## **Thierry Candresse**

# List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

 200
 7,150
 46
 78

 papers
 citations
 h-index
 g-index

 216
 8,720
 3.8
 5.66

 ext. papers
 ext. citations
 avg, IF
 L-index

#	Paper	IF	Citations
<b>2</b> 00	Sixty Years from the First Disease Description, a Novel Badnavirus Associated with Chestnut Mosaic Disease. <i>Phytopathology</i> , <b>2021</b> , 111, 1051-1058	3.8	3
199	Leaf-associated fungal and viral communities of wild plant populations differ between cultivated and natural ecosystems. <i>Plant-Environment Interactions</i> , <b>2021</b> , 2, 87-99	1.4	4
198	A Primer on the Analysis of High-Throughput Sequencing Data for Detection of Plant Viruses. <i>Microorganisms</i> , <b>2021</b> , 9,	4.9	5
197	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> , <b>2021</b> , 10,	4.5	1
196	Molecular Characterization of the Coat Protein Gene of Greek Apple Stem Pitting Virus Isolates: Evolution through Deletions, Insertions, and Recombination Events. <i>Plants</i> , <b>2021</b> , 10,	4.5	3
195	Genome characterization and diversity of trifolium virus 1: identification of a novel legume-infecting capulavirus. <i>Archives of Virology</i> , <b>2021</b> , 166, 2573-2578	2.6	1
194	Plum Pox Virus (Potyviridae) <b>2021</b> , 586-593		
193	Reassessing species demarcation criteria in viroid taxonomy by pairwise identity matrices. <i>Virus Evolution</i> , <b>2021</b> , 7, veab001	3.7	4
192	Characterization of the Mycovirome of the Phytopathogenic Fungus,. Viruses, 2021, 13,	6.2	3
191	Complete genome sequence of cherry virus T, a novel cherry-infecting tepovirus. <i>Archives of Virology</i> , <b>2020</b> , 165, 1711-1714	2.6	2
190	First Report on Detection of Three Bunya-Like Viruses in Apples in Brazil. <i>Plant Disease</i> , <b>2020</b> , 104, 3088	- <b>3.9</b> 88	1
189	Molecular diversity of grapevine Kizil Sapak virus and implications for its detection. <i>Archives of Virology</i> , <b>2020</b> , 165, 1849-1853	2.6	1
188	Complete genome sequence of a novel grapevine-infecting member of the genus Polerovirus, grapevine polerovirus 1. <i>Archives of Virology</i> , <b>2020</b> , 165, 1683-1685	2.6	2
187	Plant Viruses Infecting Family Members in the Cultivated and Wild Environments: A Review. <i>Plants</i> , <b>2020</b> , 9,	4.5	21
186	Unravelling the virome in birch: RNA-Seq reveals a complex of known and novel viruses. <i>PLoS ONE</i> , <b>2020</b> , 15, e0221834	3.7	7
185	Complete genome sequence of almond luteovirus 1, a novel luteovirus infecting almond. <i>Archives of Virology</i> , <b>2020</b> , 165, 2123-2126	2.6	О
184	Dendrobium viroid, a new monocot-infecting apscaviroid. <i>Virus Research</i> , <b>2020</b> , 282, 197958	6.4	5

