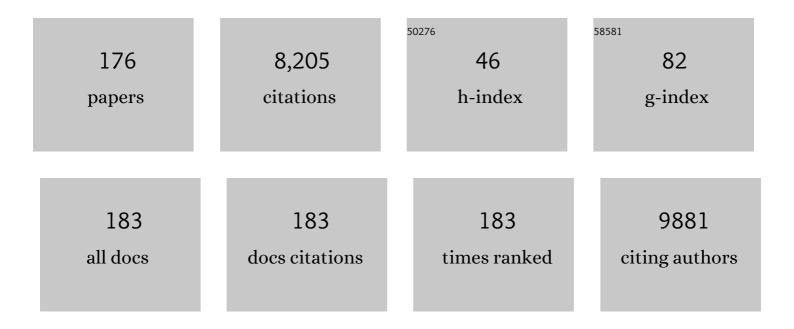
List of Publications by Year in descending order

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IENNY DENALIT

#	Article	IF	CITATIONS
1	Identification of Novel Candidate Genes Involved in Apple Cuticle Integrity and Russeting-Associated Triterpene Synthesis Using Metabolomic, Proteomic, and Transcriptomic Data. Plants, 2022, 11, 289.	3.5	8
2	Proteomic Studies of Roots in Hypoxia-Sensitive and -Tolerant Tomato Accessions Reveal Candidate Proteins Associated with Stress Priming. Cells, 2022, 11, 500.	4.1	6
3	Leaf necrosis resulting from downregulation of poplar glycosyltransferase <i>UGT72A2</i> . Tree Physiology, 2022, 42, 1084-1099.	3.1	6
4	Impact of heat treatment on the acid induced gelation of brewers' spent grain protein isolate. Food Hydrocolloids, 2021, 113, 106531.	10.7	11
5	An apoplastic fluid extraction method for the characterization of grapevine leaves proteome and metabolome from a single sample. Physiologia Plantarum, 2021, 171, 343-357.	5.2	18
6	Plant Extracellular Vesicles and Nanovesicles: Focus on Secondary Metabolites, Proteins and Lipids with Perspectives on Their Potential and Sources. International Journal of Molecular Sciences, 2021, 22, 3719.	4.1	67
7	Molecular insights into plant desiccation tolerance: transcriptomics, proteomics and targeted metabolite profiling in <i>Craterostigma plantagineum</i> . Plant Journal, 2021, 107, 377-398.	5.7	40
8	Proteomic analysis of salt-responsive proteins in the leaves of two contrasting Tunisian barley landraces. Plant Growth Regulation, 2021, 95, 65-82.	3.4	5
9	The Resistance of Oilseed Rape Microspore-Derived Embryos to Osmotic Stress Is Associated With the Accumulation of Energy Metabolism Proteins, Redox Homeostasis, Higher Abscisic Acid, and Cytokinin Contents. Frontiers in Plant Science, 2021, 12, 628167.	3.6	3
10	Stress response of lettuce (Lactuca sativa) to environmental contamination with selected pharmaceuticals: A proteomic study. Journal of Proteomics, 2021, 245, 104291.	2.4	8
11	The Cell Wall Proteome of Craterostigma plantagineum Cell Cultures Habituated to Dichlobenil and Isoxaben. Cells, 2021, 10, 2295.	4.1	4
12	Molecular investigation of Tuscan sweet cherries sampled over three years: gene expression analysis coupled to metabolomics and proteomics. Horticulture Research, 2021, 8, 12.	6.3	8
13	Gene expression and metabolite analysis in barley inoculated with net blotch fungus and plant growth-promoting rhizobacteria. Plant Physiology and Biochemistry, 2021, 168, 488-500.	5.8	5
14	Plant Proteoforms Under Environmental Stress: Functional Proteins Arising From a Single Gene. Frontiers in Plant Science, 2021, 12, 793113.	3.6	17
15	Long-Term Cd Exposure Alters the Metabolite Profile in Stem Tissue of Medicago sativa. Cells, 2020, 9, 2707.	4.1	14
16	The effects of improving low dietary protein utilization on the proteome of lamb tissues. Journal of Proteomics, 2020, 223, 103798.	2.4	7
17	Expression Analysis of Cell Wall-Related Genes in the Plant Pathogenic Fungus Drechslera teres. Genes, 2020, 11, 300.	2.4	7
18	Primary Metabolism Is Distinctly Modulated by Plant Resistance Inducers in Coffea arabica Leaves Infected by Hemileia vastatrix. Frontiers in Plant Science, 2020, 11, 309.	3.6	10

