## Paul A Haynes

List of Publications by Year in descending order

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		41258	4	6693
166	9,010	49		89
papers	citations	h-index		g-index
178	178	178		11803
all docs	docs citations	times ranked		citing authors

#	Article	IF	CITATIONS
1	Induction of Cachexia in Mice by Systemically Administered Myostatin. Science, 2002, 296, 1486-1488.	6.0	829
2	Smooth Muscle Cell Phenotypic Transition Associated With Calcification. Circulation Research, 2001, 89, 1147-1154.	2.0	753
3	Less label, more free: Approaches in labelâ€free quantitative mass spectrometry. Proteomics, 2011, 11, 535-553.	1.3	613
4	Protein Disulfide Bond Formation in the Cytoplasm during Oxidative Stress. Journal of Biological Chemistry, 2004, 279, 21749-21758.	1.6	391
5	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
6	Proteomic characterization of wheat amyloplasts using identification of proteins by tandem mass spectrometry. Proteomics, 2002, 2, 1156-1168.	1.3	195
7	Oligopeptidase B-dependent signaling mediates host cell invasion by Trypanosoma cruzi. EMBO Journal, 1998, 17, 4975-4986.	3.5	172
8	Physiological and molecular changes in Oryza meridionalis Ng., a heat-tolerant species of wild rice. Journal of Experimental Botany, 2010, 61, 191-202.	2.4	159
9	Proteome analysis: Biological assay or data archive?. Electrophoresis, 1998, 19, 1862-1871.	1.3	141
10	Multiple testing corrections in quantitative proteomics: A useful but blunt tool. Proteomics, 2016, 16, 2448-2453.	1.3	141
11	Identification of Proteins from a Cell Wall Fraction of the Diatom Thalassiosira pseudonana. Molecular and Cellular Proteomics, 2006, 5, 182-193.	2.5	131
12	Proteomic analysis indicates massive changes in metabolism prior to the inhibition of growth and photosynthesis of grapevine (Vitis vinifera L.) in response to water deficit. BMC Plant Biology, 2013, 13, 49.	1.6	122
13	Quantitative proteomic analysis of coldâ€responsive proteins in rice. Proteomics, 2011, 11, 1696-1706.	1.3	109
14	Proteomic Characterization of the Chlamydomonas reinhardtii Chloroplast Ribosome. Journal of Biological Chemistry, 2003, 278, 33774-33785.	1.6	108
15	Age-related neurodegenerative disease associated pathways identified in retinal and vitreous proteome from human glaucoma eyes. Scientific Reports, 2017, 7, 12685.	1.6	105
16	Shotgun Proteomic Analysis of Long-distance Drought Signaling in Rice Roots. Journal of Proteome Research, 2012, 11, 348-358.	1.8	92
17	Analysis of secreted proteins fromAspergillus flavus. Proteomics, 2005, 5, 3153-3161.	1.3	91
18	Proteomic analysis of temperature stress in plants. Proteomics, 2010, 10, 828-845.	1.3	91

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19	Amino acid analysis using derivatisation with 9-fluorenylmethyl chloroformate and reversed-phase high-performance liquid chromatography. Journal of Chromatography A, 1991, 540, 177-185.	1.8	90
20	Comprehensive proteomics in yeast using chromatographic fractionation, gas phase fractionation, protein gel electrophoresis, and isoelectric focusing. Proteomics, 2005, 5, 2018-2028.	1.3	90
21	Degradation of white wine haze proteins by Aspergillopepsin I and II during juice flash pasteurization. Food Chemistry, 2012, 135, 1157-1165.	4.2	89
22	Differential metabolic response of cultured rice ( <i>Oryza sativa</i> ) cells exposed to high―and lowâ€ŧemperature stress. Proteomics, 2010, 10, 3001-3019.	1.3	82
23	Applications of automated amino acid analysis using 9-fluorenylmethyl chloroformate. Journal of Chromatography A, 1991, 588, 107-114.	1.8	80
24	Root endophytic fungus Piriformospora indica improves drought stress adaptation in barley by metabolic and proteomic reprogramming. Environmental and Experimental Botany, 2019, 157, 197-210.	2.0	80
25	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
26	Roles of Grape Thaumatin-like Protein and Chitinase in White Wine Haze Formation. Journal of Agricultural and Food Chemistry, 2011, 59, 733-740.	2.4	79
27	Proteome Profiling—Pitfalls and Progress. Yeast, 2000, 1, 81-87.	0.8	78
28	Proteomic Characterization of the Small Subunit of Chlamydomonas reinhardtii Chloroplast Ribosome. Plant Cell, 2002, 14, 2957-2974.	3.1	78
29	Simultaneous Detection and Identification of O-GlcNAc-Modified Glycoproteins Using Liquid Chromatographyâ^Tandem Mass Spectrometry. Analytical Chemistry, 2000, 72, 5402-5410.	3.2	76
30	Grape and Wine Proteins: Their Fractionation by Hydrophobic Interaction Chromatography and Identification by Chromatographic and Proteomic Analysis. Journal of Agricultural and Food Chemistry, 2009, 57, 4415-4425.	2.4	76
31	Differential regulation of aquaporins, small <scp>GTP</scp> ases and <scp>V</scp> â€ <scp>ATP</scp> ases proteins in rice leaves subjected to drought stress and recovery. Proteomics, 2012, 12, 864-877.	1.3	72
32	Phosphoglycosylation: A new structural class of glycosylation?. Glycobiology, 1998, 8, 1-5.	1.3	70
33	Characterization of the Trypanosoma brucei homologue of a Trypanosoma cruzi flagellum-adhesion glycoprotein. Molecular and Biochemical Parasitology, 1996, 82, 245-255.	0.5	69
34	Identification of gel-separated proteins by liquid chromatography-electrospray tandem mass spectrometry: Comparison of methods and their limitations. Electrophoresis, 1998, 19, 939-945.	1.3	68
35	Subcellular shotgun proteomics in plants: Looking beyond the usual suspects. Proteomics, 2007, 7, 2963-2975.	1.3	64
36	Rat Liver Membrane Glycoproteome: Enrichment by Phase Partitioning and Glycoprotein Capture. Journal of Proteome Research, 2009, 8, 770-781.	1.8	63