183	ICTV Virus Taxonomy Profile:. Journal of General Virology, 2020, 101, 364-365	4.9	24
182	Metagenomic analysis of virome cross-talk between cultivated Solanum lycopersicum and wild Solanum nigrum. <i>Virology</i> , <b>2020</b> , 540, 38-44	3.6	11
181	Genetic analysis suggests a long and largely isolated evolutionary history of plum pox virus strain D in Turkey. <i>Plant Pathology</i> , <b>2020</b> , 69, 370-378	2.8	9
180	Pest categorisation of potato virus Y (non-EU isolates). <i>EFSA Journal</i> , <b>2020</b> , 18, e05938	2.3	1
179	Datamining, Genetic Diversity Analyses, and Phylogeographic Reconstructions Redefine the Worldwide Evolutionary History of Grapevine Pinot gris virus and Grapevine berry inner necrosis virus. <i>Phytobiomes Journal</i> , <b>2020</b> , 4, 165-177	4.8	18
178	Status of the current vitivirus taxonomy. <i>Archives of Virology</i> , <b>2020</b> , 165, 451-458	2.6	12
177	Molecular Characterization of the Complete Coding Sequence of Olive Leaf Yellowing-Associated Virus. <i>Plants</i> , <b>2020</b> , 9,	4.5	1
176	Illuminating an Ecological Blackbox: Using High Throughput Sequencing to Characterize the Plant Virome Across Scales. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 578064	5.7	13
175	Identification of Pomegranate as a New Host of Passiflora Edulis Symptomless Virus (PeSV) and Analysis of PeSV Diversity. <i>Agronomy</i> , <b>2020</b> , 10, 1821	3.6	1
174	A novel foveavirus identified in wild grapevine (Vitis vinifera subsp. sylvestris). <i>Archives of Virology</i> , <b>2020</b> , 165, 2999-3002	2.6	5
173	Yam asymptomatic virus 1, a novel virus infecting yams (Dioscorea spp.) with significant prevalence in a germplasm collection. <i>Archives of Virology</i> , <b>2020</b> , 165, 2653-2657	2.6	2
172	First Report of Alfalfa mosaic virus in Chayote in Italy. <i>Plant Disease</i> , <b>2020</b> ,	1.5	3
171	Next-Generation Sequencing Reveals a Novel Emaravirus in Diseased Maple Trees From a German Urban Forest. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 621179	5.7	7
170	The VirAnnot Pipeline: A Resource for Automated Viral Diversity Estimation and Operational Taxonomy Units Assignation for Virome Sequencing Data. <i>Phytobiomes Journal</i> , <b>2019</b> , 3, 256-259	4.8	11
169	First Report of Onion Yellow Dwarf Virus, Leek Yellow Stripe Virus, and Shallot Latent Virus on Garlic (Allium sativum) in Tunisia. <i>Plant Disease</i> , <b>2019</b> , 103, 2143	1.5	О
168	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> , <b>2019</b> , 164, 2193-2196	2.6	2
167	First Report of Citrus Virus A (CiVA) Infecting Pear (Pyrus communis) in France. <i>Plant Disease</i> , <b>2019</b> , 103, 2703-2703	1.5	2
166	Virus Detection by High-Throughput Sequencing of Small RNAs: Large-Scale Performance Testing of Sequence Analysis Strategies. <i>Phytopathology</i> , <b>2019</b> , 109, 488-497	3.8	54

165	Characterization of the virome of shallots affected by the shallot mild yellow stripe disease in France. <i>PLoS ONE</i> , <b>2019</b> , 14, e0219024	3.7	3
164	Phytovirome Analysis of Wild Plant Populations: Comparison of Double-Stranded RNA and Virion-Associated Nucleic Acid Metagenomic Approaches. <i>Journal of Virology</i> , <b>2019</b> , 94,	6.6	17
163	Pest categorisation of non-EU viruses and viroids of L. <i>EFSA Journal</i> , <b>2019</b> , 17, e05669	2.3	2
162	List of non-EU viruses and viroids of Mill., L., Mill., L., L., L., L. and L. <i>EFSA Journal</i> , <b>2019</b> , 17, e05501	2.3	6
161	Pest categorisation of non-EU viruses and viroids of L. <i>EFSA Journal</i> , <b>2019</b> , 17, e05735	2.3	2
160	Plant virome reconstruction and antiviral RNAi characterization by deep sequencing of small RNAs from dried leaves. <i>Scientific Reports</i> , <b>2019</b> , 9, 19268	4.9	9
159	Genetic diversity and molecular epidemiology of the T strain of Plum pox virus. <i>Plant Pathology</i> , <b>2019</b> , 68, 755-763	2.8	13
158	First Report of Peach-associated luteovirus in Nectarine (Prunus persica) in Italy. <i>Plant Disease</i> , <b>2018</b> , 102, 1465	1.5	2
157	Viral Double-Stranded RNAs (dsRNAs) from Plants: Alternative Nucleic Acid Substrates for High-Throughput Sequencing. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1746, 45-53	1.4	18
156	Complete genomic sequence of Raphanus sativus cryptic virus 4 (RsCV4), a novel alphapartitivirus from radish. <i>Archives of Virology</i> , <b>2018</b> , 163, 1097-1100	2.6	6
155	Complete genome sequence of lettuce chordovirus 1 isolated from cultivated lettuce in France. <i>Archives of Virology</i> , <b>2018</b> , 163, 2543-2545	2.6	2
154	Biological and Genetic Characterization of New and Known Necroviruses Causing an Emerging Systemic Necrosis Disease of Corn Salad (Valerianella locusta) in France. <i>Phytopathology</i> , <b>2018</b> , 108, 10	02: <sup>8</sup> 01	0 <sup>O</sup>
153	Metagenomic-based impact study of transgenic grapevine rootstock on its associated virome and soil bacteriome. <i>Plant Biotechnology Journal</i> , <b>2018</b> , 16, 208-220	11.6	14
152	Molecular characterization of a novel fusarivirus infecting the plant-pathogenic fungus Neofusicoccum luteum. <i>Archives of Virology</i> , <b>2018</b> , 163, 559-562	2.6	6
151	Determination of the complete genomic sequence of grapevine virus H, a novel vitivirus infecting grapevine. <i>Archives of Virology</i> , <b>2018</b> , 163, 277-280	2.6	23
150	High-throughput sequencing technologies for plant pest diagnosis: challenges and opportunities. <i>EPPO Bulletin</i> , <b>2018</b> , 48, 219-224	1	24
149	Genome characterization of a divergent isolate of the mycovirus Botrytis virus F from a grapevine metagenome. <i>Archives of Virology</i> , <b>2018</b> , 163, 3181-3183	2.6	4
148	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> , <b>2018</b> , 163, 2937-2946	2.6	14

