

Jan F Kreuze

List of Publications by Year in descending order

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99
papers

6,040
citations

117625

34
h-index

79698

73
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105
all docs

105
docs citations

105
times ranked

4225
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete viral genome sequence and discovery of novel viruses by deep sequencing of small RNAs: A generic method for diagnosis, discovery and sequencing of viruses. <i>Virology</i> , 2009, 388, 1-7.	2.4	537
2	ICTV Virus Taxonomy Profile: Potyviridae. <i>Journal of General Virology</i> , 2017, 98, 352-354.	2.9	416
3	Methods in virus diagnostics: From ELISA to next generation sequencing. <i>Virus Research</i> , 2014, 186, 20-31.	2.2	326
4	FamilyFlexiviridae: A Case Study in Virion and Genome Plasticity. <i>Annual Review of Phytopathology</i> , 2007, 45, 73-100.	7.8	316
5	Comparative and functional genomics of closteroviruses. <i>Virus Research</i> , 2006, 117, 38-51.	2.2	307
6	The genome of cultivated sweet potato contains <i>Agrobacterium</i> T-DNAs with expressed genes: An example of a naturally transgenic food crop. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5844-5849.	7.1	236
7	Synergistic Interactions of a Potyvirus and a Phloem-Limited Crinivirus in Sweet Potato Plants. <i>Virology</i> , 2000, 269, 26-36.	2.4	226
8	VirusDetect: An automated pipeline for efficient virus discovery using deep sequencing of small RNAs. <i>Virology</i> , 2017, 500, 130-138.	2.4	191
9	Sweetpotato Viruses: 15 Years of Progress on Understanding and Managing Complex Diseases. <i>Plant Disease</i> , 2012, 96, 168-185.	1.4	186
10	Genome sequences of two diploid wild relatives of cultivated sweetpotato reveal targets for genetic improvement. <i>Nature Communications</i> , 2018, 9, 4580.	12.8	181
11	Virgaviridae: a new family of rod-shaped plant viruses. <i>Archives of Virology</i> , 2009, 154, 1967-1972.	2.1	161
12	Viral Class 1 RNase III Involved in Suppression of RNA Silencing. <i>Journal of Virology</i> , 2005, 79, 7227-7238.	3.4	149
13	Elimination of antiviral defense by viral RNase III. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10354-10358.	7.1	128
14	Stacking three late blight resistance genes from wild species directly into African highland potato varieties confers complete field resistance to local blight races. <i>Plant Biotechnology Journal</i> , 2019, 17, 1119-1129.	8.3	126
15	RNAi-mediated resistance to diverse isolates belonging to two virus species involved in Cassava brown streak disease. <i>Molecular Plant Pathology</i> , 2011, 12, 31-41.	4.2	117
16	Self-excision of the antibiotic resistance gene nptII using a heat inducible Cre-loxP system from transgenic potato. <i>Plant Molecular Biology</i> , 2006, 62, 71-82.	3.9	107
17	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
18	Complete Genome Sequence and Analyses of the Subgenomic RNAs of Sweet Potato Chlorotic Stunt Virus Reveal Several New Features for the Genus Crinivirus. <i>Journal of Virology</i> , 2002, 76, 9260-9270.	3.4	97

