

# Arindam Ghatak

## List of Publications by Year in descending order

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96  
papers

8,296  
citations

34105

52  
h-index

48315

88  
g-index

100  
all docs

100  
docs citations

100  
times ranked

8792  
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomics for abiotic stresses in legumes: present status and future directions. <i>Critical Reviews in Biotechnology</i> , 2023, 43, 171-190.	9.0	26
2	Root exudation of contrasting drought-stressed pearl millet genotypes conveys varying biological nitrification inhibition (BNI) activity. <i>Biology and Fertility of Soils</i> , 2022, 58, 291-306.	4.3	28
3	( $\Delta$ )-Catechin $\Delta$ A Mass-Spectrometry-Based Exploration Coordination Complex Formation with Fell and Fell. <i>Cells</i> , 2022, 11, 958.	4.1	1
4	Editorial: Sorghum and Pearl Millet as Climate Resilient Crops for Food and Nutrition Security. <i>Frontiers in Plant Science</i> , 2022, 13, 851970.	3.6	12
5	Magnetic Field Induced Changes in the Shoot and Root Proteome of Barley ( <i>Hordeum vulgare</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 622795.	3.6	10
6	Heat stress response mechanisms in pollen development. <i>New Phytologist</i> , 2021, 231, 571-585.	7.3	84
7	Systems biology for crop improvement. <i>Plant Genome</i> , 2021, 14, e20098.	2.8	48
8	Spatial distribution of proteins and metabolites in developing wheat grain and their differential regulatory response during the grain filling process. <i>Plant Journal</i> , 2021, 107, 669-687.	5.7	34
9	Fast-forward breeding for a food-secure world. <i>Trends in Genetics</i> , 2021, 37, 1124-1136.	6.7	82
10	Lessons Learned from the Studies of Roots Shaded from Direct Root Illumination. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12784.	4.1	14
11	Genomic footprints of repeated evolution of <i>CAM</i> photosynthesis in a Neotropical species radiation. <i>Plant, Cell and Environment</i> , 2020, 43, 2987-3001.	5.7	15
12	Biological nitrification inhibition in the rhizosphere: determining interactions and impact on microbially mediated processes and potential applications. <i>FEMS Microbiology Reviews</i> , 2020, 44, 874-908.	8.6	73
13	Structural and Functional Heat Stress Responses of Chloroplasts of <i>Arabidopsis thaliana</i> . <i>Genes</i> , 2020, 11, 650.	2.4	14
14	Adjustment of photosynthetic activity to drought and fluctuating light in wheat. <i>Plant, Cell and Environment</i> , 2020, 43, 1484-1500.	5.7	45
15	PANOMICS meets germplasm. <i>Plant Biotechnology Journal</i> , 2020, 18, 1507-1525.	8.3	78
16	Multimiomics approach unravels fertility transition in a pigeonpea line for a two-line hybrid system. <i>Plant Genome</i> , 2020, 13, e20028.	2.8	14
17	Physiological and Proteomic Signatures Reveal Mechanisms of Superior Drought Resilience in Pearl Millet Compared to Wheat. <i>Frontiers in Plant Science</i> , 2020, 11, 600278.	3.6	44
18	Male Sterility in Maize after Transient Heat Stress during the Tetrad Stage of Pollen Development. <i>Plant Physiology</i> , 2019, 181, 683-700.	4.8	139

