

Randeep Rakwal

List of Publications by Year in descending order

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221
papers

8,492
citations

30070

54
h-index

58581

82
g-index

234
all docs

234
docs citations

234
times ranked

8738
citing authors

#	ARTICLE	IF	CITATIONS
1	A comprehensive insight into the biology of <i>Rhizoctonia solani</i> AG1-IA K ¹ 4hn, the causal organism of the sheath blight disease of rice. <i>Journal of Plant Pathology</i> , 2022, 104, 79-98.	1.2	4
2	Unravelling the <i>Helianthus tuberosus</i> L. (Jerusalem Artichoke, Kiku-Imo) Tuber Proteome by Label-Free Quantitative Proteomics. <i>Molecules</i> , 2022, 27, 1111.	3.8	5
3	Proteomics as a tool to understand the biology of agricultural crops. , 2022, , 107-122.		0
4	Reactive Oxygen Species (ROS) and Reactive Nitrogen Species (RNS) in plantsâ€™ maintenance of structural individuality and functional blend. <i>Advances in Redox Research</i> , 2022, 5, 100039.	2.1	48
5	Trends in Summer-Time Tropospheric Ozone during COVID-19 Lockdown in Indian Cities Might Forecast a Higher Future Risk. <i>Atmosphere</i> , 2022, 13, 1115.	2.3	4
6	Estimating Total Energy Expenditure for Fire-Fighters during Large Scale Disaster Response Training Using a Tri-Axial Accelerometer. <i>Nutrients</i> , 2021, 13, 2789.	4.1	2
7	Molecular Mechanism for PACAP 38-Induced Neurite Outgrowth in PC12 Cells. <i>Neural Plasticity</i> , 2021, 2021, 1-12.	2.2	3
8	Correlation of Kinematics and Kinetics of Changing Sagittal Plane Body Position during Landing and the Risk of Non-Contact Anterior Cruciate Ligament Injury. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 7773.	2.5	1
9	An Integrated Approach for the Efficient Extraction and Solubilization of Rice Microsomal Membrane Proteins for High-Throughput Proteomics. <i>Frontiers in Plant Science</i> , 2021, 12, 723369.	3.6	6
10	Effect of PACAP on sweat secretion by immortalized human sweat gland cells. <i>Peptides</i> , 2021, 146, 170647.	2.4	1
11	Physiological and Multi-Omics Approaches for Explaining Drought Stress Tolerance and Supporting Sustainable Production of Rice. <i>Frontiers in Plant Science</i> , 2021, 12, 803603.	3.6	9
12	Ethylene mediated physiological response for in vitro development of salinity tolerant tomato. <i>Journal of Plant Interactions</i> , 2020, 15, 406-416.	2.1	5
13	Transcriptomics of Mature Rice (<i>Oryza Sativa</i> L. Koshihikari) Seed under Hot Conditions by DNA Microarray Analyses. <i>Atmosphere</i> , 2020, 11, 528.	2.3	5
14	In-Depth Investigation of Low-Abundance Proteins in Matured and Filling Stages Seeds of <i>Glycine max</i> Employing a Combination of Protamine Sulfate Precipitation and TMT-Based Quantitative Proteomic Analysis. <i>Cells</i> , 2020, 9, 1517.	4.1	19
15	Concepts and strategies of soybean seed proteomics using the shotgun proteomics approach. <i>Expert Review of Proteomics</i> , 2019, 16, 795-804.	3.0	21
16	Towards identification of bioactive compounds in cold vacuum extracted double cherry blossom (Gosen-Sakura) leaves. <i>Plant Signaling and Behavior</i> , 2019, 14, e1644594.	2.4	2
17	Proteomics of Riceâ€™Magnaporthe oryzae Interaction: What Have We Learned So Far?. <i>Frontiers in Plant Science</i> , 2019, 10, 1383.	3.6	42
18	Leptin in hippocampus mediates benefits of mild exercise by an antioxidant on neurogenesis and memory. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10988-10993.	7.1	51

