

# Simon Roux

## List of Publications by Year in descending order

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Version: 2024-02-01

114  
papers

16,287  
citations

34105

52  
h-index

24982

109  
g-index

156  
all docs

156  
docs citations

156  
times ranked

12208  
citing authors

#	ARTICLE	IF	CITATIONS
1	VirSorter: mining viral signal from microbial genomic data. PeerJ, 2015, 3, e985.	2.0	949
2	Microbiota Transfer Therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. Microbiome, 2017, 5, 10.	11.1	901
3	Determinants of community structure in the global plankton interactome. Science, 2015, 348, 1262073.	12.6	842
4	Plankton networks driving carbon export in the oligotrophic ocean. Nature, 2016, 532, 465-470.	27.8	670
5	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. Nature, 2016, 537, 689-693.	27.8	629
6	Patterns and ecological drivers of ocean viral communities. Science, 2015, 348, 1261498.	12.6	617
7	Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. Nature Biotechnology, 2019, 37, 632-639.	17.5	569
8	CheckV assesses the quality and completeness of metagenome-assembled viral genomes. Nature Biotechnology, 2021, 39, 578-585.	17.5	569
9	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. Cell, 2019, 177, 1109-1123.e14.	28.9	541
10	A genomic catalog of Earth's microbiomes. Nature Biotechnology, 2021, 39, 499-509.	17.5	457
11	VirSorter2: a multi-classifier, expert-guided approach to detect diverse DNA and RNA viruses. Microbiome, 2021, 9, 37.	11.1	441
12	Minimum Information about an Uncultivated Virus Genome (MIUViG). Nature Biotechnology, 2019, 37, 29-37.	17.5	414
13	DRAM for distilling microbial metabolism to automate the curation of microbiome function. Nucleic Acids Research, 2020, 48, 8883-8900.	14.5	410
14	Viral dark matter and virus-host interactions resolved from publicly available microbial genomes. ELife, 2015, 4, .	6.0	400
15	Host-linked soil viral ecology along a permafrost thaw gradient. Nature Microbiology, 2018, 3, 870-880.	13.3	372
16	The IMG/M data management and analysis system v.6.0: new tools and advanced capabilities. Nucleic Acids Research, 2021, 49, D751-D763.	14.5	332
17	Phages rarely encode antibiotic resistance genes: a cautionary tale for virome analyses. ISME Journal, 2017, 11, 237-247.	9.8	298
18	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. Cell, 2019, 179, 1068-1083.e21.	28.9	268

#	ARTICLE	IF	CITATIONS
19	IMG/VR v3: an integrated ecological and evolutionary framework for interrogating genomes of uncultivated viruses. <i>Nucleic Acids Research</i> , 2021, 49, D764-D775.	14.5	240
20	Benchmarking viromics: an <i>in silico</i> evaluation of metagenome-enabled estimates of viral community composition and diversity. <i>PeerJ</i> , 2017, 5, e3817.	2.0	235
21	Genomic insights into the <i>Acidobacteria</i> reveal strategies for their success in terrestrial environments. <i>Environmental Microbiology</i> , 2018, 20, 1041-1063.	3.8	228
22	Assessing the Diversity and Specificity of Two Freshwater Viral Communities through Metagenomics. <i>PLoS ONE</i> , 2012, 7, e33641.	2.5	227
23	vConTACT: an iVirus tool to classify double-stranded DNA viruses that infect <i>Archaea</i> and <i>Bacteria</i> . <i>PeerJ</i> , 2017, 5, e3243.	2.0	219
24	Metavir 2: new tools for viral metagenome comparison and assembled virome analysis. <i>BMC Bioinformatics</i> , 2014, 15, 76.	2.6	217
25	Giant virus diversity and host interactions through global metagenomics. <i>Nature</i> , 2020, 578, 432-436.	27.8	207
26	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , 2019, 4, 1895-1906.	13.3	206
27	Soil Viruses Are Underexplored Players in Ecosystem Carbon Processing. <i>MSystems</i> , 2018, 3, .	3.8	189
28	Ecology and evolution of viruses infecting uncultivated SUP05 bacteria as revealed by single-cell- and meta-genomics. <i>ELife</i> , 2014, 3, e03125.	6.0	186
29	Towards quantitative viromics for both double-stranded and single-stranded DNA viruses. <i>PeerJ</i> , 2016, 4, e2777.	2.0	185
30	Evolution and Diversity of the Microviridae Viral Family through a Collection of 81 New Complete Genomes Assembled from Virome Reads. <i>PLoS ONE</i> , 2012, 7, e40418.	2.5	177
31	IMG/VR v.2.0: an integrated data management and analysis system for cultivated and environmental viral genomes. <i>Nucleic Acids Research</i> , 2019, 47, D678-D686.	14.5	174
32	Environmental characteristics of Agulhas rings affect interocean plankton transport. <i>Science</i> , 2015, 348, 1261447.	12.6	158
33	Metavir: a web server dedicated to virome analysis. <i>Bioinformatics</i> , 2011, 27, 3074-3075.	4.1	147
34	Interspecies cross-feeding orchestrates carbon degradation in the rumen ecosystem. <i>Nature Microbiology</i> , 2018, 3, 1274-1284.	13.3	144
35	Functional and genetic markers of niche partitioning among enigmatic members of the human oral microbiome. <i>Genome Biology</i> , 2020, 21, 292.	8.8	132
36	Assessment of viral community functional potential from viral metagenomes may be hampered by contamination with cellular sequences. <i>Open Biology</i> , 2013, 3, 130160.	3.6	123

