

Thierry Candresse

List of Publications by Year in descending order

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207
papers

9,748
citations

38720
50
h-index

46771
89
g-index

216
all docs

216
docs citations

216
times ranked

4991
citing authors

#	ARTICLE	IF	CITATIONS
1	Top 10 plant viruses in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2011, 12, 938-954.	2.0	936
2	Virology Division News: The new plant virus family Flexiviridae and assessment of molecular criteria for species demarcation. <i>Archives of Virology</i> , 2004, 149, 1045-1060.	0.9	400
3	A highly sensitive immunocapture polymerase chain reaction method for plum pox potyvirus detection. <i>Journal of Virological Methods</i> , 1992, 39, 27-37.	1.0	256
4	The Eukaryotic Translation Initiation Factor 4E Controls Lettuce Susceptibility to the Potyvirus Lettuce mosaic virus. <i>Plant Physiology</i> , 2003, 132, 1272-1282.	2.3	255
5	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
6	A polymerase chain reaction assay adapted to plum pox potyvirus detection. <i>Journal of Virological Methods</i> , 1991, 33, 355-365.	1.0	227
7	The family Closteroviridae revised. <i>Archives of Virology</i> , 2002, 147, 2039-2044.	0.9	203
8	Current impact and future directions of high throughput sequencing in plant virus diagnostics. <i>Virus Research</i> , 2014, 188, 90-96.	1.1	196
9	New Advances in Understanding the Molecular Biology of Plant/Potyvirus Interactions. <i>Molecular Plant-Microbe Interactions</i> , 1999, 12, 367-376.	1.4	194
10	Frequent occurrence of recombinant potyvirus isolates. <i>Journal of General Virology</i> , 1996, 77, 1953-1965.	1.3	191
11	Plum pox virus and sharka: a model potyvirus and a major disease. <i>Molecular Plant Pathology</i> , 2014, 15, 226-241.	2.0	178
12	A Framework for the Evaluation of Biosecurity, Commercial, Regulatory, and Scientific Impacts of Plant Viruses and Viroids Identified by NGS Technologies. <i>Frontiers in Microbiology</i> , 2017, 8, 45.	1.5	165
13	Next-Generation Sequencing and Genome Editing in Plant Virology. <i>Frontiers in Microbiology</i> , 2016, 7, 1325.	1.5	142
14	POLYVALENT DETECTION OF FRUIT TREE TRICHO, CAPILLO AND FOVEAVIRUSES BY NESTED RT-PCR USING DEGENERATED AND INOSINE CONTAINING PRIMERS (PDO RT-PCR). <i>Acta Horticulturae</i> , 2001, , 37-44.	0.1	133
15	Studies on the diagnosis of hop stunt viroid in fruit trees: Identification of new hosts and application of a nucleic acid extraction procedure based on non-organic solvents. <i>European Journal of Plant Pathology</i> , 1996, 102, 837-846.	0.8	128
16	The ubiquitin/26S proteasome system in plant-pathogen interactions: a never-ending hide-and-seek game. <i>Molecular Plant Pathology</i> , 2010, 11, 293-308.	2.0	126
17	Geographically and temporally distant natural recombinant isolates of Plum pox virus (PPV) are genetically very similar and form a unique PPV subgroup. <i>Journal of General Virology</i> , 2004, 85, 2671-2681.	1.3	120
18	Identification of multiple structural domains regulating viroid pathogenicity.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 10104-10108.	3.3	119

