

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	First Report of Grapevine Virus L Infecting Grapevine in Southeast France. <i>Plant Disease</i> , 2022, 106, .	1.4	11
2	VirHunter: A Deep Learning-Based Method for Detection of Novel RNA Viruses in Plant Sequencing Data. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	2.1	11
3	First report of Apium virus Y in wild carrot (<i>Daucus carota</i> ssp. <i>carota</i>) in Spain. <i>New Disease Reports</i> , 2022, 45, .	0.8	0
4	Molecular characterization of Cordyline virus 1 isolates infecting yam (<i>Dioscorea</i> spp). <i>Archives of Virology</i> , 2022, 167, 2275-2280.	2.1	3
5	Sixty Years from the First Disease Description, a Novel Badnavirus Associated with Chestnut Mosaic Disease. <i>Phytopathology</i> , 2021, 111, 1051-1058.	2.2	6
6	Plum Pox Virus (Potyviridae)., 2021, , 586-593.		0
7	First Report of Alfalfa Mosaic Virus in Chayote in Italy. <i>Plant Disease</i> , 2021, 105, 698-698.	1.4	5
8	Reassessing species demarcation criteria in viroid taxonomy by pairwise identity matrices. <i>Virus Evolution</i> , 2021, 7, veab001.	4.9	13
9	Characterization of the Mycovirome of the Phytopathogenic Fungus, <i>Neofusicoccum parvum</i> . <i>Viruses</i> , 2021, 13, 375.	3.3	9
10	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
11	First Report of Lettuce Necrotic Leaf Curl Virus Infecting Cultivated Lettuce in France. <i>Plant Disease</i> , 2021, 105, 1233.	1.4	0
12	A Primer on the Analysis of High-Throughput Sequencing Data for Detection of Plant Viruses. <i>Microorganisms</i> , 2021, 9, 841.	3.6	36
13	Molecular Characterization of Potato Virus Y (PVY) Using High-Throughput Sequencing: Constraints on Full Genome Reconstructions Imposed by Mixed Infection Involving Recombinant PVY Strains. <i>Plants</i> , 2021, 10, 753.	3.5	6
14	Molecular Characterization of the Coat Protein Gene of Greek Apple Stem Pitting Virus Isolates: Evolution through Deletions, Insertions, and Recombination Events. <i>Plants</i> , 2021, 10, 917.	3.5	4
15	Novel Ampeloviruses Infecting Cassava in Central Africa and the South-West Indian Ocean Islands. <i>Viruses</i> , 2021, 13, 1030.	3.3	8
16	Genome characterization and diversity of trifolium virus 1: identification of a novel legume-infecting capulavirus. <i>Archives of Virology</i> , 2021, 166, 2573-2578.	2.1	2
17	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
18	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

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19	Pest categorisation of potato virus Y (non-EU isolates). <i>EFSA Journal</i> , 2020, 18, e05938.	1.8	2
20	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
21	Status of the current vitivirus taxonomy. <i>Archives of Virology</i> , 2020, 165, 451-458.	2.1	21
22	Molecular Characterization of the Complete Coding Sequence of Olive Leaf Yellowing-Associated Virus. <i>Plants</i> , 2020, 9, 1272.	3.5	8
23	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
24	Identification of Pomegranate as a New Host of <i>Passiflora Edulis</i> Symptomless Virus (PeSV) and Analysis of PeSV Diversity. <i>Agronomy</i> , 2020, 10, 1821.	3.0	5
25	A novel foveavirus identified in wild grapevine (<i>Vitis vinifera</i> subsp. <i>sylvestris</i>). <i>Archives of Virology</i> , 2020, 165, 2999-3002.	2.1	8
26	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.	2.1	10
27	Complete genome sequence of cherry virus T, a novel cherry-infecting teppovirus. <i>Archives of Virology</i> , 2020, 165, 1711-1714.	2.1	3
28	First Report on Detection of Three Bunya-Like Viruses in Apples in Brazil. <i>Plant Disease</i> , 2020, 104, 3088-3088.	1.4	8
29	Molecular diversity of grapevine Kizil Sapak virus and implications for its detection. <i>Archives of Virology</i> , 2020, 165, 1849-1853.	2.1	1
30	Complete genome sequence of a novel grapevine-infecting member of the genus Polerovirus, grapevine polerovirus 1. <i>Archives of Virology</i> , 2020, 165, 1683-1685.	2.1	5
31	Plant Viruses Infecting Solanaceae Family Members in the Cultivated and Wild Environments: A Review. <i>Plants</i> , 2020, 9, 667.	3.5	49
32	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
33	Complete genome sequence of almond luteovirus 1, a novel luteovirus infecting almond. <i>Archives of Virology</i> , 2020, 165, 2123-2126.	2.1	2
34	Dendrobium viroid, a new monocot-infecting apscaviroid. <i>Virus Research</i> , 2020, 282, 197958.	2.2	8
35	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
36	ICTV Virus Taxonomy Profile: Closteroviridae. <i>Journal of General Virology</i> , 2020, 101, 364-365.	2.9	56

