

Thierry Candresse

List of Publications by Year in descending order

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207
papers

9,748
citations

38742

50
h-index

46799

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.	4.2	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.	2.1	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.	2.1	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.	4.8	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.	3.9	237
6	A polymerase chain reaction assay adapted to plum pox potyvirus detection. <i>Journal of Virological Methods</i> , 1991, 33, 355-365.	2.1	227
7	The family Closteroviridae revised. <i>Archives of Virology</i> , 2002, 147, 2039-2044.	2.1	203
8	Current impact and future directions of high throughput sequencing in plant virus diagnostics. <i>Virus Research</i> , 2014, 188, 90-96.	2.2	196
9	New Advances in Understanding the Molecular Biology of Plant/Potyvirus Interactions. <i>Molecular Plant-Microbe Interactions</i> , 1999, 12, 367-376.	2.6	194
10	Frequent occurrence of recombinant potyvirus isolates. <i>Journal of General Virology</i> , 1996, 77, 1953-1965.	2.9	191
11	Plum pox virus and sharka: a model potyvirus and a major disease. <i>Molecular Plant Pathology</i> , 2014, 15, 226-241.	4.2	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.	3.5	165
13	Next-Generation Sequencing and Genome Editing in Plant Virology. <i>Frontiers in Microbiology</i> , 2016, 7, 1325.	3.5	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.	0.2	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.	1.7	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.	4.2	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.	2.9	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.	7.1	119

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19	Simultaneous detection and typing of plum pox potyvirus (PPV) isolates by heminested-PCR and PCR-ELISA. <i>Journal of Virological Methods</i> , 1997, 68, 127-137.	2.1	118
20	The Determinant of Potyvirus Ability to Overcome the RTM Resistance of <i>Arabidopsis thaliana</i> Maps to the N-Terminal Region of the Coat Protein. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1302-1311.	2.6	114
21	Application of HTS for Routine Plant Virus Diagnostics: State of the Art and Challenges. <i>Frontiers in Plant Science</i> , 2018, 9, 1082.	3.6	110
22	Coordinated and selective recruitment of eIF4E and eIF4G factors for potyvirus infection in <i>Arabidopsis thaliana</i> . <i>FEBS Letters</i> , 2007, 581, 1041-1046.	2.8	109
23	Virus Detection by High-Throughput Sequencing of Small RNAs: Large-Scale Performance Testing of Sequence Analysis Strategies. <i>Phytopathology</i> , 2019, 109, 488-497.	2.2	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. <i>Phytopathology</i> , 1998, 88, 198-204.	2.2	104
25	Polyvalent Degenerate Oligonucleotides Reverse Transcription-Polymerase Chain Reaction: A Polyvalent Detection and Characterization Tool for Trichoviruses, Capilloviruses, and Foveaviruses. <i>Phytopathology</i> , 2005, 95, 617-625.	2.2	103
26	Multiple Resistance Traits Control Plum pox virus Infection in <i>Arabidopsis thaliana</i> . <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 541-549.	2.6	101
27	Nucleotide sequence and genomic organization of apple chlorotic leaf spot closterovirus. <i>Virology</i> , 1990, 179, 104-112.	2.4	96
28	Nucleotide sequence of the 3'-terminal region of the RNA of the E1 Amar strain of plum pox potyvirus. <i>Journal of General Virology</i> , 1991, 72, 1741-1746.	2.9	96
29	Print-capture PCR: a simple and highly sensitive method for the detection of plum pox virus (PPV) in plant tissues. <i>Nucleic Acids Research</i> , 1996, 24, 2192-2193.	14.5	92
30	<i>RTM3</i>, 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. <i>Plant Physiology</i> , 2010, 154, 222-232.	4.8	91
31	Appearances Can Be Deceptive: Revealing a Hidden Viral Infection with Deep Sequencing in a Plant Quarantine Context. <i>PLoS ONE</i> , 2014, 9, e102945.	2.5	89
32	HcPro, a multifunctional protein encoded by a plant RNA virus, targets the 20S proteasome and affects its enzymic activities. <i>Journal of General Virology</i> , 2005, 86, 2595-2603.	2.9	87
33	Association of Little cherry virus 1 (LChV1) with the Shirofugen Stunt Disease and Characterization of the Genome of a Divergent LChV1 Isolate. <i>Phytopathology</i> , 2013, 103, 293-298.	2.2	83
34	<i>Plum pox virus</i> capsid protein suppresses plant pathogen-associated molecular pattern (PAMP)-triggered immunity. <i>Molecular Plant Pathology</i> , 2017, 18, 878-886.	4.2	75
35	<i>Agrobacterium</i> -mediated genetic transformation of grapevine somatic embryos and regeneration of transgenic plants expressing the coat protein of grapevine chrome mosaic nepovirus (GCMV). <i>Plant Science</i> , 1994, 102, 161-170.	3.6	74
36	Quantitative trait loci meta-analysis of <i>Plum pox virus</i> resistance in apricot (<i>Prunus</i> Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 67 factors. <i>Molecular Plant Pathology</i> , 2009, 10, 347-360.	4.2	71