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19	Cyanide produced with ethylene by ACS and its incomplete detoxification by Î²-CAS in mango inflorescence leads to malformation. <i>Scientific Reports</i> , 2019, 9, 18361.	3.3	6
20	A Multi-omics Analysis of <i>Glycine max</i> Leaves Reveals Alteration in Flavonoid and Isoflavonoid Metabolism Upon Ethylene and Abscisic Acid Treatment. <i>Proteomics</i> , 2018, 18, e1700366.	2.2	38
21	Progress Toward Rice Seed OMICS in Low-Level Gamma Radiation Environment in Iitate Village, Fukushima. <i>Journal of Heredity</i> , 2018, 109, 206-211.	2.4	17
22	Comparative phosphoproteome analysis upon ethylene and abscisic acid treatment in <i>Glycine max</i> leaves. <i>Plant Physiology and Biochemistry</i> , 2018, 130, 173-180.	5.8	12
23	Effects of slope gradient on runoff from bare-fallow purple soil in China under natural rainfall conditions. <i>Journal of Mountain Science</i> , 2018, 15, 738-751.	2.0	13
24	Label-free quantitative secretome analysis of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> highlights the involvement of a novel cysteine protease in its pathogenicity. <i>Journal of Proteomics</i> , 2017, 169, 202-214.	2.4	25
25	Advances in proteomic technologies and their scope of application in understanding plant-pathogen interactions. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2017, 26, 371-386.	1.7	23
26	Aquaporins as potential drought tolerance inducing proteins: Towards instigating stress tolerance. <i>Journal of Proteomics</i> , 2017, 169, 233-238.	2.4	92
27	Proteomics survey of Solanaceae family: Current status and challenges ahead. <i>Journal of Proteomics</i> , 2017, 169, 41-57.	2.4	65
28	Comparative secretome analysis of <i>Colletotrichum falcatum</i> identifies a cerato-platanin protein (EPL1) as a potential pathogen-associated molecular pattern (PAMP) inducing systemic resistance in sugarcane. <i>Journal of Proteomics</i> , 2017, 169, 2-20.	2.4	30
29	Common bean proteomics: Present status and future strategies. <i>Journal of Proteomics</i> , 2017, 169, 239-248.	2.4	41
30	In-vitro secretomic analysis identifies putative pathogenicity-related proteins of <i>Sporisorium scitamineum</i> – The sugarcane smut fungus. <i>Fungal Biology</i> , 2017, 121, 199-211.	2.5	11
31	In-depth proteomic analysis of <i>Glycine max</i> seeds during controlled deterioration treatment reveals a shift in seed metabolism. <i>Journal of Proteomics</i> , 2017, 169, 125-135.	2.4	61
32	Expect the Unexpected Enrichment of “Hidden Proteome” of Seeds and Tubers by Depletion of Storage Proteins. <i>Frontiers in Plant Science</i> , 2016, 7, 761.	3.6	8
33	An Integrated Biochemical, Proteomics, and Metabolomics Approach for Supporting Medicinal Value of <i>Panax ginseng</i> Fruits. <i>Frontiers in Plant Science</i> , 2016, 7, 994.	3.6	23
34	Proteomic analysis of a compatible interaction between sugarcane and <i>Sporisorium scitamineum</i> . <i>Proteomics</i> , 2016, 16, 1111-1122.	2.2	39
35	Astaxanthin supplementation enhances adult hippocampal neurogenesis and spatial memory in mice. <i>Molecular Nutrition and Food Research</i> , 2016, 60, 589-599.	3.3	37
36	Proteome data associated with the leaf senescence in <i>Glycine max</i> . <i>Data in Brief</i> , 2016, 9, 90-95.	1.0	4