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37	Environmental Viral Genomes Shed New Light on Virus-Host Interactions in the Ocean. MSphere, 2017, 2, .	2.9	114
38	iVirus: facilitating new insights in viral ecology with software and community data sets imbedded in a cyberinfrastructure. ISME Journal, 2017, 11, 7-14.	9.8	109
39	Ecogenomics of virophages and their giant virus hosts assessed through time series metagenomics. Nature Communications, 2017, 8, 858.	12.8	107
40	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. Communications Biology, 2021, 4, 604.	4.4	107
41	Ecology of inorganic sulfur auxiliary metabolism in widespread bacteriophages. Nature Communications, 2021, 12, 3503.	12.8	97
42	Illuminating structural proteins in viral "dark matter" with metaproteomics. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2436-2441.	7.1	95
43	Chimeric viruses blur the borders between the major groups of eukaryotic single-stranded DNA viruses. Nature Communications, 2013, 4, 2700.	12.8	90
44	Numerous cultivated and uncultivated viruses encode ribosomal proteins. Nature Communications, 2019, 10, 752.	12.8	82
45	Viruses control dominant bacteria colonizing the terrestrial deep biosphere after hydraulic fracturing. Nature Microbiology, 2019, 4, 352-361.	13.3	78
46	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. Global Biogeochemical Cycles, 2019, 33, 391-419.	4.9	76
47	Metagenomic characterization of viral communities in corals: mining biological signal from methodological noise. Environmental Microbiology, 2015, 17, 3440-3449.	3.8	75
48	Diversity of environmental single-stranded DNA phages revealed by PCR amplification of the partial major capsid protein. ISME Journal, 2014, 8, 2093-2103.	9.8	71
49	Potential virus-mediated nitrogen cycling in oxygen-depleted oceanic waters. ISME Journal, 2021, 15, 981-998.	9.8	71
50	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.	7.1	69
51	Viral and metabolic controls on high rates of microbial sulfur and carbon cycling in wetland ecosystems. Microbiome, 2018, 6, 138.	11.1	63
52	Diversity and comparative genomics of Microviridae in Sphagnum- dominated peatlands. Frontiers in Microbiology, 2015, 6, 375.	3.5	62
53	Coming-of-Age Characterization of Soil Viruses: A User's Guide to Virus Isolation, Detection within Metagenomes, and Viromics. Soil Systems, 2020, 4, 23.	2.6	61
54	Analysis of metagenomic data reveals common features of halophilic viral communities across continents. Environmental Microbiology, 2016, 18, 889-903.	3.8	59