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19	Simultaneous detection and typing of plum pox potyvirus (PPV) isolates by heminested-PCR and PCR-ELISA. Journal of Virological Methods, 1997, 68, 127-137.	1.0	118
20	The Determinant of Potyvirus Ability to Overcome the RTM Resistance of Arabidopsis thaliana Maps to the N-Terminal Region of the Coat Protein. Molecular Plant-Microbe Interactions, 2009, 22, 1302-1311.	1.4	114
21	Application of HTS for Routine Plant Virus Diagnostics: State of the Art and Challenges. Frontiers in Plant Science, 2018, 9, 1082.	1.7	110
22	Coordinated and selective recruitment of eIF4E and eIF4G factors for potyvirus infection in Arabidopsis thaliana. FEBS Letters, 2007, 581, 1041-1046.	1.3	109
23	Virus Detection by High-Throughput Sequencing of Small RNAs: Large-Scale Performance Testing of Sequence Analysis Strategies. Phytopathology, 2019, 109, 488-497.	1.1	106
24	Comparison of Monoclonal Antibodies and Polymerase Chain Reaction Assays for the Typing of Isolates Belonging to the D and M Serotypes of Plum Pox Potyvirus. Phytopathology, 1998, 88, 198-204.	1.1	104
25	Polyvalent Degenerate Oligonucleotides Reverse Transcription-Polymerase Chain Reaction: A Polyvalent Detection and Characterization Tool for Trichoviruses, Capilloviruses, and Foveaviruses. Phytopathology, 2005, 95, 617-625.	1.1	103
26	Multiple Resistance Traits Control Plum pox virus Infection in Arabidopsis thaliana. Molecular Plant-Microbe Interactions, 2006, 19, 541-549.	1.4	101
27	Nucleotide sequence and genomic organization of apple chlorotic leaf spot closterovirus. Virology, 1990, 179, 104-112.	1.1	96
28	Nucleotide sequence of the 3'-terminal region of the RNA of the E1 Amar strain of plum pox potyvirus. Journal of General Virology, 1991, 72, 1741-1746.	1.3	96
29	Print-capture PCR: a simple and highly sensitive method for the detection of plum pox virus (PPV) in plant tissues. Nucleic Acids Research, 1996, 24, 2192-2193.	6.5	92
30	RTM3, Which Controls Long-Distance Movement of Potyviruses, Is a Member of a New Plant Gene Family Encoding a Meprin and TRAF Homology Domain-Containing Protein. Plant Physiology, 2010, 154, 222-232.	2.3	91
31	Appearances Can Be Deceptive: Revealing a Hidden Viral Infection with Deep Sequencing in a Plant Quarantine Context. PLoS ONE, 2014, 9, e102945.	1.1	89
32	HcPro, a multifunctional protein encoded by a plant RNA virus, targets the 20S proteasome and affects its enzymic activities. Journal of General Virology, 2005, 86, 2595-2603.	1.3	87
33	Association of Little cherry virus 1 (LChV1) with the Shirofugen Stunt Disease and Characterization of the Genome of a Divergent LChV1 Isolate. Phytopathology, 2013, 103, 293-298.	1.1	83
34	Plum pox virus capsid protein suppresses plant pathogen-associated molecular pattern (PAMP)-triggered immunity. Molecular Plant Pathology, 2017, 18, 878-886.	2.0	75
35	Agrobacterium-mediated genetic transformation of grapevine somatic embryos and regeneration of transgenic plants expressing the coat protein of grapevine chrome mosaic nepovirus (GCMV). Plant Science, 1994, 102, 161-170.	1.7	74
36	Quantitative trait loci meta-analysis of Plum pox virus resistance in apricot (Prunus) factors. Molecular Plant Pathology, 2009, 10, 347-360.	2.0	71

