Simon Roux

List of Publications by Year
in descending order

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114 papers	16,287 citations	41627 51 h-index	28425 109 g-index
156 all docs	156 docs citations	156 times ranked	13478 citing authors

#	Article	IF	Citations
1	Viral community analysis in a marine oxygen minimum zone indicates increased potential for viral manipulation of microbial physiological state. ISME Journal, 2022, 16, 972-982.	4.4	17
2	Metagenome-assembled genomes of phytoplankton microbiomes from the Arctic and Atlantic Oceans. Microbiome, 2022, 10, 67.	4.9	17
3	Virus-Host Interactions and Genetic Diversity of Antarctic Sea Ice Bacteriophages. MBio, 2022, 13, e0065122.	1.8	8
4	Diversity in the soil virosphere: to infinity and beyond?. Trends in Microbiology, 2022, 30, 1025-1035.	3.5	35
5	A genomic catalog of Earthâ€™s microbiomes. Nature Biotechnology, 2021, 39, 499-509.	9.4	457
6	Virus Bioinformatics. , 2021, , 124-132.		12
7	The IMG/M data management and analysis system v.6.0: new tools and advanced capabilities. Nucleic Acids Research, 2021, 49, D751-D763.	6.5	332
8	IMG/VR v3: an integrated ecological and evolutionary framework for interrogating genomes of uncultivated viruses. Nucleic Acids Research, 2021, 49, D764-D775.	6.5	240
9	Potential virus-mediated nitrogen cycling in oxygen-depleted oceanic waters. ISME Journal, 2021, 15, 981-998.	4.4	71
10	CheckV assesses the quality and completeness of metagenome-assembled viral genomes. Nature Biotechnology, 2021, 39, 578-585.	9.4	569
11	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. ISME Journal, 2021, 15, 421-434.	4.4	46
12	Metagenomics in Virology. , 2021, , 133-140.		23
13	Host population diversity as a driver of viral infection cycle in wild populations of green sulfur bacteria with long standing virus-host interactions. ISME Journal, 2021, 15, 1569-1584.	4.4	16
14	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborativeâ€™s Workshop and Follow-On Activities. MSystems, 2021, 6, .	1.7	28
15	VirSorter2: a multi-classifier, expert-guided approach to detect diverse DNA and RNA viruses. Microbiome, 2021, 9, 37.	4.9	441
16	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. Communications Biology, 2021, 4, 604.	2.0	107
17	Ecology and molecular targets of hypermutation in the global microbiome. Nature Communications, 2021, 12, 3076.	5.8	35
18	Extreme dimensions â€” how big (or small) can tailed phages be?. Nature Reviews Microbiology, 2021, 19, 407-407.	13.6	4

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19	Viruses infecting a warm water picoeukaryote shed light on spatial co-occurrence dynamics of marine viruses and their hosts. ISME Journal, 2021, 15, 3129-3147.	4.4	10
20	Metagenome Sequencing to Explore Phylogenomics of Terrestrial Cyanobacteria. Microbiology Resource Announcements, 2021, 10, e0025821.	0.3	15
21	Ecogenomics of Groundwater Phages Suggests Niche Differentiation Linked to Specific Environmental Tolerance. MSystems, 2021, 6, e0053721.	1.7	8
22	DOE JGI Metagenome Workflow. MSystems, 2021, 6, .	1.7	56
23	Expanding standards in viromics: in silico evaluation of dsDNA viral genome identification, classification, and auxiliary metabolic gene curation. PeerJ, 2021, 9, e11447.	0.9	51
24	Ecology of inorganic sulfur auxiliary metabolism in widespread bacteriophages. Nature Communications, 2021, 12, 3503.	5.8	97
25	efam: an <i>e</i>xpanded, metaproteome-supported HMM profile database of viral protein <i>fam</i>ilies. Bioinformatics, 2021, 37, 4202-4208.	1.8	15
26	Glacier ice archives nearly 15,000-year-old microbes and phages. Microbiome, 2021, 9, 160.	4.9	59
27	Global overview and major challenges of host prediction methods for uncultivated phages. Current Opinion in Virology, 2021, 49, 117-126.	2.6	49
28	Virus-associated organosulfur metabolism in human and environmental systems. Cell Reports, 2021, 36, 109471.	2.9	38
29	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. Nature Communications, 2021, 12, 5483.	5.8	29
30	Diversity, taxonomy, and evolution of archaeal viruses of the class Caudoviricetes. PLoS Biology, 2021, 19, e3001442.	2.6	44
31	Perspective on taxonomic classification of uncultivated viruses. Current Opinion in Virology, 2021, 51, 207-215.	2.6	31
32	iVirus 2.0: Cyberinfrastructure-supported tools and data to power DNA virus ecology. ISME Communications, 2021, 1, .	1.7	13
33	Insights into the dynamics between viruses and their hosts in a hot spring microbial mat. ISME Journal, 2020, 14, 2527-2541.	4.4	42
34	Diversity and Distribution of a Novel Genus of Hyperthermophilic Aquificae Viruses Encoding a Proof-Reading Family-A DNA Polymerase. Frontiers in Microbiology, 2020, 11, 583361.	1.5	7
35	Metagenomes from Experimental Hydrologic Manipulation of Restored Coastal Plain Wetland Soils (Tyrell County, North Carolina). Microbiology Resource Announcements, 2020, 9, .	0.3	1
36	DRAM for distilling microbial metabolism to automate the curation of microbiome function. Nucleic Acids Research, 2020, 48, 8883-8900.	6.5	410

