Judith K Brown

List of Publications by Year in descending order

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117571 102432 4,732 92 34 66 h-index citations g-index papers 95 95 95 2769 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Revision of Begomovirus taxonomy based on pairwise sequence comparisons. Archives of Virology, 2015, 160, 1593-1619.	0.9	664
2	Whitefly-Transmitted Geminiviruses and Associated Disorders in the Americas and the Caribbean Basin. Plant Disease, 1992, 76, 220.	0.7	259
3	Establishment of three new genera in the family Geminiviridae: Becurtovirus, Eragrovirus and Turncurtovirus. Archives of Virology, 2014, 159, 2193-2203.	0.9	218
4	A genome-wide pairwise-identity-based proposal for the classification of viruses in the genus Mastrevirus (family Geminiviridae). Archives of Virology, 2013, 158, 1411-1424.	0.9	216
5	THE INTRODUCTION OF THE EXOTIC Q BIOTYPE OF BEMISIA TABACI FROM THE MEDITERRANEAN REGION INTO CHINA ON ORNAMENTAL CROPS. Florida Entomologist, 2006, 89, 168-174.	0.2	212
6	Molecular markers for the identification and global tracking of whitefly vector–Begomovirus complexes. Virus Research, 2000, 71, 233-260.	1.1	166
7	Change in the Biotype Composition of <i>Bemisia tabaci < /i>i > in Shandong Province of China From 2005 to 2008. Environmental Entomology, 2010, 39, 1028-1036.</i>	0.7	162
8	Whitefly transmission of plant viruses. Advances in Botanical Research, 2002, , 65-100.	0.5	137
9	Implication of Bemisia tabaci Heat Shock Protein 70 in Begomovirus-Whitefly Interactions. Journal of Virology, 2012, 86, 13241-13252.	1.5	120
10	Rapid Spread of Tomato Yellow Leaf Curl Virus in China Is Aided Differentially by Two Invasive Whiteflies. PLoS ONE, 2012, 7, e34817.	1,1	120
11	Analysis of Morphological Variation in Distinct Populations of Bemisia tabaci (Homoptera:) Tj ETQq1 1 0.784314 r	rgBJ /Over	lock 10 Tf 50
12	Spatio-temporal patterns of genetic change amongst populations of cassava Bemisia tabaci whiteflies driving virus pandemics in East and Central Africa. Virus Research, 2014, 186, 61-75.	1.1	109
13	Molecular Evidence for Five Distinct <i>Bemisia tabaci</i> (Homoptera: Aleyrodidae) Geographic Haplotypes Associated with Cassava Plants in Sub-Saharan Africa. Annals of the Entomological Society of America, 2004, 97, 852-859.	1.3	105
14	The core region of the coat protein gene is highly useful for establishing the provisional identification and classification of begomoviruses. Archives of Virology, 2001, 146, 1581-1598.	0.9	97
15	Extraordinary Resistance to Insecticides Reveals Exotic Q Biotype of Bemisia tabaci in the New World. Journal of Economic Entomology, 2010, 103, 2174-2186.	0.8	91
16	Revisiting the classification of curtoviruses based on genome-wide pairwise identity. Archives of Virology, 2014, 159, 1873-1882.	0.9	89
17	Asian Citrus Psyllid Expression Profiles Suggest Candidatus Liberibacter Asiaticus-Mediated Alteration of Adult Nutrition and Metabolism, and of Nymphal Development and Immunity. PLoS ONE, 2015, 10, e0130328.	1.1	85
18	Life History Traits of the Whitefly, Bemisia tabaci (Homoptera: Aleyrodidae) on Six Virus-Infected or Healthy Plant Species. Environmental Entomology, 1991, 20, 1102-1107.	0.7	84