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37	Trichovirus, a new genus of plant viruses. Archives of Virology, 1994, 134, 451-455.	0.9	69
38	Further characterization of a new recombinant group of Plum pox virus isolates, PPV-T, found in orchards in the Ankara province of Turkey. Virus Research, 2009, 142, 121-126.	1.1	69
39	Illuminating an Ecological Blackbox: Using High Throughput Sequencing to Characterize the Plant Virome Across Scales. Frontiers in Microbiology, 2020, 11, 578064.	1.5	67
40	Effects of Green Fluorescent Protein or β -Glucuronidase Tagging on the Accumulation and Pathogenicity of a Resistance-Breaking Lettuce mosaic virus Isolate in Susceptible and Resistant Lettuce Cultivars. Molecular Plant-Microbe Interactions, 2000, 13, 316-324.	1.4	66
41	strategies for simultaneous detection of multiple plant viruses. Canadian Journal of Plant Pathology, 2006, 28, 16-29.	0.8	64
42	High-throughput sequencing technologies for plant pest diagnosis: challenges and opportunities. EPPO Bulletin, 2018, 48, 219-224.	0.6	62
43	Biological and Molecular Variability of Lettuce Mosaic Virus Isolates. Phytopathology, 1997, 87, 397-403.	1.1	60
44	High-Throughput Sequencing and the Viomic Study of Grapevine Leaves: From the Detection of Grapevine-Infecting Viruses to the Description of a New Environmental Tymovirales Member. Frontiers in Microbiology, 2018, 9, 1782.	1.5	60
45	Nucleotide sequence and genetic organization of Hungarian grapevine chrome mosaic nepovirus RNA2. Nucleic Acids Research, 1989, 17, 7809-7819.	6.5	59
46	Nanopore-based detection and characterization of yam viruses. Scientific Reports, 2018, 8, 17879.	1.6	57
47	Analysis of gene expression changes in peach leaves in response to plum pox virus infection using RNA-seq. Molecular Plant Pathology, 2015, 16, 164-176.	2.0	56
48	ICTV Virus Taxonomy Profile: Closteroviridae. Journal of General Virology, 2020, 101, 364-365.	1.3	56
49	The RTM Resistance to Potyviruses in Arabidopsis thaliana: Natural Variation of the RTM Genes and Evidence for the Implication of Additional Genes. PLoS ONE, 2012, 7, e39169.	1.1	55
50	Causal agent of sharka disease: historical perspective and current status of Plum pox virus strains. EPPO Bulletin, 2006, 36, 239-246.	0.6	54
51	Pathogenicity Determinants in the Complex Virus Population of a Plum pox virus Isolate. Molecular Plant-Microbe Interactions, 2001, 14, 278-287.	1.4	53
52	Survey of Prunus necrotic ringspot virus in Rose and Its Variability in Rose and Prunus spp.. Phytopathology, 2001, 91, 84-91.	1.1	53
53	Potyvirus Helper Component-Proteinase Self-Interaction in the Yeast Two-Hybrid System and Delineation of the Interaction Domain Involved. Virology, 1999, 258, 95-99.	1.1	51
54	Lettuce mosaic virus Pathogenicity Determinants in Susceptible and Tolerant Lettuce Cultivars Map to Different Regions of the Viral Genome. Molecular Plant-Microbe Interactions, 2001, 14, 804-810.	1.4	51

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55	Molecular and Biological Characterization of Lettuce mosaic virus (LMV) Isolates Reveals a Distinct and Widespread Type of Resistance-Breaking Isolate: LMV-Most. <i>Phytopathology</i> , 2002, 92, 563-572.	1.1	49
56	Plant Viruses Infecting Solanaceae Family Members in the Cultivated and Wild Environments: A Review. <i>Plants</i> , 2020, 9, 667.	1.6	49
57	Interaction between potyvirus helper component-proteinase and capsid protein in infected plants. <i>Journal of General Virology</i> , 2002, 83, 1765-1770.	1.3	48
58	The 20S proteasome α 5 subunit of <i>Arabidopsis thaliana</i> carries an RNase activity and interacts in planta with the Lettuce mosaic potyvirus HcPro protein. <i>Molecular Plant Pathology</i> , 2011, 12, 137-150.	2.0	47
59	Viral Double-Stranded RNAs (dsRNAs) from Plants: Alternative Nucleic Acid Substrates for High-Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1746, 45-53.	0.4	47
60	Characterization of Sour Cherry Isolates of Plum pox virus from the Volga Basin in Russia Reveals a New Cherry Strain of the Virus. <i>Phytopathology</i> , 2013, 103, 972-979.	1.1	46
61	Recent advances and prospects in <i>Prunus</i> virology. <i>Annals of Applied Biology</i> , 2017, 171, 125-138.	1.3	45
62	Analysis of the population structure of three phenotypically different PSTVd isolates. <i>Archives of Virology</i> , 1994, 138, 233-245.	0.9	41
63	Comparison of the complete nucleotide sequences of two isolates of lettuce mosaic virus differing in their biological properties. <i>Virus Research</i> , 1997, 47, 167-177.	1.1	41
64	Multiple Resistance Phenotypes to Lettuce mosaic virus Among <i>Arabidopsis thaliana</i> Accessions. <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 608-616.	1.4	41
65	Family-based linkage and association mapping reveals novel genes affecting Plum pox virus infection in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2012, 196, 873-886.	3.5	41
66	Characterization by Deep Sequencing of Divergent Plum bark necrosis stem pitting-associated virus (PBNSPaV) Isolates and Development of a Broad-Spectrum PBNSPaV Detection Assay. <i>Phytopathology</i> , 2014, 104, 660-666.	1.1	41
67	Characterization by Deep Sequencing of <i>Prunus</i> virus T, a Novel Tepovirus Infecting <i>Prunus</i> Species. <i>Phytopathology</i> , 2015, 105, 135-140.	1.1	41
68	ANALYSIS OF PLUM POX VIRUS VARIABILITY AND DEVELOPMENT OF STRAIN-SPECIFIC PCR ASSAYS. <i>Acta Horticulturae</i> , 1995, , 357-369.	0.1	41
69	Genetically engineered resistance against grapevine chrome mosaic nepovirus. <i>Plant Molecular Biology</i> , 1993, 21, 89-97.	2.0	40
70	Characterization of New Isolates of Apricot vein clearing-associated virus and of a New <i>Prunus</i> -Infecting Virus: Evidence for Recombination as a Driving Force in Betaflexiviridae Evolution. <i>PLoS ONE</i> , 2015, 10, e0129469.	1.1	40
71	A Eukaryotic Translation Initiation Factor 4E (eIF4E) is Responsible for the Tobacco Recessive Resistance to Potyviruses. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 609-623.	1.0	40
72	Molecular characterization and prevalence of two capulaviruses: Alfalfa leaf curl virus from France and <i>Euphorbia caput-medusae</i> latent virus from South Africa. <i>Virology</i> , 2016, 493, 142-153.	1.1	40

