

# Philippe Roumagnac

## List of Publications by Year in descending order

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83  
papers

6,433  
citations

182225

30  
h-index

81351

76  
g-index

86  
all docs

86  
docs citations

86  
times ranked

7217  
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete genome sequence of a novel marafivirus infecting pearl millet in Burkina Faso. <i>Archives of Virology</i> , 2022, 167, 245-248.	0.9	2
2	Establishment of five new genera in the family Geminiviridae: Citlodavirus, Maldovirus, Mulcrilevirus, Opunvirus, and Topilevirus. <i>Archives of Virology</i> , 2022, 167, 695-710.	0.9	43
3	Host range and molecular variability of the sadwavirus dioscorea mosaic associated virus. <i>Archives of Virology</i> , 2022, 167, 917-922.	0.9	3
4	Virion-Associated Nucleic Acid-Based Metagenomics: A Decade of Advances in Molecular Characterization of Plant Viruses. <i>Phytopathology</i> , 2022, 112, 2253-2272.	1.1	7
5	Molecular characterization of Cordyline virus 1 isolates infecting yam ( <i>Dioscorea</i> spp). <i>Archives of Virology</i> , 2022, 167, 2275-2280.	0.9	3
6	metaXplor: an interactive viral and microbial metagenomic data manager. <i>GigaScience</i> , 2021, 10, .	3.3	4
7	Nanopore Sequencing Is a Credible Alternative to Recover Complete Genomes of Geminiviruses. <i>Microorganisms</i> , 2021, 9, 903.	1.6	18
8	Genetic Diversity of Rice stripe necrosis virus and New Insights into Evolution of the Genus Benyvirus. <i>Viruses</i> , 2021, 13, 737.	1.5	9
9	New World Cactaceae Plants Harbor Diverse Geminiviruses. <i>Viruses</i> , 2021, 13, 694.	1.5	8
10	Characterisation of the Viral Community Associated with the Alfalfa Weevil ( <i>Hypera postica</i> ) and Its Host Plant, Alfalfa ( <i>Medicago sativa</i> ). <i>Viruses</i> , 2021, 13, 791.	1.5	10
11	Identification of the Begomoviruses Squash Leaf Curl Virus and Watermelon Chlorotic Stunt Virus in Various Plant Samples in North America. <i>Viruses</i> , 2021, 13, 810.	1.5	6
12	Comparison of the Virome of Quarantined Sugarcane Varieties and the Virome of Grasses Growing near the Quarantine Station. <i>Viruses</i> , 2021, 13, 922.	1.5	3
13	Genome characterization and diversity of trifolium virus 1: identification of a novel legume-infecting capulavirus. <i>Archives of Virology</i> , 2021, 166, 2573-2578.	0.9	2
14	First historical genome of a crop bacterial pathogen from herbarium specimen: Insights into citrus canker emergence. <i>PLoS Pathogens</i> , 2021, 17, e1009714.	2.1	8
15	Taxonomy update for the family Alphasatellitidae: new subfamily, genera, and species. <i>Archives of Virology</i> , 2021, 166, 3503-3511.	0.9	15
16	RDP5: a computer program for analyzing recombination in, and removing signals of recombination from, nucleotide sequence datasets. <i>Virus Evolution</i> , 2021, 7, veaa087.	2.2	257
17	Novel circular DNA virus identified in <i>Opuntia discolor</i> (Cactaceae) that codes for proteins with similarity to those of geminiviruses. <i>Journal of General Virology</i> , 2021, 102, .	1.3	1
18	Large-scale survey reveals pervasiveness and potential function of endogenous geminiviral sequences in plants. <i>Virus Evolution</i> , 2020, 6, veaa071.	2.2	15