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37	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
38	<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
39	Mass spectrometric analysis of the editosome and other multiprotein complexes in Trypanosoma brucei. Journal of the American Society for Mass Spectrometry, 2003, 14, 728-735.	1.2	59
40	Mammalian forebrain ketimine reductase identified as μâ€crystallin; potential regulation by thyroid hormones. Journal of Neurochemistry, 2011, 118, 379-387.	2.1	59
41	Differential proteomic response of rice ( <i>Oryza sativa</i> ) leaves exposed to high―and low―emperature stress. Proteomics, 2011, 11, 2839-2850.	1.3	59
42	Proteomic discovery of biomarkers of metal contamination in Sydney Rock oysters (Saccostrea) Tj ETQq0 0 0 rgl	BT <u> O</u> verlo	ck 10 Tf 50 5
43	Post-translational modifications of the Dictyostelium discoideum glycoprotein PsA. Glycosylphosphatidylinositol membrane anchor and composition of O-linked oligosaccharides. FEBS Journal, 1993, 216, 729-737.	0.2	58
44	Label-Free Quantitative Shotgun Proteomics Using Normalized Spectral Abundance Factors. Methods in Molecular Biology, 2013, 1002, 205-222.	0.4	56
45	Comparative Protein Expression in Different Strains of the Bloom-forming Cyanobacterium Microcystis aeruginosa. Molecular and Cellular Proteomics, 2011, 10, M110.003749.	2.5	54
46	Shotgun Proteomic Analysis of the Mexican Lime Tree Infected with " <i>CandidatusPhytoplasma aurantifolia</i> ― Journal of Proteome Research, 2013, 12, 785-795.	1.8	54
47	A proteomic analysis of the effects of metal contamination on Sydney Rock Oyster (Saccostrea) Tj ETQq $1\ 1\ 0.78$	4314 rgB <sup>-</sup>	Г/Qyerlock 1
48	Post-translational processing targets functionally diverse proteins in <i>Mycoplasma hyopneumoniae</i> . Open Biology, 2016, 6, 150210.	1.5	53
49	NF45 and NF90 Regulate HS4-dependent Interleukin-13 Transcription in T Cells. Journal of Biological Chemistry, 2010, 285, 8256-8267.	1.6	52
50	A Fresh Look at the Male-specific Region of the Human Y Chromosome. Journal of Proteome Research, 2013, 12, 6-22.	1.8	52
51	Manipulating Root Water Supply Elicits Major Shifts in the Shoot Proteome. Journal of Proteome Research, 2014, 13, 517-526.	1.8	52
52	Characterization of the Rat Liver Membrane Proteome Using Peptide Immobilized pH Gradient Isoelectric Focusing. Journal of Proteome Research, 2008, 7, 1036-1045.	1.8	51
53	Quantitative proteomics of heavy metal stress responses in Sydney rock oysters. Proteomics, 2012, 12, 906-921.	1.3	51
54	Proteomic analysis of Drosophila mojavensis male accessory glands suggests novel classes of seminal fluid proteins. Insect Biochemistry and Molecular Biology, 2009, 39, 366-371.	1.2	50