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55	Glacier ice archives nearly 15,000-year-old microbes and phages. <i>Microbiome</i> , 2021, 9, 160.	11.1	59
56	Characteristics of Wetting-Induced Bacteriophage Blooms in Biological Soil Crust. <i>MBio</i> , 2019, 10, .	4.1	56
57	DOE JGI Metagenome Workflow. <i>MSystems</i> , 2021, 6, .	3.8	56
58	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , 2019, 7, 157.	11.1	53
59	On the Origin of Reverse Transcriptase-Using CRISPR-Cas Systems and Their Hyperdiverse, Enigmatic Spacer Repertoires. <i>MBio</i> , 2017, 8, .	4.1	52
60	Comparison of 16S rRNA and protein-coding genes as molecular markers for assessing microbial diversity (Bacteria and Archaea) in ecosystems. <i>FEMS Microbiology Ecology</i> , 2011, 78, 617-628.	2.7	51
61	Expanding standards in viromics: in silico evaluation of dsDNA viral genome identification, classification, and auxiliary metabolic gene curation. <i>PeerJ</i> , 2021, 9, e11447.	2.0	51
62	Global overview and major challenges of host prediction methods for uncultivated phages. <i>Current Opinion in Virology</i> , 2021, 49, 117-126.	5.4	49
63	Towards optimized viral metagenomes for double-stranded and single-stranded DNA viruses from challenging soils. <i>PeerJ</i> , 2019, 7, e7265.	2.0	48
64	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. <i>ISME Journal</i> , 2021, 15, 421-434.	9.8	46
65	Putative archaeal viruses from the mesopelagic ocean. <i>PeerJ</i> , 2017, 5, e3428.	2.0	46
66	Diversity, taxonomy, and evolution of archaeal viruses of the class Caudoviricetes. <i>PLoS Biology</i> , 2021, 19, e3001442.	5.6	44
67	Insights into the dynamics between viruses and their hosts in a hot spring microbial mat. <i>ISME Journal</i> , 2020, 14, 2527-2541.	9.8	42
68	Regulation of infection efficiency in a globally abundant marine <i>Bacteriodes</i> virus. <i>ISME Journal</i> , 2017, 11, 284-295.	9.8	40
69	Virus-associated organosulfur metabolism in human and environmental systems. <i>Cell Reports</i> , 2021, 36, 109471.	6.4	38
70	Microbial metagenomes and metatranscriptomes during a coastal phytoplankton bloom. <i>Scientific Data</i> , 2019, 6, 129.	5.3	36
71	A high-throughput sequencing ecotoxicology study of freshwater bacterial communities and their responses to tebuconazole. <i>FEMS Microbiology Ecology</i> , 2014, 90, 563-574.	2.7	35
72	Ecology and molecular targets of hypermutation in the global microbiome. <i>Nature Communications</i> , 2021, 12, 3076.	12.8	35

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73	Diversity in the soil virosphere: to infinity and beyond?. Trends in Microbiology, 2022, 30, 1025-1035.	7.7	35
74	Comparative Omics and Trait Analyses of Marine Pseudoalteromonas Phages Advance the Phage OTU Concept. Frontiers in Microbiology, 2017, 8, 1241.	3.5	34
75	Terabase-scale metagenome coassembly with MetaHipMer. Scientific Reports, 2020, 10, 10689.	3.3	34
76	Genomic variation and biogeography of Antarctic haloarchaea. Microbiome, 2018, 6, 113.	11.1	32
77	Influence of the polar light cycle on seasonal dynamics of an Antarctic lake microbial community. Microbiome, 2020, 8, 116.	11.1	32
78	Perspective on taxonomic classification of uncultivated viruses. Current Opinion in Virology, 2021, 51, 207-215.	5.4	31
79	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. Nature Communications, 2021, 12, 5483.	12.8	29
80	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative's Workshop and Follow-On Activities. MSystems, 2021, 6, .	3.8	28
81	Optimizing <i>de novo</i> genome assembly from PCR-amplified metagenomes. PeerJ, 2019, 7, e6902.	2.0	28
82	Genomic characteristics and environmental distributions of the uncultivated Far-T4 phages. Frontiers in Microbiology, 2015, 6, 199.	3.5	24
83	Metagenomics in Virology. , 2021, , 133-140.		23
84	Diversity and comparative genomics of chimeric viruses in <i>Sphagnum</i> -dominated peatlands. Virus Evolution, 2016, 2, vew025.	4.9	18
85	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.	9.8	17
86	Metagenome-assembled genomes of phytoplankton microbiomes from the Arctic and Atlantic Oceans. Microbiome, 2022, 10, 67.	11.1	17
87	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.	9.8	16
88	Closely related viruses of the marine picoeukaryotic alga <i>Ostreococcus lucimarinus</i> exhibit different ecological strategies. Environmental Microbiology, 2019, 21, 2148-2170.	3.8	15
89	Ecological Assembly Processes Are Coordinated between Bacterial and Viral Communities in Fractured Shale Ecosystems. MSystems, 2020, 5, .	3.8	15
90	Metagenome Sequencing to Explore Phylogenomics of Terrestrial Cyanobacteria. Microbiology Resource Announcements, 2021, 10, e0025821.	0.6	15

