Aakash Chawade

List of Publications by Year
in descending order

71 papers	2,565 citations	304368 22 h-index	223531 46 g-index
73 all docs	73 docs citations	73 times ranked	3437 citing authors

#	Article	IF	Citations
1	Unraveling the Genetic Basis of Key Agronomic Traits of Wrinkled Vining Pea (Pisum sativum L.) for Sustainable Production. Frontiers in Plant Science, 2022, 13, 844450.	1.7	6
2	Climate Change Impact on Wheat Performanceâ€"Effects on Vigour, Plant Traits and Yield from Early and Late Drought Stress in Diverse Lines. International Journal of Molecular Sciences, 2022, 23, 3333.	1.8	20
3	Identification of Genomic Regions and Sources for Wheat Blast Resistance through GWAS in Indian Wheat Genotypes. Genes, 2022, 13, 596.	1.0	6
4	Predicting yellow rust in wheat breeding trials by proximal phenotyping and machine learning. Plant Methods, 2022, 18, 30.	1.9	16
5	Genetic dissection for head blast resistance in wheat using two mapping populations. Heredity, 2022, 128, 402-410.	1.2	9
6	Functional phenomics for improved climate resilience in Nordic agriculture. Journal of Experimental Botany, 2022, 73, 5111-5127.	2.4	10
7	Beating the beast-wheat blast disease. , 2021, , 205-223.		1
8	GIS Application for the Estimation of Bioenergy Potential from Agriculture Residues: An Overview. Energies, 2021, 14, 898.	1.6	24
9	Genome-Wide Association Analysis and Genomic Prediction for Adult-Plant Resistance to Septoria Tritici Blotch and Powdery Mildew in Winter Wheat. Frontiers in Genetics, 2021, 12, 661742.	1.1	34
10	Screening and Mapping for Head Blast Resistance in a Panel of CIMMYT and South Asian Bread Wheat Germplasm. Frontiers in Genetics, 2021, 12, 679162.	1.1	16
11	Evaluation of elite bread wheat lines for resistance to blast disease in Bangladesh. Euphytica, 2021, 217, 1.	0.6	2
12	Wheat Blast: A Disease Spreading by Intercontinental Jumps and Its Management Strategies. Frontiers in Plant Science, 2021, 12, 710707.	1.7	51
13	Transcriptome profiling by combined machine learning and statistical R analysis identifies TMEM236 as a potential novel diagnostic biomarker for colorectal cancer. Scientific Reports, 2021, 11, 14304.	1.6	22
14	Frontiers in the Solicitation of Machine Learning Approaches in Vegetable Science Research. Sustainability, 2021, 13, 8600.	1.6	6
15	Phenocave: An Automated, Standalone, and Affordable Phenotyping System for Controlled Growth Conditions. Plants, 2021, 10, 1817.	1.6	7
16	Characterizing Winter Wheat Germplasm for Fusarium Head Blight Resistance Under Accelerated Growth Conditions. Frontiers in Plant Science, 2021, 12, 705006.	1.7	5
17	RNA Interference and CRISPR/Cas Gene Editing for Crop Improvement: Paradigm Shift towards Sustainable Agriculture. Plants, 2021, 10, 1914.	1.6	17
18	A Bioinformatics Pipeline to Identify a Subset of SNPs for Genomics-Assisted Potato Breeding. Plants, 2021, 10, 30.	1.6	14

