

Armelle Marais

List of Publications by Year in descending order

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72
papers

1,908
citations

257450

24
h-index

276875

41
g-index

74
all docs

74
docs citations

74
times ranked

1681
citing authors

#	ARTICLE	IF	CITATIONS
1	First Report of Grapevine Virus L Infecting Grapevine in Southeast France. <i>Plant Disease</i> , 2022, 106, .	1.4	11
2	Host range and molecular variability of the sadwavirus dioscorea mosaic associated virus. <i>Archives of Virology</i> , 2022, 167, 917-922.	2.1	3
3	Molecular characterization of Cordyline virus 1 isolates infecting yam (<i>Dioscorea</i> spp). <i>Archives of Virology</i> , 2022, 167, 2275-2280.	2.1	3
4	Sixty Years from the First Disease Description, a Novel Badnavirus Associated with Chestnut Mosaic Disease. <i>Phytopathology</i> , 2021, 111, 1051-1058.	2.2	6
5	First Report of Alfalfa Mosaic Virus in Chayote in Italy. <i>Plant Disease</i> , 2021, 105, 698-698.	1.4	5
6	Characterization of the Mycovirome of the Phytopathogenic Fungus, <i>Neofusicoccum parvum</i> . <i>Viruses</i> , 2021, 13, 375.	3.3	9
7	First Report of Lettuce Necrotic Leaf Curl Virus Infecting Cultivated Lettuce in France. <i>Plant Disease</i> , 2021, 105, 1233.	1.4	0
8	Metagenomic analysis of virome cross-talk between cultivated <i>Solanum lycopersicum</i> and wild <i>Solanum nigrum</i> . <i>Virology</i> , 2020, 540, 38-44.	2.4	31
9	Molecular Viral Diagnosis and Sanitation of Yam Genetic Resources: Implications for Safe Yam Germplasm Exchange. <i>Viruses</i> , 2020, 12, 1101.	3.3	16
10	Yam asymptomatic virus 1, a novel virus infecting yams (<i>Dioscorea</i> spp.) with significant prevalence in a germplasm collection. <i>Archives of Virology</i> , 2020, 165, 2653-2657.	2.1	10
11	Molecular diversity of grapevine Kizil Sapak virus and implications for its detection. <i>Archives of Virology</i> , 2020, 165, 1849-1853.	2.1	1
12	Unravelling the virome in birch: RNA-Seq reveals a complex of known and novel viruses. <i>PLoS ONE</i> , 2020, 15, e0221834.	2.5	15
13	Complete genome sequence of almond luteovirus 1, a novel luteovirus infecting almond. <i>Archives of Virology</i> , 2020, 165, 2123-2126.	2.1	2
14	Characterization of the virome of shallots affected by the shallot mild yellow stripe disease in France. <i>PLoS ONE</i> , 2019, 14, e0219024.	2.5	7
15	Phytovirome Analysis of Wild Plant Populations: Comparison of Double-Stranded RNA and Virion-Associated Nucleic Acid Metagenomic Approaches. <i>Journal of Virology</i> , 2019, 94, .	3.4	29
16	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> , 2019, 164, 2193-2196.	2.1	7
17	Title is missing!. , 2019, 14, e0219024.		0
18	Title is missing!. , 2019, 14, e0219024.		0

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19	Title is missing!. , 2019, 14, e0219024.		0
20	Title is missing!. , 2019, 14, e0219024.		0
21	Viral Double-Stranded RNAs (dsRNAs) from Plants: Alternative Nucleic Acid Substrates for High-Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1746, 45-53.	0.9	47
22	Status of potato viruses in Tunisia and molecular characterization of Tunisian Potato Virus X (PVX) isolates. <i>European Journal of Plant Pathology</i> , 2018, 151, 735-744.	1.7	2
23	Complete genome sequence of lettuce chardovirus 1 isolated from cultivated lettuce in France. <i>Archives of Virology</i> , 2018, 163, 2543-2545.	2.1	6
24	Metagenomicâ€based impact study of transgenic grapevine rootstock on its associated virome and soil bacteriome. <i>Plant Biotechnology Journal</i> , 2018, 16, 208-220.	8.3	31
25	Molecular characterization of a novel fusarivirus infecting the plant-pathogenic fungus <i>Neofusicoccum luteum</i> . <i>Archives of Virology</i> , 2018, 163, 559-562.	2.1	10
26	Determination of the complete genomic sequence of grapevine virus H, a novel vitivirus infecting grapevine. <i>Archives of Virology</i> , 2018, 163, 277-280.	2.1	36
27	High-Throughput Sequencing Reveals <i>Cyclamen persicum</i> Mill. as a Natural Host for Fig Mosaic Virus. <i>Viruses</i> , 2018, 10, 684.	3.3	16
28	Grapevine virus T diversity as revealed by full-length genome sequences assembled from high-throughput sequence data. <i>PLoS ONE</i> , 2018, 13, e0206010.	2.5	19
29	High-Throughput Sequencing and the Viromic Study of Grapevine Leaves: From the Detection of Grapevine-Infecting Viruses to the Description of a New Environmental Tymovirales Member. <i>Frontiers in Microbiology</i> , 2018, 9, 1782.	3.5	60
30	Genome characterization of a divergent isolate of the mycovirus <i>Botrytis virus F</i> from a grapevine metagenome. <i>Archives of Virology</i> , 2018, 163, 3181-3183.	2.1	5
31	Molecular Characterization of a Novel Species of Capillovirus from Japanese Apricot (<i>Prunus mume</i>). <i>Viruses</i> , 2018, 10, 144.	3.3	15
32	High-Throughput Sequencing Reveals Further Diversity of Little Cherry Virus 1 with Implications for Diagnostics. <i>Viruses</i> , 2018, 10, 385.	3.3	19
33	A novel badnavirus discovered from <i>Betula</i> sp. affected by birch leaf-roll disease. <i>PLoS ONE</i> , 2018, 13, e0193888.	2.5	19
34	Determination of the complete genomic sequence of <i>Neofusicoccum luteum</i> mitovirus 1 (NLMV1), a novel mitovirus associated with a phytopathogenic <i>Botryosphaeriaceae</i> . <i>Archives of Virology</i> , 2017, 162, 2477-2480.	2.1	9
35	Two novel Alphaflexiviridae members revealed by deep sequencing of the Vanilla (<i>Orchidaceae</i>) virome. <i>Archives of Virology</i> , 2017, 162, 3855-3861.	2.1	13
36	Identification of a viroid-like RNA in a lychee Transcriptome Shotgun Assembly. <i>Virus Research</i> , 2017, 240, 1-7.	2.2	12