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37	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
38	Characterization of the virome of shallots affected by the shallot mild yellow stripe disease in France. <i>PLoS ONE</i> , 2019, 14, e0219024.	2.5	7
39	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
40	Pest categorisation of non-EU viruses and viroids of <i>Vitis</i> L.. <i>EFSA Journal</i> , 2019, 17, e05669.	1.8	6
41	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
42	Pest categorisation of non-EU viruses and viroids of <i>Prunus</i> L.. <i>EFSA Journal</i> , 2019, 17, e05735.	1.8	5
43	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
44	First Report of Onion Yellow Dwarf Virus, Leek Yellow Stripe Virus, and Shallot Latent Virus on Garlic (<i>Allium sativum</i>) in Tunisia. <i>Plant Disease</i> , 2019, 103, 2143.	1.4	8
45	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.	2.1	7
46	First Report of Citrus Virus A (CiVA) Infecting Pear (<i>Pyrus communis</i>) in France. <i>Plant Disease</i> , 2019, 103, 2703-2703.	1.4	9
47	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
48	Genetic diversity and molecular epidemiology of the T strain of Plum pox virus. <i>Plant Pathology</i> , 2019, 68, 755-763.	2.4	17
49	First Report of Peach-associated luteovirus in Nectarine (<i>Prunus persica</i>) in Italy. <i>Plant Disease</i> , 2018, 102, 1465.	1.4	10
50	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
51	Complete genomic sequence of <i>Raphanus sativus</i> cryptic virus 4 (RsCV4), a novel alphapartitivirus from radish. <i>Archives of Virology</i> , 2018, 163, 1097-1100.	2.1	7
52	Complete genome sequence of lettuce chordovirus 1 isolated from cultivated lettuce in France. <i>Archives of Virology</i> , 2018, 163, 2543-2545.	2.1	6
53	Biological and Genetic Characterization of New and Known Necroviruses Causing an Emerging Systemic Necrosis Disease of Corn Salad (<i>Valerianella locusta</i>) in France. <i>Phytopathology</i> , 2018, 108, 1002-1010.	2.2	5
54	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

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55	Molecular characterization of a novel fusarivirus infecting the plant-pathogenic fungus <i>Neofusicoccum luteum</i> . <i>Archives of Virology</i> , 2018, 163, 559-562.	2.1	10
56	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
57	Complete genome sequence of a novel bromovirus infecting elderberry (<i>Sambucus nigra</i> L.) in the Czech Republic. <i>Archives of Virology</i> , 2018, 163, 567-570.	2.1	6
58	Nanopore-based detection and characterization of yam viruses. <i>Scientific Reports</i> , 2018, 8, 17879.	3.3	57
59	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
60	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
61	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
62	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
63	High-throughput sequencing technologies for plant pest diagnosis: challenges and opportunities. <i>EPPO Bulletin</i> , 2018, 48, 219-224.	0.8	62
64	Genome characterization of a divergent isolate of the mycovirus <i>Botrytis virus F</i> from a grapevine metagenome. <i>Archives of Virology</i> , 2018, 163, 3181-3183.	2.1	5
65	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
66	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
67	Molecular Characterization of a Novel Species of Capillovirus from Japanese Apricot (<i>Prunus mume</i>). <i>Viruses</i> , 2018, 10, 144.	3.3	15
68	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
69	High-Throughput Sequencing Reveals Further Diversity of Little Cherry Virus 1 with Implications for Diagnostics. <i>Viruses</i> , 2018, 10, 385.	3.3	19
70	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
71	<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
72	Complete Nucleotide Sequence of an Isolate of Grapevine Satellite Virus and Evidence for the Presence of Multimeric Forms in an Infected Grapevine. <i>Genome Announcements</i> , 2017, 5, .	0.8	9

