

Subhra Chakraborty

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

2,143
citations

218677

26
h-index

233421

45
g-index

60
all docs

60
docs citations

60
times ranked

2100
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomic dissection of rice cytoskeleton reveals the dominance of microtubule and microfilament proteins, and novel components in the cytoskeleton-bound polysome. <i>Plant Physiology and Biochemistry</i> , 2022, 170, 75-86.	5.8	1
2	The small heat shock proteins, chaperonin 10, in plants: An evolutionary view and emerging functional diversity. <i>Environmental and Experimental Botany</i> , 2021, 182, 104323.	4.2	11
3	Wheat 2â€Cys peroxiredoxin plays a dual role in chlorophyll biosynthesis and adaptation to high temperature. <i>Plant Journal</i> , 2021, 105, 1374-1389.	5.7	17
4	Grasspea, a critical recruit among neglected and underutilized legumes, for tapping genomic resources. <i>Current Plant Biology</i> , 2021, 26, 100200.	4.7	11
5	High temperature stress responses and wheat: Impacts and alleviation strategies. <i>Environmental and Experimental Botany</i> , 2021, 190, 104589.	4.2	25
6	Chitosanâ€Triggered immunity to <i>Fusarium</i> in chickpea is associated with changes in the plant extracellular matrix architecture, stomatal closure and remodeling of the plant metabolome and proteome. <i>Plant Journal</i> , 2020, 103, 561-583.	5.7	29
7	Integrated Seed Proteome and Phosphoproteome Analyses Reveal Interplay of Nutrient Dynamics, Carbonâ€Nitrogen Partitioning, and Oxidative Signaling in Chickpea. <i>Proteomics</i> , 2020, 20, 1900267.	2.2	4
8	Extracellular Matrix Proteome: Isolation of ECM Proteins for Proteomics Studies. <i>Methods in Molecular Biology</i> , 2020, 2057, 155-172.	0.9	3
9	Dehydrationâ€responsive nuclear proteome landscape of chickpea (<i>Cicer arietinum</i> L.) reveals phosphorylationâ€mediated regulation of stress response. <i>Plant, Cell and Environment</i> , 2019, 42, 230-244.	5.7	23
10	Physiological plasticity to high temperature stress in chickpea: Adaptive responses and variable tolerance. <i>Plant Science</i> , 2019, 289, 110258.	3.6	24
11	Metabolite signatures of grasspea suspension-cultured cells illustrate the complexity of dehydration response. <i>Planta</i> , 2019, 250, 857-871.	3.2	7
12	Transcriptome profiling illustrates expression signatures of dehydration tolerance in developing grasspea seedlings. <i>Planta</i> , 2019, 250, 839-855.	3.2	14
13	Dehydration-responsive alterations in the chloroplast proteome and cell metabolomic profile of rice reveals key stress adaptation responses. <i>Environmental and Experimental Botany</i> , 2019, 160, 12-24.	4.2	27
14	Dehydration-induced proteomic landscape of mitochondria in chickpea reveals large-scale coordination of key biological processes. <i>Journal of Proteomics</i> , 2019, 192, 267-279.	2.4	9
15	Heat Shock Proteins and Abiotic Stress Tolerance in Plants. <i>Heat Shock Proteins</i> , 2018, , 41-69.	0.2	49
16	Integrative network analyses of wilt transcriptome in chickpea reveal genotype dependent regulatory hubs in immunity and susceptibility. <i>Scientific Reports</i> , 2018, 8, 6528.	3.3	14
17	Nuclear Proteome: Isolation of Intact Nuclei, Extraction of Nuclear Proteins, and 2-DE Analysis. <i>Methods in Molecular Biology</i> , 2018, 1696, 41-55.	0.9	10
18	Carboxylate clamp tetratricopeptide repeat (TPR) domain containing Hsp90 cochaperones in Triticeae: An insight into structural and functional diversification. <i>Environmental and Experimental Botany</i> , 2018, 155, 31-44.	4.2	4