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37	First Report of Nectarine stem pitting-associated virus Infecting <i>Prunus mume</i> in Japan. Plant Disease, 2017, 101, 393-393.	1.4	21
38	Classical and next generation sequencing approaches unravel Bymovirus diversity in barley crops in France. PLoS ONE, 2017, 12, e0188495.	2.5	15
39	First Report of <i>American plum line pattern virus</i> Infecting Flowering Cherry (<i>Prunus</i>) Tj ETQq1 1 0.784314 ^{1.4} /Overlock 10	1.4	7
40	First Report of <i>Kalanchoe mosaic virus</i> and <i>Kalanchoe latent virus</i> Infecting Ghost Plant (<i>Graptopetalum paraguayense</i>) in Italy. Plant Disease, 2017, 101, 1560-1560.	1.4	5
41	Beet western yellows virus infects the carnivorous plant <i>Nepenthes mirabilis</i> . Archives of Virology, 2016, 161, 2273-2278.	2.1	6
42	Molecular characterization and prevalence of two capulaviruses: Alfalfa leaf curl virus from France and <i>Euphorbia caput-medusae</i> latent virus from South Africa. Virology, 2016, 493, 142-153.	2.4	40
43	Complete genomic sequence of barley (<i>Hordeum vulgare</i>) endornavirus (HvEV) determined by next-generation sequencing. Archives of Virology, 2016, 161, 741-743.	2.1	18
44	First Report of <i>Little cherry virus 1</i> on Plum in France. Plant Disease, 2016, 100, 2544.	1.4	11
45	New Insights into Asian <i>Prunus</i> Viruses in the Light of NGS-Based Full Genome Sequencing. PLoS ONE, 2016, 11, e0146420.	2.5	26
46	Characterization of New Isolates of Apricot vein clearing-associated virus and of a New <i>Prunus</i> -Infecting Virus: Evidence for Recombination as a Driving Force in Betaflexiviridae Evolution. PLoS ONE, 2015, 10, e0129469.	2.5	40
47	Complete Nucleotide Sequence of <i>Artichoke latent virus</i> Shows it to be a Member of the Genus <i>Macluravirus</i> in the Family <i>Potyviridae</i> . Phytopathology, 2015, 105, 1155-1160.	2.2	15
48	Characterization by Deep Sequencing of <i>Prunus</i> virus T, a Novel <i>Tepovirus</i> Infecting <i>Prunus</i> Species. Phytopathology, 2015, 105, 135-140.	2.2	41
49	Molecular characterization of yam virus X, a new potexvirus infecting yams (<i>Dioscorea</i> spp) and evidence for the existence of at least three distinct potexviruses infecting yams. Archives of Virology, 2014, 159, 3421-3426.	2.1	21
50	Characterization by Deep Sequencing of Divergent <i>Plum bark necrosis stem pitting-associated virus</i> (PBNSPaV) Isolates and Development of a Broad-Spectrum PBNSPaV Detection Assay. Phytopathology, 2014, 104, 660-666.	2.2	41
51	Adaptation of <i>Lettuce mosaic virus</i> to <i>Catharanthus roseus</i> Involves Mutations in the Central Domain of the VPg. Molecular Plant-Microbe Interactions, 2014, 27, 491-497.	2.6	11
52	Partial sequence of a new Partitivirus-infecting <i>Podosphaera tridactyla</i> , the <i>Prunus</i> powdery mildew agent. Virus Genes, 2013, 46, 199-200.	1.6	2
53	Association of Little cherry virus 1 (LChV1) with the Shirofugen Stunt Disease and Characterization of the Genome of a Divergent LChV1 Isolate. Phytopathology, 2013, 103, 293-298.	2.2	83
54	Distribution of Barley yellow dwarf virus-PAV in the Sub-Antarctic Kerguelen Islands and Characterization of Two New Luteovirus Species. PLoS ONE, 2013, 8, e67231.	2.5	27

