Ulrich Melcher

List of Publications by Year
in descending order

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Version: 2024-02-01

88 papers	3,517 citations	172457 29 h-index	144013 57 g-index
89 all docs	89 docs citations	89 times ranked	2770 citing authors

#	ARTICLE	IF	CITATIONS
1	Forensic plant pathology. , 2020, , 49-70.		3
2	Special Issue â€œPlant Virus Ecology and Biodiversityâ€. Viruses, 2019, 11, 676.	3.3	0
3	Modeling of Mutational Events in the Evolution of Viruses. Viruses, 2019, 11, 418.	3.3	4
4	Annotation and analysis of the mitochondrial genome of Coniothyrium glycines, causal agent of red leaf blotch of soybean, reveals an abundance of homing endonucleases. PLoS ONE, 2018, 13, e0207062.	2.5	15
5	ICTV Virus Taxonomy Profile: Virgaviridae. Journal of General Virology, 2017, 98, 1999-2000.	2.9	134
6	Influences of Plant Species, Season and Location on Leaf Endophytic Bacterial Communities of Non-Cultivated Plants. PLoS ONE, 2016, 11, e0150895.	2.5	96
7	Adaptation and Validation of E-Probe Diagnostic Nucleic Acid Analysis for Detection of Escherichia coli O157:H7 in Metagenomic Data from Complex Food Matrices. Journal of Food Protection, 2016, 79, 574-581.	1.7	8
8	Determinants of taxonomic composition of plant viruses at the Nature Conservancyâ€™s Tallgrass Prairie Preserve, Oklahoma. Virus Evolution, 2015, 1, vev007.	4.9	28
9	Metagenomic search strategies for interactions among plants and multiple microbes. Frontiers in Plant Science, 2014, 5, 268.	3.6	19
10	Genomic characterization of Ambrosia asymptomatic virus 1 and evidence of other Tymovirales members in the Oklahoma tallgrass prairie revealed by sequence analysis. Archives of Virology, 2014, 159, 1755-1764.	2.1	9
11	Evaluating the impacts of stressors of Pseudomonas syringae pathovar tomato on the effectiveness of multi-locus variable number tandem repeat analysis and multi-locus sequence typing in microbial forensic investigations. Investigative Genetics, 2014, 5, 10.	3.3	2
12	Community terminal restriction fragment length polymorphisms reveal insights into the diversity and dynamics of leaf endophytic bacteria. BMC Microbiology, 2013, 13, 1.	3.3	257
13	An Analysis of the Genomic Variability of the Phytopathogenic Mollicute <i>Spiroplasma kunkelii</i>. Phytopathology, 2013, 103, 129-134.	2.2	5
14	Biosecurity Implications of New Technology and Discovery in Plant Virus Research. PLoS Pathogens, 2013, 9, e1003337.	4.7	66
15	Molecular Characterization, Ecology, and Epidemiology of a Novel Tymovirus in<i>Asclepias viridis</i>from Oklahoma. Phytopathology, 2012, 102, 166-176.	2.2	35
16	Population genetic analysis of grapevine fanleaf virus. Archives of Virology, 2012, 157, 1919-1929.	2.1	22
17	Detection of members of the Secoviridae in the Tallgrass Prairie Preserve, Osage County, Oklahoma, USA. Virus Research, 2012, 167, 34-42.	2.2	26
18	Virus Operation Control Centers. Signaling and Communication in Plants, 2012, , 231-254.	0.7	0

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19	Co-divergence and host-switching in the evolution of tobamoviruses. Journal of General Virology, 2012, 93, 408-418.	2.9	31
20	Selection and characterization of<i>Spiroplasma citri</i>mutants by random transposome mutagenesis. Canadian Journal of Microbiology, 2011, 57, 525-532.	1.7	5
21	The expanding field of plant virus ecology: Historical foundations, knowledge gaps, and research directions. Virus Research, 2011, 159, 84-94.	2.2	113
22	Detection of members of the Tombusviridae in the Tallgrass Prairie Preserve, Osage County, Oklahoma, USA. Virus Research, 2011, 160, 256-263.	2.2	27
23	Forensic Plant Pathology. , 2011, , 89-724.		7
24	Plectrovirus. , 2011, , 749-755.		0
25	Citrus Stubborn Severity Is Associated with <i>Spiroplasma citri</i> Titer But Not with Bacterial Genotype. Plant Disease, 2010, 94, 75-82.	1.4	11
26	Oligonucleotide-based microarray for detection of plant viruses employing sequence-independent amplification of targets. Journal of Virological Methods, 2010, 163, 57-67.	2.1	15
27	Assessing constancy of substitution rates in viruses over evolutionary time. BMC Bioinformatics, 2010, 11, S3.	2.6	7
28	New Perspectives on the Epidemiology of Citrus Stubborn Disease in California Orchards. Plant Health Progress, 2010, 11, 37.	1.4	3
29	Non-cultivated plants of the Tallgrass Prairie Preserve of northeastern Oklahoma frequently contain virus-like sequences in particulate fractions. Virus Research, 2009, 141, 169-173.	2.2	74
30	Assessment of codivergence of Mastreviruses with their plant hosts. BMC Evolutionary Biology, 2008, 8, 335.	3.2	43
31	Evidence for novel viruses by analysis of nucleic acids in virus-like particle fractions from Ambrosia psilostachya. Journal of Virological Methods, 2008, 152, 49-55.	2.1	46
32	Evolution of the Spiroplasma P58 Multigene Family. Biochemical Genetics, 2007, 45, 25-32.	1.7	6
33	Plant Pathogen Forensics: Capabilities, Needs, and Recommendations. Microbiology and Molecular Biology Reviews, 2006, 70, 450-471.	6.6	143
34	Plant Virus Biodiversity and Ecology. PLoS Biology, 2006, 4, e80.	5.6	123
35	The Phytopathogenic Spiroplasmas. , 2006, , 905-947.		10
36	Sequence comparisons of plasmids pBJS-O of Spiroplasma citri and pSKU146 of S. kunkelii: implications for plasmid evolution. BMC Genomics, 2005, 6, 175.	2.8	25