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91	efam: an expanded, metaproteome-supported HMM profile database of viral protein families. Bioinformatics, 2021, 37, 4202-4208.	4.1	15
92	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.	2.7	14
93	Role of diversity-generating retroelements for regulatory pathway tuning in cyanobacteria. BMC Genomics, 2020, 21, 664.	2.8	13
94	iVirus 2.0: Cyberinfrastructure-supported tools and data to power DNA virus ecology. ISME Communications, 2021, 1, .	4.2	13
95	Virus Bioinformatics. , 2021, , 124-132.		12
96	Microbiomes of Velloziaceae from phosphorus-impooverished soils of the campos rupestres, a biodiversity hotspot. Scientific Data, 2019, 6, 140.	5.3	10
97	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.	9.8	10
98	A Viral Ecogenomics Framework To Uncover the Secrets of Nature's "Microbe Whisperers". MSystems, 2019, 4, .	3.8	8
99	Ecogenomics of Groundwater Phages Suggests Niche Differentiation Linked to Specific Environmental Tolerance. MSystems, 2021, 6, e0053721.	3.8	8
100	Virus-Host Interactions and Genetic Diversity of Antarctic Sea Ice Bacteriophages. MBio, 2022, 13, e0065122.	4.1	8
101	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.	3.5	7
102	Philympics 2021: Prophage Predictions Perplex Programs. F1000Research, 0, 10, 758.	1.6	7
103	Metagenomes and metatranscriptomes from boreal potential and actual acid sulfate soil materials. Scientific Data, 2019, 6, 207.	5.3	6
104	Philympics 2021: Prophage Predictions Perplex Programs. F1000Research, 0, 10, 758.	1.6	6
105	A viral reckoning: viruses emerge as essential manipulators of global ecosystems. Environmental Microbiology Reports, 2019, 11, 3-8.	2.4	5
106	Marine DNA Viral Macro-and Micro-Diversity From Pole to Pole. SSRN Electronic Journal, 2019, , .	0.4	4
107	Extreme dimensions " how big (or small) can tailed phages be?. Nature Reviews Microbiology, 2021, 19, 407-407.	28.6	4
108	The International Virus Bioinformatics Meeting 2020. Viruses, 2020, 12, 1398.	3.3	3

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109	Study of Prokaryotes and Viruses in Aquatic Ecosystems by Metagenetic and Metagenomic Approaches. , 2016, , 245-254.		2
110	Future-Proofing Your <i>Microbiology Resource Announcements</i> Genome Assembly for Reproducibility and Clarity. Microbiology Resource Announcements, 2019, 8, .	0.6	2
111	Metagenomes from Experimental Hydrologic Manipulation of Restored Coastal Plain Wetland Soils (Tyrell County, North Carolina). Microbiology Resource Announcements, 2020, 9, .	0.6	1
112	Metatranscriptomic Sequencing of a Cyanobacterial Soil-Surface Consortium with and without a Diverse Underlying Soil Microbiome. Microbiology Resource Announcements, 2020, 9, .	0.6	1
113	Best Practices for Successfully Writing and Publishing a Genome Announcement in <i>Microbiology Resource Announcements</i>. Microbiology Resource Announcements, 2020, 9, .	0.6	0
114	Metagenomics applied to environmental viral communities. Virologie, 2013, 17, 229-242.	0.1	0