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37	Impact of Soil Salinity on the Cowpea Nodule-Microbiome and the Isolation of Halotolerant PGPR Strains to Promote Plant Growth under Salinity Stress. Phytobiomes Journal, 2020, 4, 364-374.	1.4	14
38	Influence of the polar light cycle on seasonal dynamics of an Antarctic lake microbial community. Microbiome, 2020, 8, 116.	4.9	32
39	Best Practices for Successfully Writing and Publishing a Genome Announcement in <i>Microbiology Resource Announcements</i>. Microbiology Resource Announcements, 2020, 9, .	0.3	0
40	Functional and genetic markers of niche partitioning among enigmatic members of the human oral microbiome. Genome Biology, 2020, 21, 292.	3.8	132
41	The International Virus Bioinformatics Meeting 2020. Viruses, 2020, 12, 1398.	1.5	3
42	Terabase-scale metagenome coassembly with MetaHipMer. Scientific Reports, 2020, 10, 10689.	1.6	34
43	Ecological Assembly Processes Are Coordinated between Bacterial and Viral Communities in Fractured Shale Ecosystems. MSystems, 2020, 5, .	1.7	15
44	Giant virus diversity and host interactions through global metagenomics. Nature, 2020, 578, 432-436.	13.7	207
45	Coming-of-Age Characterization of Soil Viruses: A Userâ€™s Guide to Virus Isolation, Detection within Metagenomes, and Viromics. Soil Systems, 2020, 4, 23.	1.0	61
46	Metatranscriptomic Sequencing of a Cyanobacterial Soil-Surface Consortium with and without a Diverse Underlying Soil Microbiome. Microbiology Resource Announcements, 2020, 9, .	0.3	1
47	Role of diversity-generating retroelements for regulatory pathway tuning in cyanobacteria. BMC Genomics, 2020, 21, 664.	1.2	13
48	Microbiomes of Velloziaceae from phosphorus-impoverished soils of the campos rupestres, a biodiversity hotspot. Scientific Data, 2019, 6, 140.	2.4	10
49	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earthâ€™s biomes. Nature Microbiology, 2019, 4, 1895-1906.	5.9	206
50	Microbial metagenomes and metatranscriptomes during a coastal phytoplankton bloom. Scientific Data, 2019, 6, 129.	2.4	36
51	Metagenomes and metatranscriptomes from boreal potential and actual acid sulfate soil materials. Scientific Data, 2019, 6, 207.	2.4	6
52	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. Cell, 2019, 179, 1068-1083.e21.	13.5	268
53	A Viral Ecogenomics Framework To Uncover the Secrets of Natureâ€™s â€œMicrobe Whisperersâ€• MSystems, 2019, 4, .	1.7	8
54	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. Cell, 2019, 177, 1109-1123.e14.	13.5	541

