

# 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	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
2	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
3	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
4	Association of Little cherry virus 1 (LChV1) with the Shirofugen Stunt Disease and Characterization of the Genome of a Divergent LChV1 Isolate. <i>Phytopathology</i> , 2013, 103, 293-298.	2.2	83
5	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
6	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
7	<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
8	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
9	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
10	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
11	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
12	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
13	Characterization by Deep Sequencing of Divergent Plum bark necrosis stem pitting-associated virus (PBNSPaV) Isolates and Development of a Broad-Spectrum PBNSPaV Detection Assay. <i>Phytopathology</i> , 2014, 104, 660-666.	2.2	41
14	Characterization by Deep Sequencing of Prunus virus T, a Novel Tepovirus Infecting Prunus Species. <i>Phytopathology</i> , 2015, 105, 135-140.	2.2	41
15	Characterization of New Isolates of Apricot vein clearing-associated virus and of a New Prunus-Infecting Virus: Evidence for Recombination as a Driving Force in Betaflexiviridae Evolution. <i>PLoS ONE</i> , 2015, 10, e0129469.	2.5	40
16	Molecular characterization and prevalence of two capulaviruses: Alfalfa leaf curl virus from France and Euphorbia caput-medusae latent virus from South Africa. <i>Virology</i> , 2016, 493, 142-153.	2.4	40
17	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
18	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

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19	Metagenomic-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
20	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
21	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
22	Phytovirus 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
23	Characterization of <i>Prunus</i> -infecting Apricot latent virus-like Foveaviruses: Evolutionary and taxonomic implications. <i>Virus Research</i> , 2011, 155, 440-445.	2.2	27
24	Distribution of Barley yellow dwarf virus-PAV in the Sub-Antarctic Kerguelen Islands and Characterization of Two New Luteovirus Species. <i>PLoS ONE</i> , 2013, 8, e67231.	2.5	27
25	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
26	New Insights into Asian <i>Prunus</i> Viruses in the Light of NGS-Based Full Genome Sequencing. <i>PLoS ONE</i> , 2016, 11, e0146420.	2.5	26
27	<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
28	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
29	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 for region A, AF326607 for region A, AF326608 for region B, AF326617 for region B, AF326625 for region C, AF326626 for region C, AF326634 for region D, AF327212 for region D, AF327220 for region E, AF328909 for region E, AF328911 for region E. <i>Microbiology (United Kingdom)</i> , 2002, 148, 3671-3680.		22
30	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. <i>Archives of Virology</i> , 2014, 159, 3421-3426.	2.1	21
31	First Report of Nectarine stem pitting-associated virus Infecting <i>Prunus mume</i> in Japan. <i>Plant Disease</i> , 2017, 101, 393-393.	1.4	21
32	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
33	High-Throughput Sequencing Reveals Further Diversity of Little Cherry Virus 1 with Implications for Diagnostics. <i>Viruses</i> , 2018, 10, 385.	3.3	19
34	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
35	Complete genomic sequence of barley ( <i>Hordeum vulgare</i> ) endornavirus (HvEV) determined by next-generation sequencing. <i>Archives of Virology</i> , 2016, 161, 741-743.	2.1	18
36	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