### (2017-2018)

147	A genome-wide diversity study of grapevine rupestris stem pitting-associated virus. <i>Archives of Virology</i> , <b>2018</b> , 163, 3105-3111	2.6	13	
146	Molecular Characterization of a Novel Species of Capillovirus from Japanese Apricot (Prunus mume). <i>Viruses</i> , <b>2018</b> , 10,	6.2	6	
145	Variability Studies of Two -Infecting Fabaviruses with the Aid of High-Throughput Sequencing. <i>Viruses</i> , <b>2018</b> , 10,	6.2	10	
144	High-Throughput Sequencing Reveals Further Diversity of with Implications for Diagnostics. <i>Viruses</i> , <b>2018</b> , 10,	6.2	10	
143	A novel badnavirus discovered from Betula sp. affected by birch leaf-roll disease. <i>PLoS ONE</i> , <b>2018</b> , 13, e0193888	3.7	8	
142	Complete genome sequence of a novel bromovirus infecting elderberry (Sambucus nigra L.) in the Czech Republic. <i>Archives of Virology</i> , <b>2018</b> , 163, 567-570	2.6	4	
141	Nanopore-based detection and characterization of yam viruses. Scientific Reports, 2018, 8, 17879	4.9	27	
140	High-Throughput Sequencing Reveals Mill. as a Natural Host for Fig Mosaic Virus. Viruses, 2018, 10,	6.2	5	
139	Grapevine virus T diversity as revealed by full-length genome sequences assembled from high-throughput sequence data. <i>PLoS ONE</i> , <b>2018</b> , 13, e0206010	3.7	9	
138	High-Throughput Sequencing and the Viromic Study of Grapevine Leaves: From the Detection of Grapevine-Infecting Viruses to the Description of a New Environmental Member. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 1782	5.7	24	
137	Application of HTS for Routine Plant Virus Diagnostics: State of the Art and Challenges. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 1082	6.2	45	
136	Plum pox virus capsid protein suppresses plant pathogen-associated molecular pattern (PAMP)-triggered immunity. <i>Molecular Plant Pathology</i> , <b>2017</b> , 18, 878-886	5.7	50	
135	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> , <b>2017</b> , 5,		4	
134	Determination of the complete genomic sequence of Neofusicoccum luteum mitovirus 1 (NLMV1), a novel mitovirus associated with a phytopathogenic Botryosphaeriaceae. <i>Archives of Virology</i> , <b>2017</b> , 162, 2477-2480	2.6	5	
133	Two novel Alphaflexiviridae members revealed by deep sequencing of the Vanilla (Orchidaceae) virome. <i>Archives of Virology</i> , <b>2017</b> , 162, 3855-3861	2.6	6	
132	Identification of a viroid-like RNA in a lychee Transcriptome Shotgun Assembly. <i>Virus Research</i> , <b>2017</b> , 240, 1-7	6.4	8	
131	First Report of Grapevine hammerhead viroid-like RNA Infecting Grapevine (Vitis vinifera) in France. <i>Plant Disease</i> , <b>2017</b> , 101, 2155-2155	1.5	3	
130	Recent advances and prospects in Prunus virology. <i>Annals of Applied Biology</i> , <b>2017</b> , 171, 125-138	2.6	27	