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37	Trichovirus, a new genus of plant viruses. <i>Archives of Virology</i> , 1994, 134, 451-455.	2.1	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. <i>Virus Research</i> , 2009, 142, 121-126.	2.2	69
39	Illuminating an Ecological Blackbox: Using High Throughput Sequencing to Characterize the Plant Virome Across Scales. <i>Frontiers in Microbiology</i> , 2020, 11, 578064.	3.5	67
40	Effects of Green Fluorescent Protein or Î²-Glucuronidase Tagging on the Accumulation and Pathogenicity of a Resistance-Breaking Lettuce mosaic virus isolate in Susceptible and Resistant Lettuce Cultivars. <i>Molecular Plant-Microbe Interactions</i> , 2000, 13, 316-324.	2.6	66
41	strategies for simultaneous detection of multiple plant viruses. <i>Canadian Journal of Plant Pathology</i> , 2006, 28, 16-29.	1.4	64
42	High-throughput sequencing technologies for plant pest diagnosis: challenges and opportunities. <i>EPPO Bulletin</i> , 2018, 48, 219-224.	0.8	62
43	Biological and Molecular Variability of Lettuce Mosaic Virus Isolates. <i>Phytopathology</i> , 1997, 87, 397-403.	2.2	60
44	High-Throughput Sequencing and the Viromic Study of Grapevine Leaves: From the Detection of Grapevine-Infecting Viruses to the Description of a New Environmental Tymovirales Member. <i>Frontiers in Microbiology</i> , 2018, 9, 1782.	3.5	60
45	Nucleotide sequence and genetic organization of Hungarian grapevine chrome mosaic nepovirus RNA2. <i>Nucleic Acids Research</i> , 1989, 17, 7809-7819.	14.5	59
46	Nanopore-based detection and characterization of yam viruses. <i>Scientific Reports</i> , 2018, 8, 17879.	3.3	57
47	Analysis of gene expression changes in peach leaves in response to plum pox virus infection using RNA-seq. <i>Molecular Plant Pathology</i> , 2015, 16, 164-176.	4.2	56
48	ICTV Virus Taxonomy Profile: Closteroviridae. <i>Journal of General Virology</i> , 2020, 101, 364-365.	2.9	56
49	The RTM Resistance to Potyviruses in <i>Arabidopsis thaliana</i> : Natural Variation of the RTM Genes and Evidence for the Implication of Additional Genes. <i>PLoS ONE</i> , 2012, 7, e39169.	2.5	55
50	Causal agent of sharka disease: historical perspective and current status of Plum pox virus strains. <i>EPPO Bulletin</i> , 2006, 36, 239-246.	0.8	54
51	Pathogenicity Determinants in the Complex Virus Population of a Plum pox virus Isolate. <i>Molecular Plant-Microbe Interactions</i> , 2001, 14, 278-287.	2.6	53
52	Survey of <i>Prunus</i> necrotic ringspot virus in Rose and Its Variability in Rose and <i>Prunus</i> spp.. <i>Phytopathology</i> , 2001, 91, 84-91.	2.2	53
53	Potyvirus Helper Component-Proteinase Self-Interaction in the Yeast Two-Hybrid System and Delineation of the Interaction Domain Involved. <i>Virology</i> , 1999, 258, 95-99.	2.4	51