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37	Behavioral and omics analyses study on potential involvement of dipeptide balenine through supplementation in diet of senescence-accelerated mouse prone 8. <i>Genomics Data</i> , 2016, 10, 38-50.	1.3	13
38	Methyl jasmonate elicits the biotransformation of geraniol stored as its glucose conjugate into methyl geranate in <i>Achyranthes bidentata</i> plant. <i>Plant Physiology and Biochemistry</i> , 2016, 109, 166-170.	5.8	5
39	Coupling of gel-based 2-DE and 1-DE shotgun proteomics approaches to dig deep into the leaf senescence proteome of <i>Glycine max</i> . <i>Journal of Proteomics</i> , 2016, 148, 65-74.	2.4	30
40	Unraveling the rat blood genome-wide transcriptome after oral administration of lavender oil by a two-color dye-swap DNA microarray approach. <i>Genomics Data</i> , 2016, 8, 139-145.	1.3	0
41	DNA microarray-based experimental strategy for trustworthy expression profiling of the hippocampal genes by astaxanthin supplementation in adult mouse. <i>Genomics Data</i> , 2016, 7, 32-37.	1.3	2
42	Proteomic analysis of lipid body from the alkenone-producing marine haptophyte alga <i>Tisochrysis lutea</i> . <i>Proteomics</i> , 2015, 15, 4145-4158.	2.2	28
43	Two-color Dye-swap DNA Microarray approach toward confident gene expression profiling in PMCAO mouse model for ischemia-related and PACAP38-influenced genes. <i>Genomics Data</i> , 2015, 3, 148-154.	1.3	12
44	Unraveling the seed endosperm proteome of the lotus (<i>Nelumbo nucifera</i> Gaertn.) utilizing 1DE and 2DE separation in conjunction with tandem mass spectrometry. <i>Proteomics</i> , 2015, 15, 1717-1735.	2.2	7
45	DNA microarray unravels rapid changes in transcriptome of MK-801 treated rat brain. <i>World Journal of Biological Chemistry</i> , 2015, 6, 389.	4.3	5
46	Immature Seed Endosperm and Embryo Proteomics of the Lotus (<i>Nelumbo Nucifera</i> Gaertn.) by One-Dimensional Gel-Based Tandem Mass Spectrometry and a Comparison with the Mature Endosperm Proteome. <i>Proteomes</i> , 2015, 3, 184-235.	3.5	4
47	Unraveling the Rat Intestine, Spleen and Liver Genome-Wide Transcriptome after the Oral Administration of Lavender Oil by a Two-Color Dye-Swap DNA Microarray Approach. <i>PLoS ONE</i> , 2015, 10, e0129951.	2.5	10
48	Gamma-glutamyl cycle in plants: a bridge connecting the environment to the plant cell?. <i>Frontiers in Plant Science</i> , 2015, 6, 252.	3.6	32
49	Understanding the plant-pathogen interactions in the context of proteomics-generated apoplastic proteins inventory. <i>Frontiers in Plant Science</i> , 2015, 6, 352.	3.6	88
50	Quantitative proteomics reveals role of sugar in decreasing photosynthetic activity due to Fe deficiency. <i>Frontiers in Plant Science</i> , 2015, 6, 592.	3.6	30
51	Protamine sulfate precipitation method depletes abundant plant seed-storage proteins: A case study on legume plants. <i>Proteomics</i> , 2015, 15, 1760-1764.	2.2	25
52	Unraveling the Specific Ischemic Core and Penumbra Transcriptome in the Permanent Middle Cerebral Artery Occlusion Mouse Model Brain Treated with the Neuropeptide PACAP38. <i>Microarrays (Basel)</i> , Tj ETQq0 0 0 rgBT /Overlap 10 Tf 50		
53	Comparative investigation of seed coats of brown versus yellow colored soybean seeds using an integrated proteomics and metabolomics approach. <i>Proteomics</i> , 2015, 15, 1706-1716.	2.2	32
54	Methyl jasmonate elicits the production of methyl hexenoate from hexenol via hexenal in <i>Achyranthes bidentata</i> plant. <i>FEBS Letters</i> , 2015, 589, 390-395.	2.8	4