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19	Toward a Unification of System-Theoretical Principles in Biology and Ecology—The Stochastic Lyapunov Matrix Equation and Its Inverse Application. <i>Frontiers in Applied Mathematics and Statistics</i> , 2019, 5, .	1.3	21
20	Molecular response of <i>Deinococcus radiodurans</i> to simulated microgravity explored by proteometabolomic approach. <i>Scientific Reports</i> , 2019, 9, 18462.	3.3	20
21	Metabolomics in Plant Stress Physiology. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2018, 164, 187-236.	1.1	63
22	Proteomics of Heat-Stress and Ethylene-Mediated Thermotolerance Mechanisms in Tomato Pollen Grains. <i>Frontiers in Plant Science</i> , 2018, 9, 1558.	3.6	62
23	Microscopic and Proteomic Analysis of Dissected Developing Barley Endosperm Layers Reveals the Starchy Endosperm as Prominent Storage Tissue for ER-Derived Hordeins Alongside the Accumulation of Barley Protein Disulfide Isomerase (HvPDIL1-1). <i>Frontiers in Plant Science</i> , 2018, 9, 1248.	3.6	18
24	Eco-Metabolomics and Metabolic Modeling: Making the Leap From Model Systems in the Lab to Native Populations in the Field. <i>Frontiers in Plant Science</i> , 2018, 9, 1556.	3.6	28
25	Using RT-qPCR, Proteomics, and Microscopy to Unravel the Spatio-Temporal Expression and Subcellular Localization of Hordoindolines Across Development in Barley Endosperm. <i>Frontiers in Plant Science</i> , 2018, 9, 775.	3.6	26
26	Proteomics survey of Solanaceae family: Current status and challenges ahead. <i>Journal of Proteomics</i> , 2017, 169, 41-57.	2.4	65
27	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	17.5	356
28	Cereal Crop Proteomics: Systemic Analysis of Crop Drought Stress Responses Towards Marker-Assisted Selection Breeding. <i>Frontiers in Plant Science</i> , 2017, 8, 757.	3.6	131
29	System-Level and Granger Network Analysis of Integrated Proteomic and Metabolomic Dynamics Identifies Key Points of Grape Berry Development at the Interface of Primary and Secondary Metabolism. <i>Frontiers in Plant Science</i> , 2017, 8, 1066.	3.6	58
30	Pollen Metabolome Dynamics: Biochemistry, Regulation and Analysis. , 2017, , 319-336.		2
31	Protocol for Enrichment of the Membrane Proteome of Mature Tomato Pollen. <i>Bio-protocol</i> , 2017, 7, e2315.	0.4	3
32	Pro- and Antioxidant Activity of Three Selected Flavan Type Flavonoids: Catechin, Eriodictyol and Taxifolin. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1986.	4.1	39
33	Metabolomic and Proteomic Profiles Reveal the Dynamics of Primary Metabolism during Seed Development of Lotus ( <i>Nelumbo nucifera</i> ). <i>Frontiers in Plant Science</i> , 2016, 7, 750.	3.6	43
34	Exploring natural variation of <i>Pinus pinaster</i> Aiton using metabolomics: Is it possible to identify the region of origin of a pine from its metabolites?. <i>Molecular Ecology</i> , 2016, 25, 959-976.	3.9	82
35	System level analysis of cacao seed ripening reveals a sequential interplay of primary and secondary metabolism leading to polyphenol accumulation and preparation of stress resistance. <i>Plant Journal</i> , 2016, 87, 318-332.	5.7	48
36	Proteomics and comparative genomics of <i>Nitrososphaera viennensis</i> reveal the core genome and adaptations of archaeal ammonia oxidizers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7937-E7946.	7.1	178

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37	Quantitative phosphoproteomics reveals the role of the AMPK plant ortholog SnRK1 as a metabolic master regulator under energy deprivation. <i>Scientific Reports</i> , 2016, 6, 31697.	3.3	252
38	Pollen proteomics: from stress physiology to developmental priming. <i>Plant Reproduction</i> , 2016, 29, 119-132.	2.2	58
39	Comprehensive tissue-specific proteome analysis of drought stress responses in <i>Pennisetum glaucum</i> (L.) R. Br. (Pearl millet). <i>Journal of Proteomics</i> , 2016, 143, 122-135.	2.4	81
40	Induction and quantitative proteomic analysis of cell dedifferentiation during callus formation of lotus ( <i>Nelumbo nucifera</i> Gaertn.spp. <i>baijianlian</i> ). <i>Journal of Proteomics</i> , 2016, 131, 61-70.	2.4	25
41	The membrane proteome of male gametophyte in <i>Solanum lycopersicum</i> . <i>Journal of Proteomics</i> , 2016, 131, 48-60.	2.4	25
42	Integrative molecular profiling indicates a central role of transitory starch breakdown in establishing a stable C/N homeostasis during cold acclimation in two natural accessions of <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2015, 15, 284.	3.6	41
43	Heat-Treatment-Responsive Proteins in Different Developmental Stages of Tomato Pollen Detected by Targeted Mass Accuracy Precursor Alignment (tMAPA). <i>Journal of Proteome Research</i> , 2015, 14, 4463-4471.	3.7	56
44	Characterization of Indian beers: chemical composition and antioxidant potential. <i>Journal of Food Science and Technology</i> , 2015, 52, 1414-1423.	2.8	49
45	Solving the Differential Biochemical Jacobian from Metabolomics Covariance Data. <i>PLoS ONE</i> , 2014, 9, e92299.	2.5	53
46	System-level network analysis of nitrogen starvation and recovery in <i>Chlamydomonas reinhardtii</i> reveals potential new targets for increased lipid accumulation. <i>Biotechnology for Biofuels</i> , 2014, 7, 171.	6.2	103
47	Mathematical modeling reveals that metabolic feedback regulation of SnRK1 and hexokinase is sufficient to control sugar homeostasis from energy depletion to full recovery. <i>Frontiers in Plant Science</i> , 2014, 5, 365.	3.6	28
48	Comprehensive Cell-specific Protein Analysis in Early and Late Pollen Development from Diploid Microsporocytes to Pollen Tube Growth. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 295-310.	3.8	71
49	A universal protocol for the combined isolation of metabolites, <scp>DNA</scp>, long <scp>RNA</scp>s, small <scp>RNA</scp>s, and proteins from plants and microorganisms. <i>Plant Journal</i> , 2014, 79, 173-180.	5.7	132
50	Indian Grape Wines: A Potential Source of Phenols, Polyphenols, and Antioxidants. <i>International Journal of Food Properties</i> , 2014, 17, 818-828.	3.0	18
51	From Proteomics to Systems Biology: MAPA, MASS WESTERN, PROMEX, and COVAIN as a User-Oriented Platform. <i>Methods in Molecular Biology</i> , 2014, 1072, 15-27.	0.9	10
52	An Improved Detergent-Compatible Gel-Fractionation LC-LTQ-Orbitrap-MS Workflow for Plant and Microbial Proteomics. <i>Methods in Molecular Biology</i> , 2014, 1072, 347-358.	0.9	63
53	mzGroupAnalyzer-Predicting Pathways and Novel Chemical Structures from Untargeted High-Throughput Metabolomics Data. <i>PLoS ONE</i> , 2014, 9, e96188.	2.5	58
54	Cell-specific Analysis of the Tomato Pollen Proteome from Pollen Mother Cell to Mature Pollen Provides Evidence for Developmental Priming. <i>Journal of Proteome Research</i> , 2013, 12, 4892-4903.	3.7	97