54	Lettuce mosaic virus Pathogenicity Determinants in Susceptible and Tolerant Lettuce Cultivars Map to Different Regions of the Viral Genome. <i>Molecular Plant-Microbe Interactions</i> , 2001, 14, 804-810.	2.6	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.	2.2	49
56	Plant Viruses Infecting Solanaceae Family Members in the Cultivated and Wild Environments: A Review. <i>Plants</i> , 2020, 9, 667.	3.5	49
57	Interaction between potyvirus helper component-proteinase and capsid protein in infected plants. <i>Journal of General Virology</i> , 2002, 83, 1765-1770.	2.9	48
58	The 20S proteasome $\hat{\pm}$ ₅ subunit of <i>Arabidopsis thaliana</i> carries an RNase activity and interacts <i>in planta</i> with the <i>Lettuce mosaic potyvirus</i> HcPro protein. <i>Molecular Plant Pathology</i> , 2011, 12, 137-150.	4.2	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.	0.9	47
60	Characterization of Sour Cherry Isolates of <i>Plum pox virus</i> from the Volga Basin in Russia Reveals a New Cherry Strain of the Virus. <i>Phytopathology</i> , 2013, 103, 972-979.	2.2	46
61	Recent advances and prospects in <i>Prunus</i> virology. <i>Annals of Applied Biology</i> , 2017, 171, 125-138.	2.5	45
62	Analysis of the population structure of three phenotypically different PSTVd isolates. <i>Archives of Virology</i> , 1994, 138, 233-245.	2.1	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.	2.2	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.	2.6	41
65	Family-based linkage and association mapping reveals novel genes affecting <i>Plum pox virus</i> infection in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2012, 196, 873-886.	7.3	41
66	Characterization by Deep Sequencing of Divergent <i>Plum bark necrosis stem pitting-associated virus</i> (PBNSPaV) Isolates and Development of a Broad-Spectrum PBNSPaV Detection Assay. <i>Phytopathology</i> , 2014, 104, 660-666.	2.2	41
67	Characterization by Deep Sequencing of <i>Prunus virus T</i> , a Novel <i>Tepovirus</i> Infecting <i>Prunus</i> Species. <i>Phytopathology</i> , 2015, 105, 135-140.	2.2	41
68	ANALYSIS OF PLUM POX VIRUS VARIABILITY AND DEVELOPMENT OF STRAIN-SPECIFIC PCR ASSAYS. <i>Acta Horticulturae</i> , 1995, , 357-369.	0.2	41
69	Genetically engineered resistance against grapevine chrome mosaic nepovirus. <i>Plant Molecular Biology</i> , 1993, 21, 89-97.	3.9	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 <i>Betaflexiviridae</i> Evolution. <i>PLoS ONE</i> , 2015, 10, e0129469.	2.5	40
71	A Eukaryotic Translation Initiation Factor 4E (eIF4E) is Responsible for the $\hat{\pm}$ -Tobacco Recessive Resistance to Potyviruses. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 609-623.	1.8	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.	2.4	40