129	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> , <b>2017</b> , 8, 45	5.7	90
128	Classical and next generation sequencing approaches unravel Bymovirus diversity in barley crops in France. <i>PLoS ONE</i> , <b>2017</b> , 12, e0188495	3.7	10
127	First Report of Little cherry virus 1 Infecting Apricot in the Czech Republic. <i>Plant Disease</i> , <b>2017</b> , 101, 84	151.5	13
126	First Report of Nectarine stem pitting-associated virus Infecting Prunus mume in Japan. <i>Plant Disease</i> , <b>2017</b> , 101, 393-393	1.5	9
125	First Report of Kalanchoe mosaic virus and Kalanchoe latent virus Infecting Ghost Plant (Graptopetalum paraguayense) in Italy. <i>Plant Disease</i> , <b>2017</b> , 101, 1560-1560	1.5	O
124	Complete genomic sequence of barley (Hordeum vulgare) endornavirus (HvEV) determined by next-generation sequencing. <i>Archives of Virology</i> , <b>2016</b> , 161, 741-3	2.6	11
123	New Insights into Asian Prunus Viruses in the Light of NGS-Based Full Genome Sequencing. <i>PLoS ONE</i> , <b>2016</b> , 11, e0146420	3.7	21
122	Next-Generation Sequencing and Genome Editing in Plant Virology. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 1325	5.7	75
121	Complete Nucleotide Sequence of a French Isolate of Maize rough dwarf virus, a Fijivirus Member in the Family Reoviridae. <i>Genome Announcements</i> , <b>2016</b> , 4,		3
120	Beet western yellows virus infects the carnivorous plant Nepenthes mirabilis. <i>Archives of Virology</i> , <b>2016</b> , 161, 2273-8	2.6	4
119	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> , <b>2016</b> , 493, 142-53	3.6	33
118	Evidence for different, host-dependent functioning of Rx against both wild-type and recombinant Pepino mosaic virus. <i>Molecular Plant Pathology</i> , <b>2016</b> , 17, 120-6	5.7	5
117	A Eukaryotic Translation Initiation Factor 4E (eIF4E) is Responsible for the Dal Tobacco Recessive Resistance to Potyviruses. <i>Plant Molecular Biology Reporter</i> , <b>2015</b> , 33, 609-623	1.7	29
116	First Report of Grapevine Pinot gris virus (GPGV) in grapevine in France. <i>Plant Disease</i> , <b>2015</b> , 99, 293	1.5	28
115	Complete Nucleotide Sequence of Artichoke latent virus Shows it to be a Member of the Genus Macluravirus in the Family Potyviridae. <i>Phytopathology</i> , <b>2015</b> , 105, 1155-60	3.8	12
114	Characterization by Deep Sequencing of Prunus virus T, a Novel Tepovirus Infecting Prunus Species. <i>Phytopathology</i> , <b>2015</b> , 105, 135-40	3.8	29
113	Analysis of gene expression changes in peach leaves in response to Plum pox virus infection using RNA-Seq. <i>Molecular Plant Pathology</i> , <b>2015</b> , 16, 164-76	5.7	49
112	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.	3.7	30

