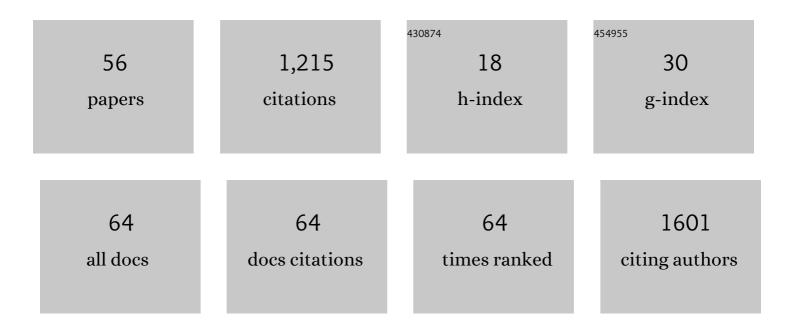
Parwinder Kaur

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7276839/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	3D genomics across the tree of life reveals condensin II as a determinant of architecture type. Science, 2021, 372, 984-989.	12.6	132
2	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
3	Microchromosomes are building blocks of bird, reptile, and mammal chromosomes. Proceedings of the United States of America, 2021, 118, .	7.1	84
4	Genetic improvement of subterranean clover (Trifolium subterraneum L.). 1. Germplasm, traits and future prospects. Crop and Pasture Science, 2013, 64, 312.	1.5	82
5	Next-Generation Breeding Strategies for Climate-Ready Crops. Frontiers in Plant Science, 2021, 12, 620420.	3.6	61
6	Airway Epithelial Cell Immunity Is Delayed During Rhinovirus Infection in Asthma and COPD. Frontiers in Immunology, 2020, 11, 974.	4.8	60
7	Proteome analysis of the Albugo candida–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
8	An advanced reference genome of <i>Trifolium subterraneum</i> L. reveals genes related to agronomic performance. Plant Biotechnology Journal, 2017, 15, 1034-1046.	8.3	38
9	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
10	Draft genome sequence of subterranean clover, a reference for genus Trifolium. Scientific Reports, 2016, 6, 30358.	3.3	33
11	CRISPR-Cas systems: ushering in the new genome editing era. Bioengineered, 2018, 9, 214-221.	3.2	30
12	Synthetic Biology towards Improved Flavonoid Pharmacokinetics. Biomolecules, 2021, 11, 754.	4.0	29
13	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
14	Changes in gene expression during germination reveal pea genotypes with either "quiescence―or "escape―mechanisms of waterlogging tolerance. Plant, Cell and Environment, 2019, 42, 245-258.	5.7	26
15	Host Range and Phylogenetic Relationships of <i>Albugo candida</i> from Cruciferous Hosts in Western Australia, with Special Reference to <i>Brassica juncea</i> . Plant Disease, 2011, 95, 712-718.	1.4	25
16	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
17	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
18	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

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19	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
20	Waterlogging tolerance of pea at germination. Journal of Agronomy and Crop Science, 2018, 204, 155-164.	3.5	19
21	High-quality reference genome for Clonorchis sinensis. Genomics, 2021, 113, 1605-1615.	2.9	19
22	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
23	Pathogenic behaviour of strains of <i>Albugo candida</i> from <i>Brassica juncea</i> (Indian mustard) and <i>Raphanus raphanistrum</i> (wild radish) in Western Australia. Australasian Plant Pathology, 2008, 37, 353.	1.0	17
24	Waterlogging Tolerance at Germination in Field Pea: Variability, Genetic Control, and Indirect Selection. Frontiers in Plant Science, 2019, 10, 953.	3.6	15
25	Applications of CRISPR systems in respiratory health: Entering a new â€~red pen' era in genome editing. Respirology, 2019, 24, 628-637.	2.3	13
26	Morphological diversity within a core collection of subterranean clover (Trifolium subterraneum) Tj ETQq0 0 0 rg	BT /Qverlo	ock ₁ 30 Tf 50 4
27	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
28	Chromosome-level genome of Schistosoma haematobium underpins genome-wide explorations of molecular variation. PLoS Pathogens, 2022, 18, e1010288.	4.7	13
29	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
30	State of Shark and Ray Genomics in an Era of Extinction. Frontiers in Marine Science, 2021, 8, .	2.5	12
31	First Report of Powdery Mildew Caused by <i>Erysiphe cruciferarum</i> on <i>Brassica juncea</i> in Australia. Plant Disease, 2008, 92, 650-650.	1.4	11
32	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
33	Large-Scale Structural Variation Detection in Subterranean Clover Subtypes Using Optical Mapping. Frontiers in Plant Science, 2018, 9, 971.	3.6	10
34	Mapping the landscape of chromatin dynamics during naÃ⁻ve CD4+ T-cell activation. Scientific Reports, 2021, 11, 14101.	3.3	10
35	Globular structures in roots accumulate phosphorus to extremely high concentrations following phosphorus addition. Plant, Cell and Environment, 2019, 42, 1987-2002.	5.7	9
36	Microbial Metabolomics Interaction and Ecological Challenges of Trichoderma Species as Biocontrol Inoculant in Crop Rhizosphere. Agronomy, 2022, 12, 900.	3.0	9

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37	Transforming traditional nutrition paradigms with synthetic biology driven microbial production platforms. Current Research in Biotechnology, 2021, 3, 260-268.	3.7	8
38	Chromosome-length genome assembly and linkage map of a critically endangered Australian bird: the helmeted honeyeater. GigaScience, 2022, 11, .	6.4	8
39	Status and Potential of Single ell 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
40	Small investments with big returns: environmental genomic bioprospecting of microbial life. Critical Reviews in Microbiology, 2022, 48, 641-655.	6.1	7
41	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
42	In Vitro-Assisted Compression of Breeding Cycles. , 2018, , 463-486.		5
43	An Improved Protocol for Agrobacterium-Mediated Transformation in Subterranean Clover (Trifolium subterraneum L.). International Journal of Molecular Sciences, 2021, 22, 4181.	4.1	5
44	New vision on the new era of genome study. Functional and Integrative Genomics, 2022, 22, 1-2.	3.5	5
45	Developing Bioprospecting Strategies for Bioplastics Through the Large-Scale Mining of Microbial Genomes. Frontiers in Microbiology, 2021, 12, 697309.	3.5	4
46	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
47	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
48	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
49	Genome Sequence of the Fungus Nannizziopsis barbatae, an Emerging Reptile Pathogen. Microbiology Resource Announcements, 2021, 10, .	0.6	2
50	Contribution of the Immune Response in the lleum 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
51	Title is missing!. , 2020, 15, e0223699.		0
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