P Lava Kumar

List of Publications by Year
in descending order

108	4,344	159585 30	128289 60
papers	citations	h-index	g-index

110	110	110	3718
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	First Report of Banana Bunchy Top Virus in Banana and Plantain (Musa spp.) in Tanzania. Plant Disease, 2022, 106, 1312.	1.4	8
2	Toolbox for Working with Root, Tuber, and Banana Seed Systems. , 2022, , 319-352.		4
3	Transforming Yam Seed Systems in West Africa. , 2022, , 421-451.		1
4	Innovative Digital Technologies to Monitor and Control Pest and Disease Threats in Root, Tuber, and Banana (RT&B) Cropping Systems: Progress and Prospects. , 2022, , 261-288.		4
5	Commercially Sustainable Cassava Seed Systems in Africa. , 2022, , 453-482.		4
6	Identification of QTLs Controlling Resistance to Anthracnose Disease in Water Yam (Dioscorea alata). Genes, 2022, 13, 347.	2.4	4
7	The role of CGIAR Germplasm Health Units in averting endemic crop diseases: the example of rice blast in Bangladesh. CABI Agriculture and Bioscience, 2022, 3, .	2.4	1
8	A newly emerging alphasatellite affects banana bunchy top virus replication, transcription, siRNA production and transmission by aphids. PLoS Pathogens, 2022, 18, e1010448.	4.7	11
9	Musa Germplasm A and B Genomic Composition Differentially Affects Their Susceptibility to Banana Bunchy Top Virus and Its Aphid Vector, Pentalonia nigronervosa. Plants, 2022, 11, 1206.	3.5	10
10	Homing in on Endogenous Badnaviral Elements: Development of Multiplex PCR-DGGE for Detection and Rapid Identification of Badnavirus Sequences in Yam Germplasm. Frontiers in Plant Science, 2022, 13, .	3.6	1
11	Sustainable management of transboundary pests requires holistic and inclusive solutions. Food Security, 2022, 14, 1449-1457.	5.3	10
12	Disease incidence and severity in cowpea lines evaluated for resistance to single and multiple infections of endemic viruses in Nigeria. Journal of Crop Improvement, 2021, 35, 427-452.	1.7	6
13	â€œBreaking through the 40% adoption ceiling: Mind the seed system gaps.â€•A perspective on seed systems research for development in One CGIAR. Outlook on Agriculture, 2021, 50, 5-12.	3.4	35
14	Phytosanitary Interventions for Safe Global Germplasm Exchange and the Prevention of Transboundary Pest Spread: The Role of CGIAR Germplasm Health Units. Plants, 2021, 10, 328.	3.5	35
15	Validation of Diagnostic Markers for Streak Virus Disease Resistance in Maize. Agriculture (Switzerland), 2021, 11, 130.	3.1	6
16	Gender Roles in Sourcing and Sharing of Banana Planting Material in Communities with and without Banana Bunchy Top Disease in Nigeria. Sustainability, 2021, 13, 3310.	3.2	9
17	Inheritance of Pod Length and Other Yield Components in Two Cowpea and Yard-Long Bean Crosses. Agronomy, 2021, 11, 682.	3.0	3
18	First Report of Banana Bunchy Top Virus in Banana (Musa spp.) and Its Eradication in Togo. Plant Disease, 2021, 105, 3312.	1.4	9

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19	Seed Yam Production Using High-Quality Minitubers Derived from Plants Established with Vine Cuttings. Agronomy, 2021, 11, 978.	3.0	9
20	Enhancing farmersâ€™ agency in the global crop commons through use of biocultural community protocols. Agriculture and Human Values, 2021, 38, 579-594.	3.0	12
21	Evidence of expanded diversity in weeds as reservoir host of viruses in pepper fields across southwestern Nigeria. Archives of Phytopathology and Plant Protection, 2021, 54, 2345-2355.	1.3	0
22	How Maize Seed Systems Can Contribute to the Control of Mycotoxigenic Fungal Infection: A Perspective. Agronomy, 2021, 11, 2168.	3.0	5