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55	Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. Nature Biotechnology, 2019, 37, 632-639.	9.4	569
56	Communityâ€Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. Global Biogeochemical Cycles, 2019, 33, 391-419.	1.9	76
57	Closely related viruses of the marine picoeukaryotic alga <i>Ostreococcus lucimarinus</i> exhibit different ecological strategies. Environmental Microbiology, 2019, 21, 2148-2170.	1.8	15
58	Numerous cultivated and uncultivated viruses encode ribosomal proteins. Nature Communications, 2019, 10, 752.	5.8	82
59	Marine DNA Viral Macro-and Micro-Diversity From Pole to Pole. SSRN Electronic Journal, 2019, , .	0.4	4
60	Characteristics of Wetting-Induced Bacteriophage Blooms in Biological Soil Crust. MBio, 2019, 10, .	1.8	56
61	Diversity, evolution, and classification of virophages uncovered through global metagenomics. Microbiome, 2019, 7, 157.	4.9	53
62	Minimum Information about an Uncultivated Virus Genome (MIUViG). Nature Biotechnology, 2019, 37, 29-37.	9.4	414
63	IMG/VR v.2.0: an integrated data management and analysis system for cultivated and environmental viral genomes. Nucleic Acids Research, 2019, 47, D678-D686.	6.5	174
64	Viruses control dominant bacteria colonizing the terrestrial deep biosphere after hydraulic fracturing. Nature Microbiology, 2019, 4, 352-361.	5.9	78
65	A viral reckoning: viruses emerge as essential manipulators of global ecosystems. Environmental Microbiology Reports, 2019, 11, 3-8.	1.0	5
66	Future-Proofing Your <i>Microbiology Resource Announcements</i> Genome Assembly for Reproducibility and Clarity. Microbiology Resource Announcements, 2019, 8, .	0.3	2
67	Optimizing <i>de novo</i> genome assembly from PCR-amplified metagenomes. PeerJ, 2019, 7, e6902.	0.9	28
68	Towards optimized viral metagenomes for double-stranded and single-stranded DNA viruses from challenging soils. PeerJ, 2019, 7, e7265.	0.9	48
69	Genomic insights into the <i>Acidobacteria</i> reveal strategies for their success in terrestrial environments. Environmental Microbiology, 2018, 20, 1041-1063.	1.8	228
70	Soil Viruses Are Underexplored Players in Ecosystem Carbon Processing. MSystems, 2018, 3, .	1.7	189
71	Interspecies cross-feeding orchestrates carbon degradation in the rumen ecosystem. Nature Microbiology, 2018, 3, 1274-1284.	5.9	144
72	Host-linked soil viral ecology along a permafrost thaw gradient. Nature Microbiology, 2018, 3, 870-880.	5.9	372

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73	Coupled laboratory and field investigations resolve microbial interactions that underpin persistence in hydraulically fractured shales. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6585-E6594.	3.3	69
74	Genomic variation and biogeography of Antarctic haloarchaea. Microbiome, 2018, 6, 113.	4.9	32
75	Viral and metabolic controls on high rates of microbial sulfur and carbon cycling in wetland ecosystems. Microbiome, 2018, 6, 138.	4.9	63
76	Phages rarely encode antibiotic resistance genes: a cautionary tale for virome analyses. ISME Journal, 2017, 11, 237-247.	4.4	298
77	Regulation of infection efficiency in a globally abundant marine <i>Bacteriodetes</i> virus. ISME Journal, 2017, 11, 284-295.	4.4	40
78	Microbiota Transfer Therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. Microbiome, 2017, 5, 10.	4.9	901
79	Ecogenomics of virophages and their giant virus hosts assessed through time series metagenomics. Nature Communications, 2017, 8, 858.	5.8	107
80	Environmental Viral Genomes Shed New Light on Virus-Host Interactions in the Ocean. MSphere, 2017, 2, .	1.3	114
81	On the Origin of Reverse Transcriptase-Using CRISPR-Cas Systems and Their Hyperdiverse, Enigmatic Spacer Repertoires. MBio, 2017, 8, .	1.8	52
82	iVirus: facilitating new insights in viral ecology with software and community data sets imbedded in a cyberinfrastructure. ISME Journal, 2017, 11, 7-14.	4.4	109
83	Comparative Omics and Trait Analyses of Marine Pseudoalteromonas Phages Advance the Phage OTU Concept. Frontiers in Microbiology, 2017, 8, 1241.	1.5	34
84	vConTACT: an iVirus tool to classify double-stranded DNA viruses that infect<i>Archaea</i>and<i>Bacteria</i>. PeerJ, 2017, 5, e3243.	0.9	219
85	Putative archaeal viruses from the mesopelagic ocean. PeerJ, 2017, 5, e3428.	0.9	46
86	Benchmarking viromics: an <i>in silico</i> evaluation of metagenome-enabled estimates of viral community composition and diversity. PeerJ, 2017, 5, e3817.	0.9	235
87	Diversity and comparative genomics of chimeric viruses in<i>Sphagnum-</i>dominated peatlands. Virus Evolution, 2016, 2, vew025.	2.2	18
88	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. Nature, 2016, 537, 689-693.	13.7	629
89	Study of Prokaryotes and Viruses in Aquatic Ecosystems by Metagenetic and Metagenomic Approaches. , 2016, , 245-254.		2
90	Analysis of metagenomic data reveals common features of halophilic viral communities across continents. Environmental Microbiology, 2016, 18, 889-903.	1.8	59

