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List of Publications by Year in descending order

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414414 361413 33 1,438 20 32 citations g-index h-index papers 33 33 33 1413 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	A new grapevine virus discovered by deep sequencing of virus- and viroid-derived small RNAs in Cv Pinot gris. Virus Research, 2012, 163, 262-268.	2.2	227
2	Roles and Programming of Arabidopsis ARGONAUTE Proteins during Turnip Mosaic Virus Infection. PLoS Pathogens, $2015,11,e1004755.$	4.7	175
3	Transcriptome profiling of two olive cultivars in response to infection by the CoDiRO strain of Xylella fastidiosa subsp. pauca. BMC Genomics, 2016, 17, 475.	2.8	118
4	Deep sequencing analysis of viral short RNAs from an infected Pinot Noir grapevine. Virology, 2010, 408, 49-56.	2.4	109
5	Identification and Characterization of <i>Citrus yellow vein clearing virus</i> , A Putative New Member of the Genus <i>Mandarivirus</i> . Phytopathology, 2012, 102, 1168-1175.	2.2	90
6	Genetic Variability of <i>Grapevine Pinot gris virus</i> and Its Association with Grapevine Leaf Mottling and Deformation. Phytopathology, 2015, 105, 555-563.	2.2	79
7	Genome-Wide Analysis Provides Evidence on the Genetic Relatedness of the Emergent <i>Xylella fastidiosa</i> Genotype in Italy to Isolates from Central America. Phytopathology, 2017, 107, 816-827.	2.2	61
8	Transmission of grapevine Pinot gris virus by Colomerus vitis (Acari: Eriophyidae) to grapevine. Archives of Virology, 2016, 161, 2595-2599.	2.1	60
9	Emergence of a Plant Pathogen in Europe Associated with Multiple Intercontinental Introductions. Applied and Environmental Microbiology, 2020, 86, .	3.1	57
10	Draft Genome Sequence of the Xylella fastidiosa CoDiRO Strain. Genome Announcements, 2015, 3, .	0.8	51
11	Differences in the Endophytic Microbiome of Olive Cultivars Infected by Xylella fastidiosa across Seasons. Pathogens, 2020, 9, 723.	2.8	39
12	Ionomic Differences between Susceptible and Resistant Olive Cultivars Infected by Xylella fastidiosa in the Outbreak Area of Salento, Italy. Pathogens, 2019, 8, 272.	2.8	37
13	Complete Genome Sequence of the Olive-Infecting Strain Xylella fastidiosa subsp. <i>pauca</i> De Donno. Genome Announcements, 2017, 5, .	0.8	34
14	Identification and Characterization of <i>Citrus tristeza virus</i> Isolates Breaking Resistance in Trifoliate Orange in California. Phytopathology, 2017, 107, 901-908.	2.2	33
15	Molecular and biological characterization of a novel mild strain of citrus tristeza virus in California. Archives of Virology, 2018, 163, 1795-1804.	2.1	31
16	Deep sequencing and analysis of small RNAs in sweet orange grafted on sour orange infected with two citrus tristeza virus isolates prevalent in Sicily. Archives of Virology, 2015, 160, 2583-2589.	2.1	28
17	Deep-sequencing analysis of an apricot tree with vein clearing symptoms reveals the presence of a novel betaflexivirus. Virus Research, 2014, 181, 1-5.	2.2	27
18	Identification and characterization of an isolate of apple green crinkle associated virus involved in a severe disease of quince (Cydonia oblonga, Mill.). Archives of Virology, 2017, 162, 299-306.	2.1	25

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19	Draft Genome Resources of Two Strains ("ESVL―and "IVIA5901â€) of <i>Xylella fastidiosa</i> Associated with Almond Leaf Scorch Disease in Alicante, Spain. Phytopathology, 2019, 109, 219-221.	2.2	24
20	Identification and characterization of privet leaf blotchâ€associated virus, a novel <i>idaeovirus</i> . Molecular Plant Pathology, 2017, 18, 925-936.	4.2	22
21	<i>Xylella fastidiosa</i> >'s relationships: the bacterium, the host plants, and the plant microbiome. New Phytologist, 2022, 234, 1598-1605.	7.3	17
22	Introduction and adaptation of an emerging pathogen to olive trees in Italy. Microbial Genomics, 2021 , 7 , .	2.0	14
23	Draft Genome Sequence of Xylella fastidiosa subsp. <i>fastidiosa</i> Strain IVIA5235, Isolated from Prunus avium in Mallorca Island, Spain. Microbiology Resource Announcements, 2018, 7, .	0.6	13
24	Infections of the Xylella fastidiosa subsp. pauca Strain "De Donno―in Alfalfa (Medicago sativa) Elicits an Overactive Immune Response. Plants, 2019, 8, 335.	3.5	12
25	An assay for the detection of grapevine leafroll-associated virus 3 using a single-chain fragment variable antibody. Archives of Virology, 2009, 154, 19-26.	2.1	11
26	Draft Genome Sequence Resources of Three Strains (TOS4, TOS5, and TOS14) of Xylella fastidiosa Infecting Different Host Plants in the Newly Discovered Outbreak in Tuscany, Italy. Phytopathology, 2019, 109, 1516-1518.	2.2	11
27	Draft Genome Sequence of CO33, a Coffee-Infecting Isolate of Xylella fastidiosa. Genome Announcements, 2015, 3, .	0.8	10
28	Detection and molecular characterization of a Grapevine Roditis leaf discoloration-associated virus (GRLDaV) variant in an autochthonous grape from Apulia (Italy). Virus Genes, 2016, 52, 428-431.	1.6	9
29	Grapevine Pinot gris virus variants in vines with chlorotic mottling and leaf deformation. Journal of Plant Pathology, 2020, 102, 531-531.	1.2	8
30	Coding-Complete Genome Sequence of a <i>Black Queen Cell Virus</i> Isolate from Honey Bees (Apis) Tj ETQq0 0) 8.gBT /C	yerlock 10 ⁻
31	Small RNA Isolation from Tissues of Grapevine and Woody Plants. Methods in Molecular Biology, 2018, 1746, 27-36.	0.9	2
32	Identification and Characterization of Resistance-Breaking (RB) Isolates of Citrus tristeza virus. Methods in Molecular Biology, 2019, 2015, 105-126.	0.9	1
33	DEEP SEQUENCING OF SMALL RNAS FROM CITRUS AFFECTED BY GRAFT-TRANSMISSIBLE DISEASES OF UNKNOWN AETIOLOGY LEADS TO DISCOVERY OF TWO NOVEL VIRUSES. Acta Horticulturae, 2015, , 817-824.	0.2	O