

Mohsen Mehrvar

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7680432/publications.pdf>

Version: 2024-02-01

26
papers

195
citations

1163117

8
h-index

1125743

13
g-index

27
all docs

27
docs citations

27
times ranked

203
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular characterization of two highly divergent Iranian johnsongrass mosaic virus isolates from <i>Zea mays</i> . <i>VirusDisease</i> , 2021, 32, 155-160.	2.0	2
2	Complete Genomic Characterization of Two Beet Soil-Borne Virus Isolates from Turkey: Implications of Comparative Analysis of Genome Sequences. <i>Plant Pathology Journal</i> , 2021, 37, 152-161.	1.7	1
3	Analysis of the molecular and biological variability of Zucchini yellow mosaic virus isolates from Iran and Iraq. <i>Gene</i> , 2021, 788, 145674.	2.2	1
4	Identification of garlic-infecting leek yellow stripe virus through deep-sequencing analyses from Iran. <i>VirusDisease</i> , 2021, 32, 595-600.	2.0	1
5	Whole genome characterization of wisteria vein mosaic virus from Iran and its relationship to other members of bean common mosaic virus group. <i>3 Biotech</i> , 2021, 11, 407.	2.2	2
6	Whole-Genome Characterization of Alfalfa Mosaic Virus Obtained from Metagenomic Analysis of <i>Vinca minor</i> and <i>Wisteria sinensis</i> in Iran: with Implications for the Genetic Structure of the Virus. <i>Plant Pathology Journal</i> , 2021, 37, 619-631.	1.7	6
7	Analysis of the complete genome sequence of cucumber mosaic virus from <i>Vinca minor</i> and <i>Wisteria sinensis</i> in Iran. <i>Journal of Plant Pathology</i> , 2020, 102, 1263-1268.	1.2	1
8	Distribution and phylogenetic analysis of the 3'UTR and coat protein gene of Iranian Beet black scorch virus. <i>Journal of Plant Diseases and Protection</i> , 2019, 126, 535-542.	2.9	0
9	Genetic variability and molecular evolution of Bean common mosaic virus populations in Iran: comparison with the populations in the world. <i>European Journal of Plant Pathology</i> , 2019, 154, 673-690.	1.7	10
10	Identification of the experimental herbaceous host range of the Apscaviroids infecting citrus species. <i>Acta Virologica</i> , 2019, 63, 415-422.	0.8	0
11	Identification and characterization of a phytoplasma associated with black locust yellow disease in two provinces of Iran. <i>Crop Protection</i> , 2018, 110, 261-268.	2.1	7
12	Genetic diversity and biological characterization of sugarcane streak mosaic virus isolates from Iran. <i>VirusDisease</i> , 2018, 29, 316-323.	2.0	7
13	First report of <i>Wisteria vein mosaic virus</i> on <i>Wisteria sinensis</i> in Iran. <i>New Disease Reports</i> , 2018, 38, 18-18.	0.8	4
14	Nucleotide sequence analyses of coat protein gene of peanut stunt virus isolates from alfalfa and different hosts show a new tentative subgroup from Iran. <i>VirusDisease</i> , 2017, 28, 295-302.	2.0	7
15	Iranian johnsongrass mosaic virus: the complete genome sequence, molecular and biological characterization, and comparison of coat protein gene sequences. <i>Virus Genes</i> , 2017, 53, 77-88.	1.6	13
16	Comparative genetic diversity of potato virus Y populations based on coat protein gene. <i>Acta Virologica</i> , 2017, 61, 161-174.	0.8	3
17	Dynamics of the population structure and genetic variability within Iranian isolates of grapevine fanleaf virus: evidence for polyphyletic origin. <i>Acta Virologica</i> , 2017, 61, 324-335.	0.8	2
18	Molecular characterization of two sugarcane streak mosaic virus isolates from Iran with emphasis on its population structure. <i>Acta Virologica</i> , 2017, 61, 428-437.	0.8	3

#	ARTICLE	IF	CITATIONS
19	Occurrence and Evolutionary Analysis of Coat Protein Gene Sequences of Iranian Isolates of Sugarcane mosaic virus. <i>Plant Pathology Journal</i> , 2017, 33, 296-306.	1.7	25
20	The complete genome sequences of two naturally occurring recombinant isolates of Sugarcane mosaic virus from Iran. <i>Virus Genes</i> , 2016, 52, 270-280.	1.6	22
21	Molecular variability in the cysteine rich protein of potato virus M. <i>VirusDisease</i> , 2015, 26, 117-122.	2.0	3
22	Genetic structure and molecular variability of potato virus M populations. <i>Archives of Virology</i> , 2014, 159, 2081-2090.	2.1	13
23	Growth analysis of rhizomania infected and healthy sugar beet. <i>Journal of Crop Science and Biotechnology</i> , 2014, 17, 59-69.	1.5	4
24	Diversity of Beet curly top Iran virus isolated from different hosts in Iran. <i>Virus Genes</i> , 2013, 46, 571-575.	1.6	29
25	Iranian beet necrotic yellow vein virus (BNYVV): pronounced diversity of the p25 coding region in A-type BNYVV and identification of P-type BNYVV lacking a fifth RNA species. <i>Archives of Virology</i> , 2009, 154, 501-506.	2.1	18
26	A full-length infectious clone of beet soil-borne virus indicates the dispensability of the RNA-2 for virus survival in planta and symptom expression on <i>Chenopodium quinoa</i> leaves. <i>Journal of General Virology</i> , 2009, 90, 3051-3056.	2.9	11