

Paul A Haynes

List of Publications by Year in descending order

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166
papers

9,010
citations

41258

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h-index

46693

89
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178
all docs

178
docs citations

178
times ranked

11803
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomics study reveals the molecular mechanisms underlying cryotolerance induced by mild sublethal stress in human sperm. <i>Cell and Tissue Research</i> , 2022, 387, 143-157.	1.5	9
2	Patterns of gene expression in pollen of cotton (<i>Gossypium hirsutum</i>) indicate downregulation as a feature of thermotolerance. <i>Plant Journal</i> , 2022, 109, 965-979.	2.8	4
3	Genome survey sequencing of wild cotton (<i>Gossypium robinsonii</i>) reveals insights into proteomic responses of pollen to extreme heat. <i>Plant, Cell and Environment</i> , 2022, 45, 1242-1256.	2.8	4
4	Development of a novel minimally invasive sampling and analysis technique using skin sampling tape strips for bioarchaeological proteomics. <i>Journal of Archaeological Science</i> , 2022, 139, 105548.	1.2	8
5	Multiple Abiotic Stresses Applied Simultaneously Elicit Distinct Responses in Two Contrasting Rice Cultivars. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1739.	1.8	11
6	Comparative <i>Pistacia vera</i> leaf proteomics in response to herbivory of the common pistachio psylla (<i>Agonoscaena pistaciae</i>). <i>Arthropod-Plant Interactions</i> , 2022, 16, 215-226.	0.5	4
7	Key Genes and Biochemical Networks in Various Brain Regions Affected in Alzheimer's Disease. <i>Cells</i> , 2022, 11, 987.	1.8	16
8	Pollen development in cotton (<i>Gossypium hirsutum</i>) is highly sensitive to heat exposure during the tetrad stage. <i>Plant, Cell and Environment</i> , 2021, 44, 2150-2166.	2.8	29
9	Quantitative proteomics analysis of high and low polyphenol expressing recombinant inbred lines (RILs) of peanut (<i>Arachis hypogaea</i> L.). <i>Food Chemistry</i> , 2021, 334, 127517.	4.2	3
10	Comparison of protein and peptide fractionation approaches in protein identification and quantification from <i>Saccharomyces cerevisiae</i> . <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2021, 1162, 122453.	1.2	4
11	PeptideMind – Applying machine learning algorithms to assess replicate quality in shotgun proteomic data. <i>SoftwareX</i> , 2021, 13, 100644.	1.2	0
12	The phosphoproteome of rice leaves responds to water and nitrogen supply. <i>Molecular Omics</i> , 2021, 17, 706-718.	1.4	5
13	Mouse model of Alzheimer's disease demonstrates differential effects of early disease pathology on various brain regions. <i>Proteomics</i> , 2021, 21, e2000213.	1.3	5
14	Mitochondrial dysfunction in Alzheimer's disease - a proteomics perspective. <i>Expert Review of Proteomics</i> , 2021, 18, 295-304.	1.3	27
15	A Proteomic View of Cellular and Molecular Effects of Cannabis. <i>Biomolecules</i> , 2021, 11, 1411.	1.8	11
16	Comparative Analysis of Aducanumab, Zaganemab and Pioglitazone as Targeted Treatment Strategies for Alzheimer's Disease. , 2021, 12, 1964.		35
17	Retinal proteomics of experimental glaucoma model reveal intraocular pressure-induced mediators of neurodegenerative changes. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 4931-4944.	1.2	21
18	Wild and Cultivated Species of Rice Have Distinctive Proteomic Responses to Drought. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5980.	1.8	14