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91	Illuminating structural proteins in viral â€œdark matterâ€•with metaproteomics. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2436-2441.	3.3	95
92	Plankton networks driving carbon export in the oligotrophic ocean. Nature, 2016, 532, 465-470.	13.7	670
93	Towards quantitative viromics for both double-stranded and single-stranded DNA viruses. PeerJ, 2016, 4, e2777.	0.9	185
94	Diversity and comparative genomics of Microviridae in Sphagnum- dominated peatlands. Frontiers in Microbiology, 2015, 6, 375.	1.5	62
95	Viral dark matter and virusâ€"host interactions resolved from publicly available microbial genomes. ELife, 2015, 4, .	2.8	400
96	Determinants of community structure in the global plankton interactome. Science, 2015, 348, 1262073.	6.0	842
97	Patterns and ecological drivers of ocean viral communities. Science, 2015, 348, 1261498.	6.0	617
98	Environmental characteristics of Agulhas rings affect interocean plankton transport. Science, 2015, 348, 1261447.	6.0	158
99	Metagenomic characterization of viral communities in corals: mining biological signal from methodological noise. Environmental Microbiology, 2015, 17, 3440-3449.	1.8	75
100	VirSorter: mining viral signal from microbial genomic data. PeerJ, 2015, 3, e985.	0.9	949
101	Genomic characteristics and environmental distributions of the uncultivated Far-T4 phages. Frontiers in Microbiology, 2015, 6, 199.	1.5	24
102	A high-throughput sequencing ecotoxicology study of freshwater bacterial communities and their responses to tebuconazole. FEMS Microbiology Ecology, 2014, 90, 563-574.	1.3	35
103	Diversity of environmental single-stranded DNA phages revealed by PCR amplification of the partial major capsid protein. ISME Journal, 2014, 8, 2093-2103.	4.4	71
104	Metavir 2: new tools for viral metagenome comparison and assembled virome analysis. BMC Bioinformatics, 2014, 15, 76.	1.2	217
105	Ecology and evolution of viruses infecting uncultivated SUP05 bacteria as revealed by single-cell- and meta-genomics. ELife, 2014, 3, e03125.	2.8	186
106	Chimeric viruses blur the borders between the major groups of eukaryotic single-stranded DNA viruses. Nature Communications, 2013, 4, 2700.	5.8	90
107	Assessment of viral community functional potential from viral metagenomes may be hampered by contamination with cellular sequences. Open Biology, 2013, 3, 130160.	1.5	123
108	Metagenomics applied to environmental viral communities. Virologie, 2013, 17, 229-242.	0.1	0

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109	Evolution and Diversity of the Microviridae Viral Family through a Collection of 81 New Complete Genomes Assembled from Virome Reads. PLoS ONE, 2012, 7, e40418.	1.1	177
110	Assessing the Diversity and Specificity of Two Freshwater Viral Communities through Metagenomics. PLoS ONE, 2012, 7, e33641.	1.1	227
111	Comparison of 16S rRNA and protein-coding genes as molecular markers for assessing microbial diversity (Bacteria and Archaea) in ecosystems. FEMS Microbiology Ecology, 2011, 78, 617-628.	1.3	51
112	Metavir: a web server dedicated to virome analysis. Bioinformatics, 2011, 27, 3074-3075.	1.8	147
113	Philympics 2021: Prophage Predictions Perplex Programs. F1000Research, 0, 10, 758.	0.8	7
114	Philympics 2021: Prophage Predictions Perplex Programs. F1000Research, 0, 10, 758.	0.8	6