23	Adoption of Roguing to Contain Banana Bunchy Top Disease in South-East BÃ©nin: Role of Farmersâ€™ Knowledge and Perception. International Journal of Fruit Science, 2020, 20, 720-736.	2.4	9
24	Germplasm Acquisition and Distribution by CGIAR Genebanks. Plants, 2020, 9, 1296.	3.5	31
25	Genotyping-by-Sequencing to Unlock Genetic Diversity and Population Structure in White Yam (Dioscorea rotundata Poir.). Agronomy, 2020, 10, 1437.	3.0	16
26	Global Cropland Connectivity: A Risk Factor for Invasion and Saturation by Emerging Pathogens and Pests. BioScience, 2020, 70, 744-758.	4.9	30
27	Assessment of Yam mild mosaic virus coat protein gene sequence diversity reveals the prevalence of cosmopolitan and African group of isolates in Ghana and Nigeria. Current Plant Biology, 2020, 23, 100156.	4.7	7
28	Quantitative trait loci mapping for resistance to maize streak virus in F2:3 population of tropical maize. Cereal Research Communications, 2020, 48, 195-202.	1.6	3
29	Application of CRISPR/Cas for Diagnosis and Management of Viral Diseases of Banana. Frontiers in Microbiology, 2020, 11, 609784.	3.5	29
30	Tissue culture and next-generation sequencing: A combined approach for detecting yam (Dioscorea) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.5	23
31	Open data kit (ODK) in crop farming: mobile data collection for seed yam tracking in Ibadan, Nigeria. Journal of Crop Improvement, 2019, 33, 605-619.	1.7	9
32	Why interventions in the seed systems of roots, tubers and bananas crops do not reach their full potential. Food Security, 2019, 11, 23-42.	5.3	68
33	Molecular Characterization of a New Virus Species Identified in Yam (Dioscorea spp.) by High-Throughput Sequencing. Plants, 2019, 8, 167.	3.5	20
34	CGIAR Operations under the Plant Treaty Framework. Crop Science, 2019, 59, 819-832.	1.8	22
35	Gender Norms and Their Implications for Banana Production and Recovery in West Africa. Advances in Gender Research, 2019, , 61-75.	0.2	0
36	Detection and diversity of maize yellow mosaic virus infecting maize in Nigeria. VirusDisease, 2019, 30, 538-544.	2.0	6

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37	Monitoring Aspergillus flavus Genotypes in a Multi-Genotype Aflatoxin Biocontrol Product With Quantitative Pyrosequencing. Frontiers in Microbiology, 2019, 10, 2529.	3.5	8
38	Distribution and diversity of viruses infecting yams (Dioscorea spp.) in Cameroon. VirusDisease, 2019, 30, 526-537.	2.0	10
39	Impact of single and double infection with Cucumber mosaic virus and Potato virus Y on growth and yield of pepper. International Journal of Vegetable Science, 2019, 25, 529-541.	1.3	3
40	Prevalence and Genome Characterization of Field Isolates of Sugarcane Mosaic Virus (SCMV) in Nigeria. Plant Disease, 2019, 103, 818-824.	1.4	8
41	Rapid detection of potyviruses from crude plant extracts. Analytical Biochemistry, 2018, 546, 17-22.	2.4	65
42	Chromogenic detection of yam mosaic virus by closed-tube reverse transcription loop-mediated isothermal amplification (CT-RT-LAMP). Archives of Virology, 2018, 163, 1057-1061.	2.1	25
43	First Report of Passion fruit woodiness virus Associated with Passion Fruit Woodiness Disease of Passion Fruit in Nigeria. Plant Disease, 2018, 102, 1181-1181.	1.4	5
44	An EST-SSR based genetic linkage map and identification of QTLs for anthracnose disease resistance in water yam (Dioscorea alata L.). PLoS ONE, 2018, 13, e0197717.	2.5	28
45	Understanding root, tuber, and banana seed systems and coordination breakdown: a multi-stakeholder framework. Journal of Crop Improvement, 2018, 32, 599-621.	1.7	37