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19	Review of the cultivation program within the National Alliance for Advanced Biofuels and Bioproducts. Algal Research, 2017, 22, 166-186.	2.4	72
20	Viral Metagenomics: Analysis of Begomoviruses by Illumina High-Throughput Sequencing. Viruses, 2014, 6, 1219-1236.	1.5	69
21	Review of the algal biology program within the National Alliance for Advanced Biofuels and Bioproducts. Algal Research, 2017, 22, 187-215.	2.4	69
22	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2021, 166, 3513-3566.	0.9	62
23	Genetic analysis of Bemisia (Hemiptera: Aleyrodidae) populations by isoelectric focusing electrophoresis. Biochemical Genetics, 2000, 38, 13-25.	0.8	59
24	Global Population Structure of a Worldwide Pest and Virus Vector: Genetic Diversity and Population History of the Bemisia tabaci Sibling Species Group. PLoS ONE, 2016, 11, e0165105.	1.1	58
25	Note: First report of the Q biotype of Bemisia tabaci in Southern Sonora, Mexico. Phytoparasitica, 2007, 35, 282-284.	0.6	53
26	Knock down of Whitefly Gut Gene Expression and Mortality by Orally Delivered Gut Gene-Specific dsRNAs. PLoS ONE, 2017, 12, e0168921.	1.1	52
27	Chocolate Under Threat from Old and New Cacao Diseases. Phytopathology, 2019, 109, 1331-1343.	1.1	50
28	Potato Zebra Chip Disease: A Phytopathological Tale. Plant Health Progress, 2010, 11, .	0.8	49
29	Colonization and Intrusive Invasion of Potato Psyllid by <i>Candidatus</i> Liberibacter solanacearum'. Phytopathology, 2017, 107, 36-49.	1.1	46
30	Host range, distribution, and natural enemies of Bemisia tabaci â€ ⁻ B biotypeâ€ [™] (Hemiptera: Aleyrodidae) in Turkey. Journal of Pest Science, 2006, 79, 233-240.	1.9	43
31	Ingestion, transmission, and persistence of Chino del tomate virus (CdTV), a New World begomovirus, by Old and New World biotypes of the whitefly vector Bemisia tabaci. Annals of Applied Biology, 2001, 139, 145-154.	1.3	41
32	Molecular analysis of Cotton leaf curl virus-Sudan reveals an evolutionary history of recombination. Virus Genes, 2002, 24, 249-256.	0.7	41
33	Localization of <i>Candidatus</i> Liberibacter solanacearum' and Evidence for Surface Appendages in the Potato Psyllid Vector. Phytopathology, 2016, 106, 142-154.	1.1	39
34	Nuclear Orthologs Derived from Whole Genome Sequencing Indicate Cryptic Diversity in the Bemisia tabaci (Insecta: Aleyrodidae) Complex of Whiteflies. Diversity, 2019, 11, 151.	0.7	39
35	Phylogenetic relationships, recombination analysis, and genetic variability among diverse variants of tomato yellow leaf curl virus in Iran and the Arabian Peninsula: further support for a TYLCV center of diversity. Archives of Virology, 2014, 159, 485-497.	0.9	38
36	Comparison of Potato and Asian Citrus Psyllid Adult and Nymph Transcriptomes Identified Vector Transcripts with Potential Involvement in Circulative, Propagative Liberibacter Transmission. Pathogens, 2014, 3, 875-907.	1.2	37

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37	Phylogenetic relationship of native and introduced Bemisia tabaci (Homoptera: Aleyrodidae) from China and India based on mtCOI DNA sequencing and host plant comparisons. Progress in Natural Science: Materials International, 2007, 17, 645-654.	1.8	36
38	Molecular characterization of begomoviruses and DNA satellites associated with okra leaf curl disease in Cameroon. Virus Research, 2013, 174, 116-125.	1.1	32
39	The Bemisia Tabaci Complex: Genetic and Phenotypic Variation and Relevance to TYLCV-Vector Interactions., 2007,, 25-56.		31
40	Nuclear DNA content of the whitefly Bemisia tabaci (Aleyrodidae: Hemiptera) estimated by flow cytometry. Bulletin of Entomological Research, 2005, 95, 309-312.	0.5	30
41	Host-free biofilm culture of "Candidatus Liberibacter asiaticus,―the bacterium associated with Huanglongbing. Biofilm, 2019, 1, 100005.	1.5	29
42	Molecular characterization of previously elusive badnaviruses associated with symptomatic cacao in the New World. Archives of Virology, 2017, 162, 1363-1371.	0.9	28
43	Diversity and Distribution of Cryptic Species of the Bemisia tabaci (Hemiptera: Aleyrodidae) complex in Pakistan. Journal of Economic Entomology, 2017, 110, 2295-2300.	0.8	27
44	Reproduction of the whitefly <i>Bemisia tabaci</i> (Hemiptera: Aleyrodidae) B biotype in maize fields (<i>Zea mays</i> L.) in Brazil. Pest Management Science, 2016, 72, 2181-2187.	1.7	26
45	Molecular characterization and phylogenetic relationships of two new bipartite begomovirus infecting malvaceous plants in Yucatan, Mexico. Virus Genes, 2007, 35, 369-377.	0.7	24
46	Characterization of the Complete Genome and PO Protein for a Previously Unreported Genotype of Cotton Leafroll Dwarf Virus, an Introduced Polerovirus in the United States. Plant Disease, 2020, 104, 780-786.	0.7	24
47	First Report of <i>Cotton leafroll dwarf virus</i> Infecting Upland Cotton (<i>Gossypium) Tj ETQq1 1 0.784314</i>	FrgBT/Ove	erlock 10 Tf 5
48	Exploiting somatic piRNAs in <i>Bemisia tabac</i> i enables novel gene silencing through RNA feeding. Life Science Alliance, 2020, 3, e202000731.	1.3	21
49	The Molecular Epidemiology of Begomoviruses. , 2001, , 279-316.		20
50	Demographic Expansion of the Predominant Bemisia tabaci (Gennadius) (Hemiptera: Aleyrodidae) Mitotypes Associated With the Cotton Leaf Curl Virus Epidemic in Pakistan. Annals of the Entomological Society of America, 2019, 112, 265-280.	1.3	19
51	A Complex of Badnavirus Species Infecting Cacao Reveals Mixed Infections, Extensive Genomic Variability, and Interspecific Recombination. Viruses, 2020, 12, 443.	1.5	19
52	Association between algal productivity and phycosphere composition in an outdoor <i>Chlorella sorokiniana</i> reactor based on multiple longitudinal analyses. Microbial Biotechnology, 2020, 13, 1546-1561.	2.0	17
53	Anatomy of Accessory Salivary Glands of the Whitefly Bemisia tabaci (Hemiptera: Aleyrodidae) and Correlations to Begomovirus Transmission. Annals of the Entomological Society of America, 2011, 104, 280-286.	1.3	16
54	Genetic diversification of penaeid shrimp infectious myonecrosis virus between Indonesia and Brazil. Virus Research, 2014, 189, 97-105.	1.1	16