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37	Molecular Viral Diagnosis and Sanitation of Yam Genetic Resources: Implications for Safe Yam Germplasm Exchange. <i>Viruses</i> , 2020, 12, 1101.	3.3	16
38	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> . <i>Phytopathology</i> , 2015, 105, 1155-1160.	2.2	15
39	Molecular Characterization of a Novel Species of Capillovirus from Japanese Apricot ( <i>Prunus mume</i> ). <i>Viruses</i> , 2018, 10, 144.	3.3	15
40	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
41	Classical and next generation sequencing approaches unravel Bymovirus diversity in barley crops in France. <i>PLoS ONE</i> , 2017, 12, e0188495.	2.5	15
42	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
43	Identification of a viroid-like RNA in a lychee Transcriptome Shotgun Assembly. <i>Virus Research</i> , 2017, 240, 1-7.	2.2	12
44	Adaptation of <i>Lettuce mosaic virus</i> to <i>Catharanthus roseus</i> Involves Mutations in the Central Domain of the VPg. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 491-497.	2.6	11
45	First Report of <i>Little cherry virus 1</i> on Plum in France. <i>Plant Disease</i> , 2016, 100, 2544.	1.4	11
46	First Report of Grapevine Virus L Infecting Grapevine in Southeast France. <i>Plant Disease</i> , 2022, 106, .	1.4	11
47	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
48	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
49	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
50	Characterization of the Mycovirome of the Phytopathogenic Fungus, <i>Neofusicoccum parvum</i> . <i>Viruses</i> , 2021, 13, 375.	3.3	9
51	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
52	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
53	First Report of <i>American plum line pattern virus</i> Infecting Flowering Cherry ( <i>Prunus</i> ) Tj ETQq1 1 0.784314 <a href="#">rgBT /Overlock 10 T</a>	1.4	7
54	Beet western yellows virus infects the carnivorous plant <i>Nepenthes mirabilis</i> . <i>Archives of Virology</i> , 2016, 161, 2273-2278.	2.1	6

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55	Complete genome sequence of lettuce chardovirus 1 isolated from cultivated lettuce in France. Archives of Virology, 2018, 163, 2543-2545.	2.1	6
56	Sixty Years from the First Disease Description, a Novel Badnavirus Associated with Chestnut Mosaic Disease. Phytopathology, 2021, 111, 1051-1058.	2.2	6
57	Genome characterization of a divergent isolate of the mycovirus Botrytis virus F from a grapevine metagenome. Archives of Virology, 2018, 163, 3181-3183.	2.1	5
58	First Report of Alfalfa Mosaic Virus in Chayote in Italy. Plant Disease, 2021, 105, 698-698.	1.4	5
59	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
60	Discriminatory Power of RAPD,PCR-RFLP and Southern Blot Analyses of ureCD or ureA Gene Probes on Helicobacter pylori Isolates. Zeitschrift Fur Naturforschung - Section C Journal of Biosciences, 2002, 57, 516-521.	1.4	4
61	Host range and molecular variability of the sadwavirus dioscorea mosaic associated virus. Archives of Virology, 2022, 167, 917-922.	2.1	3
62	Molecular characterization of Cordyline virus 1 isolates infecting yam (Dioscorea spp). Archives of Virology, 2022, 167, 2275-2280.	2.1	3
63	Partial sequence of a new Partitivirus-infecting Podosphaera tridactyla, the Prunus powdery mildew agent. Virus Genes, 2013, 46, 199-200.	1.6	2
64	Status of potato viruses in Tunisia and molecular characterization of Tunisian Potato Virus X (PVX) isolates. European Journal of Plant Pathology, 2018, 151, 735-744.	1.7	2
65	Complete genome sequence of almond luteovirus 1, a novel luteovirus infecting almond. Archives of Virology, 2020, 165, 2123-2126.	2.1	2
66	Construction of replicative and integrative plasmids for setting up the in vivo expression technology in Helicobacter pylori. Plasmid, 2004, 51, 101-107.	1.4	1
67	Molecular diversity of grapevine Kizil Sapak virus and implications for its detection. Archives of Virology, 2020, 165, 1849-1853.	2.1	1
68	First Report of Lettuce Necrotic Leaf Curl Virus Infecting Cultivated Lettuce in France. Plant Disease, 2021, 105, 1233.	1.4	0
69	Title is missing!. , 2019, 14, e0219024.		0
70	Title is missing!. , 2019, 14, e0219024.		0
71	Title is missing!. , 2019, 14, e0219024.		0
72	Title is missing!. , 2019, 14, e0219024.		0