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73	Nucleotide sequence of Hungarian grapevine chrome mosaic nepovirus RNA1. Nucleic Acids Research, 1989, 17, 7795-7807.	6.5	39
74	First Report of <i>Grapevine Pinot gris virus</i> (GPGV) in grapevine in France. Plant Disease, 2015, 99, 293-293.	0.7	39
75	Transcriptomic Analysis of <i>Prunus domestica</i> Undergoing Hypersensitive Response to Plum Pox Virus Infection. PLoS ONE, 2014, 9, e100477.	1.1	38
76	A complex virome unveiled by deep sequencing analysis of RNAs from a French Pinot Noir grapevine exhibiting strong leafroll symptoms.. Archives of Virology, 2018, 163, 2937-2946.	0.9	38
77	Construction of full-length cDNA clones of lettuce mosaic virus (LMV) and the effects of intron-insertion on their viability in <i>Escherichia coli</i> and on their infectivity to plants. Archives of Virology, 1998, 143, 2443-2451.	0.9	36
78	Determination of the complete genomic sequence of grapevine virus H, a novel vitivirus infecting grapevine. Archives of Virology, 2018, 163, 277-280.	0.9	36
79	A Primer on the Analysis of High-Throughput Sequencing Data for Detection of Plant Viruses. Microorganisms, 2021, 9, 841.	1.6	36
80	Molecular mapping of the viral determinants of systemic wilting induced by a Lettuce mosaic virus (LMV) isolate in some lettuce cultivars. Virus Research, 2005, 109, 175-180.	1.1	35
81	The <i>Rx</i> Gene Confers Resistance to a Range of <i>Potexviruses</i> in Transgenic <i>Nicotiana</i> Plants. Molecular Plant-Microbe Interactions, 2008, 21, 1154-1164.	1.4	35
82	High genetic variability and evidence for plant-to-plant transfer of Banana mild mosaic virus. Journal of General Virology, 2005, 86, 3179-3187.	1.3	34
83	Datamining, Genetic Diversity Analyses, and Phylogeographic Reconstructions Redefine the Worldwide Evolutionary History of <i>Grapevine Pinot gris virus</i> and <i>Grapevine berry inner necrosis virus</i> . Phytobiomes Journal, 2020, 4, 165-177.	1.4	33
84	Sequence Variability, Recombination Analysis, and Specific Detection of the W Strain of <i>Plum pox virus</i> . Phytopathology, 2011, 101, 980-985.	1.1	31
85	Metagenomic-based impact study of transgenic grapevine rootstock on its associated virome and soil bacteriome. Plant Biotechnology Journal, 2018, 16, 208-220.	4.1	31
86	Metagenomic analysis of virome cross-talk between cultivated <i>Solanum lycopersicum</i> and wild <i>Solanum nigrum</i> . Virology, 2020, 540, 38-44.	1.1	31
87	PECULIAR PLUM POX POTYVIRUS D-POPULATIONS ARE EPIDEMIC IN PEACH TREES. Acta Horticulturae, 1998, , 355-366.	0.1	30
88	The C terminus of lettuce mosaic potyvirus cylindrical inclusion helicase interacts with the viral VPg and with lettuce translation eukaryotic initiation factor 4E. Journal of General Virology, 2012, 93, 184-193.	1.3	30
89	A genome-wide diversity study of grapevine <i>rupestris</i> stem pitting-associated virus. Archives of Virology, 2018, 163, 3105-3111.	0.9	29
90	Phytovirome Analysis of Wild Plant Populations: Comparison of Double-Stranded RNA and Virion-Associated Nucleic Acid Metagenomic Approaches. Journal of Virology, 2019, 94, .	1.5	29