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55	Time to dig deep into the plant proteome: a hunt for low-abundance proteins. <i>Frontiers in Plant Science</i> , 2015, 6, 22.	3.6	47
56	Comparative Biochemical and Proteomic Analyses of Soybean Seed Cultivars Differing in Protein and Oil Content. <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 7134-7142.	5.2	22
57	Towards a common bean proteome atlas: looking at the current state of research and the need for a comprehensive proteome. <i>Frontiers in Plant Science</i> , 2015, 6, 201.	3.6	12
58	Abundant storage protein depletion from tuber proteins using ethanol precipitation method: Suitability to proteomics study. <i>Proteomics</i> , 2015, 15, 1765-1769.	2.2	17
59	2D-DIGE-based proteome expression changes in leaves of rice seedlings exposed to low-level gamma radiation at Iitate village, Fukushima. <i>Plant Signaling and Behavior</i> , 2015, 10, e1103406.	2.4	30
60	Peptide Separation Methodologies for In-depth Proteomics. <i>Methods in Molecular Biology</i> , 2015, 1242, 195-209.	0.9	0
61	Long-Term Mild, rather than Intense, Exercise Enhances Adult Hippocampal Neurogenesis and Greatly Changes the Transcriptomic Profile of the Hippocampus. <i>PLoS ONE</i> , 2015, 10, e0128720.	2.5	108
62	Hsp90 and ECM29 Are Important to Maintain the Integrity of Mammalian 26S Proteasome. <i>Advances in Biological Chemistry</i> , 2015, 05, 255-265.	0.6	2
63	Analyzing Waste Problems in Developing Countries: Lessons for Kathmandu, Nepal through Analysis of the Waste System in Tsukuba City, Japan. <i>Journal of Scientific Research and Reports</i> , 2015, 8, 1-13.	0.2	5
64	PACAP38 Differentially Effects Genes and CRMP2 Protein Expression in Ischemic Core and Penumbra Regions of Permanent Middle Cerebral Artery Occlusion Model Mice Brain. <i>International Journal of Molecular Sciences</i> , 2014, 15, 17014-17034.	4.1	21
65	Comprehensive Analysis of Neonatal versus Adult Unilateral Decortication in a Mouse Model Using Behavioral, Neuroanatomical, and DNA Microarray Approaches. <i>International Journal of Molecular Sciences</i> , 2014, 15, 22492-22517.	4.1	7
66	Seeking genes responsible for developmental origins of health and disease from the fetal mouse liver following maternal food restriction. <i>Congenital Anomalies (discontinued)</i> , 2014, 54, n/a-n/a.	0.6	13
67	Genomic Methods for Improving Abiotic Stress Tolerance in Crops. , 2014, , 35-42.		1
68	Unraveling Low-Level Gamma Radiation-Responsive Changes in Expression of Early and Late Genes in Leaves of Rice Seedlings at Iitate Village, Fukushima. <i>Journal of Heredity</i> , 2014, 105, 723-738.	2.4	41
69	Rice proteomics: A model system for crop improvement and food security. <i>Proteomics</i> , 2014, 14, 593-610.	2.2	68
70	Proteomics of rice and <i>Cochliobolus miyabeanus</i> fungal interaction: Insight into proteins at intracellular and extracellular spaces. <i>Proteomics</i> , 2014, 14, 2307-2318.	2.2	45
71	Transcriptome Analysis of Early Responsive Genes in Rice during <i>Magnaporthe oryzae</i> Infection. <i>Plant Pathology Journal</i> , 2014, 30, 343-354.	1.7	40
72	Correction: Transcriptomics and proteomics analyses of the PACAP38 influenced ischemic brain in permanent middle cerebral artery occlusion model mice. <i>Journal of Neuroinflammation</i> , 2013, 10, .	7.2	5