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55	Granger causality in integrated GC-MS and LC-MS metabolomics data reveals the interface of primary and secondary metabolism. <i>Metabolomics</i> , 2013, 9, 564-574.	3.0	118
56	Using ProtMAX to create high-mass-accuracy precursor alignments from label-free quantitative mass spectrometry data generated in shotgun proteomics experiments. <i>Nature Protocols</i> , 2013, 8, 595-601.	12.0	44
57	Identification of Novel in vivo MAP Kinase Substrates in <i>Arabidopsis thaliana</i> Through Use of Tandem Metal Oxide Affinity Chromatography. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 369-380.	3.8	122
58	A workflow for mathematical modeling of subcellular metabolic pathways in leaf metabolism of <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 541.	3.6	16
59	Dynamic Adaption of Metabolic Pathways during Germination and Growth of Lily Pollen Tubes after Inhibition of the Electron Transport Chain. <i>Plant Physiology</i> , 2013, 162, 1822-1833.	4.8	79
60	Systemic Cold Stress Adaptation of <i>Chlamydomonas reinhardtii</i> . <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2032-2047.	3.8	122
61	Proteome and metabolome profiling of cytokinin action in <i>Arabidopsis</i> identifying both distinct and similar responses to cytokinin down- and up-regulation. <i>Journal of Experimental Botany</i> , 2013, 64, 4193-4206.	4.8	58
62	ProMEX – a mass spectral reference database for plant proteomics. <i>Frontiers in Plant Science</i> , 2012, 3, 125.	3.6	36
63	The different proteomes of <i>Chlamydomonas reinhardtii</i> . <i>Journal of Proteomics</i> , 2012, 75, 5883-5887.	2.4	16
64	COVAIn: a toolbox for uni- and multivariate statistics, time-series and correlation network analysis and inverse estimation of the differential Jacobian from metabolomics covariance data. <i>Metabolomics</i> , 2012, 8, 81-93.	3.0	168
65	Evaluation of radical scavenging potential and total phenol content in <i>Woodfordia fruticosa</i> from different altitudes. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2012, 21, 17-22.	1.7	11
66	MAPA Distinguishes Genotype-Specific Variability of Highly Similar Regulatory Protein Isoforms in Potato Tuber. <i>Journal of Proteome Research</i> , 2011, 10, 2979-2991.	3.7	42
67	Green systems biology – From single genomes, proteomes and metabolomes to ecosystems research and biotechnology. <i>Journal of Proteomics</i> , 2011, 75, 284-305.	2.4	189
68	Functional analysis of proteins and protein species using shotgun proteomics and linear mathematics. <i>Amino Acids</i> , 2011, 41, 329-341.	2.7	10
69	Unpredictability of metabolism – the key role of metabolomics science in combination with next-generation genome sequencing. <i>Analytical and Bioanalytical Chemistry</i> , 2011, 400, 1967-1978.	3.7	87
70	<i>Arabidopsis thaliana</i> as a model organism for plant proteome research. <i>Journal of Proteomics</i> , 2010, 73, 2239-2248.	2.4	65
71	Comparative analysis of phytohormone-responsive phosphoproteins in <i>Arabidopsis thaliana</i> using TiO <sub>2</sub> -phosphopeptide enrichment and mass accuracy precursor alignment. <i>Plant Journal</i> , 2010, 63, no-no.	5.7	190
72	Metabolomics: an integral technique in systems biology. <i>Bioanalysis</i> , 2010, 2, 829-836.	1.5	89