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91	CHAPTER 36: <i>Plum pox virus</i> , 2011, , 185-197.		29
92	Analysis of recombinant Plum pox virus (PPV) isolates from Serbia confirms genetic homogeneity and supports a regional origin for the PPV-Rec subgroup. Archives of Virology, 2005, 150, 2051-2060.	0.9	28
93	Partial sequence analysis of an atypical Turkish isolate provides further information on the evolutionary history of Plum pox virus (PPV). Virus Research, 2005, 108, 199-206.	1.1	28
94	Biochemical identification of proteasome-associated endonuclease activity in sunflower. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2003, 1645, 30-39.	1.1	27
95	Characterization of Prunus-infecting Apricot latent virus-like Foveaviruses: Evolutionary and taxonomic implications. Virus Research, 2011, 155, 440-445.	1.1	27
96	Distribution of Barley yellow dwarf virus-PAV in the Sub-Antarctic Kerguelen Islands and Characterization of Two New Luteovirus Species. PLoS ONE, 2013, 8, e67231.	1.1	27
97	Multiple Coat Protein Mutations Abolish Recognition of <i>Pepino mosaic potexvirus</i> (PepMV) by the Potato <i>Rx</i> Resistance Gene in Transgenic Tomatoes. Molecular Plant-Microbe Interactions, 2010, 23, 376-383.	1.4	26
98	Development of a polyvalent RT-PCR detection assay covering the genetic diversity of <i>Cherry capillovirus A</i> . Plant Pathology, 2012, 61, 195-204.	1.2	26
99	The VirAnnot Pipeline: A Resource for Automated Viral Diversity Estimation and Operational Taxonomy Units Assignment for Virome Sequencing Data. Phytobiomes Journal, 2019, 3, 256-259.	1.4	26
100	Plant virome reconstruction and antiviral RNAi characterization by deep sequencing of small RNAs from dried leaves. Scientific Reports, 2019, 9, 19268.	1.6	26
101	New Insights into Asian Prunus Viruses in the Light of NGS-Based Full Genome Sequencing. PLoS ONE, 2016, 11, e0146420.	1.1	26
102	Detection and characterization of Plum pox virus: molecular methods. EPPO Bulletin, 2006, 36, 262-266.	0.6	23
103	A naturally occurring recombinant isolate of Lettuce mosaic virus. Archives of Virology, 2003, 149, 191-197.	0.9	22
104	Characterization of Apricot pseudo-chlorotic leaf spot virus, A Novel Trichovirus Isolated from Stone Fruit Trees. Phytopathology, 2005, 95, 420-426.	1.1	22
105	Enzyme-Linked Immunosorbent Assay Testing of Shoots Crown In Vitro and the Use of Immunocapture-Reverse Transcription-Polymerase Chain Reaction Improve the Detection of Prunus necrotic ringspot virus in Rose. Phytopathology, 2000, 90, 522-528.	1.1	21
106	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. Archives of Virology, 2014, 159, 3421-3426.	0.9	21
107	Status of the current vitivirus taxonomy. Archives of Virology, 2020, 165, 451-458.	0.9	21
108	First Report of <i>Little cherry virus 1</i> Infecting Apricot in the Czech Republic. Plant Disease, 2017, 101, 845.	0.7	21