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55	Molecular diagnostic development for begomovirus-betasatellite complexes undergoing diversification: A case study. Virus Research, 2017, 241, 29-41.	1.1	16
56	Complete genome sequence of a new bipartite begomovirus infecting cotton in the Republic of Benin in West Africa. Archives of Virology, 2016, 161, 2329-2333.	0.9	15
57	Engineered Disease Resistance in Cotton Using RNA-Interference to Knock down Cotton leaf curl Kokhran virus-Burewala and Cotton leaf curl Multan betasatellite Expression. Viruses, 2017, 9, 257.	1.5	15
58	Systematics of Bemisia and Bemisia Relatives: Can Molecular Techniques Solve the Bemisia tabaci Complex Conundrum – A Taxonomist's Viewpoint. , 2009, , 5-29.		14
59	Characterization of Rhynchosia yellow mosaic Yucatan virus, a new recombinant begomovirus associated with two fabaceous weeds in Yucatan, Mexico. Archives of Virology, 2010, 155, 1571-1579.	0.9	14
60	The proposed new species, cacao red vein virus, and three previously recognized badnavirus species are associated with cacao swollen shoot disease. Virology Journal, 2017, 14, 199.	1.4	14
61	Cotton Leafroll Dwarf Virus US Genomes Comprise Divergent Subpopulations and Harbor Extensive Variability. Viruses, 2021, 13, 2230.	1.5	14
62	Preliminary identification and coat protein gene phylogenetic relationships of begomoviruses associated with native flora and cultivated plants from the Yucatan Peninsula of Mexico. Virus Genes, 2007, 35, 825-833.	0.7	13
63	Single-Target and Multiplex Discrimination of Whiteflies (Hemiptera: Aleyrodidae) Bemisia tabaci and Trialeurodes vaporariorum With Modified Priming Oligonucleotide Thermodynamics. Journal of Economic Entomology, 2017, 110, 1821-1830.	0.8	13
64	Real-time quantitative detection of Vampirovibrio chlorellavorus, an obligate bacterial pathogen of Chlorella sorokiniana. Journal of Applied Phycology, 2019, 31, 1117-1129.	1,5	13
65	Association of Vampirovibrio chlorellavorus with decline and death of Chlorella sorokiniana in outdoor reactors. Journal of Applied Phycology, 2019, 31, 1131-1142.	1.5	13
66	Phyloâ€biogeographical distribution of whitefly Bemisia tabaci (Insecta: Aleyrodidae) mitotypes in Ecuador. Ecosphere, 2020, 11, e03154.	1.0	13
67	Size Limitations in the Filter Chamber and Digestive Tract of Nymphal and Adult <1>Bemisia tabaci 1 Whiteflies (Hemiptera: Aleyrodidae). Annals of the Entomological Society of America, 2003, 96, 544-552.	1.3	12
68	Functional Anatomy of the Oral Region of the Potato Psyllid (Hemiptera: Psylloidea: Triozidae). Annals of the Entomological Society of America, 2015, 108, 743-761.	1.3	12
69	Phylogeographic and SNPs Analyses of Bemisia tabaci B Mitotype Populations Reveal Only Two of Eight Haplotypes Are Invasive. Biology, 2021, 10, 1048.	1.3	12
70	Characterization of <i>Tomato curly stunt virus</i> : a new tomatoâ€infecting begomovirus from South Africa. Plant Pathology, 2008, 57, 809-818.	1,2	11
71	Genetic variability, community structure, and horizontal transfer of endosymbionts among three Asia Il―Bemisia tabaci mitotypes in Pakistan. Ecology and Evolution, 2020, 10, 2928-2943.	0.8	11
72	Population Structure of the Greenhouse Whitefly, Trialeurodes vaporariorum (Westwood), an Invasive Species from the Americas, 60 Years after Invading China. International Journal of Molecular Sciences, 2014, 15, 13514-13528.	1.8	11