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19	Deep Sequencing of Virus-Derived Small Interfering RNAs and RNA from Viral Particles Shows Highly Similar Mutational Landscapes of a Plant Virus Population. <i>Journal of Virology</i> , 2015, 89, 4760-4769.	3.4	84
20	Ortervirales: New Virus Order Unifying Five Families of Reverse-Transcribing Viruses. <i>Journal of Virology</i> , 2018, 92, .	3.4	79
21	Phylogenetic Analysis of 16S rRNA Genes and PCR Analysis of the <i>nec1</i> Gene from <i>Streptomyces</i> spp. Causing Common Scab, Pitted Scab, and Netted Scab in Finland. <i>Phytopathology</i> , 1999, 89, 462-469.	2.2	78
22	Viral Diseases in Potato. , 2020, , 389-430.		78
23	Occurrence and survival of potato scab pathogens (<i>Streptomyces</i> species) on tuber lesions: quick diagnosis based on a PCR-based assay. <i>Plant Pathology</i> , 2004, 53, 280-287.	2.4	71
24	Biological, Serological, and Molecular Differences Among Isolates of Potato A Potyvirus. <i>Phytopathology</i> , 1998, 88, 311-321.	2.2	67
25	Analysis of gene content in sweet potato chlorotic stunt virus RNA1 reveals the presence of the p22 RNA silencing suppressor in only a few isolates: implications for viral evolution and synergism. <i>Journal of General Virology</i> , 2008, 89, 573-582.	2.9	67
26	Comparisons of coat protein gene sequences show that East African isolates of Sweet potato feathery mottle virus form a genetically distinct group. <i>Archives of Virology</i> , 2000, 145, 567-574.	2.1	66
27	RNA silencing-mediated resistance to a crinivirus (Closteroviridae) in cultivated sweetpotato (<i>Ipomoea batatas</i> L.) and development of sweetpotato virus disease following co-infection with a potyvirus. <i>Molecular Plant Pathology</i> , 2008, 9, 589-598.	4.2	61
28	Degeneration in sweetpotato due to viruses, virus-cleaned planting material and reversion: a review. <i>Plant Pathology</i> , 2015, 64, 1-15.	2.4	61
29	A novel sweet potato potyvirus open reading frame (ORF) is expressed via polymerase slippage and suppresses RNA silencing. <i>Molecular Plant Pathology</i> , 2016, 17, 1111-1123.	4.2	61
30	Synergistic interactions of begomoviruses with Sweet potato chlorotic stunt virus (genus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3 <i>Molecular Plant Pathology</i> , 2015, 16, 459-471.	4.2	51
31	ICTV Virus Taxonomy Profile: Caulimoviridae. <i>Journal of General Virology</i> , 2020, 101, 1025-1026.	2.9	49
32	Molecular variability of sweet potato feathery mottle virus and other potyviruses infecting sweet potato in Peru. <i>Archives of Virology</i> , 2008, 153, 473-483.	2.1	48
33	Horizontal Gene Transfer Contributes to Plant Evolution: The Case of <i>Agrobacterium</i> T-DNAs. <i>Frontiers in Plant Science</i> , 2017, 8, 2015.	3.6	44
34	Some molecular characteristics of three viruses from SPVD-affected sweet potato plants in Egypt. <i>Archives of Virology</i> , 2003, 148, 2449-2460.	2.1	41
35	Salicylic Acid Perturbs sRNA-Gibberellin Regulatory Network in Immune Response of Potato to Potato virus Y Infection. <i>Frontiers in Plant Science</i> , 2017, 8, 2192.	3.6	41
36	A Primer on the Analysis of High-Throughput Sequencing Data for Detection of Plant Viruses. <i>Microorganisms</i> , 2021, 9, 841.	3.6	36

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37	ICTV Virus Taxonomy Profile: Alphaflexiviridae. <i>Journal of General Virology</i> , 2020, 101, 699-700.	2.9	36
38	Two Serotypes of Sweetpotato feathery mottle virus in Uganda and Their Interaction with Resistant Sweetpotato Cultivars. <i>Phytopathology</i> , 2000, 90, 1250-1255.	2.2	35
39	Phytosanitary Interventions for Safe Global Germplasm Exchange and the Prevention of Transboundary Pest Spread: The Role of CGIAR Germplasm Health Units. <i>Plants</i> , 2021, 10, 328.	3.5	35
40	Analysis of complete genomic sequences of isolates of the Sweet potato feathery mottle virus strains C and EA: molecular evidence for two distinct potyvirus species and two P1 protein domains. <i>Archives of Virology</i> , 2010, 155, 2059-2063.	2.1	34
41	Complete genome sequences of new divergent potato virus X isolates and discrimination between strains in a mixed infection using small RNAs sequencing approach. <i>Virus Research</i> , 2014, 191, 45-50.	2.2	34
42	Potato virus Y; the Andean connection. <i>Virus Evolution</i> , 2019, 5, vez037.	4.9	34
43	Transgenic Resistance to PVYO Associated with Post-Transcriptional Silencing of P1 Transgene Is Overcome by PVYN Strains That Carry Highly Homologous P1 Sequences and Recover Transgene Expression at Infection. <i>Molecular Plant-Microbe Interactions</i> , 2000, 13, 366-373.	2.6	33
44	Sequence characterization of a Peruvian isolate of Sweet potato chlorotic stunt virus: Further variability and a model for p22 acquisition. <i>Virus Research</i> , 2011, 157, 111-115.	2.2	33
45	Using Small RNA Deep Sequencing Data to Detect Human Viruses. <i>BioMed Research International</i> , 2016, 2016, 1-9.	1.9	33
46	Distinct cavemoviruses interact synergistically with sweet potato chlorotic stunt virus (genus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382	2.9	31
47	Diversity, Pathogenicity, and Current Occurrence of Bacterial Wilt Bacterium <i>Ralstonia solanacearum</i> in Peru. <i>Frontiers in Plant Science</i> , 2017, 8, 1221.	3.6	31
48	The linear mitochondrial genome of the quarantine chytrid <i>Synchytrium endobioticum</i> ; insights into the evolution and recent history of an obligate biotrophic plant pathogen. <i>BMC Evolutionary Biology</i> , 2018, 18, 136.	3.2	30
49	Global Cropland Connectivity: A Risk Factor for Invasion and Saturation by Emerging Pathogens and Pests. <i>BioScience</i> , 2020, 70, 744-758.	4.9	30
50	The complete genome sequences of a Peruvian and a Colombian isolate of Andean potato latent virus and partial sequences of further isolates suggest the existence of two distinct potato-infecting tymovirus species. <i>Virus Research</i> , 2013, 173, 431-435.	2.2	29
51	Rpi-blb2 gene from <i>Solanum bulbocastanum</i> confers extreme resistance to late blight disease in potato. <i>Plant Cell, Tissue and Organ Culture</i> , 2016, 125, 269-281.	2.3	26
52	Utilization of engineered resistance to viruses in crops of the developing world, with emphasis on sub-Saharan Africa. <i>Current Opinion in Virology</i> , 2017, 26, 90-97.	5.4	26
53	The complete nucleotide sequence of sweet potato C6 virus: a carlavirus lacking a cysteine-rich protein. <i>Archives of Virology</i> , 2013, 158, 1393-1396.	2.1	25
54	Complete genome sequence of a potyvirus infecting yam beans (<i>Pachyrhizus</i> spp.) in Peru. <i>Archives of Virology</i> , 2012, 157, 773-776.	2.1	24

