

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	MALATIN1 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
2	Plant secretome: Unlocking secrets of the secreted proteins. <i>Proteomics</i> , 2010, 10, 799-827.	2.2	255
3	A hydroponic rice seedling culture model system for investigating proteome of salt stress in rice leaf. <i>Electrophoresis</i> , 2005, 26, 4521-4539.	2.4	195
4	High-resolution two-dimensional electrophoresis separation of proteins from metal-stressed rice (<i>Oryza sativa</i> L.) leaves: Drastic reductions/ fragmentation of ribulose-1,5-bisphosphate carboxylase/oxygenase and induction of stress-related proteins. <i>Electrophoresis</i> , 2001, 22, 2824-2831.	2.4	180
5	Proteome analysis of differentially displayed proteins as a tool for investigating ozone stress in rice (<i>Oryza sativa</i> L.) seedlings. <i>Proteomics</i> , 2002, 2, 947.	2.2	180
6	Isolation of novel rice (<i>Oryza sativa</i> L.) multiple stress responsive MAP kinase gene, OsMSRMK2, whose mRNA accumulates rapidly in response to environmental cues. <i>Biochemical and Biophysical Research Communications</i> , 2002, 294, 1009-1016.	2.1	164
7	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
8	Chitosan activates defense/stress response(s) in the leaves of <i>Oryza sativa</i> seedlings. <i>Plant Physiology and Biochemistry</i> , 2002, 40, 1061-1069.	5.8	149
9	Rice proteomics: A cornerstone for cereal food crop proteomes. <i>Mass Spectrometry Reviews</i> , 2006, 25, 1-53.	5.4	148
10	Role of jasmonate in the rice (<i>Oryza sativa</i> L.) self-defense mechanism using proteome analysis. <i>Electrophoresis</i> , 2000, 21, 2492-2500.	2.4	147
11	Molecular Cloning and Characterization of a Novel Jasmonate Inducible Pathogenesis-Related Class 10 Protein Gene, JIOsPR10, from Rice (<i>Oryza sativa</i> L.) Seedling Leaves. <i>Biochemical and Biophysical Research Communications</i> , 2001, 286, 973-983.	2.1	146
12	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
13	Signalling molecules and blast pathogen attack activates rice OsPR1a and OsPR1b genes: A model illustrating components participating during defence/stress response. <i>Plant Physiology and Biochemistry</i> , 2001, 39, 1095-1103.	5.8	126
14	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
15	Separation of proteins from stressed rice (<i>Oryza sativa</i> L.) leaf tissues by two-dimensional polyacrylamide gel electrophoresis: Induction of pathogenesis-related and cellular protectant proteins by jasmonic acid, UV irradiation and copper chloride. <i>Electrophoresis</i> , 1999, 20, 3472-3478.	2.4	119
16	Octadecanoid signaling component bursts in rice (<i>Oryza sativa</i> L.) seedling leaves upon wounding by cut and treatment with fungal elicitor chitosan. <i>Biochemical and Biophysical Research Communications</i> , 2002, 295, 1041-1045.	2.1	115
17	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
18	Separation and characterization of proteins from green and etiolated shoots of rice (<i>Oryza sativa</i> L.): Towards a rice proteome. <i>Electrophoresis</i> , 1999, 20, 630-636.	2.4	107