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19	Genome-Wide Identification of the Alba Gene Family in Plants and Stress-Responsive Expression of the Rice Alba Genes. <i>Genes</i> , 2018, 9, 183.	2.4	29
20	Variety-specific nutrient acquisition and dehydration-induced proteomic landscape of grasspea (<i>Cicer arietinum</i> L.) Tj ETQq0 0 0 rgBTj/Overlock 10 Tf 50 7	2.4	8
21	Dissecting the chloroplast proteome of chickpea (<i>Cicer arietinum</i> L.) provides new insights into classical and non-classical functions. <i>Journal of Proteomics</i> , 2017, 165, 11-20.	2.4	20
22	Cultivar-specific high temperature stress responses in bread wheat (<i>Triticum aestivum</i> L.) associated with physicochemical traits and defense pathways. <i>Food Chemistry</i> , 2017, 221, 1077-1087.	8.2	37
23	Molecular Dissection of Extracellular Matrix Proteome Reveals Discrete Mechanism Regulating <i>Verticillium Dahliae</i> Triggered Vascular Wilt Disease in Potato. <i>Proteomics</i> , 2017, 17, 1600373.	2.2	3
24	Quantitative Extracellular Matrix Proteomics Suggests Cell Wall Reprogramming in Host-Specific Immunity During Vascular Wilt Caused by <i>Fusarium oxysporum</i> in Chickpea. <i>Proteomics</i> , 2017, 17, 1600374.	2.2	10
25	Extracellular Matrix Proteome and Phosphoproteome of Potato Reveals Functionally Distinct and Diverse Canonical and Non-Canonical Proteoforms. <i>Proteomes</i> , 2016, 4, 20.	3.5	9
26	Plant Organellar Proteomics in Response to Dehydration: Turning Protein Repertoire into Insights. <i>Frontiers in Plant Science</i> , 2016, 7, 460.	3.6	13
27	Comparative Proteomics of Oxalate Downregulated Tomatoes Points toward Cross Talk of Signal Components and Metabolic Consequences during Post-harvest Storage. <i>Frontiers in Plant Science</i> , 2016, 7, 1147.	3.6	7
28	Ectopic expression of amaranth seed storage albumin modulates photoassimilate transport and nutrient acquisition in sweetpotato. <i>Scientific Reports</i> , 2016, 6, 25384.	3.3	13
29	Improving nutritional quality and fungal tolerance in soya bean and grass pea by expressing an oxalate decarboxylase. <i>Plant Biotechnology Journal</i> , 2016, 14, 1394-1405.	8.3	50
30	Legume proteomics: Progress, prospects, and challenges. <i>Proteomics</i> , 2016, 16, 310-327.	2.2	35
31	Seed Proteomics: An Overview. , 2016, , 31-52.		0
32	Proteometabolomic analysis of transgenic tomato overexpressing oxalate decarboxylase uncovers novel proteins potentially involved in defense mechanism against <i>Sclerotinia</i> . <i>Journal of Proteomics</i> , 2016, 143, 242-253.	2.4	24
33	Comparison of proteomic and metabolomic profiles of two contrasting ecotypes of sweetpotato (<i>Ipomoea batatas</i> L.) Tj ETQq1 1 0.784314 rgBTj/Overlock 27	2.4	27
34	Proteomics of an Orphan Legume, Grasspea: Current Status and Future Strategy. <i>Plant Tissue Culture and Biotechnology</i> , 2015, 25, 117-141.	0.2	6
35	Proteomics of Important Food Crops in the Asia Oceania Region: Current Status and Future Perspectives. <i>Journal of Proteome Research</i> , 2015, 14, 2723-2744.	3.7	16
36	Birth of plant proteomics in India: A new horizon. <i>Journal of Proteomics</i> , 2015, 127, 34-43.	2.4	2