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73	Biofuels as a sustainable energy source: An update of the applications of proteomics in bioenergy crops and algae. <i>Journal of Proteomics</i> , 2013, 93, 234-244.	2.4	66
74	Deuterium labeling for investigating de novo synthesis of terpene volatiles in <i>Achyranthes bidentata</i> . <i>Biotechnology Letters</i> , 2013, 35, 1247-1252.	2.2	5
75	Plant proteomics in India and Nepal: current status and challenges ahead. <i>Physiology and Molecular Biology of Plants</i> , 2013, 19, 461-477.	3.1	7
76	Depletion of abundant plant RuBisCO protein using the protamine sulfate precipitation method. <i>Proteomics</i> , 2013, 13, 2176-2179.	2.2	61
77	Rice Proteomic Analysis: Sample Preparation for Protein Identification. <i>Methods in Molecular Biology</i> , 2013, 956, 151-184.	0.9	6
78	In-depth insight into in vivo apoplastic secretome of rice-Magnaporthe oryzae interaction. <i>Journal of Proteomics</i> , 2013, 78, 58-71.	2.4	104
79	Genome-wide mapping of the ozone-responsive transcriptomes in rice panicle and seed tissues reveals novel insight into their regulatory events. <i>Biotechnology Letters</i> , 2013, 35, 647-656.	2.2	13
80	Secretome analysis of the rice bacterium <i>Xanthomonas oryzae</i> using in vitro and in planta systems. <i>Proteomics</i> , 2013, 13, 1901-1912.	2.2	38
81	A decade of plant proteomics and mass spectrometry: Translation of technical advancements to food security and safety issues. <i>Mass Spectrometry Reviews</i> , 2013, 32, 335-365.	5.4	70
82	Biomarker discovery and applications for foods and beverages: Proteomics to nanoproteomics. <i>Journal of Proteomics</i> , 2013, 93, 74-92.	2.4	49
83	INPPO Actions and Recognition as a Driving Force for Progress in Plant Proteomics: Change of Guard, INPPO Update, and Upcoming Activities. <i>Proteomics</i> , 2013, 13, 3093-3100.	2.2	0
84	Comparative analysis of seed transcriptomes of ambient ozone-fumigated 2 different rice cultivars. <i>Plant Signaling and Behavior</i> , 2013, 8, e26300.	2.4	9
85	Lotus – A Source of Food and Medicine: Current Status and Future Perspectives in Context of the Seed Proteomics. <i>International Journal of Life Sciences</i> , 2013, 7, 1-5.	0.2	24
86	Rice Mitogen-Activated Protein Kinase Interactome Analysis Using the Yeast Two-Hybrid System. <i>Plant Physiology</i> , 2012, 160, 477-487.	4.8	81
87	Unraveling the ischemic brain transcriptome in a permanent middle cerebral artery occlusion mouse model by DNA microarray analysis. <i>DMM Disease Models and Mechanisms</i> , 2012, 5, 270-283.	2.4	62
88	Methyl jasmonate is transported to distal leaves via vascular process metabolizing itself into JA-Ile and triggering VOCs emission as defensive metabolites. <i>Plant Signaling and Behavior</i> , 2012, 7, 1378-1381.	2.4	22
89	Translational plant proteomics: A perspective. <i>Journal of Proteomics</i> , 2012, 75, 4588-4601.	2.4	63
90	Transcriptomics and proteomics analyses of the PACAP38 influenced ischemic brain in permanent middle cerebral artery occlusion model mice. <i>Journal of Neuroinflammation</i> , 2012, 9, 256.	7.2	36

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91	ADHD Animal Model Characterization: Transcriptomics and Proteomics Analyses. <i>Methods in Molecular Biology</i> , 2012, 829, 505-530.	0.9	4
92	Global identification of potential gene biomarkers associated with ozone-induced foliar injury in rice seedling leaves by correlating their symptom severity with transcriptome profiling. <i>International Journal of Life Sciences</i> , 2012, 6, 1-13.	0.2	5
93	Boosting the Globalization of Plant Proteomics through INPPO: Current Developments and Future Prospects. <i>Proteomics</i> , 2012, 12, 359-368.	2.2	10
94	Secretome analysis of <i>Magnaporthe oryzae</i> using in vitro systems. <i>Proteomics</i> , 2012, 12, 878-900.	2.2	30
95	Characterization of Grain Amino Acid Composition and Proteome Profile of a High-lysine Barley Mutant Line M98. <i>Hang'uk Jakmul Hakhoe Chi</i> , 2012, 57, 171-181.	0.2	1
96	Science, Scientists, and Journal. <i>International Journal of Life Sciences</i> , 2012, 5, .	0.2	0
97	Comparative Secretome Investigation of <i>Magnaporthe oryzae</i> Proteins Responsive to Nitrogen Starvation. <i>Journal of Proteome Research</i> , 2011, 10, 3136-3148.	3.7	62
98	The <i>Arabidopsis</i> aminopeptidase LAP2 regulates plant growth, leaf longevity and stress response. <i>New Phytologist</i> , 2011, 191, 958-969.	7.3	30
99	Seeking gene candidates responsible for developmental origins of health and disease. <i>Congenital Anomalies (discontinued)</i> , 2011, 51, 110-125.	0.6	19
100	Conversion of airborne nerolidol to DMNT emission requires additional signals in <i>Achyranthes bidentata</i> . <i>FEBS Letters</i> , 2011, 585, 1807-1813.	2.8	7
101	A comparative proteomics survey of proteins responsive to phosphorous starvation in roots of hydroponically-grown rice seedlings. <i>Journal of the Korean Society for Applied Biological Chemistry</i> , 2011, 54, 667-677.	0.9	28
102	The RNase Activity of Rice Probenazole-Induced Protein1 (PBZ1) Plays a Key Role in Cell Death in Plants. <i>Molecules and Cells</i> , 2011, 31, 25-32.	2.6	70
103	Biotic Stress-Responsive Rice Proteome: An Overview. <i>Journal of Plant Biology</i> , 2011, 54, 219-226.	2.1	22
104	Time to articulate a vision for the future of plant proteomics – A global perspective: An initiative for establishing the International Plant Proteomics Organization (INPPO). <i>Proteomics</i> , 2011, 11, 1559-1568.	2.2	31
105	Rice proteomics: A move toward expanded proteome coverage to comparative and functional proteomics uncovers the mysteries of rice and plant biology. <i>Proteomics</i> , 2011, 11, 1630-1649.	2.2	96
106	Plant organelle proteomics: Collaborating for optimal cell function. <i>Mass Spectrometry Reviews</i> , 2011, 30, 772-853.	5.4	89
107	Tropospheric Ozone and Plants: Absorption, Responses, and Consequences. <i>Reviews of Environmental Contamination and Toxicology</i> , 2011, 212, 61-111.	1.3	42
108	MALDI Imaging Mass Spectrometry for Investigating the Brain. , 2011, , 765-783.		0