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19	PeptideWitchâ€”A Software Package to Produce High-Stringency Proteomics Data Visualizations from Label-Free Shotgun Proteomics Data. <i>Proteomes</i> , 2020, 8, 21.	1.7	3
20	Comparative Leaf Proteomics of Brassica napus Genotypes with Distinctive Levels of Early Cold Acclimation. <i>Plant Molecular Biology Reporter</i> , 2020, 39, 317.	1.0	3
21	Proteomic Responses to Drought Vary Widely Among Eight Diverse Genotypes of Rice (<i>Oryza sativa</i>). <i>International Journal of Molecular Sciences</i> , 2020, 21, 363.	1.8	23
22	Statistics in Proteomics: A Meta-analysis of 100 Proteomics Papers Published in 2019. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1337-1343.	1.2	4
23	Amyloid-beta peptide neurotoxicity in human neuronal cells is associated with modulation of insulin-like growth factor transport, lysosomal machinery and extracellular matrix receptor interactions. <i>Neural Regeneration Research</i> , 2020, 15, 2131.	1.6	8
24	Front Cover: Plantâ€”Microbe Symbiosis: What Has Proteomics Taught Us?. <i>Proteomics</i> , 2019, 19, 1970141.	1.3	1
25	Front Cover: Proteomes of Leafâ€”Growing Zones in Rice Genotypes with Contrasting Drought Tolerance. <i>Proteomics</i> , 2019, 19, 1970071.	1.3	1
26	Upregulation of Proteolytic Pathways and Altered Protein Biosynthesis Underlie Retinal Pathology in a Mouse Model of Alzheimerâ€™s Disease. <i>Molecular Neurobiology</i> , 2019, 56, 6017-6034.	1.9	41
27	Plantâ€”Microbe Symbiosis: What Has Proteomics Taught Us?. <i>Proteomics</i> , 2019, 19, e1800105.	1.3	22
28	Proteomes of Leafâ€”Growing Zones in Rice Genotypes with Contrasting Drought Tolerance. <i>Proteomics</i> , 2019, 19, 1800310.	1.3	9
29	Amyloid β Induces Early Changes in the Ribosomal Machinery, Cytoskeletal Organization and Oxidative Phosphorylation in Retinal Photoreceptor Cells. <i>Frontiers in Molecular Neuroscience</i> , 2019, 12, 24.	1.4	28
30	Evidence from the proteome for local adaptation to extreme heat in a widespread tree species. <i>Functional Ecology</i> , 2019, 33, 436-446.	1.7	9
31	The Quest for Missing Proteins in Rice. <i>Molecular Plant</i> , 2019, 12, 4-6.	3.9	8
32	Label-free and isobaric tandem mass tag (TMT) multiplexed quantitative proteomic data of two contrasting rice cultivars exposed to drought stress and recovery. <i>Data in Brief</i> , 2019, 22, 697-702.	0.5	5
33	Root endophytic fungus <i>Piriformospora indica</i> improves drought stress adaptation in barley by metabolic and proteomic reprogramming. <i>Environmental and Experimental Botany</i> , 2019, 157, 197-210.	2.0	80
34	Prospective Isolation of ISL1+ Cardiac Progenitors from Human ESCs for Myocardial Infarction Therapy. <i>Stem Cell Reports</i> , 2018, 10, 848-859.	2.3	23
35	Differential protein expression and post-translational modifications in metronidazole-resistant <i>Giardia duodenalis</i> . <i>GigaScience</i> , 2018, 7, .	3.3	41
36	Surface markers of human embryonic stem cells: a meta analysis of membrane proteomics reports. <i>Expert Review of Proteomics</i> , 2018, 15, 911-922.	1.3	8