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109	First Report of Nectarine stem pitting-associated virus Infecting <i>Prunus mume</i> in Japan. Plant Disease, 2017, 101, 393-393.	0.7	21
110	First Report of the Presence of Plum pox virus Rec Strain in Turkey. Plant Disease, 2007, 91, 331-331.	0.7	21
111	Analysis of the dsRNAs of apple chlorotic leaf spot virus. Journal of General Virology, 1992, 73, 767-773.	1.3	20
112	Evaluation of the genetic diversity of Plum pox virus in a single plum tree. Virus Research, 2012, 167, 112-117.	1.1	20
113	The Use of Green Fluorescent Protein-Tagged Recombinant Viruses to Test Lettuce mosaic virus Resistance in Lettuce. Phytopathology, 2002, 92, 169-176.	1.1	19
114	A simple and efficient method for testing Lettuce mosaic virus resistance in in vitro cultivated lettuce. Journal of Virological Methods, 2004, 116, 123-131.	1.0	19
115	Identification of Quantitative Trait Loci Controlling Symptom Development During Viral Infection in <i>Arabidopsis thaliana</i> . Molecular Plant-Microbe Interactions, 2008, 21, 198-207.	1.4	19
116	Finding and identifying the viral needle in the metagenomic haystack: trends and challenges. Frontiers in Microbiology, 2015, 5, 739.	1.5	19
117	Grapevine virus T diversity as revealed by full-length genome sequences assembled from high-throughput sequence data. PLoS ONE, 2018, 13, e0206010.	1.1	19
118	High-Throughput Sequencing Reveals Further Diversity of Little Cherry Virus 1 with Implications for Diagnostics. Viruses, 2018, 10, 385.	1.5	19
119	A novel badnavirus discovered from <i>Betula</i> sp. affected by birch leaf-roll disease. PLoS ONE, 2018, 13, e0193888.	1.1	19
120	Analysis of the Epitope Structure of <i>Plum pox virus</i> Coat Protein. Phytopathology, 2011, 101, 611-619.	1.1	18
121	Complete genomic sequence of barley (<i>Hordeum vulgare</i>) endornavirus (HvEV) determined by next-generation sequencing. Archives of Virology, 2016, 161, 741-743.	0.9	18
122	Molecular characterization of foveaviruses associated with the cherry necrotic mottle leaf disease and complete sequencing of an European isolate of cherry green ring mottle virus. Archives of Virology, 2002, 147, 1033-1042.	0.9	17
123	Genetic diversity and molecular epidemiology of the T strain of <i>Plum pox virus</i> . Plant Pathology, 2019, 68, 755-763.	1.2	17
124	Characterization of two different apricot latent virus variants associated with peach asteroid spot and peach sooty ringspot diseases. Archives of Virology, 2001, 146, 1453-1464.	0.9	16
125	High-Throughput Sequencing Reveals <i>Cyclamen persicum</i> Mill. as a Natural Host for Fig Mosaic Virus. Viruses, 2018, 10, 684.	1.5	16
126	Variability Studies of Two <i>Prunus</i> -Infecting Fabaviruses with the Aid of High-Throughput Sequencing. Viruses, 2018, 10, 204.	1.5	16