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19	Plant phosphoproteomics: An update. <i>Proteomics</i> , 2009, 9, 964-988.	2.2	107
20	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
21	Role of Jasmonic Acid as a Signaling Molecule in Copper Chloride-elicited Rice Phytoalexin Production. <i>Bioscience, Biotechnology and Biochemistry</i> , 1996, 60, 1046-1048.	1.3	102
22	Rice MAPKs. <i>Biochemical and Biophysical Research Communications</i> , 2003, 302, 171-180.	2.1	96
23	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
24	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
25	Molecular cloning and mRNA expression analysis of a novel rice (<i>Oryzasativa L.</i>) MAPK kinase kinase, OsEDR1, an ortholog of <i>ArabidopsisAtEDR1</i> , reveal its role in defense/stress signalling pathways and development. <i>Biochemical and Biophysical Research Communications</i> , 2003, 300, 868-876.	2.1	94
26	Rice octadecanoid pathway. <i>Biochemical and Biophysical Research Communications</i> , 2004, 317, 1-15.	2.1	94
27	Aquaporins as potential drought tolerance inducing proteins: Towards instigating stress tolerance. <i>Journal of Proteomics</i> , 2017, 169, 233-238.	2.4	92
28	Phytoalexin production elicited by exogenously applied jasmonic acid in rice leaves (<i>Oryza sativa L.</i>) is under the control of cytokinins and ascorbic acid. <i>FEBS Letters</i> , 1997, 412, 61-64.	2.8	90
29	Plant organelle proteomics: Collaborating for optimal cell function. <i>Mass Spectrometry Reviews</i> , 2011, 30, 772-853.	5.4	89
30	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
31	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
32	Importance of ascorbate peroxidases OsAPX1 and OsAPX2 in the rice pathogen response pathways and growth and reproduction revealed by their transcriptional profiling. <i>Gene</i> , 2003, 322, 93-103.	2.2	84
33	Plant phosphoproteomics: A long road ahead. <i>Proteomics</i> , 2006, 6, 5517-5528.	2.2	83
34	Rice Mitogen-Activated Protein Kinase Interactome Analysis Using the Yeast Two-Hybrid System. <i>Plant Physiology</i> , 2012, 160, 477-487.	4.8	81
35	Rice proteomics: Current status and future perspectives. <i>Electrophoresis</i> , 2003, 24, 3378-3389.	2.4	75
36	Small GTPase Rop TM : molecular switch for plant defense responses. <i>FEBS Letters</i> , 2003, 546, 173-180.	2.8	73

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37	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
38	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
39	Rice proteomics: Ending phase I and the beginning of phase II. <i>Proteomics</i> , 2009, 9, 935-963.	2.2	69
40	Rice proteomics: A model system for crop improvement and food security. <i>Proteomics</i> , 2014, 14, 593-610.	2.2	68
41	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
42	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
43	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
44	Proteomics survey of Solanaceae family: Current status and challenges ahead. <i>Journal of Proteomics</i> , 2017, 169, 41-57.	2.4	65
45	A Methyltransferase for Synthesis of the Flavanone Phytoalexin Sakuranetin in Rice Leaves. <i>Biochemical and Biophysical Research Communications</i> , 1996, 222, 732-735.	2.1	63
46	Translational plant proteomics: A perspective. <i>Journal of Proteomics</i> , 2012, 75, 4588-4601.	2.4	63
47	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
48	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
49	Depletion of abundant plant RuBisCO protein using the protamine sulfate precipitation method. <i>Proteomics</i> , 2013, 13, 2176-2179.	2.2	61
50	In-depth proteomic analysis of Glycine max seeds during controlled deterioration treatment reveals a shift in seed metabolism. <i>Journal of Proteomics</i> , 2017, 169, 125-135.	2.4	61
51	The rice (<i>Oryza sativa</i>) Blast Lesion Mimic Mutant, blm, may confer resistance to blast pathogens by triggering multiple defense-associated signaling pathways. <i>Plant Physiology and Biochemistry</i> , 2005, 43, 397-406.	5.8	60
52	Differential induction of three pathogenesis-related genes, PR10, PR1b and PR5 by the ethylene generator ethephon under light and dark in rice (<i>Oryza sativa</i> L.) seedlings. <i>Journal of Plant Physiology</i> , 2001, 158, 133-137.	3.5	59
53	Rejuvenating rice proteomics: Facts, challenges, and visions. <i>Proteomics</i> , 2006, 6, 5549-5576.	2.2	58
54	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

