133	Evolutionary Study of the Crassphage Virus at Gene Level. Viruses, 2020, 12, 1035.	3.3	8
134	Copper tolerance and distribution of epibiotic bacteria associated with giant kelp <i>Macrocystis pyrifera</i> in southern California. Ecotoxicology, 2015, 24, 1131-1140.	2.4	7
135	Integrating Computational Methods to Investigate the Macroecology of Microbiomes. Frontiers in Genetics, 2019, 10, 1344.	2.3	7
136	Genome-wide screening in human growth plates during puberty in one patient suggests a role for RUNX2 in epiphyseal maturation. Journal of Endocrinology, 2011, 209, 245-254.	2.6	6
137	Bioinformatics Meets Virology: The European Virus Bioinformatics Center's Second Annual Meeting. Viruses, 2018, 10, 256.	3.3	6
138	OGRE: Overlap Graph-based metagenomic Read clustering. Bioinformatics, 2021, 37, 905-912.	4.1	6
139	Immunoglobulin rearrangement analysis from multiple lesions in the same patient using next-generation sequencing. Histopathology, 2015, 67, 843-858.	2.9	5
140	ITN-VIROINF: Understanding (Harmful) Virus-Host Interactions by Linking Virology and Bioinformatics. Viruses, 2021, 13, 766.	3.3	5
141	Preservation of bacterial DNA in 10-year-old guaiac FOBT cards and FIT tubes. Journal of Clinical Pathology, 2017, 70, 994-996.	2.0	4
142	Ecogenomics of the Marine Benthic Filamentous Cyanobacterium <i>Adonisia</i> . Microbial Ecology, 2020, 80, 249-265.	2.8	4
143	Development of Styrene Maleic Acid Lipid Particles as a Tool for Studies of Phage-Host Interactions. Journal of Virology, 2020, 94, .	3.4	3
144	Reply to: Caution in inferring viral strategies from abundance correlations in marine metagenomes. Nature Communications, 2019, 10, 502.	12.8	2

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145	Finding functional associations between prokaryotic virus orthologous groups: a proof of concept. BMC Bioinformatics, 2021, 22, 438.	2.6	2
146	Editorial: Computational Methods for Microbiome Analysis. Frontiers in Genetics, 2020, 11, 623897.	2.3	0
147	Colorectal Cancer-Associated Microbiota. , 2013, , 1-8.		0