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37	Markov model recognition and classification of DNA/protein sequences within large text databases. Bioinformatics, 2005, 21, 4046-4053.	4.1	16
38	Soilborne wheat mosaic virus (SBWMV) 19K protein belongs to a class of cysteine rich proteins that suppress RNA silencing. Virology Journal, 2005, 2, 18.	3.4	34
39	Selection for 3â€² end triplets for polymerase chain reaction primers. Molecular and Cellular Probes, 2004, 18, 369-372.	2.1	13
40	Turnip vein-clearing virus, from pathogen to host expression profile. Molecular Plant Pathology, 2003, 4, 133-140.	4.2	19
41	Evidence that the 37â€…kDa protein of Soil-borne wheat mosaic virus is a virus movement protein. Journal of General Virology, 2003, 84, 3153-3163.	2.9	22
42	Molecular Detection and Identification of Influenza Viruses by Oligonucleotide Microarray Hybridization. Journal of Clinical Microbiology, 2003, 41, 4542-4550.	3.9	98
43	Serratia marcescens, a Phloem-Colonizing, Squash Bug -Transmitted Bacterium: Causal Agent of Cucurbit Yellow Vine Disease. Plant Disease, 2003, 87, 937-944.	1.4	83
44	VirOligo: a database of virus-specific oligonucleotides. Nucleic Acids Research, 2002, 30, 203-204.	14.5	24
45	Predominance of six different hexanucleotide recoding signals 3' of read-through stop codons. Nucleic Acids Research, 2002, 30, 2011-2017.	14.5	110
46	Nylon Membrane-Immobilized PCR for Detection of Bovine Viruses. BioTechniques, 2002, 32, 74-80.	1.8	10
47	Characterization of Spiroplasma citri adhesion related protein SARP1, which contains a domain of a novel family designated sarpin. Gene, 2001, 275, 57-64.	2.2	53
48	Common elements of spiroplasma plectroviruses revealed by nucleotide sequence of SVTS2. Virus Genes, 2000, 20, 47-56.	1.6	20
49	The â€˜30Kâ€™ superfamily of viral movement proteins. Microbiology (United Kingdom), 2000, 81, 257-266.	1.8	265
50	Historical importance of TMV. Trends in Plant Science, 2000, 5, 268.	8.8	0
51	Mechanisms of Spiroplasma Genome Variation Associated with SpVl-like Viral DNA Inferred from Sequence Comparisons. Microbial & Comparative Genomics, 1999, 4, 29-46.	0.4	25
52	Sequence changes in six variants of rice tungro bacilliform virus and their phylogenetic relationships. Journal of General Virology, 1999, 80, 2229-2237.	2.9	19
53	The Phytopathogenic Mollicute-Insect Vector Interface: A Closer Look. Phytopathology, 1998, 88, 1351-1358.	2.2	92
54	Polymerase Chain Reaction Detection and Phylogenetic Characterization of an Agent Associated with Yellow Vine Disease of Cucurbits. Phytopathology, 1998, 88, 428-436.	2.2	20