111	Finding and identifying the viral needle in the metagenomic haystack: trends and challenges. <i>Frontiers in Microbiology</i> , <b>2014</b> , 5, 739	5.7	12
110	Current impact and future directions of high throughput sequencing in plant virus diagnostics. <i>Virus Research</i> , <b>2014</b> , 188, 90-6	6.4	141
109	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> , <b>2014</b> , 104, 660-6	3.8	31
108	Shifting the paradigm from pathogens to pathobiome: new concepts in the light of meta-omics. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2014</b> , 4, 29	5.9	163
107	Transcriptomic analysis of Prunus domestica undergoing hypersensitive response to plum pox virus infection. <i>PLoS ONE</i> , <b>2014</b> , 9, e100477	3.7	34
106	Molecular characterization of yam virus X, a new potexvirus infecting yams (Dioscorea spp) and evidence for the existence of at least three distinct potexviruses infecting yams. <i>Archives of Virology</i> , <b>2014</b> , 159, 3421-6	2.6	13
105	Closteroviridae <b>2014</b> ,		1
104	Plum pox virus and sharka: a model potyvirus and a major disease. <i>Molecular Plant Pathology</i> , <b>2014</b> , 15, 226-41	5.7	137
103	Appearances can be deceptive: revealing a hidden viral infection with deep sequencing in a plant quarantine context. <i>PLoS ONE</i> , <b>2014</b> , 9, e102945	3.7	65
102	Diagnosis of Plant Pathogens and Implications for Plant Quarantine: A Risk Assessment Perspective <b>2014</b> , 167-193		3
101	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> , <b>2013</b> , 103, 293-8	3.8	71
100	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> , <b>2013</b> , 103, 972-9	3.8	36
99	Distribution of Barley yellow dwarf virus-PAV in the Sub-Antarctic Kerguelen Islands and Characterization of Two New Luteovirus Species. <i>PLoS ONE</i> , <b>2013</b> , 8, e67231	3.7	15
98	Cydonia japonica, Pyrus calleryana and P. amygdaliformis: three new ornamental or wild hosts of Apple stem pitting virus. <i>Virus Genes</i> , <b>2012</b> , 44, 319-22	2.3	4
97	Identification and characterization of tomato mutants affected in the Rx-mediated resistance to PVX isolates. <i>Molecular Plant-Microbe Interactions</i> , <b>2012</b> , 25, 341-54	3.6	5
96	Family-based linkage and association mapping reveals novel genes affecting Plum pox virus infection in Arabidopsis thaliana. <i>New Phytologist</i> , <b>2012</b> , 196, 873-886	9.8	33
95	Evaluation of the genetic diversity of Plum pox virus in a single plum tree. <i>Virus Research</i> , <b>2012</b> , 167, 112-7	6.4	17
94	Development of a polyvalent RT-PCR detection assay covering the genetic diversity of Cherry capillovirus A. <i>Plant Pathology</i> , <b>2012</b> , 61, 195-204	2.8	18