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19	Physiological and proteomic response of Escherichia coli O157:H7 to a bioprotective lactic acid bacterium in a meat environment. Food Research International, 2019, 125, 108622.	6.2	9
20	Distribution of cell-wall polysaccharides and proteins during growth of the hemp hypocotyl. Planta, 2019, 250, 1539-1556.	3.2	12
21	Phellem Cell-Wall Components Are Discriminants of Cork Quality in Quercus suber. Frontiers in Plant Science, 2019, 10, 944.	3.6	10
22	The Dynamics of the Cell Wall Proteome of Developing Alfalfa Stems. Biology, 2019, 8, 60.	2.8	16
23	The muscular, hepatic and adipose tissues proteomes in muskox (Ovibos moschatus): Differences between males and females. Journal of Proteomics, 2019, 208, 103480.	2.4	9
24	Does long-term cadmium exposure influence the composition of pectic polysaccharides in the cell wall of Medicago sativa stems?. BMC Plant Biology, 2019, 19, 271.	3.6	56
25	Insights into Lignan Composition and Biosynthesis in Stinging Nettle (Urtica dioica L.). Molecules, 2019, 24, 3863.	3.8	9
26	Specialisation events of fungal metacommunities exposed to a persistent organic pollutant are suggestive of augmented pathogenic potential. Microbiome, 2018, 6, 208.	11.1	16
27	Changes in the Proteome of Medicago sativa Leaves in Response to Long-Term Cadmium Exposure Using a Cell-Wall Targeted Approach. International Journal of Molecular Sciences, 2018, 19, 2498.	4.1	41
28	Proteome response of dental pulp cells to exogenous FGF8. Journal of Proteomics, 2018, 183, 14-24.	2.4	11
29	Proteomic responses of carotenoid and retinol administration to Mongolian gerbils. Food and Function, 2018, 9, 3835-3844.	4.6	8
30	Plant Abiotic Stress Proteomics: The Major Factors Determining Alterations in Cellular Proteome. Frontiers in Plant Science, 2018, 9, 122.	3.6	240
31	Differential Proteomic Analysis of Lactic Acid Bacteria—Escherichia coli O157:H7 Interaction and Its Contribution to Bioprotection Strategies in Meat. Frontiers in Microbiology, 2018, 9, 1083.	3.5	20
32	Insights into the molecular regulation of monolignol-derived product biosynthesis in the growing hemp hypocotyl. BMC Plant Biology, 2018, 18, 1.	3.6	368
33	Genetical genomics of quality related traits in potato tubers using proteomics. BMC Plant Biology, 2018, 18, 20.	3.6	18
34	Salinity effect on germination, seedling growth and cotyledon membrane complexes of a Portuguese salt marsh wild beet ecotype. Theoretical and Experimental Plant Physiology, 2018, 30, 113-127.	2.4	14
35	Longâ€ŧerm cadmium exposure influences the abundance of proteins that impact the cell wall structure in <i>Medicago sativa</i> stems. Plant Biology, 2018, 20, 1023-1035.	3.8	54
36	2D-DIGE in Proteomics. Methods in Molecular Biology, 2017, 1654, 245-254.	0.9	12

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37	Environmental stress is the major cause of transcriptomic and proteomic changes in GM and non-GM plants. Scientific Reports, 2017, 7, 10624.	3.3	18
38	A Cell Wall Proteome and Targeted Cell Wall Analyses Provide Novel Information on Hemicellulose Metabolism in Flax. Molecular and Cellular Proteomics, 2017, 16, 1634-1651.	3.8	23
39	Identification of chickpea seed proteins resistant to simulated in vitro human digestion. Journal of Proteomics, 2017, 169, 143-152.	2.4	23
40	Membrane-enriched proteome changes and prion protein expression during neural differentiation and in neuroblastoma cells. BMC Genomics, 2017, 18, 319.	2.8	2