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55	Molecular Epidemiology of <i>Ralstonia solanacearum</i> Species Complex Strains Causing Bacterial Wilt of Potato in Uganda. <i>Phytopathology</i> , 2019, 109, 1922-1931.	2.2	24
56	Potato Virus A Isolates from Three Continents: Their Biological Properties, Phylogenetics, and Prehistory. <i>Phytopathology</i> , 2021, 111, 217-226.	2.2	24
57	Breeding Progress for Vitamin A, Iron and Zinc Biofortification, Drought Tolerance, and Sweetpotato Virus Disease Resistance in Sweetpotato. <i>Frontiers in Sustainable Food Systems</i> , 2021, 5, .	3.9	23
58	Using Small RNA-seq Data to Detect siRNA Duplexes Induced by Plant Viruses. <i>Genes</i> , 2017, 8, 163.	2.4	22
59	Coat protein sequence analysis reveals occurrence of new strains of Sweet potato feathery mottle virus in Uganda and Tanzania. <i>Virus Genes</i> , 2003, 27, 49-56.	1.6	21
60	Marker-free PLRV resistant potato mediated by Cre-loxP excision and RNAi. <i>Transgenic Research</i> , 2016, 25, 813-828.	2.4	18
61	The horizontal gene transfer of <i>Agrobacterium</i> T-DNAs into the series <i>Batatas</i> (Genus <i>Ipomoea</i>) genome is not confined to hexaploid sweetpotato. <i>Scientific Reports</i> , 2019, 9, 12584.	3.3	18
62	Badnaviruses of Sweet Potato: Symptomless Coinhabitants on a Global Scale. <i>Frontiers in Plant Science</i> , 2020, 11, 313.	3.6	18
63	R/Avr gene expression study of Rpi-vnt1.1 transgenic potato resistant to the <i>Phytophthora infestans</i> clonal lineage EC-1. <i>Plant Cell, Tissue and Organ Culture</i> , 2017, 131, 259-268.	2.3	16
64	Complete sequence and variability of a new subgroup B nepovirus infecting potato in central Peru. <i>Archives of Virology</i> , 2017, 162, 885-889.	2.1	16
65	The complete genome sequences of two isolates of potato black ringspot virus and their relationship to other isolates and nepoviruses. <i>Archives of Virology</i> , 2014, 159, 811-815.	2.1	15
66	Molecular and pathobiological characterization of 61 <i>Potato mopâ€štop virus</i> fullâ€šlength cDNAs reveals great variability of the virus in the centre of potato domestication, novel genotypes and evidence for recombination. <i>Molecular Plant Pathology</i> , 2017, 18, 864-877.	4.2	14
67	Extreme salinity as a challenge to grow potatoes under Mars-like soil conditions: targeting promising genotypes. <i>International Journal of Astrobiology</i> , 2019, 18, 18-24.	1.6	14
68	Transcriptome analysis provides insights into the responses of sweet potato to sweet potato virus disease (SPVD). <i>Virus Research</i> , 2021, 295, 198293.	2.2	14
69	A temperature-dependent phenology model for the greenhouse whitefly <i>Trialeurodes vaporariorum</i> (Hemiptera: Aleyrodidae). <i>Virus Research</i> , 2020, 289, 198107.	2.2	13
70	Storage Root Yield of Sweetpotato as Influenced by <i>Sweetpotato leaf curl virus</i> and Its Interaction With <i>Sweetpotato feathery mottle virus</i> and <i>Sweetpotato chlorotic stunt virus</i> in Kenya. <i>Plant Disease</i> , 2020, 104, 1477-1486.	1.4	12
71	The Phylogeography of Potato Virus X Shows the Fingerprints of Its Human Vector. <i>Viruses</i> , 2021, 13, 644.	3.3	12
72	Interlaboratory Comparison Study on Ribodepleted Total RNA High-Throughput Sequencing for Plant Virus Diagnostics and Bioinformatic Competence. <i>Pathogens</i> , 2021, 10, 1174.	2.8	12