93	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> , <b>2012</b> , 93, 184-19	9 <b>3</b> 4.9	29
92	The RTM resistance to potyviruses in Arabidopsis thaliana: natural variation of the RTM genes and evidence for the implication of additional genes. <i>PLoS ONE</i> , <b>2012</b> , 7, e39169	3.7	41
91	Sequence variability, recombination analysis, and specific detection of the W strain of Plum pox virus. <i>Phytopathology</i> , <b>2011</b> , 101, 980-5	3.8	27
90	Characterization of Prunus-infecting apricot latent virus-like Foveaviruses: evolutionary and taxonomic implications. <i>Virus Research</i> , <b>2011</b> , 155, 440-5	6.4	17
89	Analysis of the epitope structure of Plum pox virus coat protein. <i>Phytopathology</i> , <b>2011</b> , 101, 611-9	3.8	15
88	The 20S proteasome B subunit of Arabidopsis thaliana carries an RNase activity and interacts in planta with the lettuce mosaic potyvirus HcPro protein. <i>Molecular Plant Pathology</i> , <b>2011</b> , 12, 137-50	5.7	42
87	Top 10 plant viruses in molecular plant pathology. <i>Molecular Plant Pathology</i> , <b>2011</b> , 12, 938-54	5.7	637
86	CHAPTER 36: Plum pox virus <b>2011</b> , 185-197		21
85	The ubiquitin/26S proteasome system in plant-pathogen interactions: a never-ending hide-and-seek game. <i>Molecular Plant Pathology</i> , <b>2010</b> , 11, 293-308	5.7	98
84	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. <i>Plant Physiology</i> , <b>2010</b> , 154, 222-32	6.6	80
83	Multiple coat protein mutations abolish recognition of Pepino mosaic potexvirus (PepMV) by the potato rx resistance gene in transgenic tomatoes. <i>Molecular Plant-Microbe Interactions</i> , <b>2010</b> , 23, 376-8	3 <sup>3.6</sup>	22
82	Quantitative trait loci meta-analysis of Plum pox virus resistance in apricot (Prunus armeniaca L.): new insights on the organization and the identification of genomic resistance factors. <i>Molecular Plant Pathology</i> , <b>2009</b> , 10, 347-60	5.7	62
81	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> , <b>2009</b> , 142, 121-6	6.4	62
80	The determinant of potyvirus ability to overcome the RTM resistance of Arabidopsis thaliana maps to the N-terminal region of the coat protein. <i>Molecular Plant-Microbe Interactions</i> , <b>2009</b> , 22, 1302-11	3.6	85
79	Identification of quantitative trait loci controlling symptom development during viral infection in Arabidopsis thaliana. <i>Molecular Plant-Microbe Interactions</i> , <b>2008</b> , 21, 198-207	3.6	19
78	The Rx gene confers resistance to a range of potexviruses in transgenic Nicotiana plants. <i>Molecular Plant-Microbe Interactions</i> , <b>2008</b> , 21, 1154-64	3.6	32
77	Partial genome sequence of Bidens mottle virus sheds light on its taxonomy. <i>Archives of Virology</i> , <b>2008</b> , 153, 227-8	2.6	1
76	INVESTIGATION ON OCCURRENCE OF TRICHO-, FOVEA- AND CAPILLOVIRUSES IN ANCIENT FRUIT TREE CULTIVARS IN CAMPANIA. <i>Acta Horticulturae</i> , <b>2008</b> , 53-58	0.3	5

#### (2004-2007)

75	Coordinated and selective recruitment of eIF4E and eIF4G factors for potyvirus infection in Arabidopsis thaliana. <i>FEBS Letters</i> , <b>2007</b> , 581, 1041-6	3.8	88
74	First Report of the Presence of Plum pox virus Rec Strain in Turkey. <i>Plant Disease</i> , <b>2007</b> , 91, 331	1.5	19
73	trategies for simultaneous detection of multiple plant viruses. <i>Canadian Journal of Plant Pathology</i> , <b>2006</b> , 28, 16-29	1.6	59
72	Asian prunus viruses: New related members of the family Flexiviridae in Prunus germplasm of Asian origin. <i>Virus Research</i> , <b>2006</b> , 120, 176-83	6.4	11
71	Multiple resistance traits control Plum pox virus infection in Arabidopsis thaliana. <i>Molecular Plant-Microbe Interactions</i> , <b>2006</b> , 19, 541-9	3.6	88
7°	Causal agent of sharka disease: historical perspective and current status of Plum pox virus strains. <i>EPPO Bulletin</i> , <b>2006</b> , 36, 239-246	1	45
69	Detection and characterization of Plum pox virus: molecular methods. <i>EPPO Bulletin</i> , <b>2006</b> , 36, 262-266	1	19
68	Virus Susceptibility and Resistance in Lettuce <b>2006</b> , 383-397		1
67	Characterization and partial genome sequence of stocky prune virus, a new member of the genus Cheravirus. <i>Archives of Virology</i> , <b>2006</b> , 151, 1179-88	2.6	8
66	The complete nucleotide sequence of the Plum pox virus El Amar isolate. <i>Archives of Virology</i> , <b>2006</b> , 151, 1679-82	2.6	8
65	Partial sequence analysis of an atypical Turkish isolate provides further information on the evolutionary history of Plum pox virus (PPV). <i>Virus Research</i> , <b>2005</b> , 108, 199-206	6.4	28
64	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> , <b>2005</b> , 109, 175-80	6.4	34
63	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> , <b>2005</b> , 86, 2595-2603	4.9	81
62	Polyvalent degenerate oligonucleotides reverse transcription-polymerase chain reaction: a polyvalent detection and characterization tool for trichoviruses, capilloviruses, and foveaviruses. <i>Phytopathology</i> , <b>2005</b> , 95, 617-25	3.8	8o
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