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55	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. Journal of Proteomics, 2016, 143, 73-82.	1.2	50
56	Two-Step Purification of Pathogenesis-Related Proteins from Grape Juice and Crystallization of Thaumatin-like Proteins. Journal of Agricultural and Food Chemistry, 2009, 57, 11376-11382.	2.4	49
57	Induction of virulence factors in Giardia duodenalis independent of host attachment. Scientific Reports, 2016, 6, 20765.	1.6	47
58	Structural characterization of novel oligosaccharides of cell-surface glycoproteins of Trypanosoma cruzi. Glycobiology, 1996, 6, 869-878.	1.3	46
59	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
60	Protein Expression Profiling of Coccidioides posadasii 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
61	Five omic technologies are concordant in differentiating the biochemical characteristics of the berries of five grapevine (Vitis vinifera L.) cultivars. BMC Genomics, 2015, 16, 946.	1.2	41
62	Differential protein expression and post-translational modifications in metronidazole-resistant Giardia duodenalis. GigaScience, 2018, 7, .	3.3	41
63	Upregulation of Proteolytic Pathways and Altered Protein Biosynthesis Underlie Retinal Pathology in a Mouse Model of Alzheimer's Disease. Molecular Neurobiology, 2019, 56, 6017-6034.	1.9	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	Liver Membrane Proteome Glycosylation Changes in Mice Bearing an Extra-hepatic Tumor. Molecular and Cellular Proteomics, 2011, 10, M900538-MCP200.	2.5	38
66	High-throughput functional affinity purification of mannose binding proteins from Oryza sativa. Proteomics, 2003, 3, 1270-1278.	1.3	37
67	PlantPReS: A database for plant proteome response to stress. Journal of Proteomics, 2016, 143, 69-72.	1.2	37
68	Methamphetamine-Induced Sensitization Is Associated with Alterations to the Proteome of the Prefrontal Cortex: Implications for the Maintenance of Psychotic Disorders. Journal of Proteome Research, 2015, 14, 397-410.	1.8	36
69	Effects of low temperature on tropical and temperate isolates of marine <i>Synechococcus</i> Journal, 2016, 10, 1252-1263.	4.4	36
70	Conservation of the lipooligosaccharide synthesis locus lgt among strains of Neisseria gonorrhoeae: requirement for lgtE in synthesis of the 2C7 epitope and of the beta chain of strain 15253 Journal of Experimental Medicine, 1996, 184, 1233-1241.	4.2	35
71	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
72	Comparative Analysis of Aducanumab, Zagotenemab and Pioglitazone as Targeted Treatment Strategies for Alzheimer's Disease. , 2021, 12, 1964.		35

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73	Comparative proteomic analysis of a sea urchin (Heliocidaris erythrogramma) antibacterial response revealed the involvement of apextrin and calreticulin. Journal of Invertebrate Pathology, 2011, 106, 223-229.	1.5	34
74	Composition and Structure of the 80S Ribosome from the Green Alga Chlamydomonas reinhardtii: 80S Ribosomes are Conserved in Plants and Animals. Journal of Molecular Biology, 2005, 351, 266-279.	2.0	33
75	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
76	Time to articulate a vision for the future of plant proteomics $\hat{a} \in A$ global perspective: An initiative for establishing the International Plant Proteomics Organization (INPPO). Proteomics, 2011, 11, 1559-1568.	1.3	31
77	Shotgun Label-Free Quantitative Proteomics of Water-Deficit-Stressed Midmature Peanut (Arachis) Tj ETQq1 1 0.	.784314 r	gBŢ <sub>1</sub> /Overloc
78	Proteome Analysis of Ground State Pluripotency. Scientific Reports, 2016, 5, 17985.	1.6	31
79	PloGO: Plotting gene ontology annotation and abundance in multiâ€condition proteomics experiments. Proteomics, 2012, 12, 406-410.	1.3	30
80	Crystal Structure of Lsm3 Octamer from Saccharomyces cerevisiae: Implications for Lsm Ring Organisation and Recruitment. Journal of Molecular Biology, 2008, 377, 1357-1371.	2.0	29
81	Pollen development in cotton ( <scp><i>Gossypium hirsutum</i></scp> ) is highly sensitive to heat exposure during the tetrad stage. Plant, Cell and Environment, 2021, 44, 2150-2166.	2.8	29
82	Amyloid $\hat{l}^2$ Induces Early Changes in the Ribosomal Machinery, Cytoskeletal Organization and Oxidative Phosphorylation in Retinal Photoreceptor Cells. Frontiers in Molecular Neuroscience, 2019, 12, 24.	1.4	28
83	A Simplified Gradient Solvent Delivery System for Capillary Liquid Chromatography–Electrospray Ionization Mass Spectrometry. Analytical Biochemistry, 1998, 265, 129-138.	1.1	27
84	A Combination of Immobilised pH Gradients Improves Membrane Proteomics. Journal of Proteome Research, 2008, 7, 4974-4981.	1.8	27
85	Shotgun proteomics of coelomic fluid from the purple sea urchin, Strongylocentrotus purpuratus. Developmental and Comparative Immunology, 2013, 40, 35-50.	1.0	27
86	Proteomic analysis in Giardia duodenalisyields insights into strain virulence and antigenic variation. Proteomics, 2014, 14, 2523-2534.	1.3	27
87	Mitochondrial dysfunction in Alzheimer's disease - a proteomics perspective. Expert Review of Proteomics, 2021, 18, 295-304.	1.3	27
88	Proteomic analysis of the dorsal and ventral hippocampus of rats maintained on a high fat and refined sugar diet. Proteomics, 2013, 13, 3076-3091.	1.3	25
89	The Art of Validating Quantitative Proteomics Data. Proteomics, 2018, 18, e1800222.	1.3	25
90	Quantitative proteomic analysis of human testis reveals system-wide molecular and cellular pathways associated with non-obstructive azoospermia. Journal of Proteomics, 2017, 162, 141-154.	1.2	24