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37	Comparative analysis of phytochemicals and nutrient availability in two contrasting cultivars of sweet potato (<i>Ipomoea batatas</i> L.). <i>Food Chemistry</i> , 2015, 173, 957-965.	8.2	95
38	Nuclear phosphoproteome of developing chickpea seedlings (<i>Cicer arietinum</i> L.) and protein-kinase interaction network. <i>Journal of Proteomics</i> , 2014, 105, 58-73.	2.4	30
39	OsAlba1, a dehydration-responsive nuclear protein of rice (<i>Oryza sativa</i> L. ssp. indica), participates in stress adaptation. <i>Phytochemistry</i> , 2014, 100, 16-25.	2.9	29
40	Membrane-associated proteomics of chickpea identifies Sad1/UNC-84 protein (CaSUN1), a novel component of dehydration signaling. <i>Scientific Reports</i> , 2014, 4, 4177.	3.3	29
41	Characterisation of the nuclear proteome of a dehydration-sensitive cultivar of chickpea and comparative proteomic analysis with a tolerant cultivar. <i>Proteomics</i> , 2013, 13, 1973-1992.	2.2	61
42	Comparative proteomics of dehydration response in the rice nucleus: New insights into the molecular basis of genotype-specific adaptation. <i>Proteomics</i> , 2013, 13, 3478-3497.	2.2	24
43	Phosphoproteomic Dynamics of Chickpea (<i>Cicer arietinum</i> L.) Reveals Shared and Distinct Components of Dehydration Response. <i>Journal of Proteome Research</i> , 2013, 12, 5025-5047.	3.7	37
44	Comparative Proteomics Reveals a Role for Seed Storage Protein AmA1 in Cellular Growth, Development, and Nutrient Accumulation. <i>Journal of Proteome Research</i> , 2013, 12, 4904-4930.	3.7	35
45	Comparative analyses of nuclear proteome: extending its function. <i>Frontiers in Plant Science</i> , 2013, 4, 100.	3.6	33
46	Reduction of Oxalate Levels in Tomato Fruit and Consequent Metabolic Remodeling Following Overexpression of a Fungal Oxalate Decarboxylase. <i>Plant Physiology</i> , 2013, 162, 364-378.	4.8	62
47	Dehydration-Responsive Reversible and Irreversible Changes in the Extracellular Matrix: Comparative Proteomics of Chickpea Genotypes with Contrasting Tolerance. <i>Journal of Proteome Research</i> , 2011, 10, 2027-2046.	3.7	40
48	Characterization of the Secretome of Chickpea Suspension Culture Reveals Pathway Abundance and the Expected and Unexpected Secreted Proteins. <i>Journal of Proteome Research</i> , 2011, 10, 5006-5015.	3.7	26
49	Analysis of the grasspea proteome and identification of stress-responsive proteins upon exposure to high salinity, low temperature, and abscisic acid treatment. <i>Phytochemistry</i> , 2011, 72, 1293-1307.	2.9	85
50	Next-generation protein-rich potato expressing the seed protein gene <i>AmA1</i> is a result of proteome rebalancing in transgenic tuber. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17533-17538.	7.1	91
51	Identification of Extracellular Matrix Proteins of Rice (<i>Oryza sativa</i> L.) Involved in Dehydration-Responsive Network: A Proteomic Approach. <i>Journal of Proteome Research</i> , 2010, 9, 3443-3464.	3.7	97
52	Dehydration-responsive Nuclear Proteome of Rice (<i>Oryza sativa</i> L.) Illustrates Protein Network, Novel Regulators of Cellular Adaptation, and Evolutionary Perspective. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1579-1598.	3.8	131
53	Comparative analyses of genotype dependent expressed sequence tags and stress-responsive transcriptome of chickpea wilt illustrate predicted and unexpected genes and novel regulators of plant immunity. <i>BMC Genomics</i> , 2009, 10, 415.	2.8	57
54	Active site geometry of oxalate decarboxylase from <i>Flammulina velutipes</i> : Role of histidine-coordinated manganese in substrate recognition. <i>Protein Science</i> , 2009, 11, 2138-2147.	7.6	17

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55	Comparative Proteomics of Tuber Induction, Development and Maturation Reveal the Complexity of Tuberization Process in Potato (<i>Solanum tuberosum</i> L.). <i>Journal of Proteome Research</i> , 2008, 7, 3803-3817.	3.7	62
56	Proteomics Approach to Identify Dehydration Responsive Nuclear Proteins from Chickpea (<i>Cicer</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 7	3.8	166
57	Comparative Proteomics Analysis of Differentially Expressed Proteins in Chickpea Extracellular Matrix during Dehydration Stress. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1868-1884.	3.8	183
58	The Nuclear Proteome of Chickpea (<i>Cicer arietinum</i> L.) Reveals Predicted and Unexpected Proteins. <i>Journal of Proteome Research</i> , 2006, 5, 3301-3311.	3.7	81
59	Extracellular Matrix Proteome of Chickpea (<i>Cicerarietinum</i> L.) Illustrates Pathway Abundance, Novel Protein Functions and Evolutionary Perspect. <i>Journal of Proteome Research</i> , 2006, 5, 1711-1720.	3.7	57
60	Cloning and characterization of the 5' flanking region of the oxalate decarboxylase gene from <i>Flammulina velutipes</i> . <i>Biochemical Journal</i> , 2002, 367, 67-75.	3.7	24