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73	Targeted proteomics for <i>Chlamydomonas reinhardtii</i> combined with rapid subcellular protein fractionation, metabolomics and metabolic flux analyses. <i>Molecular BioSystems</i> , 2010, 6, 1018.	2.9	94
74	Metabolomics Unravel Contrasting Effects of Biodiversity on the Performance of Individual Plant Species. <i>PLoS ONE</i> , 2010, 5, e12569.	2.5	114
75	An automated GCxGC-TOF-MS protocol for batch-wise extraction and alignment of mass isotopomer matrixes from differential <sup>13</sup> C labelling experiments: a case study for photoautotrophic-mixotrophic grown <i>Chlamydomonas reinhardtii</i> cells. <i>Journal of Basic Microbiology</i> , 2009, 49, 82-91.	3.3	62
76	Immunoproteomics approach for prediction of antigenic epitope of Tertiapin from <i>Apis mellifera</i> . <i>International Journal of Drug Discovery</i> , 2009, 1, 14-17.	0.2	2
77	A rapid approach for phenotype screening and database independent detection of cSNP/protein polymorphism using mass accuracy precursor alignment. <i>Proteomics</i> , 2008, 8, 4214-4225.	2.2	78
78	If the antibody fails – a mass Western approach. <i>Plant Journal</i> , 2008, 55, 1039-1046.	5.7	77
79	Integration of metabolomics and proteomics in molecular plant physiology – coping with the complexity by data-dimensionality reduction. <i>Physiologia Plantarum</i> , 2008, 132, 176-189.	5.2	88
80	Absolute quantification of <i>Medicago truncatula</i> sucrose synthase isoforms and N-metabolism enzymes in symbiotic root nodules and the detection of novel nodule phosphoproteins by mass spectrometry. <i>Journal of Experimental Botany</i> , 2008, 59, 3307-3315.	4.8	40
81	Integration of Metabolomic and Proteomic Phenotypes. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1725-1736.	3.8	155
82	Metabolomics- and Proteomics-Assisted Genome Annotation and Analysis of the Draft Metabolic Network of <i>Chlamydomonas reinhardtii</i> . <i>Genetics</i> , 2008, 179, 157-166.	2.9	141
83	Proteome Analysis of <i>Arabidopsis</i> Leaf Peroxisomes Reveals Novel Targeting Peptides, Metabolic Pathways, and Defense Mechanisms. <i>Plant Cell</i> , 2007, 19, 3170-3193.	6.6	324
84	ProMEX: a mass spectral reference database for proteins and protein phosphorylation sites. <i>BMC Bioinformatics</i> , 2007, 8, 216.	2.6	96
85	Integrative Profiling of Metabolites and Proteins. <i>Methods in Molecular Biology</i> , 2007, 358, 57-75.	0.9	33
86	Relative and absolute quantitative shotgun proteomics: targeting low-abundance proteins in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2006, 57, 1529-1535.	4.8	81
87	Stable isotope-free quantitative shotgun proteomics combined with sample pattern recognition for rapid diagnostics. <i>Journal of Separation Science</i> , 2006, 29, 2793-2801.	2.5	48
88	The role of mass spectrometry in plant systems biology. <i>Mass Spectrometry Reviews</i> , 2006, 25, 173-214.	5.4	140
89	Multisite Protein Phosphorylation in Plants - Technical Considerations and Biological Implications. <i>Current Proteomics</i> , 2006, 3, 217-231.	0.3	2
90	Metabolomics: from pattern recognition to biological interpretation. <i>Drug Discovery Today</i> , 2005, 10, 1551-1558.	6.4	274

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91	Correlative GC-TOF-MS-based metabolite profiling and LC-MS-based protein profiling reveal time-related systemic regulation of metabolite-protein networks and improve pattern recognition for multiple biomarker selection. <i>Metabolomics</i> , 2005, 1, 109-121.	3.0	97
92	Differential metabolic networks unravel the effects of silent plant phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7809-7814.	7.1	376
93	Process for the integrated extraction, identification and quantification of metabolites, proteins and RNA to reveal their co-regulation in biochemical networks. <i>Proteomics</i> , 2004, 4, 78-83.	2.2	398
94	Cell-specific protein profiling in <i>Arabidopsis thaliana</i> trichomes: identification of trichome-located proteins involved in sulfur metabolism and detoxification. <i>Phytochemistry</i> , 2004, 65, 1641-1649.	2.9	90
95	METABOLOMICS IN SYSTEMS BIOLOGY. <i>Annual Review of Plant Biology</i> , 2003, 54, 669-689.	18.7	614
96	Can we discover novel pathways using metabolomic analysis?. <i>Current Opinion in Biotechnology</i> , 2002, 13, 156-160.	6.6	170