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109	Proteomics of ionic stresses in rice: An overview. <i>Journal of Plant Biotechnology</i> , 2011, 38, 130-136.	0.4	1
110	MALAT1 enhances cell motility of lung adenocarcinoma cells by influencing the expression of motility-related genes. <i>FEBS Letters</i> , 2010, 584, 4575-4580.	2.8	391
111	Sugarcane proteomics: Establishment of a protein extraction method for 2-DE in stalk tissues and initiation of sugarcane proteome reference map. <i>Electrophoresis</i> , 2010, 31, 1959-1974.	2.4	57
112	Plant secretome: Unlocking secrets of the secreted proteins. <i>Proteomics</i> , 2010, 10, 799-827.	2.2	255
113	Investigating the Impact of Elevated Levels of Ozone on Tropical Wheat Using Integrated Phenotypical, Physiological, Biochemical, and Proteomics Approaches. <i>Journal of Proteome Research</i> , 2010, 9, 4565-4584.	3.7	88
114	An in planta technique for cis-/trans-stereochemical analysis of jasmonoyl isoleucine. <i>Journal of Plant Physiology</i> , 2010, 167, 933-937.	3.5	8
115	Ultra Low-Dose Radiation: Stress Responses and Impacts Using Rice as a Grass Model. <i>International Journal of Molecular Sciences</i> , 2009, 10, 1215-1225.	4.1	17
116	Gel-based proteomics approach for detecting low nitrogen-responsive proteins in cultivated rice species. <i>Physiology and Molecular Biology of Plants</i> , 2009, 15, 31-41.	3.1	19
117	Plant phosphoproteomics: An update. <i>Proteomics</i> , 2009, 9, 964-988.	2.2	107
118	Secretome analysis of differentially induced proteins in rice suspension-cultured cells triggered by rice blast fungus and elicitor. <i>Proteomics</i> , 2009, 9, 1302-1313.	2.2	65
119	Rice proteomics: Ending phase I and the beginning of phase II. <i>Proteomics</i> , 2009, 9, 935-963.	2.2	69
120	Physiology and proteomics of the water deficit stress response in three contrasting peanut genotypes. <i>Plant, Cell and Environment</i> , 2009, 32, 380-407.	5.7	127
121	Developing Rice Embryo Proteomics Reveals Essential Role for Embryonic Proteins in Regulation of Seed Germination. <i>Journal of Proteome Research</i> , 2009, 8, 3598-3605.	3.7	66
122	Integrated Transcriptomics, Proteomics, and Metabolomics Analyses To Survey Ozone Responses in the Leaves of Rice Seedling. <i>Journal of Proteome Research</i> , 2008, 7, 2980-2998.	3.7	159
123	Systematic Secretome Analyses of Rice Leaf and Seed Callus Suspension-Cultured Cells: Workflow Development and Establishment of High-Density Two-Dimensional Gel Reference Maps. <i>Journal of Proteome Research</i> , 2008, 7, 5187-5210.	3.7	58
124	Proteomics analysis of mature seed of four peanut cultivars using two-dimensional gel electrophoresis reveals distinct differential expression of storage, anti-nutritional, and allergenic proteins. <i>Plant Science</i> , 2008, 175, 321-329.	3.6	53
125	Interplant communication: Airborne methyl jasmonate is essentially converted into JA and JA-Ile activating jasmonate signaling pathway and VOCs emission. <i>Biochemical and Biophysical Research Communications</i> , 2008, 376, 723-727.	2.1	96
126	Proteomics- and Transcriptomics-Based Screening of Differentially Expressed Proteins and Genes in Brain of Wig Rat: A Model for Attention Deficit Hyperactivity Disorder (ADHD) Research. <i>Journal of Proteome Research</i> , 2008, 7, 2471-2489.	3.7	27