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55	Molecular characterization of a gene encoding a membrane protein of Spiroplasma citri. Gene, 1997, 189, 95-100.	2.2	31
56	Tobamovirus evolution: gene overlaps, recombination, and taxonomic implications. Molecular Biology and Evolution, 1996, 13, 1327-1338.	8.9	103
57	Extensive chromosome aberrations inSpiroplasma citri strain BR3. Biochemical Genetics, 1996, 34, 269-286.	1.7	49
58	Extensive chromosome aberrations inSpiroplasma citri strain BR3. Biochemical Genetics, 1996, 34, 269-286.	1.7	4
59	Completion of a cDNA sequence from a tobamovirus pathogenic to crucifers. Gene, 1995, 166, 331-332.	2.2	36
60	Graphic Representations of Amino Acid Sequences. , 1995, , 6-14.		2
61	Phylogenetic relationships reveal recombination among isolates of cauliflower mosaic virus. Journal of Molecular Evolution, 1994, 39, 496-505.	1.8	42
62	HIV-1 Proteinase as Structural Model of Intercellular Transport Proteins of Plant Viruses. Journal of Theoretical Biology, 1993, 162, 61-74.	1.7	9
63	In Planta Deletion of DNA Inserts from the Large Intergenic Region of Cauliflower Mosaic Virus DNA. Virology, 1993, 192, 188-196.	2.4	16
64	The complete nucleotide sequence of cauliflower mosaic virus isolate BBC. Gene, 1993, 123, 255-257.	2.2	15
65	Nucleotide Sequence of Cauliflower Mosaic Virus Isolate NY8153. Plant Physiology, 1992, 100, 542-545.	4.8	11
66	Recombination sites in cauliflower mosaic virus DNAs: Implications for mechanisms of recombination. Virology, 1990, 177, 717-726.	2.4	53
67	Symptoms of Cauliflower Mosaic Virus Infection in Arabidopsis thaliana and Turnip. Botanical Gazette, 1989, 150, 139-147.	0.6	42
68	Inactivation of cauliflower mosaic virus by a photoactivatable cotton phytoalexin. Physiological and Molecular Plant Pathology, 1988, 33, 115-126.	2.5	20
69	A readable and space-efficient DNA sequence representation: application to caulimoviral DNAs. Bioinformatics, 1988, 4, 93-96.	4.1	1
70	Replication of Cauliflower Mosaic Virus DNA in Leaves and Suspension Culture Protoplasts of Cotton. Plant Physiology, 1987, 83, 633-639.	4.8	10
71	Selective allele loss and interference between cauliflower mosaic virus DNAs. Molecular Genetics and Genomics, 1986, 203, 230-236.	2.4	9
72	Infection of evacuolated turnip protoplasts with liposome-packaged cauliflower mosaic virus. Plant Cell Reports, 1985, 4, 58-62.	5.6	10

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73	Recombination between mutant cauliflower mosaic virus DNAs. Plant Molecular Biology, 1985, 5, 281-289.	3.9	29
74	Complementary DNA â€“ 25S ribosomal RNA hybridization: an improved method for phylogenetic studies. Canadian Journal of Microbiology, 1983, 29, 546-551.	1.7	8
75	Helper component for aphid transmission encoded by region II of cauliflower mosaic virus DNA. Virology, 1983, 129, 25-30.	2.4	106
76	Clones of cauliflower mosaic virus identified by molecular hybridization in turnip leaves. Plant Molecular Biology, 1981, 1, 63-73.	3.9	29
77	Heterogeneity of Zea mays protein body messenger RNA. Plant Science Letters, 1980, 18, 133-141.	1.8	6
78	Methionine-rich protein fraction prepared by cryoprecipitation from extracts of corn meal. Journal of Agricultural and Food Chemistry, 1980, 28, 1334-1336.	5.2	14
79	<i>In Vitro</i> Synthesis of a Precursor to the Methionine-rich Polypeptide of the Zein Fraction of Corn. Plant Physiology, 1979, 63, 354-358.	4.8	26
80	Possible palindromes in immunoglobulin heavy-chain genes: Their role in membrane attachment. Immunogenetics, 1978, 7, 1-12.	2.4	2
81	Density differences between membrane and secreted immunoglobulins of murine splenocytes. Biochemistry, 1977, 16, 145-152.	2.5	32
82	The purification of Î²-galactosidase-specific polysomes by affinity chromatography. Analytical Biochemistry, 1975, 64, 461-465.	2.4	6
83	Are immunoglobulins integral membrane proteins?. Nature, 1975, 258, 434-435.	27.8	64
84	Cell surface immunoglobulin. XI. The appearance of an IgD-like molecule on murine lymphoid cells during ontogeny.. Journal of Experimental Medicine, 1975, 141, 206-215.	8.5	196
85	CELL SURFACE IMMUNOGLOBULIN. Journal of Experimental Medicine, 1974, 140, 1427-1431.	8.5	141
86	AN ELECTROPHORETIC DIFFERENCE BETWEEN SURFACE AND SECRETED IGM OF MURINE SPLENOCYTES. Journal of Experimental Medicine, 1973, 138, 1282-1287.	8.5	20
87	Metabolism of puromycin by yeast cells. Nucleic Acids and Protein Synthesis, 1971, 246, 216-224.	1.7	7
88	PROTEIN RELEASE BY BARLEY ALEURONE LAYERS. Journal of the Institute of Brewing, 1971, 77, 456-461.	2.3	25