46	Mapping of QTLs associated with recovery resistance to streak virus disease in maize. Annals of Agricultural Sciences, 2018, 63, 115-121.	2.9	7
47	Recovering banana production in bunchy top-affected areas in Sub-Saharan Africa: developing gender-responsive approaches. Acta Horticulturae, 2018, , 219-228.	0.2	11
48	Rolling Circle Amplification to Screen Yam Germplasm for Badnavirus Infections and to Amplify and Characterise Novel Badnavirus Genomes. Bio-protocol, 2018, 8, e2672.	0.4	3
49	Comparative Reliability of Screening Parameters for Anthracnose Resistance in Water Yam (Dioscorea alata). Plant Disease, 2017, 101, 209-216.	1.4	11
50	Identification and molecular characterization of a novel sugarcane streak mastrevirus and an isolate of the A-strain of maize streak virus from sugarcane in Nigeria. Archives of Virology, 2017, 162, 597-602.	2.1	14
51	Incidence and diversity of viruses in cowpeas and weeds in the unmanaged farming systems of savanna zones in Nigeria. Archives of Phytopathology and Plant Protection, 2017, 50, 1-12.	1.3	13
52	Morphological and molecular characterisation of Scutellonema species from yam (Dioscorea spp.) and a key to the species ofÂtheÂgenus. Nematology, 2017, 19, 751-787.	0.6	9
53	PCR-DGGE Analysis: Unravelling Complex Mixtures of Badnavirus Sequences Present in Yam Germplasm. Viruses, 2017, 9, 181.	3.3	11
54	Genome sequencing of the staple food crop white Guinea yam enables the development of a molecular marker for sex determination. BMC Biology, 2017, 15, 86.	3.8	114

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55	Diversity of Root-knot Nematodes Associated with Tubers of Yam (Dioscorea spp.) Established Using Isozyme Analysis and Mitochondrial DNA-based Identification. Journal of Nematology, 2017, 49, 177-188.	0.9	16
56	First Report of Outbreaks of the Fall Armyworm Spodoptera frugiperda (J E Smith) (Lepidoptera,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7	2.5	931
57	A Sequence-Independent Strategy for Amplification and Characterisation of Episomal Badnavirus Sequences Reveals Three Previously Uncharacterised Yam Badnaviruses. Viruses, 2016, 8, 188.	3.3	26
58	Evaluation of isolates of Trichoderma, Pseudomonas and Bacillus species as treatment for the control of post-harvest fungal rot disease of yam (Dioscorea spp.). Archives of Phytopathology and Plant Protection, 2016, 49, 456-470.	1.3	4
59	First Report of Meloidogyne enterolobii Causing Tuber Galling Damage on White Yam (Dioscorea rotundata) in Nigeria. Plant Disease, 2016, 100, 2173.	1.4	10
60	Maize Lethal Necrosis (MLN), an Emerging Threat to Maize-Based Food Security in Sub-Saharan Africa. Phytopathology, 2015, 105, 956-965.	2.2	222
61	Biology, Etiology, and Control of Virus Diseases of Banana and Plantain. Advances in Virus Research, 2015, 91, 229-269.	2.1	73
62	Pigeonpea sterility mosaic virus: a legumeâ€infecting Emaravirus from <scp>S</scp>outh <scp>A</scp>sia. Molecular Plant Pathology, 2015, 16, 775-786.	4.2	61
63	Fine mapping of Msv1, a major QTL for resistance to Maize Streak Virus leads to development of production markers for breeding pipelines. Theoretical and Applied Genetics, 2015, 128, 1839-1854.	3.6	61
64	Diversity, Distribution and Effects on Cassava Cultivars of Cassava Brown Streak Viruses in Malawi. Journal of Phytopathology, 2015, 163, 433-443.	1.0	17
65	Rapid and specific detection of Yam mosaic virus by reverse-transcription recombinase polymerase amplification. Journal of Virological Methods, 2015, 222, 138-144.	2.1	72
66	Cassava Virus Diseases. Advances in Virus Research, 2015, 91, 85-142.	2.1	196