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55	System, trends and perspectives of proteomics in dicot plantsPart III: Unraveling the proteomes influenced by the environment, and at the levels of function and genetic relationships. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2005, 815, 137-145.	2.3	57
56	Sugarcane proteomics: Establishment of a protein extraction method for 2â€œDE in stalk tissues and initiation of sugarcane proteome reference map. <i>Electrophoresis</i> , 2010, 31, 1959-1974.	2.4	57
57	Proteomics Analysis of Rice Lesion Mimic Mutant (<i>spl</i>1) 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
58	System, trends and perspectives of proteomics in dicot plantsPart I: Technologies in proteome establishment. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2005, 815, 109-123.	2.3	54
59	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
60	Gelâ€œbased 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
61	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
62	Light-dependent induction of OsPR10 in rice (<i>Oryza sativa</i> L.) seedlings by the global stress signaling molecule jasmonic acid and protein phosphatase 2A inhibitors. <i>Plant Science</i> , 2001, 161, 469-479.	3.6	50
63	Biomarker discovery and applications for foods and beverages: Proteomics to nanoproteomics. <i>Journal of Proteomics</i> , 2013, 93, 74-92.	2.4	49
64	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
65	Reactive Oxygen Species (ROS) and Reactive Nitrogen Species (RNS) in plantsâ€œ maintenance of structural individuality and functional blend. <i>Advances in Redox Research</i> , 2022, 5, 100039.	2.1	48
66	Protein phosphatase inhibitors activate defense responses in rice (<i>Oryza sativa</i>) leaves. <i>Physiologia Plantarum</i> , 2001, 111, 151-157.	5.2	47
67	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
68	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
69	Naringenin 7-O-methyltransferase involved in the biosynthesis of the flavanone phytoalexin sakuranetin from rice (<i>Oryza sativa</i> L.). <i>Plant Science</i> , 2000, 155, 213-221.	3.6	44
70	Chitinase induced by jasmonic acid, methyl jasmonate, ethylene and protein phosphatase inhibitors in rice. <i>Molecular Biology Reports</i> , 2004, 31, 113-119.	2.3	43
71	Functional characterization ofÂOsRacB GTPase â€œ aÂpotentially negative regulator ofÂbasal disease resistance inÂrice. <i>Plant Physiology and Biochemistry</i> , 2006, 44, 68-77.	5.8	43
72	Proteomics of Riceâ€œMagnaporthe oryzae Interaction: What Have We Learned So Far?. <i>Frontiers in Plant Science</i> , 2019, 10, 1383.	3.6	42

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73	Tropospheric Ozone and Plants: Absorption, Responses, and Consequences. Reviews of Environmental Contamination and Toxicology, 2011, 212, 61-111.	1.3	42
74	Unraveling Low-Level Gamma Radiation-Responsive Changes in Expression of Early and Late Genes in Leaves of Rice Seedlings at Iitate Village, Fukushima. Journal of Heredity, 2014, 105, 723-738.	2.4	41
75	Common bean proteomics: Present status and future strategies. Journal of Proteomics, 2017, 169, 239-248.	2.4	41
76	Proteomics of Two Cultivated Mushrooms <i>Sparassis crispa</i> and <i>Hericium erinaceum</i> Provides Insight into their Numerous Functional Protein Components and Diversity. Journal of Proteome Research, 2008, 7, 1819-1835.	3.7	40
77	Transcriptome Analysis of Early Responsive Genes in Rice during <i>Magnaporthe oryzae</i> Infection. Plant Pathology Journal, 2014, 30, 343-354.	1.7	40
78	Proteomic analysis of a compatible interaction between sugarcane and <i>Sporisorium scitamineum</i> . Proteomics, 2016, 16, 1111-1122.	2.2	39
79	Secretome analysis of the rice bacterium <i>Xanthomonas oryzae</i> (<i>Xoo</i>) using in vitro and in planta systems. Proteomics, 2013, 13, 1901-1912.	2.2	38
80	A Multi-Omics Analysis of <i>Glycine max</i> Leaves Reveals Alteration in Flavonoid and Isoflavonoid Metabolism Upon Ethylene and Abscisic Acid Treatment. Proteomics, 2018, 18, e1700366.	2.2	38
81	Differential Expression of Defense/Stress-Related Marker Proteins in Leaves of a Unique Rice Blast Lesion Mimic Mutant (<i>blm</i>). Journal of Proteome Research, 2006, 5, 2586-2598.	3.7	37
82	Astaxanthin supplementation enhances adult hippocampal neurogenesis and spatial memory in mice. Molecular Nutrition and Food Research, 2016, 60, 589-599.	3.3	37
83	Transcriptomics and proteomics analyses of the PACAP38 influenced ischemic brain in permanent middle cerebral artery occlusion model mice. Journal of Neuroinflammation, 2012, 9, 256.	7.2	36
84	System, trends and perspectives of proteomics in dicot plants Part II: Proteomes of the complex developmental stages. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2005, 815, 125-136.	2.3	35
85	Protein extraction/solubilization protocol for monocot and dicot plant gel-based proteomics. Journal of Plant Biology, 2006, 49, 413-420.	2.1	35
86	New protein extraction/solubilization protocol for gel-based proteomics of rat (female) whole brain and brain regions. Molecules and Cells, 2006, 22, 119-25.	2.6	34
87	Transcriptional profiling of indica rice cultivar IET8585 (Ajaya) infected with bacterial leaf blight pathogen <i>Xanthomonas oryzae</i> pv <i>oryzae</i> . Plant Physiology and Biochemistry, 2007, 45, 834-850.	5.8	33
88	Gamma-glutamyl cycle in plants: a bridge connecting the environment to the plant cell?. Frontiers in Plant Science, 2015, 6, 252.	3.6	32
89	Comparative investigation of seed coats of brown versus yellow colored soybean seeds using an integrated proteomics and metabolomics approach. Proteomics, 2015, 15, 1706-1716.	2.2	32
90	Time to articulate a vision for the future of plant proteomics – A global perspective: An initiative for establishing the International Plant Proteomics Organization (INPPO). Proteomics, 2011, 11, 1559-1568.	2.2	31

