Parwinder Kaur

List of Publications by Year
in descending order

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56 papers	1,215 citations	430874 18 h-index	454955 30 g-index
64 all docs	64 docs citations	64 times ranked	1601 citing authors

#	Article	IF	Citations
1	Chromosome-length genome assemblies of six legume species provide insights into genome organization, evolution, and agronomic traits for crop improvement. Journal of Advanced Research, 2022, 42, 315-329.	9.5	20
2	New vision on the new era of genome study. Functional and Integrative Genomics, 2022, 22, 1-2.	3.5	5
3	Small investments with big returns: environmental genomic bioprospecting of microbial life. Critical Reviews in Microbiology, 2022, 48, 641-655.	6.1	7
4	Investigating the development of diarrhoea through gene expression analysis in sheep genetically resistant to gastrointestinal helminth infection. Scientific Reports, 2022, 12, 2207.	3.3	4
5	Protection against severe infant lower respiratory tract infections by immune training: Mechanistic studies. Journal of Allergy and Clinical Immunology, 2022, 150, 93-103.	2.9	11
6	Chromosome-level genome of Schistosoma haematobium underpins genome-wide explorations of molecular variation. PLoS Pathogens, 2022, 18, e1010288.	4.7	13
7	From rags to enriched: metagenomic insights into ammoniaâ€oxidizing archaea following ammonia enrichment of a denuded oligotrophic soil ecosystem. Environmental Microbiology, 2022, 24, 3097-3110.	3.8	4
8	Microbial Metabolomics Interaction and Ecological Challenges of Trichoderma Species as Biocontrol Inoculant in Crop Rhizosphere. Agronomy, 2022, 12, 900.	3.0	9
9	Chromosome-length genome assembly and linkage map of a critically endangered Australian bird: the helmeted honeyeater. GigaScience, 2022, 11, .	6.4	8
10	Contribution of the Immune Response in the Ileum to the Development of Diarrhoea caused by Helminth Infection: Studies with the Sheep Model. Functional and Integrative Genomics, 2022, 22, 865-877.	3.5	2
11	The Key to the Future Lies in the Past: Insights from Grain Legume Domestication and Improvement Should Inform Future Breeding Strategies. Plant and Cell Physiology, 2022, 63, 1554-1572.	3.1	13
12	Transforming traditional nutrition paradigms with synthetic biology driven microbial production platforms. Current Research in Biotechnology, 2021, 3, 260-268.	3.7	8
13	Delineating the Tnt1 Insertion Landscape of the Model Legume Medicago truncatula cv. R108 at the Hi-C Resolution Using a Chromosome-Length Genome Assembly. International Journal of Molecular Sciences, 2021, 22, 4326.	4.1	13
14	An Improved Protocol for Agrobacterium-Mediated Transformation in Subterranean Clover (Trifolium subterraneum L.). International Journal of Molecular Sciences, 2021, 22, 4181.	4.1	5
15	High-quality reference genome for Clonorchis sinensis. Genomics, 2021, 113, 1605-1615.	2.9	19
16	3D genomics across the tree of life reveals condensin II as a determinant of architecture type. Science, 2021, 372, 984-989.	12.6	132
17	Synthetic Biology towards Improved Flavonoid Pharmacokinetics. Biomolecules, 2021, 11, 754.	4.0	29
18	Developing Bioprospecting Strategies for Bioplastics Through the Large-Scale Mining of Microbial Genomes. Frontiers in Microbiology, 2021, 12, 697309.	3.5	4

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19	Next-Generation Breeding Strategies for Climate-Ready Crops. Frontiers in Plant Science, 2021, 12, 620420.	3.6	61
20	Recent Advances in Heterologous Synthesis Paving Way for Future Green-Modular Bioindustries: A Review With Special Reference to Isoflavonoids. Frontiers in Bioengineering and Biotechnology, 2021, 9, 673270.	4.1	28
21	Mapping the landscape of chromatin dynamics during naÃ¯ve CD4+â€‰T-cell activation. Scientific Reports, 2021, 11, 14101.	3.3	10
22	Genome Sequence of the Fungus Nannizziopsis barbatae, an Emerging Reptile Pathogen. Microbiology Resource Announcements, 2021, 10, .	0.6	2
23	State of Shark and Ray Genomics in an Era of Extinction. Frontiers in Marine Science, 2021, 8, .	2.5	12
24	Microchromosomes are building blocks of bird, reptile, and mammal chromosomes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	84
25	RNA-sequencing based gene expression landscape of guava cv. Allahabad Safeda and comparative analysis to colored cultivars. BMC Genomics, 2020, 21, 484.	2.8	18
26	Status and Potential of Singleâ€Cell Transcriptomics for Understanding Plant Development and Functional Biology. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 97, 997-1006.	1.5	7
27	Airway Epithelial Cell Immunity Is Delayed During Rhinovirus Infection in Asthma and COPD. Frontiers in Immunology, 2020, 11, 974.	4.8	60
28	Morphological diversity within a core collection of subterranean clover (Trifolium subterraneum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	2.5	13
29	Title is missing!. , 2020, 15, e0223699.		0
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33	Title is missing!. , 2020, 15, e0223699.		0
34	Title is missing!. , 2020, 15, e0223699.		0
35	Changes in gene expression during germination reveal pea genotypes with either â€œquiescenceâ€•or â€œescapeâ€•mechanisms of waterlogging tolerance. Plant, Cell and Environment, 2019, 42, 245-258.	5.7	26
36	Waterlogging Tolerance at Germination in Field Pea: Variability, Genetic Control, and Indirect Selection. Frontiers in Plant Science, 2019, 10, 953.	3.6	15