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37	The Art of Validating Quantitative Proteomics Data. <i>Proteomics</i> , 2018, 18, e1800222.	1.3	25
38	Potential protein biomarkers of QX disease resistance in selectively bred Sydney Rock Oysters. <i>Aquaculture</i> , 2018, 495, 144-152.	1.7	10
39	Discovery of Novel Cell Surface Markers for Purification of Embryonic Dopamine Progenitors for Transplantation in Parkinson's Disease Animal Models. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1670-1684.	2.5	23
40	Shotgun proteomic analysis of photoperiod regulated dormancy induction in grapevine. <i>Journal of Proteomics</i> , 2018, 187, 13-24.	1.2	14
41	Quantitative proteomic analysis of human testis reveals system-wide molecular and cellular pathways associated with non-obstructive azoospermia. <i>Journal of Proteomics</i> , 2017, 162, 141-154.	1.2	24
42	Age-related neurodegenerative disease associated pathways identified in retinal and vitreous proteome from human glaucoma eyes. <i>Scientific Reports</i> , 2017, 7, 12685.	1.6	105
43	Low Focal Adhesion Signaling Promotes Ground State Pluripotency of Mouse Embryonic Stem Cells. <i>Journal of Proteome Research</i> , 2017, 16, 3585-3595.	1.8	23
44	Proteomics of Rice—Our Most Valuable Food Crop. , 2017, , 17-33.		2
45	Proteomic Analysis of Disease in Sydney Rock Oysters. , 2017, , 343-357.		1
46	Quantitative shotgun proteomics reveals extensive changes to the proteome of the orbitofrontal cortex in rats that are hyperactive following withdrawal from a high sugar diet. <i>Proteomics</i> , 2016, 16, 657-673.	1.3	10
47	Induction of virulence factors in <i>Giardia duodenalis</i> independent of host attachment. <i>Scientific Reports</i> , 2016, 6, 20765.	1.6	47
48	Proteome Analysis of Ground State Pluripotency. <i>Scientific Reports</i> , 2016, 5, 17985.	1.6	31
49	Relative quantification of phosphoproteomic changes in grapevine (<i>Vitis vinifera</i> L.) leaves in response to abscisic acid. <i>Horticulture Research</i> , 2016, 3, 16029.	2.9	15
50	Quantitative proteomic analysis of two different rice varieties reveals that drought tolerance is correlated with reduced abundance of photosynthetic machinery and increased abundance of ClpD1 protease. <i>Journal of Proteomics</i> , 2016, 143, 73-82.	1.2	50
51	Extended exposure to sugar and/or caffeine produces distinct behavioral and neurochemical profiles in the orbitofrontal cortex of rats: Implications for neural function. <i>Proteomics</i> , 2016, 16, 2894-2910.	1.3	2
52	Biomarkers of Winter Mortality resistance in selectively bred Sydney rock oysters (<i>Saccostrea</i>) Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 142	1.7	10
53	The biology of environmental stress: molecular biomarkers in Sydney rock oysters (<i>Saccostrea</i>) Tj ETQq1 1 0.784314 rgBT /Oyerlock 10	1.7	10
54	Data quality issues in proteomics - there are many paths to enlightenment. <i>Proteomics</i> , 2016, 16, 2433-2434.	1.3	2

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55	Applications of Quantitative Proteomics in Plant Research. , 2016, , 1-29.		5
56	Post-translational processing targets functionally diverse proteins in <i>Mycoplasma hyopneumoniae</i> . Open Biology, 2016, 6, 150210.	1.5	53
57	Identification of proteins from 4200-year-old skin and muscle tissue biopsies from ancient Egyptian mummies of the first intermediate period shows evidence of acute inflammation and severe immune response. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2016, 374, 20150373.	1.6	11
58	Quantitative proteomics in <i>Giardia duodenalis</i> – Achievements and challenges. Molecular and Biochemical Parasitology, 2016, 208, 96-112.	0.5	20
59	Multiple testing corrections in quantitative proteomics: A useful but blunt tool. Proteomics, 2016, 16, 2448-2453.	1.3	141
60	Quantitative Proteomic Analysis of the Orbital Frontal Cortex in Rats Following Extended Exposure to Caffeine Reveals Extensive Changes to Protein Expression: Implications for Neurological Disease. Journal of Proteome Research, 2016, 15, 1455-1471.	1.8	8
61	PlantPRoS: A database for plant proteome response to stress. Journal of Proteomics, 2016, 143, 69-72.	1.2	37
62	Effects of low temperature on tropical and temperate isolates of marine <i>Synechococcus</i> . ISME Journal, 2016, 10, 1252-1263.	4.4	36
63	Five omic technologies are concordant in differentiating the biochemical characteristics of the berries of five grapevine (<i>Vitis vinifera</i> L.) cultivars. BMC Genomics, 2015, 16, 946.	1.2	41
64	Quantitative proteomic analysis of cabernet sauvignon grape cells exposed to thermal stresses reveals alterations in sugar and phenylpropanoid metabolism. Proteomics, 2015, 15, 3048-3060.	1.3	40
65	Protein identification and quantification from riverbank grape, <i>Vitis riparia</i> : Comparing SDS-PAGE and FASP-GPF techniques for shotgun proteomic analysis. Proteomics, 2015, 15, 3061-3065.	1.3	14
66	Quantitative proteomic analysis of <i>Giardia duodenalis</i> assemblage A: A baseline for host, assemblage, and isolate variation. Proteomics, 2015, 15, 2281-2285.	1.3	20
67	Proteomics of Important Food Crops in the Asia Oceania Region: Current Status and Future Perspectives. Journal of Proteome Research, 2015, 14, 2723-2744.	1.8	16
68	Recent Advances in Proteomics Applied to Elucidate the Role of Environmental Impacts on Human Health and Organismal Function. Journal of Proteome Research, 2015, 14, 1-4.	1.8	1
69	The generation gap: Proteome changes and strain variation during encystation in <i>Giardia duodenalis</i> . Molecular and Biochemical Parasitology, 2015, 201, 47-56.	0.5	16
70	Two Splice Variants of Y Chromosome-Located Lysine-Specific Demethylase 5D Have Distinct Function in Prostate Cancer Cell Line (DU-145). Journal of Proteome Research, 2015, 14, 3492-3502.	1.8	35
71	<i>DDX3Y</i> , a Male-Specific Region of Y Chromosome Gene, May Modulate Neuronal Differentiation. Journal of Proteome Research, 2015, 14, 3474-3483.	1.8	61
72	Inter-laboratory evaluation of instrument platforms and experimental workflows for quantitative accuracy and reproducibility assessment. EuPA Open Proteomics, 2015, 8, 6-15.	2.5	32