41	Proteomic Insights on the Metabolism of Penicillium janczewskii during the Biotransformation of the Plant Terpenoid Labdanolic Acid. Frontiers in Bioengineering and Biotechnology, 2017, 5, 45.	4.1	5
42	Pathogenic Leptospires Modulate Protein Expression and Post-translational Modifications in Response to Mammalian Host Signals. Frontiers in Cellular and Infection Microbiology, 2017, 7, 362.	3.9	36
43	Didehydrophenylalanine, an abundant modification in the beta subunit of plant polygalacturonases. PLoS ONE, 2017, 12, e0171990.	2.5	7
44	Stuck at work? Quantitative proteomics of environmental wine yeast strains reveals the natural mechanism of overcoming stuck fermentation. Proteomics, 2016, 16, 593-608.	2.2	12
45	A proteomics study of colostrum and milk from the two major small ruminant dairy breeds from the Canary Islands: a bovine milk comparison perspective. Journal of Dairy Research, 2016, 83, 366-374.	1.4	42
46	2-D DIGE proteomic profiles of three strains of Fusarium graminearum grown in agmatine or glutamic acid medium. Data in Brief, 2016, 6, 985-988.	1.0	0
47	Integrated proteomics and metabolomics to unlock global and clonal responses of Eucalyptus globulus recovery from water deficit. Metabolomics, 2016, 12, 1.	3.0	41
48	Dataset of liver proteins of eu- and hypothyroid rats affected in abundance by any of three factors: in vivo exposure to hexabromocyclododecane (HBCD), thyroid status, gender differences. Data in Brief, 2016, 8, 1344-1347.	1.0	2
49	Dataset of protein changes induced by cold acclimation in red clover (Trifolium pratense L.) populations recurrently selected for improved freezing tolerance. Data in Brief, 2016, 8, 570-574.	1.0	2
50	Proteomic response of inflammatory stimulated intestinal epithelial cells to in vitro digested plums and cabbages rich in carotenoids and polyphenols. Food and Function, 2016, 7, 4388-4399.	4.6	9
51	Gender specific differences in the liver proteome of rats exposed to short term and low-concentration hexabromocyclododecane (HBCD). Toxicology Research, 2016, 5, 1273-1283.	2.1	11
52	A proteome analysis of freezing tolerance in red clover (Trifolium pratense L.). BMC Plant Biology, 2016, 16, 65.	3.6	31
53	Diagonal two-dimensional electrophoresis (D-2DE): a new approach to study the effect of osmotic stress induced by polyethylene glycol in durum wheat (Triticum durum Desf.). Molecular Biology Reports, 2016, 43, 897-909.	2.3	8
54	Dataset of liver proteins changed in eu- and hypothyroid female rats upon in vivo exposure to hexabromocyclododecane (HBCD). Data in Brief, 2016, 7, 386-392.	1.0	1

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55	Hexabromocyclododecane (HBCD) induced changes in the liver proteome of eu- and hypothyroid female rats. Toxicology Letters, 2016, 245, 40-51.	0.8	24
56	Combining -Omics to Unravel the Impact of Copper Nutrition on Alfalfa (<i>Medicago sativa</i>) Stem Metabolism. Plant and Cell Physiology, 2016, 57, 407-422.	3.1	23
57	A Fusarium graminearum strain-comparative proteomic approach identifies regulatory changes triggered by agmatine. Journal of Proteomics, 2016, 137, 107-116.	2.4	8
58	The Goat (Capra hircus) Mammary Gland Mitochondrial Proteome: A Study on the Effect of Weight Loss Using Blue-Native PAGE and Two-Dimensional Gel Electrophoresis. PLoS ONE, 2016, 11, e0151599.	2.5	21