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19	Genomic Selection for Wheat Blast in a Diversity Panel, Breeding Panel and Full-Sibs Panel. Frontiers in Plant Science, 2021, 12, 745379.	1.7	13
20	New Genotypes and Genomic Regions for Resistance to Wheat Blast in South Asian Germplasm. Plants, 2021, 10, 2693.	1.6	9
21	Mapping for adult-plant resistance against Septoria tritici blotch in a common wheat line Murga. Phytopathology, 2020, 111, 1001-1007.	1.1	3
22	Differential Gene Expression Analysis of Wheat Breeding Lines Reveal Molecular Insights in Yellow Rust Resistance under Field Conditions. Agronomy, 2020, 10, 1888.	1.3	8
23	Additives as a Support Structure for Specific Biochemical Activity Boosts in Anaerobic Digestion: A Review. Frontiers in Energy Research, 2020, 8, .	1.2	44
24	QTL Mapping for Resistance to Early Blight in a Tetraploid Potato Population. Agronomy, 2020, 10, 728.	1.3	20
25	QTL mapping for field resistance to wheat blast in the Caninde#1/Alondra population. Theoretical and Applied Genetics, 2020, 133, 2673-2683.	1.8	19
26	Affordable Phenotyping of Winter Wheat under Field and Controlled Conditions for Drought Tolerance. Agronomy, 2020, 10, 882.	1.3	23
27	Interactive proteogenomic exploration of response to Fusarium head blight in oat varieties with different resistance. Journal of Proteomics, 2020, 218, 103688.	1.2	6
28	An integrated transcriptomic- and proteomic-based approach to evaluate the human skin sensitization potential of glyphosate and its commercial agrochemical formulations. Journal of Proteomics, 2020, 217, 103647.	1.2	12
29	Breeding for Wheat Blast Resistance. , 2020, , 163-174.		5
30	Lignocellulolytic and Chitinolytic Glycoside Hydrolases: Structure, Catalytic Mechanism, Directed Evolution and Industrial Implementation. , 2020, , 97-127.		0
31	What is cost-efficient phenotyping? Optimizing costs for different scenarios. Plant Science, 2019, 282, 14-22.	1.7	103
32	GWAS-Assisted Genomic Prediction to Predict Resistance to Septoria Tritici Blotch in Nordic Winter Wheat at Seedling Stage. Frontiers in Genetics, 2019, 10, 1224.	1.1	41
33	QTL Mapping and Transcriptome Analysis to Identify Differentially Expressed Genes Induced by Septoria Tritici Blotch Disease of Wheat. Agronomy, 2019, 9, 510.	1.3	23
34	Prioritization of solid concentration and temperature for solid state anaerobic digestion of pearl millet straw employing multi-criteria assessment tool. Scientific Reports, 2019, 9, 11902.	1.6	16
35	High-Throughput Field-Phenotyping Tools for Plant Breeding and Precision Agriculture. Agronomy, 2019, 9, 258.	1.3	144
36	Clinical biomarker discovery by SWATH-MS based label-free quantitative proteomics: impact of criteria for identification of differentiators and data normalization method. Journal of Translational Medicine, 2019, 17, 184.	1.8	16

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37	NormalyzerDE: Online Tool for Improved Normalization of Omics Expression Data and High-Sensitivity Differential Expression Analysis. Journal of Proteome Research, 2019, 18, 732-740.	1.8	137
38	De-construction of major Indian cereal crop residues through chemical pretreatment for improved biogas production: An overview. Renewable and Sustainable Energy Reviews, 2018, 90, 160-170.	8.2	82
39	A transnational and holistic breeding approach is needed for sustainable wheat production in the Baltic Sea region. Physiologia Plantarum, 2018, 164, 442-451.	2.6	36
40	Scandinavian perspectives on plant gene technology: applications, policies and progress. Physiologia Plantarum, 2018, 162, 219-238.	2.6	24
41	Chitinasesâ€"Potential Candidates for Enhanced Plant Resistance towards Fungal Pathogens. Agriculture (Switzerland), 2018, 8, 88.	1.4	117
42	Comments on two recent publications on GM maize and Roundup. Scientific Reports, 2018, 8, 13338.	1.6	5
43	Practical breeding strategies to improve resistance to Septoria tritici blotch of wheat. Euphytica, 2018, 214, 1.	0.6	14
44	Affordable Imaging Lab for Noninvasive Analysis of Biomass and Early Vigour in Cereal Crops. BioMed Research International, 2018, 2018, 1-9.	0.9	20
45	Draft Genome Sequence for the Tree PathogenPhytophthora plurivora. Genome Biology and Evolution, 2018, 10, 2432-2442.	1.1	19
46	Proximal Phenotyping and Machine Learning Methods to Identify Septoria Tritici Blotch Disease Symptoms in Wheat. Frontiers in Plant Science, 2018, 9, 685.	1.7	44
47	Genetic Engineering of Energy Crops to Reduce Recalcitrance and Enhance Biomass Digestibility. Agriculture (Switzerland), 2018, 8, 76.	1.4	17
48	Nordic research infrastructures for plant phenotyping. Agricultural and Food Science, 2018, 27, .	0.3	3
49	Specalyzerâ€"an interactive online tool to analyze spectral reflectance measurements. PeerJ, 2018, 6, e5031.	0.9	2
50	Wholegrain oat diet changes the expression of genes associated with intestinal bile acid transport. Molecular Nutrition and Food Research, 2017, 61, 1600874.	1.5	9
51	Draft genome of the oomycete pathogen Phytophthora cactorum strain LV007 isolated from European beech (Fagus sylvatica). Genomics Data, 2017, 12, 155-156.	1.3	18
52	Food Waste to Energy: An Overview of Sustainable Approaches for Food Waste Management and Nutrient Recycling. BioMed Research International, 2017, 2017, 1-19.	0.9	338
53	The GARD platform for potency assessment of skin sensitizing chemicals. ALTEX: Alternatives To Animal Experimentation, 2017, 34, 539-559.	0.9	31
54	The GARD assay expanded â€" Potency assessment of skin sensitizing chemicals. Toxicology Letters, 2016, 259, S171.	0.4	2