67	Biotechnology Success Stories by the Consultative Group on International Agriculture Research (CGIAR) System. Science Policy Reports, 2014, , 95-114.	0.1	4
68	Tropical Food Legumes. Advances in Virus Research, 2014, 90, 431-505.	2.1	40
69	The association between exposure to aflatoxin, mutation in TP53, infection with hepatitis B virus, and occurrence of liver disease in a selected population in Hyderabad, India. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2014, 766, 23-28.	1.7	9
70	High-resolution mapping of resistance to cassava mosaic geminiviruses in cassava using genotyping-by-sequencing and its implications for breeding. Virus Research, 2014, 186, 87-96.	2.2	143
71	A global alliance declaring war on cassava viruses in Africa. Food Security, 2014, 6, 231-248.	5.3	81
72	The prevalence of badnaviruses in West African yams (Dioscorea cayenensis-rotundata) and evidence of endogenous pararetrovirus sequences in their genomes. Virus Research, 2014, 186, 144-154.	2.2	43

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73	Insertion/deletion polymorphism of the angiotensin-converting enzyme gene and the risk of hypertension among residents of two cities, South-South Nigeria. Advanced Biomedical Research, 2014, 3, 118.	0.5	8
74	Pathogen-derived resistance using a viral nucleocapsid gene confers only partial non-durable protection in peanut against peanut bud necrosis virus. Archives of Virology, 2013, 158, 133-143.	2.1	12
75	Does the informal seed system threaten cowpea seed health?. Crop Protection, 2013, 43, 166-174.	2.1	15
76	A study of the M235T variant of the angiotensinogen gene and hypertension in a sample population of Calabar and Uyo, Nigeria. Egyptian Journal of Medical Human Genetics, 2013, 14, 13-19.	1.0	9
77	Health of farmer-saved maize seed in north-east Nigeria. European Journal of Plant Pathology, 2013, 137, 563-572.	1.7	10
78	Angiotensin II type 1 receptor A1166C gene polymorphism and essential hypertension in Calabar and Uyo cities, Nigeria. Indian Journal of Human Genetics, 2013, 19, 213.	0.7	12
79	First Report of Banana bunchy top virus in Banana and Plantain (Musa spp.) in Nigeria. Plant Disease, 2013, 97, 290-290.	1.4	22
80	Multiplex RT-PCR assays for the simultaneous detection of both RNA and DNA viruses infecting cassava and the common occurrence of mixed infections by two cassava brown streak viruses in East Africa. Journal of Virological Methods, 2012, 179, 176-184.	2.1	53
81	First Report of Mango Malformation Disease Caused by Fusarium tupiense in Senegal. Plant Disease, 2012, 96, 1582-1582.	1.4	26
82	First Report of Leaf Blight of Taro (Colocasia esculenta) Caused by Phytophthora colocasiae in Ghana. Plant Disease, 2012, 96, 292-292.	1.4	24
83	Occurrence of Banana bunchy top virus in banana and plantain (Musa sp.) in Benin. New Disease Reports, 2012, 25, 13-13.	0.8	17
84	Comparing the regional epidemiology of the cassava mosaic and cassava brown streak virus pandemics in Africa. Virus Research, 2011, 159, 161-170.	2.2	276
85	Banana bunchy top virus in sub-Saharan Africa: Investigations on virus distribution and diversity. Virus Research, 2011, 159, 171-182.	2.2	85
86	Isolation and Characterization of Baculoviruses from Three Major Lepidopteran Pests in the Semi-Arid Tropics of India. Indian Journal of Virology: an Official Organ of Indian Virological Society, 2011, 22, 29-36.	0.7	18
87	First Report of Taro (Colocasia esculenta) Leaf Blight Caused by Phytophthora colocasiae in Nigeria. Plant Disease, 2011, 95, 618-618.	1.4	25