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127	Next-Generation Sequencing Reveals a Novel Emaravirus in Diseased Maple Trees From a German Urban Forest. <i>Frontiers in Microbiology</i> , 2020, 11, 621179.	1.5	16
128	Restoration of secondary hairpin II is associated with restoration of infectivity of a non-viable recombinant viroid. <i>Virus Research</i> , 2001, 75, 29-34.	1.1	15
129	Introduction of a Nla proteinase cleavage site between the reporter gene and HC-Pro only partially restores the biological properties of GUS- or GFP-tagged LMV. <i>Virus Research</i> , 2003, 98, 151-162.	1.1	15
130	Complete Nucleotide Sequence of <i>Artichoke latent virus</i> Shows it to be a Member of the Genus <i>Macluravirus</i> in the Family <i>Potyviridae</i>. <i>Phytopathology</i> , 2015, 105, 1155-1160.	1.1	15
131	Molecular Characterization of a Novel Species of Capillovirus from Japanese Apricot (<i>Prunus mume</i>). <i>Viruses</i> , 2018, 10, 144.	1.5	15
132	List of non-EEU viruses and viroids of <i>Cydonia</i> Mill., <i>Fragaria</i> L., <i>Malus</i> Mill., <i>Prunus</i> L., <i>Pyrus</i> L., <i>Ribes</i> L., <i>Rubus</i> L. and <i>Vitis</i> L.. <i>EFSA Journal</i> , 2019, 17, e05501.	0.9	15
133	Unravelling the virome in birch: RNA-Seq reveals a complex of known and novel viruses. <i>PLoS ONE</i> , 2020, 15, e0221834.	1.1	15
134	Classical and next generation sequencing approaches unravel Bymovirus diversity in barley crops in France. <i>PLoS ONE</i> , 2017, 12, e0188495.	1.1	15
135	Genetic analysis suggests a long and largely isolated evolutionary history of plum pox virus strain D in Turkey. <i>Plant Pathology</i> , 2020, 69, 370-378.	1.2	14
136	Leaf-associated fungal and viral communities of wild plant populations differ between cultivated and natural ecosystems. <i>Plant-Environment Interactions</i> , 2021, 2, 87-99.	0.7	14
137	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
138	Reassessing species demarcation criteria in viroid taxonomy by pairwise identity matrices. <i>Virus Evolution</i> , 2021, 7, veab001.	2.2	13
139	Asian prunus viruses: New related members of the family Flexiviridae in Prunus germplasm of Asian origin. <i>Virus Research</i> , 2006, 120, 176-183.	1.1	12
140	Characterization and partial genome sequence of stocky prune virus, a new member of the genus Cheravirus. <i>Archives of Virology</i> , 2006, 151, 1179-1188.	0.9	12
141	Identification of a viroid-like RNA in a lychee Transcriptome Shotgun Assembly. <i>Virus Research</i> , 2017, 240, 1-7.	1.1	12
142	INVESTIGATION ON OCCURRENCE OF TRICHO-, FOVEA- AND CAPILLOVIRUSES IN ANCIENT FRUIT TREE CULTIVARS IN CAMPANIA. <i>Acta Horticulturae</i> , 2008, , 53-58.	0.1	12
143	First Report of Grapevine Virus L Infecting Grapevine in Southeast France. <i>Plant Disease</i> , 2022, 106, .	0.7	11
144	VirHunter: A Deep Learning-Based Method for Detection of Novel RNA Viruses in Plant Sequencing Data. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	11

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145	First Report of <i>Peach-associated luteovirus</i> in Nectarine (<i>Prunus persica</i>) in Italy. Plant Disease, 2018, 102, 1465.	0.7	10
146	Molecular characterization of a novel fusarivirus infecting the plant-pathogenic fungus <i>Neofusicoccum luteum</i> . Archives of Virology, 2018, 163, 559-562.	0.9	10
147	Yam asymptomatic virus 1, a novel virus infecting yams (<i>Dioscorea</i> spp.) with significant prevalence in a germplasm collection. Archives of Virology, 2020, 165, 2653-2657.	0.9	10
148	Cloning full-length cDNA of grapevine chrome mosaic nepovirus. Gene, 1988, 73, 67-75.	1.0	9
149	CLOSTEROVIRUSES (CLOSTEROVIRIDAE)., 1999, , 266-273.		9
150	Complete Nucleotide Sequence of an Isolate of Grapevine Satellite Virus and Evidence for the Presence of Multimeric Forms in an Infected Grapevine. Genome Announcements, 2017, 5, .	0.8	9
151	Determination of the complete genomic sequence of <i>Neofusicoccum luteum</i> mitovirus 1 (NLMV1), a novel mitovirus associated with a phytopathogenic Botryosphaeriaceae. Archives of Virology, 2017, 162, 2477-2480.	0.9	9
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