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19	High-Throughput Sequencing for Deciphering the Virome of Alfalfa ( <i>Medicago sativa</i> L.). <i>Frontiers in Microbiology</i> , 2020, 11, 553109.	1.5	24
20	Illuminating an Ecological Blackbox: Using High Throughput Sequencing to Characterize the Plant Virome Across Scales. <i>Frontiers in Microbiology</i> , 2020, 11, 578064.	1.5	67
21	Yam asymptomatic virus 1, a novel virus infecting yams ( <i>Dioscorea</i> spp.) with significant prevalence in a germplasm collection. <i>Archives of Virology</i> , 2020, 165, 2653-2657.	0.9	10
22	Diverse genomoviruses representing twenty-nine species identified associated with plants. <i>Archives of Virology</i> , 2020, 165, 2891-2901.	0.9	13
23	Heterogeneity of the rice microbial community of the Chinese centuries-old Honghe Hani rice terraces system. <i>Environmental Microbiology</i> , 2020, 22, 3429-3445.	1.8	8
24	Sorghum mastrevirus-associated alphasatellites: new geminalphasatellites associated with an African streak mastrevirus infecting wild Poaceae plants on Reunion Island. <i>Archives of Virology</i> , 2020, 165, 1925-1928.	0.9	3
25	Improvements in Virus Detection at CIRAD's Sugarcane Quarantine Using Both Viral Metagenomics and PCR-Based Approaches. <i>Sugar Tech</i> , 2020, 22, 498-503.	0.9	7
26	Molecular detection of sugarcane striate virus and sugarcane white streak virus and their prevalence in the Miami World Collection of sugarcane and related grasses. <i>Plant Pathology</i> , 2020, 69, 1060-1069.	1.2	4
27	A Novel Divergent Geminivirus Identified in Asymptomatic New World Cactaceae Plants. <i>Viruses</i> , 2020, 12, 398.	1.5	10
28	Evolution and ecology of plant viruses. <i>Nature Reviews Microbiology</i> , 2019, 17, 632-644.	13.6	166
29	Diverse and variable virus communities in wild plant populations revealed by metagenomic tools. <i>PeerJ</i> , 2019, 7, e6140.	0.9	53
30	Exploring the diversity of Poaceae-infecting mastreviruses on Reunion Island using a viral metagenomics-based approach. <i>Scientific Reports</i> , 2019, 9, 12716.	1.6	14
31	High-throughput sequencing of complete genomes of ipomoviruses associated with an epidemic of cassava brown streak disease in the Comoros Archipelago. <i>Archives of Virology</i> , 2019, 164, 2193-2196.	0.9	7
32	A New Prevalent Densovirus Discovered in Acari. Insight from Metagenomics in Viral Communities Associated with Two-Spotted Mite ( <i>Tetranychus urticae</i> ) Populations. <i>Viruses</i> , 2019, 11, 233.	1.5	19
33	Emergence of Southern Rice Black-Streaked Dwarf Virus in the Centuries-Old Chinese Yuanyang Agrosystem of Rice Landraces. <i>Viruses</i> , 2019, 11, 985.	1.5	7
34	Novel circular DNA viruses associated with Apiaceae and Poaceae from South Africa and New Zealand. <i>Archives of Virology</i> , 2019, 164, 237-242.	0.9	12
35	Viral Metagenomics Approaches for High-Resolution Screening of Multiplexed Arthropod and Plant Viral Communities. <i>Methods in Molecular Biology</i> , 2018, 1746, 77-95.	0.4	25
36	Comparison of loop-mediated isothermal amplification, polymerase chain reaction, and selective isolation assays for detection of <i>Xanthomonas albilineans</i> from sugarcane. <i>Tropical Plant Pathology</i> , 2018, 43, 351-359.	0.8	10