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37	Genetic Diversity Linked to Haplotype Variation in the World Core Collection of Trifolium subterraneum for Boron Toxicity Tolerance Provides Valuable Markers for Pasture Breeding. Frontiers in Plant Science, 2019, 10, 1043.	3.6	2
38	Applications of CRISPR systems in respiratory health: Entering a new â€˜red penâ€™ era in genome editing. Respirology, 2019, 24, 628-637.	2.3	13
39	Globular structures in roots accumulate phosphorus to extremely high concentrations following phosphorus addition. Plant, Cell and Environment, 2019, 42, 1987-2002.	5.7	9
40	Waterlogging tolerance of pea at germination. Journal of Agronomy and Crop Science, 2018, 204, 155-164.	3.5	19
41	Large-Scale Structural Variation Detection in Subterranean Clover Subtypes Using Optical Mapping. Frontiers in Plant Science, 2018, 9, 971.	3.6	10
42	In Vitro-Assisted Compression of Breeding Cycles. , 2018, , 463-486.		5
43	CRISPR-Cas systems: ushering in the new genome editing era. Bioengineered, 2018, 9, 214-221.	3.2	30
44	2,4-D and dicamba resistance mechanisms in wild radish: subtle, complex and population specific?. Annals of Botany, 2018, 122, 627-640.	2.9	22
45	An advanced reference genome of Trifolium subterraneum L. reveals genes related to agronomic performance. Plant Biotechnology Journal, 2017, 15, 1034-1046.	8.3	38
46	Climate Clever Clovers: New Paradigm to Reduce the Environmental Footprint of Ruminants by Breeding Low Methanogenic Forages Utilizing Haplotype Variation. Frontiers in Plant Science, 2017, 8, 1463.	3.6	21
47	Draft genome sequence of subterranean clover, a reference for genus Trifolium. Scientific Reports, 2016, 6, 30358.	3.3	33
48	Mass-spectrometry data for Rhizoctonia solani proteins produced during infection of wheat and vegetative growth. Data in Brief, 2016, 8, 267-271.	1.0	5
49	Proteomic Analysis of Rhizoctonia solani Identifies Infection-specific, Redox Associated Proteins and Insight into Adaptation to Different Plant Hosts. Molecular and Cellular Proteomics, 2016, 15, 1188-1203.	3.8	37
50	Decreasing Electron Flux through the Cytochrome and/or Alternative Respiratory Pathways Triggers Common and Distinct Cellular Responses Dependent on Growth Conditions Â. Plant Physiology, 2014, 167, 228-250.	4.8	85
51	Genetic improvement of subterranean clover (Trifolium subterraneum L.). 1. Germplasm, traits and future prospects. Crop and Pasture Science, 2013, 64, 312.	1.5	82
52	Pre-inoculation with Hyaloperonospora parasitica reduces incubation period and increases severity of disease caused by Albugo candida in a Brassica juncea variety resistant to downy mildew. Journal of General Plant Pathology, 2011, 77, 101-106.	1.0	21
53	Host Range and Phylogenetic Relationships ofAlbugo candidafrom Cruciferous Hosts in Western Australia, with Special Reference toBrassica juncea. Plant Disease, 2011, 95, 712-718.	1.4	25
54	Proteome analysis of the Albugo candidaâ€“Brassica juncea pathosystem reveals that the timing of the expression of defence-related genes is a crucial determinant of pathogenesis. Journal of Experimental Botany, 2011, 62, 1285-1298.	4.8	39

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55	Pathogenic behaviour of strains ofAlbugo candidafromBrassica juncea(Indian mustard) andRaphanus raphanistrum(wild radish) in Western Australia. Australasian Plant Pathology, 2008, 37, 353.	1.0	17
56	First Report of Powdery Mildew Caused by Erysiphe cruciferarum on Brassica juncea in Australia. Plant Disease, 2008, 92, 650-650.	1.4	11