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73	Data from a proteomic baseline study of Assemblage A in <i>Giardia duodenalis</i> . <i>Data in Brief</i> , 2015, 5, 23-27.	0.5	6
74	Methamphetamine-Induced Sensitization Is Associated with Alterations to the Proteome of the Prefrontal Cortex: Implications for the Maintenance of Psychotic Disorders. <i>Journal of Proteome Research</i> , 2015, 14, 397-410.	1.8	36
75	The Hsp90 inhibitor SNX-7081 is synergistic with fludarabine nucleoside via DNA damage and repair mechanisms in human, p53-negative chronic lymphocytic leukemia. <i>Oncotarget</i> , 2015, 6, 40981-40997.	0.8	9
76	Current perspectives in proteomic analysis of abiotic stress in Grapevines. <i>Frontiers in Plant Science</i> , 2014, 5, 686.	1.7	9
77	Manipulating Root Water Supply Elicits Major Shifts in the Shoot Proteome. <i>Journal of Proteome Research</i> , 2014, 13, 517-526.	1.8	52
78	Proteomic analysis in <i>Giardia duodenalis</i> yields insights into strain virulence and antigenic variation. <i>Proteomics</i> , 2014, 14, 2523-2534.	1.3	27
79	Analysis of Rice Proteins Using SDS-PAGE Shotgun Proteomics. <i>Methods in Molecular Biology</i> , 2014, 1072, 289-302.	0.4	13
80	Proteomic analysis indicates massive changes in metabolism prior to the inhibition of growth and photosynthesis of grapevine (<i>Vitis vinifera</i> L.) in response to water deficit. <i>BMC Plant Biology</i> , 2013, 13, 49.	1.6	122
81	Proteomic analysis of the dorsal and ventral hippocampus of rats maintained on a high fat and refined sugar diet. <i>Proteomics</i> , 2013, 13, 3076-3091.	1.3	25
82	Shotgun Label-Free Quantitative Proteomics of Water-Deficit-Stressed Midmature Peanut (<i>Arachis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.8	31
83	Shotgun proteomics of coelomic fluid from the purple sea urchin, <i>Strongylocentrotus purpuratus</i> . <i>Developmental and Comparative Immunology</i> , 2013, 40, 35-50.	1.0	27
84	A Fresh Look at the Male-specific Region of the Human Y Chromosome. <i>Journal of Proteome Research</i> , 2013, 12, 6-22.	1.8	52
85	Realizing the Potential of Agricultural and Environmental Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 4651-4651.	1.8	1
86	The influence of signals from chilled roots on the proteome of shoot tissues in rice seedlings. <i>Proteomics</i> , 2013, 13, 1922-1933.	1.3	22
87	Label-Free Quantitative Shotgun Proteomics Using Normalized Spectral Abundance Factors. <i>Methods in Molecular Biology</i> , 2013, 1002, 205-222.	0.4	56
88	Plant Proteogenomics: From Protein Extraction to Improved Gene Predictions. <i>Methods in Molecular Biology</i> , 2013, 1002, 267-294.	0.4	14
89	Shotgun Proteomic Analysis of the Mexican Lime Tree Infected with <i>Candidatus Phytoplasma aurantifolia</i> . <i>Journal of Proteome Research</i> , 2013, 12, 785-795.	1.8	54
90	Promoting Agriculture Proteome Research Activities in the Asia and Oceania Region. <i>Journal of Proteome Research</i> , 2012, 11, 1461-1461.	1.8	1