59	Metabolite and transcriptome profiling of russeted and waxy apple skins highlighted genes involved in triterpene-hydroxycinnamate biosynthesis. Planta Medica, 2016, 81, S1-S381.	1.3	0
60	Animal board invited review: advances in proteomics for animal and food sciences. Animal, 2015, 9, 1-17.	3.3	143
61	Effects of silver nanoparticles and ions on a co-culture model for the gastrointestinal epithelium. Particle and Fibre Toxicology, 2015, 13, 9.	6.2	99
62	The quest for tolerant varieties: the importance of integrating "omics―techniques to phenotyping. Frontiers in Plant Science, 2015, 6, 448.	3.6	67
63	Proteomic analysis of apoplastic fluid of Coffea arabica leaves highlights novel biomarkers for resistance against Hemileia vastatrix. Frontiers in Plant Science, 2015, 6, 478.	3.6	46
64	Quantitative analysis of proteome extracted from barley crowns grown under different drought conditions. Frontiers in Plant Science, 2015, 6, 479.	3.6	53
65	Effect of temperature on the pathogenesis, accumulation of viral and satellite RNAs and on plant proteome in peanut stunt virus and satellite RNA-infected plants. Frontiers in Plant Science, 2015, 6, 903.	3.6	40
66	Ups and downs in alfalfa: Proteomic and metabolic changes occurring in the growing stem. Plant Science, 2015, 238, 13-25.	3.6	10
67	In vitro culture may be the major contributing factor for transgenic versus nontransgenic proteomic plant differences. Proteomics, 2015, 15, 124-134.	2.2	9
68	Lettuce (Lactuca sativa L.) leaf-proteome profiles after exposure to cylindrospermopsin and a microcystin-LR/cylindrospermopsin mixture: A concentration-dependent response. Phytochemistry, 2015, 110, 91-103.	2.9	20
69	An improved protocol to study the plant cell wall proteome. Frontiers in Plant Science, 2015, 6, 237.	3.6	33
70	Comparative proteomic analysis of lung tissue from guinea pigs with leptospiral pulmonary haemorrhage syndrome (LPHS) reveals a decrease in abundance of host proteins involved in cytoskeletal and cellular organization. Journal of Proteomics, 2015, 122, 55-72.	2.4	15
71	Unravelling the effect of sucrose and cold pretreatment on cryopreservation of potato through sugar analysis and proteomics. Cryobiology, 2015, 71, 432-441.	0.7	43
72	A 2-D guinea pig lung proteome map. Data in Brief, 2015, 4, 140-145.	1.0	2

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73	The old 3-oxoadipate pathway revisited: New insights in the catabolism of aromatics in the saprophytic fungus Aspergillus nidulans. Fungal Genetics and Biology, 2015, 74, 32-44.	2.1	45
74	Identification of Metabolic Pathways Expressed by Pichia anomala Kh6 in the Presence of the Pathogen Botrytis cinerea on Apple: New Possible Targets for Biocontrol Improvement. PLoS ONE, 2014, 9, e91434.	2.5	25
75	Physiological and Proteomic Responses of Different Willow Clones (<i>Salix fragilis</i> X <i>alba</i>) Exposed to Dredged Sediment Contaminated by Heavy Metals. International Journal of Phytoremediation, 2014, 16, 1148-1169.	3.1	22
76	Comparative analysis of Salmonella susceptibility and tolerance to the biocide chlorhexidine identifies a complex cellular defense network. Frontiers in Microbiology, 2014, 5, 373.	3.5	20
77	Exposure of Lycopersicon Esculentum to Microcystin-LR: Effects in the Leaf Proteome and Toxin Translocation from Water to Leaves and Fruits. Toxins, 2014, 6, 1837-1854.	3.4	50
78	Investigating Aspergillus nidulans secretome during colonisation of cork cell walls. Journal of Proteomics, 2014, 98, 175-188.	2.4	23
