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List of Publications by Year
in descending order

72	2,756	186265 28	182427 51
papers	citations	h-index	g-index

72	72	72	2168
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Three new mycoviruses identified in the apple replant disease (ARD)-associated fungus Rugonectria rugulosa. Virus Genes, 2022, 58, 423-435.	1.6	4
2	Complete genome sequence of a German isolate of spartina mottle virus supports its classification as a member of the proposed genus â€œSparmovirusâ€•within the family Potyviridae. Archives of Virology, 2020, 165, 2385-2388.	2.1	1
3	Complete genome sequence and construction of an infectious full-length cDNA clone of a German isolate of celery mosaic virus. Archives of Virology, 2018, 163, 1107-1111.	2.1	5
4	ICTV Virus Taxonomy Profile: Partitiviridae. Journal of General Virology, 2018, 99, 17-18.	2.9	202
5	Development of a molecular assay for the detection of Cucumber mosaic virus and the discrimination of its subgroups I and II. Journal of Virological Methods, 2017, 243, 35-43.	2.1	8
6	Development of a molecular assay for the general detection of tospoviruses and the distinction between tospoviral species. Archives of Virology, 2017, 162, 1519-1528.	2.1	9
7	Combining drought QTLs and bacterial blight Xa-genes to control bacterial blight disease under drought stress. Agriculture, Ecosystems and Environment, 2016, 233, 282-290.	5.3	4
8	Characterization of the Complete Genome of a Novel Polerovirus Infecting <scp>S</scp>auropus androgynus in <scp>T</scp>hailand. Journal of Phytopathology, 2015, 163, 695-702.	1.0	9
9	First full-length genome sequence of the polerovirus luffa aphid-borne yellows virus (LABYV) reveals the presence of at least two consensus sequences in an isolate from Thailand. Archives of Virology, 2015, 160, 2633-2636.	2.1	6
10	Complete genome sequences of two biologically distinct isolates of Asparagus virus 1. Archives of Virology, 2015, 160, 569-572.	2.1	5
11	Molecular diversity of poleroviruses infecting cucurbit crops in four countries reveals the presence of members of six distinct species. Archives of Virology, 2014, 159, 1459-1465.	2.1	34
12	Taxonomic reorganization of family Partitiviridae and other recent progress in partitivirus research. Virus Research, 2014, 188, 128-141.	2.2	271
13	Influence of <scp>tomato spotted wilt virus</scp> on performance and behaviour of western flower thrips (<scp>F</scp>rankliniella occidentalis). Journal of Applied Entomology, 2013, 137, 488-498.	1.8	51
14	Molecular characterization of five betacryptoviruses infecting four clover species and dill. Archives of Virology, 2013, 158, 1943-1952.	2.1	33
15	In planta Protein Interactions of Three Alphacryptoviruses and Three Betacryptoviruses from White Clover, Red Clover and Dill by Bimolecular Fluorescence Complementation Analysis. Viruses, 2013, 5, 2512-2530.	3.3	8
16	Taxonomic relatedness between Pectobacterium carotovorum subsp. carotovorum, Pectobacterium carotovorum subsp. odoriferum and Pectobacterium carotovorum subsp. brasiliense subsp. nov. Journal of Applied Microbiology, 2012, 113, 904-913.	3.1	94
17	Engineered Tobacco mosaic virus mutants with distinct physical characteristics in planta and enhanced metallization properties. Virus Research, 2011, 157, 35-46.	2.2	68
18	An optimized mRFP-based bimolecular fluorescence complementation system for the detection of proteinâ€“protein interactions in planta. Journal of Virological Methods, 2011, 174, 158-165.	2.1	19