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73	Determination of the complete genomic sequence of Neofusicoccum luteum mitovirus 1 (NLMV1), a novel mitovirus associated with a phytopathogenic Botryosphaeriaceae. Archives of Virology, 2017, 162, 2477-2480.	2.1	9
74	Two novel Alphaflexiviridae members revealed by deep sequencing of the Vanilla (Orchidaceae) virome. Archives of Virology, 2017, 162, 3855-3861.	2.1	13
75	Identification of a viroid-like RNA in a lychee Transcriptome Shotgun Assembly. Virus Research, 2017, 240, 1-7.	2.2	12
76	First Report of Grapevine hammerhead viroid-like RNA Infecting Grapevine (<i>Vitis vinifera</i>) in France. Plant Disease, 2017, 101, 2155-2155.	1.4	6
77	Recent advances and prospects in <i>Prunus</i> virology. Annals of Applied Biology, 2017, 171, 125-138.	2.5	45
78	A Framework for the Evaluation of Biosecurity, Commercial, Regulatory, and Scientific Impacts of Plant Viruses and Viroids Identified by NGS Technologies. Frontiers in Microbiology, 2017, 8, 45.	3.5	165
79	First Report of <i>Little cherry virus 1</i> Infecting Apricot in the Czech Republic. Plant Disease, 2017, 101, 845.	1.4	21
80	First Report of Nectarine stem pitting-associated virus Infecting <i>Prunus mume</i> in Japan. Plant Disease, 2017, 101, 393-393.	1.4	21
81	Classical and next generation sequencing approaches unravel Bymovirus diversity in barley crops in France. PLoS ONE, 2017, 12, e0188495.	2.5	15
82	First Report of <i>Kalanchoe mosaic virus</i> and <i>Kalanchoe latent virus</i> Infecting Ghost Plant (<i>Graptopetalum paraguayense</i>) in Italy. Plant Disease, 2017, 101, 1560-1560.	1.4	5
83	Next-Generation Sequencing and Genome Editing in Plant Virology. Frontiers in Microbiology, 2016, 7, 1325.	3.5	142
84	Complete Nucleotide Sequence of a French Isolate of <i>Maize rough dwarf virus</i> , a <i>Fijivirus</i> Member in the Family <i>Reoviridae</i>. Genome Announcements, 2016, 4, .	0.8	3
85	Beet western yellows virus infects the carnivorous plant Nepenthes mirabilis. Archives of Virology, 2016, 161, 2273-2278.	2.1	6
86	Molecular characterization and prevalence of two capulaviruses: Alfalfa leaf curl virus from France and Euphorbia caput-medusae latent virus from South Africa. Virology, 2016, 493, 142-153.	2.4	40
87	Evidence for different, hostâ€dependent functioning of <i>Rx</i> against both wildâ€type and recombinant <i>Pepino mosaic virus</i>. Molecular Plant Pathology, 2016, 17, 120-126.	4.2	8
88	Complete genomic sequence of barley (Hordeum vulgare) endornavirus (HvEV) determined by next-generation sequencing. Archives of Virology, 2016, 161, 741-743.	2.1	18
89	New Insights into Asian Prunus Viruses in the Light of NGS-Based Full Genome Sequencing. PLoS ONE, 2016, 11, e0146420.	2.5	26
90	Characterization of New Isolates of Apricot vein clearing-associated virus and of a New Prunus-Infecting Virus: Evidence for Recombination as a Driving Force in Betaflexiviridae Evolution. PLoS ONE, 2015, 10, e0129469.	2.5	40

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91	A Eukaryotic Translation Initiation Factor 4E (eIF4E) is Responsible for the <i>œva</i> Tobacco Recessive Resistance to Potyviruses. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 609-623.	1.8	40
92	Finding and identifying the viral needle in the metagenomic haystack: trends and challenges. <i>Frontiers in Microbiology</i> , 2015, 5, 739.	3.5	19
93	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
94	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
95	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
96	Analysis of gene expression changes in peach leaves in response to <i>Plum pox virus</i> infection using <i>RNA-seq</i> . <i>Molecular Plant Pathology</i> , 2015, 16, 164-176.	4.2	56
97	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
98	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
99	<i>Plum pox virus</i> and sharka: a model potyvirus and a major disease. <i>Molecular Plant Pathology</i> , 2014, 15, 226-241.	4.2	178
100	Current impact and future directions of high throughput sequencing in plant virus diagnostics. <i>Virus Research</i> , 2014, 188, 90-96.	2.2	196
101	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
102	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
103	Diagnosis of Plant Pathogens and Implications for Plant Quarantine: A Risk Assessment Perspective. , 2014, , 167-193.		4
104	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
105	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
106	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
107	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
108	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