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37	Geometagenomics illuminates the impact of agriculture on the distribution and prevalence of plant viruses at the ecosystem scale. <i>ISME Journal</i> , 2018, 12, 173-184.	4.4	132
38	Nanovirus-alphasatellite complex identified in <i>Vicia cracca</i> in the Rhône delta region of France. <i>Archives of Virology</i> , 2018, 163, 695-700.	0.9	25
39	Nanopore-based detection and characterization of yam viruses. <i>Scientific Reports</i> , 2018, 8, 17879.	1.6	57
40	The Westward Journey of Alfalfa Leaf Curl Virus. <i>Viruses</i> , 2018, 10, 542.	1.5	12
41	Notes on recombination and reassortment in multipartite/segmented viruses. <i>Current Opinion in Virology</i> , 2018, 33, 156-166.	2.6	44
42	Viral Metagenomic-Based Screening of Sugarcane from Florida Reveals Occurrence of Six Sugarcane-Infecting Viruses and High Prevalence of <i>Sugarcane yellow leaf virus</i> . <i>Plant Disease</i> , 2018, 102, 2317-2323.	0.7	20
43	First Report of Alfalfa Leaf Curl Virus Affecting Alfalfa ( <i>Medicago sativa</i> ) in Jordan, Lebanon, Syria, and Tunisia. <i>Plant Disease</i> , 2018, 102, 2052-2052.	0.7	4
44	Alphasatellitidae: a new family with two subfamilies for the classification of geminivirus- and nanovirus-associated alphasatellites. <i>Archives of Virology</i> , 2018, 163, 2587-2600.	0.9	133
45	First Report of Alfalfa Leaf Curl Virus from Alfalfa in Iran. <i>Plant Disease</i> , 2018, 102, 2385.	0.7	5
46	From Spatial Metagenomics to Molecular Characterization of Plant Viruses: A Geminivirus Case Study. <i>Advances in Virus Research</i> , 2018, 101, 55-83.	0.9	34
47	Capulavirus and Grablovirus: two new genera in the family Geminiviridae. <i>Archives of Virology</i> , 2017, 162, 1819-1831.	0.9	240
48	Genome sequences of a capulavirus infecting <i>Plantago lanceolata</i> in the Åland archipelago of Finland. <i>Archives of Virology</i> , 2017, 162, 2041-2045.	0.9	39
49	Exploiting Genetic Information to Trace Plant Virus Dispersal in Landscapes. <i>Annual Review of Phytopathology</i> , 2017, 55, 139-160.	3.5	19
50	Complete genome sequences of cowpea polerovirus 1 and cowpea polerovirus 2 infecting cowpea plants in Burkina Faso. <i>Archives of Virology</i> , 2017, 162, 2149-2152.	0.9	11
51	Two novel Alphaflexiviridae members revealed by deep sequencing of the Vanilla (Orchidaceae) virome. <i>Archives of Virology</i> , 2017, 162, 3855-3861.	0.9	13
52	Occurrence of a novel mastrevirus in sugarcane germplasm collections in Florida, Guadeloupe and Réunion. <i>Virology Journal</i> , 2017, 14, 146.	1.4	20
53	ICTV Virus Taxonomy Profile: Geminiviridae. <i>Journal of General Virology</i> , 2017, 98, 131-133.	1.3	676
54	Prevalence of <i>Sugarcane yellow leaf virus</i> in Sugarcane-Producing Regions in Kenya Revealed by Reverse-Transcription Loop-Mediated Isothermal Amplification Method. <i>Plant Disease</i> , 2016, 100, 260-268.	0.7	14

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55	Molecular characterization and prevalence of two capulaviruses: Alfalfa leaf curl virus from France and Euphorbia caput-medusae latent virus from South Africa. <i>Virology</i> , 2016, 493, 142-153.	1.1	40
56	Diverse circular replication-associated protein encoding viruses circulating in invertebrates within a lake ecosystem. <i>Infection, Genetics and Evolution</i> , 2016, 39, 304-316.	1.0	66
57	Metagenomic-Based Screening and Molecular Characterization of Cowpea-Infecting Viruses in Burkina Faso. <i>PLoS ONE</i> , 2016, 11, e0165188.	1.1	46
58	Plant Virus Metagenomics: Advances in Virus Discovery. <i>Phytopathology</i> , 2015, 105, 716-727.	1.1	340
59	The genomes of many yam species contain transcriptionally active endogenous geminiviral sequences that may be functionally expressed. <i>Virus Evolution</i> , 2015, 1, vev002.	2.2	30
60	Identification of novel Bromus- and Trifolium-associated circular DNA viruses. <i>Archives of Virology</i> , 2015, 160, 1303-1311.	0.9	28
61	Alfalfa Leaf Curl Virus: an Aphid-Transmitted Geminivirus. <i>Journal of Virology</i> , 2015, 89, 9683-9688.	1.5	62
62	Metagenomics Approaches Based on Virion-Associated Nucleic Acids (VANA): An Innovative Tool for Assessing Without A Priori Viral Diversity of Plants. <i>Methods in Molecular Biology</i> , 2015, 1302, 249-257.	0.4	23
63	Molecular characterization of yam virus X, a new potexvirus infecting yams ( <i>Dioscorea</i> spp) and evidence for the existence of at least three distinct potexviruses infecting yams. <i>Archives of Virology</i> , 2014, 159, 3421-3426.	0.9	21
64	The genome of African yam ( <i>Dioscorea cayenensis</i> <i>rotundata</i> complex) hosts endogenous sequences from four distinct badnavirus species. <i>Molecular Plant Pathology</i> , 2014, 15, 790-801.	2.0	28
65	Shifting the paradigm from pathogens to pathobiome: new concepts in the light of meta-omics. <i>Frontiers in Cellular and Infection Microbiology</i> , 2014, 4, 29.	1.8	237
66	Appearances Can Be Deceptive: Revealing a Hidden Viral Infection with Deep Sequencing in a Plant Quarantine Context. <i>PLoS ONE</i> , 2014, 9, e102945.	1.1	89
67	Identification and characterisation of a highly divergent geminivirus: Evolutionary and taxonomic implications. <i>Virus Research</i> , 2013, 177, 35-45.	1.1	76
68	Reversible oxygen-tolerant hydrogenase carried by free-living N <sub>2</sub> -fixing bacteria isolated from the rhizospheres of rice, maize, and wheat. <i>MicrobiologyOpen</i> , 2012, 1, 349-361.	1.2	5
69	Recombination in Eukaryotic Single Stranded DNA Viruses. <i>Viruses</i> , 2011, 3, 1699-1738.	1.5	188
70	Salmonella enterica Serotype Typhi with Nonclassical Quinolone Resistance Phenotype. <i>Emerging Infectious Diseases</i> , 2011, 17, 1091-1094.	2.0	16
71	Phylogeography and Molecular Epidemiology of <i>Yersinia pestis</i> in Madagascar. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1319.	1.3	80
72	<i>Salmonella enterica</i> Serotype Typhi with Nonclassical Quinolone Resistance Phenotype. <i>Emerging Infectious Diseases</i> , 2011, 17, 1091-1094.	2.0	26