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73	Nucleotide sequence of Hungarian grapevine chrome mosaic nepovirus RNA1. <i>Nucleic Acids Research</i> , 1989, 17, 7795-7807.	14.5	39
74	First Report of <i>Grapevine Pinot gris virus</i> (GPGV) in grapevine in France. <i>Plant Disease</i> , 2015, 99, 293-293.	1.4	39
75	Transcriptomic Analysis of <i>Prunus domestica</i> Undergoing Hypersensitive Response to Plum Pox Virus Infection. <i>PLoS ONE</i> , 2014, 9, e100477.	2.5	38
76	A complex virome unveiled by deep sequencing analysis of RNAs from a French Pinot Noir grapevine exhibiting strong leafroll symptoms.. <i>Archives of Virology</i> , 2018, 163, 2937-2946.	2.1	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. <i>Archives of Virology</i> , 1998, 143, 2443-2451.	2.1	36
78	Determination of the complete genomic sequence of grapevine virus H, a novel vitivirus infecting grapevine. <i>Archives of Virology</i> , 2018, 163, 277-280.	2.1	36
79	A Primer on the Analysis of High-Throughput Sequencing Data for Detection of Plant Viruses. <i>Microorganisms</i> , 2021, 9, 841.	3.6	36
80	Molecular mapping of the viral determinants of systemic wilting induced by a Lettuce mosaic virus (LMV) isolate in some lettuce cultivars. <i>Virus Research</i> , 2005, 109, 175-180.	2.2	35
81	The <i>Rx</i> Gene Confers Resistance to a Range of <i>Potexviruses</i> in Transgenic <i>Nicotiana</i> Plants. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 1154-1164.	2.6	35
82	High genetic variability and evidence for plant-to-plant transfer of Banana mild mosaic virus. <i>Journal of General Virology</i> , 2005, 86, 3179-3187.	2.9	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> . <i>Phytobiomes Journal</i> , 2020, 4, 165-177.	2.7	33
84	Sequence Variability, Recombination Analysis, and Specific Detection of the W Strain of <i>Plum pox virus</i> . <i>Phytopathology</i> , 2011, 101, 980-985.	2.2	31
85	Metagenomic-based impact study of transgenic grapevine rootstock on its associated virome and soil bacteriome. <i>Plant Biotechnology Journal</i> , 2018, 16, 208-220.	8.3	31
86	Metagenomic analysis of virome cross-talk between cultivated <i>Solanum lycopersicum</i> and wild <i>Solanum nigrum</i> . <i>Virology</i> , 2020, 540, 38-44.	2.4	31
87	PECULIAR PLUM POX POTYVIRUS D-POPULATIONS ARE EPIDEMIC IN PEACH TREES. <i>Acta Horticulturae</i> , 1998, , 355-366.	0.2	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. <i>Journal of General Virology</i> , 2012, 93, 184-193.	2.9	30
89	A genome-wide diversity study of grapevine <i>rupestris</i> stem pitting-associated virus. <i>Archives of Virology</i> , 2018, 163, 3105-3111.	2.1	29
90	Phytovirome Analysis of Wild Plant Populations: Comparison of Double-Stranded RNA and Virion-Associated Nucleic Acid Metagenomic Approaches. <i>Journal of Virology</i> , 2019, 94, .	3.4	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. <i>Archives of Virology</i> , 2005, 150, 2051-2060.	2.1	28
93	Partial sequence analysis of an atypical Turkish isolate provides further information on the evolutionary history of Plum pox virus (PPV). <i>Virus Research</i> , 2005, 108, 199-206.	2.2	28
94	Biochemical identification of proteasome-associated endonuclease activity in sunflower. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2003, 1645, 30-39.	2.3	27
95	Characterization of Prunus-infecting Apricot latent virus-like Foveaviruses: Evolutionary and taxonomic implications. <i>Virus Research</i> , 2011, 155, 440-445.	2.2	27
96	Distribution of Barley yellow dwarf virus-PAV in the Sub-Antarctic Kerguelen Islands and Characterization of Two New Luteovirus Species. <i>PLoS ONE</i> , 2013, 8, e67231.	2.5	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. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 376-383.	2.6	26
98	Development of a polyvalent RT-PCR detection assay covering the genetic diversity of <i>Cherry capillovirus A</i> . <i>Plant Pathology</i> , 2012, 61, 195-204.	2.4	26
99	The VirAnnot Pipeline: A Resource for Automated Viral Diversity Estimation and Operational Taxonomy Units Assignment for Virome Sequencing Data. <i>Phytobiomes Journal</i> , 2019, 3, 256-259.	2.7	26
100	Plant virome reconstruction and antiviral RNAi characterization by deep sequencing of small RNAs from dried leaves. <i>Scientific Reports</i> , 2019, 9, 19268.	3.3	26
101	New Insights into Asian Prunus Viruses in the Light of NGS-Based Full Genome Sequencing. <i>PLoS ONE</i> , 2016, 11, e0146420.	2.5	26
102	Detection and characterization of Plum pox virus: molecular methods. <i>EPPO Bulletin</i> , 2006, 36, 262-266.	0.8	23
103	A naturally occurring recombinant isolate of Lettuce mosaic virus. <i>Archives of Virology</i> , 2003, 149, 191-197.	2.1	22
104	Characterization of Apricot pseudo-chlorotic leaf spot virus, A Novel Trichovirus Isolated from Stone Fruit Trees. <i>Phytopathology</i> , 2005, 95, 420-426.	2.2	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. <i>Phytopathology</i> , 2000, 90, 522-528.	2.2	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. <i>Archives of Virology</i> , 2014, 159, 3421-3426.	2.1	21
107	Status of the current vitivirus taxonomy. <i>Archives of Virology</i> , 2020, 165, 451-458.	2.1	21
108	First Report of <i>Little cherry virus 1</i> Infecting Apricot in the Czech Republic. <i>Plant Disease</i> , 2017, 101, 845.	1.4	21