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19	Detection of plum pox potyviral proteinâ€“protein interactions in planta using an optimized mRFP-based bimolecular fluorescence complementation system. Journal of General Virology, 2011, 92, 2711-2723.	2.9	39
20	Molecular characterization of two alphacryptovirus dsRNAs isolated from Daucus carota. Archives of Virology, 2009, 154, 541-543.	2.1	14
21	Nucleotide sequence of a satellite RNA associated with carrot motley dwarf in parsley and carrot. Virus Genes, 2009, 38, 187-188.	1.6	7
22	Complete nucleotide sequence and experimental host range of Okra mosaic virus. Virus Genes, 2008, 36, 231-240.	1.6	18
23	Eriophyid mite transmission and host range of a Brome streak mosaic virus isolate derived from a full-length cDNA clone. Archives of Virology, 2008, 153, 181-185.	2.1	21
24	Construction of an infectious full-length cDNA clone of potato virus M. Archives of Virology, 2008, 153, 1385-1389.	2.1	21
25	Complete nucleotide sequence of a carrot isolate of Carrot mottle virus from Germany. Archives of Virology, 2008, 153, 2163-2165.	2.1	3
26	Transreplication of a Tomato yellow leaf curl Thailand virus DNA-B and replication of a DNAÃŸ component by Tomato leaf curl Vietnam virus and Tomato yellow leaf curl Vietnam virus. Virus Research, 2008, 136, 107-117.	2.2	15
27	A chimeric plum pox virus shows reduced spread and cannot compete with its parental wild-type viruses in a mixed infection. Journal of General Virology, 2007, 88, 2846-2851.	2.9	9
28	Capsid Protein-Mediated Recruitment of Host DnaJ-Like Proteins Is Required for Potato Virus Y Infection in Tobacco Plants. Journal of Virology, 2007, 81, 11870-11880.	3.4	123
29	Use of pentapeptide-insertion scanning mutagenesis for functional mapping of the plum pox virus helper component proteinase suppressor of gene silencing. Journal of General Virology, 2007, 88, 1005-1015.	2.9	44
30	The role of the coat protein region in symptom formation on Physalis floridana varies between PVY strains. Virus Research, 2007, 127, 122-125.	2.2	31
31	Application of Phi29 DNA polymerase in identification and full-length clone inoculation of tomato yellow leaf curl Thailand virus and tobacco leaf curl Thailand virus. Archives of Virology, 2007, 152, 941-954.	2.1	35
32	Molecular characterization and detection of Vicia cryptic virus in different Vicia faba cultivars. Archives of Virology, 2007, 152, 1477-1488.	2.1	29
33	No recombination detected in artificial potyvirus mixed infections and between potyvirus derived transgenes and heterologous challenging potyviruses. Environmental Biosafety Research, 2007, 6, 207-218.	1.1	9
34	The complete nucleotide sequence of a capsicum chlorosis virus isolate from Lycopersicum esculentum in Thailand. Archives of Virology, 2006, 151, 1761-1782.	2.1	38
35	Detection of 6K1 as a mature protein of 6â€…kDa in plum pox virus-infected Nicotiana benthamiana. Journal of General Virology, 2006, 87, 2381-2386.	2.9	17
36	Biological properties of Beet mild yellowing virus derived from a full-length cDNA clone. Journal of General Virology, 2006, 87, 445-449.	2.9	23

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37	Ceratothripoides claratris, a New Vector of a Capsicum chlorosis virus Isolate Infecting Tomato in Thailand. Phytopathology, 2005, 95, 659-663.	2.2	63
38	Occurrence and distribution of cassava begomoviruses in Kenya. Annals of Applied Biology, 2004, 145, 175-184.	2.5	26
39	The complete nucleotide sequence of Plum pox virus isolates from sweet (PPV-SwC) and sour (PPV-SoC) cherry and their taxonomic relationships within the species. Archives of Virology, 2003, 148, 2137-2153.	2.1	26
40	Multiplex RT-PCR-ELISA compared with bioassay for the detection of four apple viruses. Journal of Virological Methods, 2003, 110, 153-157.	2.1	39
41	Fluorescent labelling reveals spatial separation of potyvirus populations in mixed infected Nicotiana benthamiana plants. Journal of General Virology, 2003, 84, 2871-2876.	2.9	163
42	Detection of four apple viruses by multiplex RT-PCR assays with coamplification of plant mRNA as internal control. Journal of Virological Methods, 2002, 99, 81-92.	2.1	314
43	The production of a genus-specific recombinant antibody (scFv) using a recombinant potyvirus protease. Journal of Virological Methods, 2002, 106, 225-233.	2.1	57
44	Molecular and serological relationships of Spartina mottle virus (SpMV) strains from Spartina spec. and from Cynodon dactylon to other members of the Potyviridae. Archives of Virology, 2002, 147, 379-391.	2.1	8
45	The complete sequence of the genome of Cocksfoot streak virus (CSV), a grass infecting Potyvirus. Archives of Virology, 2002, 147, 1573-1583.	2.1	20
46	Transgenic or Plant Expression Vector-Mediated Recombination of Plum Pox Virus. Journal of Virology, 2000, 74, 7462-7469.	3.4	31
47	Native electrophoresis and Western blot analysis (NEWeB): a method for characterization of different forms of potyvirus particles and similar nucleoprotein complexes in extracts of infected plant tissues. Journal of General Virology, 2000, 81, 2295-2298.	2.9	27
48	Mutations in the coat protein gene of Plum pox virus suppress particle assembly, heterologous encapsidation and complementation in transgenic plants of Nicotiana benthamiana. Journal of General Virology, 2000, 81, 567-576.	2.9	58
49	Title is missing!. Molecular Breeding, 1998, 4, 155-164.	2.1	10
50	Ultrastructural localization of nonstructural and coat proteins of 19 potyviruses using antisera to bacterially expressed proteins of plum pox potyvirus. Archives of Virology, 1998, 143, 2133-2158.	2.1	58
51	Host-Controlled Cell-to-Cell Movement of a Hybrid Barley Stripe Mosaic Virus Expressing a Dianthovirus Movement Protein. Intervirology, 1997, 40, 1-6.	2.8	34
52	Expression and biochemical analyses of the recombinant potato virus X 25K movement protein. FEBS Letters, 1996, 397, 75-78.	2.8	64
53	Sour Cherry Strain of Plum Pox Potyvirus (PPV): Molecular and Serological Evidence for a New Subgroup of PPV Strains. Phytopathology, 1996, 86, 1215.	2.2	57
54	"Rattlesnake" structure of a filamentous plant RNA virus built of two capsid proteins.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 2470-2473.	7.1	132