88	Two new â€˜legumovirusesâ€™ (genus Begomovirus) naturally infecting soybean in Nigeria. Archives of Virology, 2010, 155, 643-656.	2.1	23
89	Terminal drought-tolerant pearl millet [Pennisetum glaucum (L.) R. Br.] have high leaf ABA and limit transpiration at high vapour pressure deficit. Journal of Experimental Botany, 2010, 61, 1431-1440.	4.8	199
90	First report of the East African cassava mosaic virusâ€Uganda (EACMVâ€UG) infecting cassava (Manihot esculenta) in Cameroon. New Disease Reports, 2010, 21, 22-22.	0.8	21

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91	First report of Banana bunchy top virus in banana and plantain (Musa spp.) in Angola. Plant Pathology, 2009, 58, 402-402.	2.4	5
92	First report of the occurrence of East African cassava mosaic virusâ€Uganda (EACMVâ€UG) in Angola. Plant Pathology, 2009, 58, 402-402.	2.4	14
93	Breeding Peanut for Resistance to Aflatoxin Contamination at ICRISAT. Peanut Science, 2009, 36, 42-49.	0.1	75
94	Occurrence of Banana Bunchy Top Disease Caused by the Banana bunchy top virus on Banana and Plantain (Musa sp.) in Cameroon. Plant Disease, 2009, 93, 1076-1076.	1.4	32
95	Alternate hosts of African cassava mosaic virus and East African cassava mosaic Cameroon virus in Nigeria. Archives of Virology, 2008, 153, 1743-1747.	2.1	56
96	Multiplex PCR for the detection of African cassava mosaic virus and East African cassava mosaic Cameroon virus in cassava. Journal of Virological Methods, 2008, 154, 111-120.	2.1	59
97	First Report of Cucumber mosaic virus in Yams (Dioscorea spp.) in Ghana, Togo, and Republic of Benin in West Africa. Plant Disease, 2008, 92, 833-833.	1.4	11
98	Sources of Resistance to Tobacco streak virus in Wild Arachis (Fabaceae: Papilionoidae) Germplasm. Plant Disease, 2007, 91, 1585-1590.	1.4	25
99	Broad-based resistance to pigeonpea sterility mosaic disease in wild relatives of pigeonpea (Cajanus:) Tj ETQq1 1 0.784314 rgBT /Ove	2.5	35
100	Sterility Mosaic Diseaseâ€"the â€œGreen Plagueâ€•of Pigeonpea: Advances in Understanding the Etiology, Transmission and Control of a Major Virus Disease. Plant Disease, 2004, 88, 436-445.	1.4	38
101	A Novel Mite-Transmitted Virus with a Divided RNA Genome Closely Associated with Pigeonpea Sterility Mosaic Disease. Phytopathology, 2003, 93, 71-81.	2.2	58
102	Transmission of Pigeon pea sterility mosaic virus by the Eriophyid Mite, Aceria cajani (Acari:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 302 T	1.4	64
103	Cytopathology of Plgeonpea sterility mosaic virus in pigeonpea and Nicotiana benthamiana: similarities with those of eriophyid mite-borne agents of undefined aetiology. Annals of Applied Biology, 2002, 140, 87-96.	2.5	42
104	Characterization of a Virus from Pigeonpea with Affinities to Species in the Genus Aureusvirus, Family Tombusviridae. Plant Disease, 2001, 85, 208-215.	1.4	14
105	Resistance to groundnut rosette disease in wild Arachis species. Annals of Applied Biology, 2001, 139, 45-50.	2.5	31
106	Assessment of variation in Aceria cajani using analysis of rDNA ITS regions and scanning electron microscopy: implications for the variability observed in host plant resistance to pigeonpea sterility mosaic disease. Annals of Applied Biology, 2001, 139, 61-73.	2.5	28
107	Identification of Cecidophyopsis mites (Acari: Eriophyidae) based on variable simple sequence repeats of ribosomal DNA internal transcribed spacer-1 sequences via multiplex PCR. Insect Molecular Biology, 1999, 8, 347-357.	2.0	51
108	Inheritance of resistance to three endemic viral diseases of cowpea in Nigeria. Journal of Crop Improvement, 0, , 1-18.	1.7	0