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55	Characterization of Prunus-infecting Apricot latent virus-like Foveaviruses: Evolutionary and taxonomic implications. <i>Virus Research</i> , 2011, 155, 440-445.	2.2	27
56	Strategies to facilitate the development of uncloned or cloned infectious full-length viral cDNAs: Apple chlorotic leaf spot virus as a case study. <i>Virology Journal</i> , 2011, 8, 488.	3.4	33
57	Multiple Coat Protein Mutations Abolish Recognition of <i>Pepino mosaic potexvirus</i> (PepMV) by the Potato <i>Rx</i> Resistance Gene in Transgenic Tomatoes. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 376-383.	2.6	26
58	Polyvalent Degenerate Oligonucleotides Reverse Transcription-Polymerase Chain Reaction: A Polyvalent Detection and Characterization Tool for Trichoviruses, Capilloviruses, and Foveaviruses. <i>Phytopathology</i> , 2005, 95, 617-625.	2.2	103
59	Construction of replicative and integrative plasmids for setting up the in vivo expression technology in <i>Helicobacter pylori</i> . <i>Plasmid</i> , 2004, 51, 101-107.	1.4	1
60	Characterization of the genes <i>rdxA</i> and <i>frxA</i> involved in metronidazole resistance in <i>Helicobacter pylori</i> . <i>Research in Microbiology</i> , 2003, 154, 137-144.	2.1	71
61	Natural History of <i>Helicobacter hepaticus</i> Infection in Conventional A/J Mice, with Special Reference to Liver Involvement. <i>Infection and Immunity</i> , 2003, 71, 3667-3672.	2.2	30
62	New Pathogenicity Marker Found in the Plasticity Region of the <i>Helicobacter pylori</i> Genome. <i>Journal of Clinical Microbiology</i> , 2003, 41, 1651-1655.	3.9	64
63	Identification of strain-specific genes located outside the plasticity zone in nine clinical isolates of <i>Helicobacter pylori</i> b bThe GenBank accession numbers for the <i>H. pylori</i> sequences reported in this paper are AF326599-326607 for region A, AF326608-326616 for region B, AF326617-326625 for 1.8 region C, AF326626-326634 for region D, AF327212-327220 for region E, AF328909-32891. <i>Microbiology (United Kingdom)</i> , 2002, 148, 3671-3680.		22
64	Discriminatory Power of RAPD, PCR-RFLP and Southern Blot Analyses of <i>ureCD</i> or <i>ureA</i> Gene Probes on <i>Helicobacter pylori</i> Isolates. <i>Zeitschrift Fur Naturforschung - Section C Journal of Biosciences</i> , 2002, 57, 516-521.	1.4	4
65	<i>cagA</i> Status and Eradication Treatment Outcome of Anti- <i>Helicobacter pylori</i> Triple Therapies in Patients with Nonulcer Dyspepsia. <i>Journal of Clinical Microbiology</i> , 2001, 39, 1319-1322.	3.9	71
66	Composition and Gene Expression of the <i>cag</i> Pathogenicity Island in <i>Helicobacter pylori</i> Strains Isolated from Gastric Carcinoma and Gastritis Patients in Costa Rica. <i>Infection and Immunity</i> , 2001, 69, 1902-1908.	2.2	52
67	Detection of <i>Helicobacter</i> species in the liver of patients with and without primary liver carcinoma. <i>Cancer</i> , 2000, 89, 1431-1439.	4.1	125
68	Distribution of Open Reading Frames of Plasticity Region of Strain J99 in <i>Helicobacter pylori</i> Strains Isolated from Gastric Carcinoma and Gastritis Patients in Costa Rica. <i>Infection and Immunity</i> , 2000, 68, 6240-6249.	2.2	80
69	Rapid Detection, by PCR and Reverse Hybridization, of Mutations in the <i>Helicobacter pylori</i> 23S rRNA Gene, Associated with Macrolide Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 1999, 43, 1779-1782.	3.2	73
70	<i>Helicobacter</i> Species Colonizing Pig Stomach: Molecular Characterization and Determination of Prevalence. <i>Applied and Environmental Microbiology</i> , 1999, 65, 4672-4676.	3.1	25
71	Human Embryonic Gastric Xenografts in Nude Mice: a New Model of <i>Helicobacter pylori</i> Infection. <i>Infection and Immunity</i> , 1999, 67, 1798-1805.	2.2	25
72	Metabolism and Genetics of <i>Helicobacter pylori</i> : the Genome Era. <i>Microbiology and Molecular Biology Reviews</i> , 1999, 63, 642-674.	6.6	172