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109	First Report of Nectarine stem pitting-associated virus Infecting <i>Prunus mume</i> in Japan. <i>Plant Disease</i> , 2017, 101, 393-393.	1.4	21
110	First Report of the Presence of Plum pox virus Rec Strain in Turkey. <i>Plant Disease</i> , 2007, 91, 331-331.	1.4	21
111	Analysis of the dsRNAs of apple chlorotic leaf spot virus. <i>Journal of General Virology</i> , 1992, 73, 767-773.	2.9	20
112	Evaluation of the genetic diversity of Plum pox virus in a single plum tree. <i>Virus Research</i> , 2012, 167, 112-117.	2.2	20
113	The Use of Green Fluorescent Protein-Tagged Recombinant Viruses to Test Lettuce mosaic virus Resistance in Lettuce. <i>Phytopathology</i> , 2002, 92, 169-176.	2.2	19
114	A simple and efficient method for testing Lettuce mosaic virus resistance in in vitro cultivated lettuce. <i>Journal of Virological Methods</i> , 2004, 116, 123-131.	2.1	19
115	Identification of Quantitative Trait Loci Controlling Symptom Development During Viral Infection in <i>Arabidopsis thaliana</i> . <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 198-207.	2.6	19
116	Finding and identifying the viral needle in the metagenomic haystack: trends and challenges. <i>Frontiers in Microbiology</i> , 2015, 5, 739.	3.5	19
117	Grapevine virus T diversity as revealed by full-length genome sequences assembled from high-throughput sequence data. <i>PLoS ONE</i> , 2018, 13, e0206010.	2.5	19
118	High-Throughput Sequencing Reveals Further Diversity of Little Cherry Virus 1 with Implications for Diagnostics. <i>Viruses</i> , 2018, 10, 385.	3.3	19
119	A novel badnavirus discovered from <i>Betula</i> sp. affected by birch leaf-roll disease. <i>PLoS ONE</i> , 2018, 13, e0193888.	2.5	19
120	Analysis of the Epitope Structure of Plum pox virus Coat Protein. <i>Phytopathology</i> , 2011, 101, 611-619.	2.2	18
121	Complete genomic sequence of barley (<i>Hordeum vulgare</i>) endornavirus (HvEV) determined by next-generation sequencing. <i>Archives of Virology</i> , 2016, 161, 741-743.	2.1	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. <i>Archives of Virology</i> , 2002, 147, 1033-1042.	2.1	17
123	Genetic diversity and molecular epidemiology of the T strain of Plum pox virus. <i>Plant Pathology</i> , 2019, 68, 755-763.	2.4	17
124	Characterization of two different apricot latent virus variants associated with peach asteroid spot and peach sooty ringspot diseases. <i>Archives of Virology</i> , 2001, 146, 1453-1464.	2.1	16
125	High-Throughput Sequencing Reveals <i>Cyclamen persicum</i> Mill. as a Natural Host for Fig Mosaic Virus. <i>Viruses</i> , 2018, 10, 684.	3.3	16
126	Variability Studies of Two <i>Prunus</i> -Infecting Fabaviruses with the Aid of High-Throughput Sequencing. <i>Viruses</i> , 2018, 10, 204.	3.3	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.	3.5	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.	2.2	15
129	Introduction of a NIa 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.	2.2	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.	2.2	15
131	Molecular Characterization of a Novel Species of Capillovirus from Japanese Apricot (<i>Prunus mume</i>). <i>Viruses</i> , 2018, 10, 144.	3.3	15
132	List of non-EU 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.	1.8	15
133	Unravelling the virome in birch: RNA-Seq reveals a complex of known and novel viruses. <i>PLoS ONE</i> , 2020, 15, e0221834.	2.5	15
134	Classical and next generation sequencing approaches unravel Bymovirus diversity in barley crops in France. <i>PLoS ONE</i> , 2017, 12, e0188495.	2.5	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.	2.4	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.	1.5	14
137	Two novel Alphaflexiviridae members revealed by deep sequencing of the Vanilla (Orchidaceae) virome. <i>Archives of Virology</i> , 2017, 162, 3855-3861.	2.1	13
138	Reassessing species demarcation criteria in viroid taxonomy by pairwise identity matrices. <i>Virus Evolution</i> , 2021, 7, veab001.	4.9	13
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