79	Proteomic changes in leaves of poplar exposed to both cadmium and low-temperature. Environmental and Experimental Botany, 2014, 106, 112-123.	4.2	40
80	Differential cadmium and zinc distribution in relation to their physiological impact in the leaves of the accumulating <i><scp>Z</scp>ygophyllum fabago</i> â€ <scp>L</scp> Plant, Cell and Environment, 2014, 37, 1299-1320.	5.7	75
81	Description of the mechanisms underlying geosmin production in Penicillium expansum using proteomics. Journal of Proteomics, 2014, 96, 13-28.	2.4	7
82	Changes in sugar content and proteome of potato in response to cold and dehydration stress and their implications for cryopreservation. Journal of Proteomics, 2014, 98, 99-111.	2.4	46
83	Elucidating how the saprophytic fungus Aspergillus nidulans uses the plant polyester suberin as carbon source. BMC Genomics, 2014, 15, 613.	2.8	27
84	Salicylic acid is an indispensable component of the Ny-1 resistance-gene-mediated response against Potato virus Y infection in potato. Journal of Experimental Botany, 2014, 65, 1095-1109.	4.8	117
85	Maize IgE binding proteins: each plant a different profile?. Proteome Science, 2014, 12, 17.	1.7	11
86	Effect of greenhouse conditions on the leaf apoplastic proteome of Coffea arabica plants. Journal of Proteomics, 2014, 104, 128-139.	2.4	26
87	Changes in the proteome and water state in bark and xylem of Hydrangea paniculata during loss of freezing tolerance. Environmental and Experimental Botany, 2014, 106, 99-111.	4.2	15
88	The membrane proteome of Medicago truncatula roots displays qualitative and quantitative changes in response to arbuscular mycorrhizal symbiosis. Journal of Proteomics, 2014, 108, 354-368.	2.4	49
89	A multiple-level study of metal tolerance in Salix fragilis and Salix aurita clones. Journal of Proteomics, 2014, 101, 113-129.	2.4	20
90	2DE Analysis of Forest Tree Proteins Using Fluorescent Labels and Multiplexing. Methods in Molecular Biology, 2014, 1072, 141-154.	0.9	0

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#	Article	IF	CITATIONS
91	Exploring chloroplastic changes related to chilling and freezing tolerance during cold acclimation of pea (Pisum sativum L.). Journal of Proteomics, 2013, 80, 145-159.	2.4	48
92	Physiological and proteomic changes suggest an important role of cell walls in the high tolerance to metals of Elodea nuttallii. Journal of Hazardous Materials, 2013, 263, 575-583.	12.4	37
93	A biomolecular isolation framework for eco-systems biology. ISME Journal, 2013, 7, 110-121.	9.8	97
94	Proteome Analysis of Cold Response in Spring and Winter Wheat (<i>Triticum aestivum</i>) Crowns Reveals Similarities in Stress Adaptation and Differences in Regulatory Processes between the Growth Habits. Journal of Proteome Research, 2013, 12, 4830-4845.	3.7	102
95	Plant proteomics in India and Nepal: current status and challenges ahead. Physiology and Molecular Biology of Plants, 2013, 19, 461-477.	3.1	7
96	Differential Protein Expression in Response to Abiotic Stress in Two Potato Species: Solanum commersonii Dun and Solanum tuberosum L International Journal of Molecular Sciences, 2013, 14, 4912-4933.	4.1	39
97	2 <scp>D</scp> difference gel electrophoresis reference map of a <i><scp>F</scp>usarium graminearum</i> nivalenol producing strain. Electrophoresis, 2013, 34, 505-509.	2.4	15