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109	Identification and Characterization of Tomato Mutants Affected in the <i>Rx</i> -Mediated Resistance to PVX Isolates. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 341-354.	2.6	5
110	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
111	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
112	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
113	<i>Cydonia japonica</i> , <i>Pyrus calleryana</i> and <i>P. amygdaliformis</i> : three new ornamental or wild hosts of Apple stem pitting virus. <i>Virus Genes</i> , 2012, 44, 319-322.	1.6	8
114	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
115	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
116	Characterization of <i>Prunus</i> -infecting Apricot latent virus-like Foveaviruses: Evolutionary and taxonomic implications. <i>Virus Research</i> , 2011, 155, 440-445.	2.2	27
117	Analysis of the Epitope Structure of <i>Plum pox virus</i> Coat Protein. <i>Phytopathology</i> , 2011, 101, 611-619.	2.2	18
118	The 20S proteasome α 5 subunit of <i>Arabidopsis thaliana</i> carries an RNase activity and interacts in planta with the <i>Lettuce mosaic potyvirus</i> HcPro protein. <i>Molecular Plant Pathology</i> , 2011, 12, 137-150.	4.2	47
119	Top 10 plant viruses in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2011, 12, 938-954.	4.2	936
120	CHAPTER 36: <i>Plum pox virus</i> . , 2011, , 185-197.		29
121	Multiple Coat Protein Mutations Abolish Recognition of <i>Pepino mosaic potyvirus</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
122	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
123	<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
124	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 14 factors. <i>Molecular Plant Pathology</i> , 2009, 10, 347-360.	4.2	71
125	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
126	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

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127	Partial genome sequence of Bidens mottle virus sheds light on its taxonomy. Archives of Virology, 2008, 153, 227-228.	2.1	3
128	Identification of Quantitative Trait Loci Controlling Symptom Development During Viral Infection in <i>Arabidopsis thaliana</i> . Molecular Plant-Microbe Interactions, 2008, 21, 198-207.	2.6	19
129	The <i>Rx</i> Gene Confers Resistance to a Range of Potexviruses in Transgenic <i>Nicotiana</i> Plants. Molecular Plant-Microbe Interactions, 2008, 21, 1154-1164.	2.6	35
130	INVESTIGATION ON OCCURRENCE OF TRICHO-, FOVEA- AND CAPILLOVIRUSES IN ANCIENT FRUIT TREE CULTIVARS IN CAMPANIA. Acta Horticulturae, 2008, , 53-58.	0.2	12
131	Coordinated and selective recruitment of eIF4E and eIF4G factors for potyvirus infection in <i>Arabidopsis thaliana</i> . FEBS Letters, 2007, 581, 1041-1046.	2.8	109
132	First Report of the Presence of Plum pox virus Rec Strain in Turkey. Plant Disease, 2007, 91, 331-331.	1.4	21
133	strategies for simultaneous detection of multiple plant viruses. Canadian Journal of Plant Pathology, 2006, 28, 16-29.	1.4	64
134	Asian prunus viruses: New related members of the family Flexiviridae in Prunus germplasm of Asian origin. Virus Research, 2006, 120, 176-183.	2.2	12
135	Multiple Resistance Traits Control Plum pox virus Infection in <i>Arabidopsis thaliana</i> . Molecular Plant-Microbe Interactions, 2006, 19, 541-549.	2.6	101
136	Causal agent of sharka disease: historical perspective and current status of Plum pox virus strains. EPPO Bulletin, 2006, 36, 239-246.	0.8	54
137	Detection and characterization of Plum pox virus: molecular methods. EPPO Bulletin, 2006, 36, 262-266.	0.8	23
138	Virus Susceptibility and Resistance in Lettuce. , 2006, , 383-397.		1
139	Characterization and partial genome sequence of stocky prune virus, a new member of the genus Cheravirus. Archives of Virology, 2006, 151, 1179-1188.	2.1	12
140	The complete nucleotide sequence of the Plum pox virus El Amar isolate. Archives of Virology, 2006, 151, 1679-1682.	2.1	8
141	Polyvalent Degenerate Oligonucleotides Reverse Transcription-Polymerase Chain Reaction: A Polyvalent Detection and Characterization Tool for Trichoviruses, Capilloviruses, and Foveaviruses. Phytopathology, 2005, 95, 617-625.	2.2	103
142	Characterization of Apricot pseudo-chlorotic leaf spot virus, A Novel Trichovirus Isolated from Stone Fruit Trees. Phytopathology, 2005, 95, 420-426.	2.2	22
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