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55	Dinosaur: A Refined Open-Source Peptide MS Feature Detector. Journal of Proteome Research, 2016, 15, 2143-2151.	1.8	70
56	Targeted Proteomics Approach for Precision Plant Breeding. Journal of Proteome Research, 2016, 15, 638-646.	1.8	44
57	Is labelâ€free LCâ€MS/MS ready for biomarker discovery?. Proteomics - Clinical Applications, 2015, 9, 289-294.	0.8	51
58	Deletion of glycerol channel aquaporin-9 (Aqp9) impairs long-term blood glucose control in C57BL/6 leptin receptor-deficient (db/db) obese mice. Physiological Reports, 2015, 3, e12538.	0.7	15
59	Data Processing Has Major Impact on the Outcome of Quantitative Label-Free LC-MS Analysis. Journal of Proteome Research, 2015, 14, 676-687.	1.8	33
60	Comparative Transcriptomics of Sijung and Jumli Marshi Rice during Early Chilling Stress Imply Multiple Protective Mechanisms. PLoS ONE, 2015, 10, e0125385.	1.1	14
61	Relating genes in the biosynthesis of the polyphenol composition of <scp>A</scp>ndean colored potato collection. Food Science and Nutrition, 2014, 2, 46-57.	1.5	4
62	Identification and qualitative characterization of high and low lignin lines from an oat TILLING population. Industrial Crops and Products, 2014, 59, 1-8.	2.5	21
63	Normalyzer: A Tool for Rapid Evaluation of Normalization Methods for Omics Data Sets. Journal of Proteome Research, 2014, 13, 3114-3120.	1.8	218
64	Global Expression Profiling of Low Temperature Induced Genes in the Chilling Tolerant Japonica Rice Jumli Marshi. PLoS ONE, 2013, 8, e81729.	1.1	53
65	Development of a Model System to Identify Differences in Spring and Winter Oat. PLoS ONE, 2012, 7, e29792.	1.1	14
66	Mutagenesis as a Tool in Plant Genetics, Functional Genomics, and Breeding. International Journal of Plant Genomics, 2011, 2011, 1-13.	2.2	191
67	Development and characterization of an oat TILLING-population and identification of mutations in lignin and Î²-glucan biosynthesis genes. BMC Plant Biology, 2010, 10, 86.	1.6	90
68	<i>In silico</i> analysis of promoter regions from cold-induced genes in rice (<i>Oryza sativa</i> L.) and <i>Arabidopsis thaliana</i> reveals the importance of combinatorial control. Bioinformatics, 2009, 25, 1345-1348.	1.8	23
69	Evaluation of Combining Several Statistical Methods with a Flexible Cutoff for Identifying Differentially Expressed Genes in Pairwise Comparison of EST Sets. Bioinformatics and Biology Insights, 2008, 2, BBI.S431.	1.0	2
70	Identification of Cold-Induced Genes in Cereal Crops and Arabidopsis Through Comparative Analysis of Multiple EST Sets. , 2007, , 48-65.		4
71	Putative cold acclimation pathways in Arabidopsis thaliana identified by a combined analysis of mRNA co-expression patterns, promoter motifs and transcription factors. BMC Genomics, 2007, 8, 304.	1.2	27