98	Protein actors sustaining arbuscular mycorrhizal symbiosis: underground artists break the silence. New Phytologist, 2013, 199, 26-40.	7.3	31
99	Proteomic and phenotypic analysis of triclosan tolerant verocytotoxigenic Escherichia coli O157:H19. Journal of Proteomics, 2013, 80, 78-90.	2.4	23
100	Proteomic alterations induced by ionic liquids in Aspergillus nidulans and Neurospora crassa. Journal of Proteomics, 2013, 94, 262-278.	2.4	21
101	The response of Mucor plumbeus to pentachlorophenol: A toxicoproteomics study. Journal of Proteomics, 2013, 78, 159-171.	2.4	28
102	A decade of plant proteomics and mass spectrometry: Translation of technical advancements to food security and safety issues. Mass Spectrometry Reviews, 2013, 32, 335-365.	5.4	70
103	Two Traditional Maize Inbred Lines of Contrasting Technological Abilities Are Discriminated by the Seed Flour Proteome. Journal of Proteome Research, 2013, 12, 3152-3165.	3.7	22
104	Physiological and proteome study of sunflowers exposed to a polymetallic constraint. Proteomics, 2013, 13, 1993-2015.	2.2	15
105	From Tolerance to Acute Metabolic Deregulation: Contribution of Proteomics To Dig into the Molecular Response of Alder Species under a Polymetallic Exposure. Journal of Proteome Research, 2013, 12, 5160-5179.	3.7	17
106	Proteomic changes associated with freezeâ€ŧhaw injury and postâ€ŧhaw recovery in onion (<i>Allium) Tj ETQq0</i>	0	Ovgrlock 101
107	How can plant virus satellite RNAs alter the effects of plant virus infection? A study of the changes in the <i>Nicotiana benthamiana</i> proteome after infection by <i>Peanut stunt virus</i> in the presence or absence of its satellite RNA. Proteomics, 2013, 13, 2162-2175.	2.2	21

¹⁰⁸ INPPO Actions and Recognition as a Driving Force for Progress in Plant Proteomics: Change of Guard, 2.2

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109	A physiological and proteomic study of poplar leaves during ozone exposure combined with mild drought. Proteomics, 2013, 13, 1737-1754.	2.2	27
110	Gel-Based and Gel-Free Quantitative Proteomics Approaches at a Glance. International Journal of Plant Genomics, 2012, 2012, 1-17.	2.2	148
111	Carotenoid exposure of Caco-2 intestinal epithelial cells did not affect selected inflammatory markers but altered their proteomic response. British Journal of Nutrition, 2012, 108, 963-973.	2.3	21
112	Screening for changes in leaf and cambial proteome of Populus tremula×P. alba under different heat constraints. Journal of Plant Physiology, 2012, 169, 1698-1718.	3.5	15
113	Identification of Differentially Expressed Proteins in Curcumin-Treated Prostate Cancer Cell Lines. OMICS A Journal of Integrative Biology, 2012, 16, 289-300.	2.0	41
114	Continuous thrombin infusion leads to a bleeding phenotype in sheep. Thrombosis Research, 2012, 130, 226-236.	1.7	4
115	Characterization of maize allergens — MON810 vs. its non-transgenic counterpart. Journal of Proteomics, 2012, 75, 2027-2037.	2.4	38
116	Translational plant proteomics: A perspective. Journal of Proteomics, 2012, 75, 4588-4601.	2.4	63
117	Comparative proteomic analysis of Salmonella tolerance to the biocide active agent triclosan. Journal of Proteomics, 2012, 75, 4505-4519.	2.4	35
118	Atrazine and PCB 153 and their effects on the proteome of subcellular fractions of human MCF-7 cells. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 833-841.	2.3	23