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91	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
92	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
93	Secretome analysis of <i>Magnaporthe oryzae</i> using in vitro systems. <i>Proteomics</i> , 2012, 12, 878-900.	2.2	30
94	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
95	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
96	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
97	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
98	Jasmonate, salicylate, protein phosphatase 2A inhibitors and kinetin up-regulate OsPR5 expression in cut-responsive rice (<i>Oryza sativa</i>). <i>Journal of Plant Physiology</i> , 2001, 158, 1357-1362.	3.5	29
99	Cloning and characterization of a jasmonate inducible rice (<i>Oryza sativa</i> L.) peroxidase gene, OsPOX, against global signaling molecules and certain inhibitors of kinase-signaling cascade(s). <i>Plant Science</i> , 2002, 162, 49-58.	3.6	28
100	Abscisic acid promoted changes in the protein profiles of rice seedling by proteome analysis. <i>Molecular Biology Reports</i> , 2005, 31, 217-230.	2.3	28
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	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
103	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
104	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
105	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
106	Jasmonic acid-induced necrosis and drastic decreases in ribulose-1,5-bisphosphate carboxylase/oxygenase in rice seedlings under light involves reactive oxygen species. <i>Journal of Plant Physiology</i> , 2001, 158, 679-688.	3.5	24
107	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
108	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

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109	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
110	Biotic Stress-Responsive Rice Proteome: An Overview. <i>Journal of Plant Biology</i> , 2011, 54, 219-226.	2.1	22
111	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
112	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
113	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
114	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
115	Rapid induction of defense/stress-related proteins in leaves of rice (<i>Oryza sativa</i>) seedlings exposed to ozone is preceded by newly phosphorylated proteins and changes in a 66-kDa ERK-type MAPK. <i>Journal of Plant Physiology</i> , 2002, 159, 361-369.	3.5	19
116	Gel-Based Proteomics of Unilateral Irradiated Striatum after Gamma Knife Surgery. <i>Journal of Proteome Research</i> , 2007, 6, 2656-2668.	3.7	19
117	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
118	Seeking gene candidates responsible for developmental origins of health and disease. <i>Congenital Anomalies (discontinued)</i> , 2011, 51, 110-125.	0.6	19
119	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
120	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
121	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
122	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
123	Stress signaling molecules involved in defense and protein phosphatase 2A inhibitors modulate OsCATC expression in rice (<i>Oryza sativa</i>) seedlings. <i>Journal of Plant Physiology</i> , 2001, 158, 1349-1355.	3.5	14
124	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
125	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
126	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> , 2014, 3, 1-10.	0.4	10

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127	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
128	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
129	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
130	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
131	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
132	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
133	InÂvitro secretomic analysis identifies putative pathogenicity-related proteins of <i>Sporisorium scitamineum</i> â€œ The sugarcane smut fungus. <i>Fungal Biology</i> , 2017, 121, 199-211.	2.5	11
134	Proteomics in Plant Defense Response. , 0, , 585-604.		10
135	Boosting the Globalization of Plant Proteomics through INPPO: Current Developments and Future Prospects. <i>Proteomics</i> , 2012, 12, 359-368.	2.2	10
136	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
137	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
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