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73	<i>Yersinia pestis</i> genome sequencing identifies patterns of global phylogenetic diversity. <i>Nature Genetics</i> , 2010, 42, 1140-1143.	9.4	504
74	Evolution and Population Structure of <i>Salmonella enterica</i> Serovar Newport. <i>Journal of Bacteriology</i> , 2010, 192, 6465-6476.	1.0	109
75	A multiplex single nucleotide polymorphism typing assay for detecting mutations that result in decreased fluoroquinolone susceptibility in <i>Salmonella enterica</i> serovars Typhi and Paratyphi A. <i>Journal of Antimicrobial Chemotherapy</i> , 2010, 65, 1631-1641.	1.3	36
76	High-throughput sequencing provides insights into genome variation and evolution in <i>Salmonella</i> Typhi. <i>Nature Genetics</i> , 2008, 40, 987-993.	9.4	453
77	Frequent emergence and limited geographic dispersal of methicillin-resistant <i>Staphylococcus aureus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14130-14135.	3.3	239
78	High-Throughput Genotyping of <i>Salmonella enterica</i> Serovar Typhi Allowing Geographical Assignment of Haplotypes and Pathotypes within an Urban District of Jakarta, Indonesia. <i>Journal of Clinical Microbiology</i> , 2008, 46, 1741-1746.	1.8	69
79	Clonal Expansion and Microevolution of Quinolone-Resistant <i>Salmonella enterica</i> Serotype Typhi in Vietnam from 1996 to 2004. <i>Journal of Clinical Microbiology</i> , 2007, 45, 3485-3492.	1.8	52
80	An African origin for the intimate association between humans and <i>Helicobacter pylori</i> . <i>Nature</i> , 2007, 445, 915-918.	13.7	826
81	CLONAL RECONQUEST OF ANTIBIOTIC-SUSCEPTIBLE <i>SALMONELLA ENTERICA</i> SEROTYPE TYPHI IN SON LA PROVINCE, VIETNAM. <i>American Journal of Tropical Medicine and Hygiene</i> , 2007, 76, 1174-1181.	0.6	9
82	Clonal reconquest of antibiotic-susceptible <i>Salmonella enterica</i> serotype Typhi in Son La Province, Vietnam. <i>American Journal of Tropical Medicine and Hygiene</i> , 2007, 76, 1174-81.	0.6	6
83	Evolutionary History of <i>Salmonella</i> Typhi. <i>Science</i> , 2006, 314, 1301-1304.	6.0	349