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73	Crinivirus. , 2011, , 335-342.		12
74	Sweetpotato plant regeneration via an improved somatic embryogenesis protocol. Scientia Horticulturae, 2013, 161, 95-100.	3.6	11
75	Phytotoxin produced by the netted scab pathogen, <i>Streptomyces turgidiscabies</i> strain 65, isolated in Sweden. Journal of General Plant Pathology, 2018, 84, 108-117.	1.0	11
76	siRNA Deep Sequencing and Assembly: Piecing Together Viral Infections. , 2014, , 21-38.		10
77	Variation of Resistance to Different Strains of <i>Ralstonia Solanacearum</i> in Highland Tropics Adapted Potato Genotypes. American Journal of Potato Research, 2015, 92, 258-265.	0.9	10
78	Identification and Control of Latent Bacteria in in vitro Cultures of Sweetpotato [<i>Ipomoea batatas</i> (L.) Lam]. Frontiers in Plant Science, 2020, 11, 903.	3.6	10
79	Molecular Diversity and Pathogenicity of <i>Ralstonia solanacearum</i> Species Complex Associated With Bacterial Wilt of Potato in Rwanda. Plant Disease, 2021, 105, 770-779.	1.4	9
80	Molecular Characterization of the 3'-Terminal Region of Turnip mosaic virus Isolates from Eastern China. Journal of Phytopathology, 2007, 155, 333-341.	1.0	8
81	Serological survey and metagenomic discovery of potato viruses in Rwanda and Burundi reveals absence of PVY in Burundi and first report of TRV in potatoes in sub-Saharan Africa. Virus Research, 2021, 302, 198487.	2.2	8
82	Loop-Mediated Isothermal Amplification assays for on-site detection of the main sweetpotato infecting viruses. Journal of Virological Methods, 2021, 298, 114301.	2.1	8
83	Phylogenetics and Evolution of Potato Virus V: Another Potyvirus that Originated in the Andes. Plant Disease, 2022, 106, 691-700.	1.4	8
84	Efficiency of insect-proof net tunnels in reducing virus-related seed degeneration in sweet potato. Plant Pathology, 2019, 68, 1472-1480.	2.4	7
85	A temperature-driven model for potato yellow vein virus transmission efficacy by <i>Trialeurodes vaporariorum</i> (Hemiptera: Aleyrodidae). Virus Research, 2020, 289, 198109.	2.2	7
86	Title is missing!. Euphytica, 2001, 120, 71-83.	1.2	6
87	Characterization of distinct strains of an aphid-transmitted ilarvirus (Fam. Bromoviridae) infecting different hosts from South America. Virus Research, 2020, 282, 197944.	2.2	6
88	First Report of <i>Potato virus S</i> Naturally Infecting Arracacha (<i>Arracacia xanthorrhiza</i>) in Peru. Plant Disease, 2018, 102, 460-460.	1.4	6
89	Brief Note Rapid plant DNA and RNA extraction protocol using a bench drill. Genetics and Molecular Research, 2019, 18, .	0.2	4
90	Challenge of Virus Disease Threats to Ensuring Sustained Uptake of Vitamin-A-Rich Sweetpotato in Africa. Plant Pathology in the 21st Century, 2021, , 73-94.	0.9	4

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91	Innovative Digital Technologies to Monitor and Control Pest and Disease Threats in Root, Tuber, and Banana (RT&B) Cropping Systems: Progress and Prospects. , 2022, , 261-288.		4

92	WEEVIL RESISTANT SWEETPOTATO THROUGH BIOTECHNOLOGY. Acta Horticulturae, 2013, , 91-98.	0.2	3
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