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91	Proteomic discovery of biomarkers of metal contamination in Sydney Rock oysters (<i>Saccostrea</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.9	59
92	Degradation of white wine haze proteins by Aspergillopepsin I and II during juice flash pasteurization. <i>Food Chemistry</i> , 2012, 135, 1157-1165.	4.2	89
93	Time course proteomic profiling of cellular responses to immunological challenge in the sea urchin, <i>Heliocidaris erythrogramma</i> . <i>Developmental and Comparative Immunology</i> , 2012, 37, 243-256.	1.0	17
94	Shotgun Proteomic Analysis of Long-distance Drought Signaling in Rice Roots. <i>Journal of Proteome Research</i> , 2012, 11, 348-358.	1.8	92
95	PloGO: Plotting gene ontology annotation and abundance in multi-condition proteomics experiments. <i>Proteomics</i> , 2012, 12, 406-410.	1.3	30
96	Differential regulation of aquaporins, small GTPases and V-ATPases proteins in rice leaves subjected to drought stress and recovery. <i>Proteomics</i> , 2012, 12, 864-877.	1.3	72
97	Quantitative proteomics of heavy metal stress responses in Sydney rock oysters. <i>Proteomics</i> , 2012, 12, 906-921.	1.3	51
98	Roles of Grape Thaumatin-like Protein and Chitinase in White Wine Haze Formation. <i>Journal of Agricultural and Food Chemistry</i> , 2011, 59, 733-740.	2.4	79
99	Comparative Protein Expression in Different Strains of the Bloom-forming Cyanobacterium <i>Microcystis aeruginosa</i> . <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003749.	2.5	54
100	5.26 Hsp90 Inhibitor Restores P53-Mutated MEC1 Chronic Lymphocytic Leukemia Cell Sensitivity to Fludarabine by Downregulating DNA Repair and Endoplasmic Reticulum Chaperone Proteins. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2011, 11, S260-S261.	0.2	0
101	A proteomic analysis of the effects of metal contamination on Sydney Rock Oyster (<i>Saccostrea</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.9	53
102	Comparative proteomic analysis of a sea urchin (<i>Heliocidaris erythrogramma</i>) antibacterial response revealed the involvement of apextrin and calreticulin. <i>Journal of Invertebrate Pathology</i> , 2011, 106, 223-229.	1.5	34
103	Mammalian forebrain ketimine reductase identified as β -crystallin; potential regulation by thyroid hormones. <i>Journal of Neurochemistry</i> , 2011, 118, 379-387.	2.1	59
104	Shotgun proteomic profiling of five species of New Zealand <i>Pachycladon</i> . <i>Proteomics</i> , 2011, 11, 166-171.	1.3	14
105	Less label, more free: Approaches in label-free quantitative mass spectrometry. <i>Proteomics</i> , 2011, 11, 535-553.	1.3	613
106	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.	1.3	31
107	Quantitative proteomic analysis of cold-responsive proteins in rice. <i>Proteomics</i> , 2011, 11, 1696-1706.	1.3	109
108	Differential proteomic response of rice (<i>Oryza sativa</i>) leaves exposed to high and low temperature stress. <i>Proteomics</i> , 2011, 11, 2839-2850.	1.3	59