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73	Differential Transcriptional Responses in Two Old World Bemisia tabaci Cryptic Species Post Acquisition of Old and New World Begomoviruses. Cells, 2022, 11, 2060.	1.8	11
74	The Previously Unidentified, Divergent Badnavirus Species Cacao red vein-banding virus is Associated with Cacao Swollen Shoot Disease in Nigeria. Plant Disease, 2019, 103, 1302-1308.	0.7	10
75	Complete genome sequence of a new bipartite begomovirus infecting fluted pumpkin (Telfairia) Tj ETQq1 1 0.78	4314 rgBT 0.9	- Qverlock 1
76	Knockdown of ecdysteroid synthesis genes results in impaired molting and high mortality in <i>Bactericera cockerelli</i> (Hemiptera: Triozidae). Pest Management Science, 2022, 78, 2204-2214.	1.7	8
77	Molecular characterization and phylogenetic relationships of Desmodium leaf distortion virus (DeLDV): a new begomovirus infecting Desmodium glabrum in Yucatan, Mexico. Virus Genes, 2009, 39, 371-374.	0.7	7
78	Complete genome sequences of three newly discovered cacao mild mosaic virus isolates from Theobroma cacao L. in Brazil and Puerto Rico and evidence for recombination. Archives of Virology, 2021, 166, 2027-2031.	0.9	7
79	The infection of its insect vector by bacterial plant pathogen "Candidatus Liberibacter solanacearum" is associated with altered vector physiology. Enzyme and Microbial Technology, 2019, 129, 109358.	1.6	6
80	Metabolic resistance to organophosphate insecticides in natural populations of the whitefly Bemisia tabaci (Hemiptera: Aleyrodidae) in Egypt and molecular identification of mitotypes. Phytoparasitica, 2021, 49, 443-457.	0.6	5
81	Molecular detection of cacao swollen shoot badnavirus species by amplification with four PCR primer pairs, and evidence that Cacao swollen shoot Togo B virus-like isolates are highly prevalent in Côte d'lvoire. European Journal of Plant Pathology, 2021, 159, 941-947.	0.8	4
82	Low-phosphate-selected Auxenochlorella protothecoides redirects phosphate to essential pathways while producing more biomass. PLoS ONE, 2018, 13, e0198953.	1.1	3
83	Invasion of previously unreported dicot plant hosts by chickpea chlorotic dwarf virus in Pakistan. VirusDisease, 2019, 30, 95-100.	1.0	3
84	Vampirovibrio chlorellavorus draft genome sequence, annotation, and preliminary characterization of pathogenicity determinants. Phycological Research, 2020, 68, 23-29.	0.8	3
85	A stationary tweezer platform for high throughput dissections of minute arthropods and extirpation of their minute organs. MethodsX, 2021, 8, 101317.	0.7	3
86	Earlier than expected introductions of the <i>Bemisia tabaci</i> B mitotype in Brazil reveal an unprecedented, rapid invasion history. Ecology and Evolution, 2022, 12, e8557.	0.8	3
87	Exploring the Use of High-Resolution Melting Analysis and Helicase-Dependent Amplification for Discrimination of <i>Bemisia tabaci</i> (Hemiptera: Aleyrodidae) Cryptic Species and <i>Trialeurodes vaporariorum</i> Journal of Economic Entomology, 2020, 113, 2511-2520.	0.8	2
88	Minimal genomic variability in Merremia mosaic virus isolates endemic in Merremia spp and cultivated tomato in Puerto Rico. VirusDisease, 2019, 30, 84-94.	1.0	1
89	Construction of an Infectious Clone of the Badnavirus Cacao Swollen Shoot Ghana M Virus and Infectivity by Gene Gun- and Agrobacterium-Mediated Inoculation. Frontiers in Agronomy, 2021, 3, .	1.5	1
90	Single nucleotide polymorphism-mismatch primer development for rapid molecular identification of selected microalgal species. Journal of Applied Phycology, 2021, 33, 1685-1694.	1.5	0

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91	Complete genome sequence of a previously undescribed monopartite begomovirus and betasatellite infecting Malvastrum coromandelianum in Cambodia. Archives of Virology, 2021, 166, 1789-1793.	0.9	O
92	Comparison of Auxenochlorella protothecoides and Chlorella spp. Chloroplast Genomes: Evidence for Endosymbiosis and Horizontal Virus-like Gene Transfer. Life, 2022, 12, 458.	1.1	0