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55	Molecular analyses of the coat protein region of different viruses on Poaceae belonging to the Potyviridae. Agronomy for Sustainable Development, 1995, 15, 491-494.	0.8	9
56	The Complete Nucleotide Sequence of the S RNA of a NewTospovirusSpecies, Representing Serogroup IV. Phytopathology, 1995, 85, 683.	2.2	34
57	Studies on Particle Components of Cacao Swollen Shoot Virus. Journal of Phytopathology, 1993, 139, 207-216.	1.0	7
58	Characterisation and serology of virusâ€like particles associated with faba bean necrotic yellows. Annals of Applied Biology, 1993, 123, 629-647.	2.5	68
59	Nucleotide sequence of the coat protein gene of pelargonium leaf curl virus and comparison of the deduced coat protein amino acid sequence with those of other tombusviruses. Archives of Virology, 1993, 129, 349-356.	2.1	6
60	A novel open reading frame in tobacco mosaic virus genome coding for a putative small, positively charged protein. Biochimie, 1993, 75, 659-665.	2.6	23
61	Single- and Double-Stranded RNAs Associated with an Isolate of Beet Soil-Borne Virus. Intervirology, 1992, 33, 97-102.	2.8	9
62	Nucleotide Sequence of the PPV-B Coat Protein Gene. Biotechnology and Biotechnological Equipment, 1991, 5, 52-55.	1.3	0
63	Expression of the coat protein gene of plum pox virus inEscherichia coli. Archives of Phytopathology and Plant Protection, 1990, 26, 381-388.	1.3	0
64	Nucleotide sequence of the bean leafroll luteovirus coat protein gene. Nucleic Acids Research, 1990, 18, 5544-5544.	14.5	15
65	Expression of the plum pox virus coat protein region in Escherichia coli. Virus Genes, 1989, 2, 119-127.	1.6	9
66	Nucleotide sequence of the potato leafroll virus coat protein gene. Nucleic Acids Research, 1989, 17, 1768-1768.	14.5	7
67	Molecular Cloning of DNA Complementary to the RNA-Genome of Plum Pox Virus (PPV). Journal of Phytopathology, 1988, 122, 222-231.	1.0	33
68	Cucumis sativus Cryptic Virus, a New Virus in Cucumber. Journal of Phytopathology, 1988, 121, 233-238.	1.0	5
69	Production and use of cDNA clones from arabis mosaic virus. Annals of Applied Biology, 1988, 113, 483-491.	2.5	7
70	Einsatz einer Resistenzinduktion durch Kulturfiltrate vonStachybotrys chartarum(Ehrenb. ex Link) Hughes undBacillus subtilis(Ehrenberg) Cohn gegen Virosen unter praxisÃ¼blichen Anbaubedingungen. Archives of Phytopathology and Plant Protection, 1987, 23, 275-283.	1.3	4
71	Resistenzinduktion gegen systemische Virusinfektionen durch Kulturfiltrate von Stachybotrys chartarum (Ehrenb. ex Link) Hughes. Journal of Phytopathology, 1987, 119, 175-183.	1.0	1
72	Detection of plum pox virus by isolation of double-stranded ribonucleic acid (dsRNA). EPPO Bulletin, 1987, 17, 91-95.	0.8	5