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109	Plant Proteomics. <i>Proteomics</i> , 2011, 11, 1557-1558.	1.3	10
110	Liver Membrane Proteome Glycosylation Changes in Mice Bearing an Extra-hepatic Tumor. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M900538-MCP200.	2.5	38
111	Transcript and protein profiling identify candidate gene sets of potential adaptive significance in New Zealand <i>Pachycladon</i> . <i>BMC Evolutionary Biology</i> , 2010, 10, 151.	3.2	19
112	Proteomic analysis of temperature stress in plants. <i>Proteomics</i> , 2010, 10, 828-845.	1.3	91
113	Differential metabolic response of cultured rice (<i>Oryza sativa</i>) cells exposed to high and low temperature stress. <i>Proteomics</i> , 2010, 10, 3001-3019.	1.3	82
114	NF45 and NF90 Regulate HS4-dependent Interleukin-13 Transcription in T Cells. <i>Journal of Biological Chemistry</i> , 2010, 285, 8256-8267.	1.6	52
115	Physiological and molecular changes in <i>Oryza meridionalis</i> Ng., a heat-tolerant species of wild rice. <i>Journal of Experimental Botany</i> , 2010, 61, 191-202.	2.4	159
116	Engineered Rings of Mixed Yeast Lsm Proteins Show Differential Interactions with Translation Factors and U-Rich RNA. <i>Biochemistry</i> , 2010, 49, 2335-2345.	1.2	13
117	Partial Characterization of a Vicilin-Like Glycoprotein from Seeds of Flowering Tobacco (<i>Nicotiana glauca</i>). <i>Journal of Proteome Research</i> , 2010, 9, 1078-1084.	1.2	4
118	Proteomic analysis of a filamentous fungal endophyte using EST datasets. <i>Proteomics</i> , 2009, 9, 2295-2300.	1.3	7
119	Rat Liver Membrane Glycoproteome: Enrichment by Phase Partitioning and Glycoprotein Capture. <i>Journal of Proteome Research</i> , 2009, 8, 770-781.	1.8	63
120	Two-Step Purification of Pathogenesis-Related Proteins from Grape Juice and Crystallization of Thaumatin-like Proteins. <i>Journal of Agricultural and Food Chemistry</i> , 2009, 57, 11376-11382.	2.4	49
121	Grape and Wine Proteins: Their Fractionation by Hydrophobic Interaction Chromatography and Identification by Chromatographic and Proteomic Analysis. <i>Journal of Agricultural and Food Chemistry</i> , 2009, 57, 4415-4425.	2.4	76
122	Proteomic analysis of <i>Drosophila mojavensis</i> male accessory glands suggests novel classes of seminal fluid proteins. <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 366-371.	1.2	50
123	Crystal Structure of Lsm3 Octamer from <i>Saccharomyces cerevisiae</i> : Implications for Lsm Ring Organisation and Recruitment. <i>Journal of Molecular Biology</i> , 2008, 377, 1357-1371.	2.0	29
124	Characterization of the Rat Liver Membrane Proteome Using Peptide Immobilized pH Gradient Isoelectric Focusing. <i>Journal of Proteome Research</i> , 2008, 7, 1036-1045.	1.8	51
125	A Combination of Immobilised pH Gradients Improves Membrane Proteomics. <i>Journal of Proteome Research</i> , 2008, 7, 4974-4981.	1.8	27
126	Two-Dimensional Differential In-Gel Electrophoresis (DIGE) of Leaf and Roots of <i>Lycopersicon esculentum</i> . <i>Journal of Proteome Research</i> , 2007, 6, 157-174.		7