119	Optimization of iTRAQ labelling coupled to OFFGEL fractionation as a proteomic workflow to the analysis of microsomal proteins of Medicago truncatula roots. Proteome Science, 2012, 10, 37.	1.7	34
120	The Proteome Response to Amyloid Protein Expression In Vivo. PLoS ONE, 2012, 7, e50123.	2.5	12
121	Analysis of proteome and frost tolerance in chromosome 5A and 5B reciprocal substitution lines between two winter wheats during longâ€ŧerm cold acclimation. Proteomics, 2012, 12, 68-85.	2.2	71
122	Boosting the Globalization of Plant Proteomics through INPPO: Current Developments and Future Prospects. Proteomics, 2012, 12, 359-368.	2.2	10
123	Proteomics as a Toolbox to Study the Metabolic Adjustment of Trees During Exposure to Metal Trace Elements. , 2012, , 143-164.		2
124	Physiological response and differential leaf proteome pattern in the European invasive Asteraceae Solidago canadensis colonizing a former cokery soil. Journal of Proteomics, 2012, 75, 1129-1143.	2.4	13
125	Towards a synthetic view of potato cold and salt stress response by transcriptomic and proteomic analyses. Plant Molecular Biology, 2012, 78, 503-514.	3.9	86
126	Potential Therapeutic Target Discovery by 2D-DIGE Proteomic Analysis in Mouse Models of Asthma. Journal of Proteome Research, 2011, 10, 4291-4301.	3.7	16

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127	A Difference Gel Electrophoresis Study on Thylakoids Isolated from Poplar Leaves Reveals a Negative Impact of Ozone Exposure on Membrane Proteins. Journal of Proteome Research, 2011, 10, 3003-3011.	3.7	20
128	Proteomic analysis of plasma samples from patients with acute myocardial infarction identifies haptoglobin as a potential prognostic biomarker. Journal of Proteomics, 2011, 75, 229-236.	2.4	50
129	The use of 2D-electrophoresis and de novo sequencing to characterize inter- and intra-cultivar protein polymorphisms in an allopolyploid crop. Phytochemistry, 2011, 72, 1243-1250.	2.9	33
130	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
131	Alteration of plasma membrane-bound redox systems of iron deficient pea roots by chitosan. Journal of Proteomics, 2011, 74, 1437-1449.	2.4	35
132	Proteins associated with cork formation in Quercus suber L. stem tissues. Journal of Proteomics, 2011, 74, 1266-1278.	2.4	35
133	Plant proteome changes under abiotic stress — Contribution of proteomics studies to understanding plant stress response. Journal of Proteomics, 2011, 74, 1301-1322.	2.4	700
134	One dry summer: A leaf proteome study on the response of oak to drought exposure. Journal of Proteomics, 2011, 74, 1385-1395.	2.4	49
135	Poplar under drought: Comparison of leaf and cambial proteomic responses. Journal of Proteomics, 2011, 74, 1396-1410.	2.4	46
136	Plant proteomics in Europe $\hat{a} \in \mathbb{C}$ COST action FA0603. Journal of Proteomics, 2011, 74, 1161-1164.	2.4	2
137	Proteomics research on forest trees, the most recalcitrant and orphan plant species. Phytochemistry, 2011, 72, 1219-1242.	2.9	108
138	Human Muscle Proteome Modifications after Acute or Repeated Eccentric Exercises. Medicine and Science in Sports and Exercise, 2011, 43, 2281-2296.	0.4	52
139	Poplar Proteomics. , 2011, , 128-165.		1
140	Toxin Induction and Protein Extraction from Fusarium spp. Cultures for Proteomic Studies. Journal of Visualized Experiments, 2010, , .	0.3	4