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127	Systematic Investigation of the Hemolymph Proteome of <i>Manduca sexta</i> at the Fifth Instar Larvae Stage Using One- and Two-Dimensional Proteomics Platforms. <i>Journal of Proteome Research</i> , 2008, 7, 938-959.	3.7	30
128	Proteomics of Two Cultivated Mushrooms <i>Sparassis crispa</i> and <i>Hericium erinaceum</i> Provides Insight into their Numerous Functional Protein Components and Diversity. <i>Journal of Proteome Research</i> , 2008, 7, 1819-1835.	3.7	40
129	Proteomics Analysis of Rice Lesion Mimic Mutant (<i>pl1</i>) Reveals Tightly Localized Probenazole-Induced Protein (PBZ1) in Cells Undergoing Programmed Cell Death. <i>Journal of Proteome Research</i> , 2008, 7, 1750-1760.	3.7	55
130	Omics Tools for Environmental Monitoring of Chemicals, Radiation, and Physical Stresses in <i>Saccharomyces Cerevisiae</i> . , 2008, , 325-337.		1
131	Growth retardation and death of rice plants irradiated with carbon ion beams is preceded by very early dose- and time-dependent gene expression changes. <i>Molecules and Cells</i> , 2008, 25, 272-8.	2.6	13
132	Survey of Differentially Expressed Proteins and Genes in Jasmonic Acid Treated Rice Seedling Shoot and Root at the Proteomics and Transcriptomics Levels. <i>Journal of Proteome Research</i> , 2007, 6, 3581-3603.	3.7	48
133	Gel-Based Proteomics of Unilateral Irradiated Striatum after Gamma Knife Surgery. <i>Journal of Proteome Research</i> , 2007, 6, 2656-2668.	3.7	19
134	Gel-based proteomics reveals potential novel protein markers of ozone stress in leaves of cultivated bean and maize species of Panama. <i>Electrophoresis</i> , 2007, 28, 4369-4381.	2.4	51
135	Transcriptional profiling of indica rice cultivar IET8585 (Ajaya) infected with bacterial leaf blight pathogen <i>Xanthomonas oryzae</i> pv <i>oryzae</i> . <i>Plant Physiology and Biochemistry</i> , 2007, 45, 834-850.	5.8	33
136	Differential Expression of Defense/Stress-Related Marker Proteins in Leaves of a Unique Rice Blast Lesion Mimic Mutant (blm). <i>Journal of Proteome Research</i> , 2006, 5, 2586-2598.	3.7	37
137	Plant phosphoproteomics: A long road ahead. <i>Proteomics</i> , 2006, 6, 5517-5528.	2.2	83
138	Rejuvenating rice proteomics: Facts, challenges, and visions. <i>Proteomics</i> , 2006, 6, 5549-5576.	2.2	58
139	Functional characterization of OsRacB GTPase – a potentially negative regulator of basal disease resistance in rice. <i>Plant Physiology and Biochemistry</i> , 2006, 44, 68-77.	5.8	43
140	Role of defense/stress-related marker genes, proteins and secondary metabolites in defining rice self-defense mechanisms. <i>Plant Physiology and Biochemistry</i> , 2006, 44, 261-273.	5.8	122
141	Protein extraction/solubilization protocol for monocot and dicot plant gel-based proteomics. <i>Journal of Plant Biology</i> , 2006, 49, 413-420.	2.1	35
142	Rice proteomics: A cornerstone for cereal food crop proteomes. <i>Mass Spectrometry Reviews</i> , 2006, 25, 1-53.	5.4	148
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