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127	Two-Dimensional Nanoflow Liquid Chromatography-Tandem Mass Spectrometry of Proteins Extracted from Rice Leaves and Roots. , 2007, 355, 249-266.		5
128	Proteomic Analysis of Shade-Avoidance Response in Tomato Leaves. Journal of Agricultural and Food Chemistry, 2007, 55, 8310-8318.	2.4	13
129	Subcellular shotgun proteomics in plants: Looking beyond the usual suspects. Proteomics, 2007, 7, 2963-2975.	1.3	64
130	Identification of Proteins from a Cell Wall Fraction of the Diatom <i>Thalassiosira pseudonana</i> . Molecular and Cellular Proteomics, 2006, 5, 182-193.	2.5	131
131	Protein Expression Profiling of <i>Coccidioides posadasii</i> by Two-Dimensional Differential In-Gel Electrophoresis and Evaluation of a Newly Recognized Peroxisomal Matrix Protein as a Recombinant Vaccine Candidate. Infection and Immunity, 2006, 74, 1865-1872.	1.0	44
132	The wildcat toolbox: a set of perl script utilities for use in peptide mass spectral database searching and proteomics experiments. Journal of Biomolecular Techniques, 2006, 17, 97-102.	0.8	6
133	Verification of single-peptide protein identifications by the application of complementary database search algorithms. Journal of Biomolecular Techniques, 2006, 17, 327-32.	0.8	20
134	Comprehensive proteomics in yeast using chromatographic fractionation, gas phase fractionation, protein gel electrophoresis, and isoelectric focusing. Proteomics, 2005, 5, 2018-2028.	1.3	90
135	Analysis of secreted proteins from <i>Aspergillus flavus</i> . Proteomics, 2005, 5, 3153-3161.	1.3	91
136	Composition and Structure of the 80S Ribosome from the Green Alga <i>Chlamydomonas reinhardtii</i> : 80S Ribosomes are Conserved in Plants and Animals. Journal of Molecular Biology, 2005, 351, 266-279.	2.0	33
137	Protein Disulfide Bond Formation in the Cytoplasm during Oxidative Stress. Journal of Biological Chemistry, 2004, 279, 21749-21758.	1.6	391
138	Investigative proteomics: Identification of an unknown plant virus from infected plants using mass spectrometry. Journal of the American Society for Mass Spectrometry, 2003, 14, 736-741.	1.2	79
139	Mass spectrometric analysis of the editosome and other multiprotein complexes in <i>Trypanosoma brucei</i> . Journal of the American Society for Mass Spectrometry, 2003, 14, 728-735.	1.2	59
140	High-throughput functional affinity purification of mannose binding proteins from <i>Oryza sativa</i> . Proteomics, 2003, 3, 1270-1278.	1.3	37
141	Development of a System for the Study of Protein-Protein Interactions in Plants: Characterization of a TATA-Box Binding Protein Complex in <i>Oryza sativa</i> . Journal of Proteome Research, 2003, 2, 514-522.	1.8	14
142	Proteomic Characterization of the <i>Chlamydomonas reinhardtii</i> Chloroplast Ribosome. Journal of Biological Chemistry, 2003, 278, 33774-33785.	1.6	108
143	Proteomic Characterization of the Small Subunit of <i>Chlamydomonas reinhardtii</i> Chloroplast Ribosome. Plant Cell, 2002, 14, 2957-2974.	3.1	78
144	Induction of Cachexia in Mice by Systemically Administered Myostatin. Science, 2002, 296, 1486-1488.	6.0	829

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145	Proteomic survey of metabolic pathways in rice. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11969-11974.	3.3	386
146	Proteomic characterization of wheat amyloplasts using identification of proteins by tandem mass spectrometry. Proteomics, 2002, 2, 1156-1168.	1.3	195
147	The functional proteomics toolbox: methods and applications. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2002, 782, 165-181.	1.2	62
148	Smooth Muscle Cell Phenotypic Transition Associated With Calcification. Circulation Research, 2001, 89, 1147-1154.	2.0	753
149	Proteome Profiling—Pitfalls and Progress. Yeast, 2000, 1, 81-87.	0.8	78
150	Simultaneous Detection and Identification of O-GlcNAc-Modified Glycoproteins Using Liquid Chromatography—Tandem Mass Spectrometry. Analytical Chemistry, 2000, 72, 5402-5410.	3.2	76
151	Towards an Integrated Analytical Technology for the Generation of Multidimensional Protein Expression Maps. , 2000, , 143-162.		3
152	Proteins of rat serum: III. Gender-related differences in protein concentration under baseline conditions and upon experimental inflammation as evaluated by two-dimensional electrophoresis. Electrophoresis, 1999, 20, 836-845.	1.3	46
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