141	Acute metal stress in <i>Populus tremula</i> × <i>P. alba</i> (717â€1B4 genotype): Leaf and cambial proteome changes induced by cadmium ²⁺ . Proteomics, 2010, 10, 349-368.	2.2	94
142	Proteomics of life at low temperatures: trigger factor is the primary chaperone in the Antarctic bacterium <i>Pseudoalteromonas haloplanktis</i> TAC125. Molecular Microbiology, 2010, 76, 120-132.	2.5	91
143	Differential impact of chronic ozone exposure on expanding and fully expanded poplar leaves. Tree Physiology, 2010, 30, 1415-1432.	3.1	30
144	Plant Biotic Stress and Proteomics. Current Proteomics, 2010, 7, 275-297.	0.3	24

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145	Difference Gel Electrophoresis as a Tool to Discover Stress-Regulated Proteins. Methods in Molecular Biology, 2010, 639, 207-218.	0.9	0
146	Potato (Solanum tuberosum L.) tuber ageing induces changes in the proteome and antioxidants associated with the sprouting pattern. Journal of Experimental Botany, 2009, 60, 1273-1288.	4.8	47
147	The impact of atmospheric composition on plants: A case study of ozone and poplar. Mass Spectrometry Reviews, 2009, 28, 495-516.	5.4	64
148	Proteomic evaluation of woundâ€healing processes in potato (<i>Solanum tuberosum</i> L.) tuber tissue. Proteomics, 2009, 9, 4154-4175.	2.2	39
149	Recent developments in the application of proteomics to the analysis of plant responses to heavy metals. Proteomics, 2009, 9, 2602-2621.	2.2	215
150	Proteomic and enzymatic response of poplar to cadmium stress. Journal of Proteomics, 2009, 72, 379-396.	2.4	121
151	Taking Advantage of Nonspecific Trypsin Cleavages for the Identification of Seed Storage Proteins in Cereals. Journal of Proteome Research, 2009, 8, 3182-3190.	3.7	16
152	Effects of the Endocrine Disruptors Atrazine and PCB 153 on the Protein Expression of MCF-7 Human Cells. Journal of Proteome Research, 2009, 8, 5485-5496.	3.7	94
153	Combining Proteomics and Metabolite Analyses To Unravel Cadmium Stress-Response in Poplar Leaves. Journal of Proteome Research, 2009, 8, 400-417.	3.7	142
154	The Proapoptotic C16-ceramide-Dependent Pathway Requires the Death-Promoting Factor Btf in Colon Adenocarcinoma Cells. Journal of Proteome Research, 2009, 8, 4810-4822.	3.7	43
155	Identification of proteins from potato leaves submitted to chilling temperature , 2009, , 279-292.		8
156	Quantitative proteomic analysis of short photoperiod and low-temperature responses in bark tissues of peach (Prunus persica L. Batsch). Tree Genetics and Genomes, 2008, 4, 589-600.	1.6	101
157	Embryo-specific Proteins in Cyclamen persicum Analyzed with 2-D DIGE. Journal of Plant Growth Regulation, 2008, 27, 353-369.	5.1	56
158	Quantitative changes in protein expression of cadmiumâ€exposed poplar plants. Proteomics, 2008, 8, 2514-2530.	2.2	200
159	Comparative proteomic study of arsenicâ€induced differentially expressed proteins in rice roots reveals glutathione plays a central role during As stress. Proteomics, 2008, 8, 3561-3576.	2.2	243
160	Proteome analysis of nonâ€model plants: A challenging but powerful approach. Mass Spectrometry Reviews, 2008, 27, 354-377.	5.4	180
161	Proteomic changes in rat hippocampus and adrenals following short-term sleep deprivation. Proteome Science, 2008, 6, 14.	1.7	38
162	Gene expression in potato during cold exposure: Changes in carbohydrate and polyamine metabolisms. Plant Science, 2008, 175, 839-852.	3.6	64

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