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91	Low Focal Adhesion Signaling Promotes Ground State Pluripotency of Mouse Embryonic Stem Cells. Journal of Proteome Research, 2017, 16, 3585-3595.	1.8	23
92	Prospective Isolation of ISL1+ Cardiac Progenitors from Human ESCs forÂMyocardial Infarction Therapy. Stem Cell Reports, 2018, 10, 848-859.	2.3	23
93	Discovery of Novel Cell Surface Markers for Purification of Embryonic Dopamine Progenitors for Transplantation in Parkinson's Disease Animal Models. Molecular and Cellular Proteomics, 2018, 17, 1670-1684.	2.5	23
94	Proteomic Responses to Drought Vary Widely Among Eight Diverse Genotypes of Rice (Oryza sativa). International Journal of Molecular Sciences, 2020, 21, 363.	1.8	23
95	The influence of signals from chilled roots on the proteome of shoot tissues in rice seedlings. Proteomics, 2013, 13, 1922-1933.	1.3	22
96	Plant–Microbe Symbiosis: What Has Proteomics Taught Us?. Proteomics, 2019, 19, e1800105.	1.3	22
97	Retinal proteomics of experimental glaucoma model reveal intraocular pressureâ€induced mediators of neurodegenerative changes. Journal of Cellular Biochemistry, 2020, 121, 4931-4944.	1.2	21
98	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
99	Quantitative proteomics in Giardia duodenalis —Achievements and challenges. Molecular and Biochemical Parasitology, 2016, 208, 96-112.	0.5	20
100	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
101	Transcript and protein profiling identify candidate gene sets of potential adaptive significance in New Zealand Pachycladon. BMC Evolutionary Biology, 2010, 10, 151.	3.2	19
102	A web site for the Rat Serum Protein Study Group. Electrophoresis, 1999, 20, 3599-3602.	1.3	17
103	Time course proteomic profiling of cellular responses to immunological challenge in the sea urchin, Heliocidaris erythrogramma. Developmental and Comparative Immunology, 2012, 37, 243-256.	1.0	17
104	Characterisation of oligosaccharides from a glycoprotein variant of human serum albumin (albumin) Tj ETQq0 0 0 spectroscopy. Biomedical Applications, 1992, 581, 187-193.	rgBT /Ove 1.7	rlock 10 Tf : 16
105	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
106	The generation gap: Proteome changes and strain variation during encystation in Giardia duodenalis. Molecular and Biochemical Parasitology, 2015, 201, 47-56.	0.5	16
107	Key Genes and Biochemical Networks in Various Brain Regions Affected in Alzheimer's Disease. Cells, 2022, 11, 987.	1.8	16
108	Relative quantification of phosphoproteomic changes in grapevine (Vitis vinifera L.) leaves in response to abscisic acid. Horticulture Research, 2016, 3, 16029.	2.9	15

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109	Development of a System for the Study of Proteinâ <sup>^</sup> Protein Interactionsin Planta:Â Characterization of a TATA-Box Binding Protein Complex inOryza sativa. Journal of Proteome Research, 2003, 2, 514-522.	1.8	14
110	Shotgun proteomic profiling of five species of New Zealand <i>Pachycladon</i> . Proteomics, 2011, 11, 166-171.	1.3	14
111	Plant Proteogenomics: From Protein Extraction to Improved Gene Predictions. Methods in Molecular Biology, 2013, 1002, 267-294.	0.4	14
112	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
113	Shotgun proteomic analysis of photoperiod regulated dormancy induction in grapevine. Journal of Proteomics, 2018, 187, 13-24.	1.2	14
114	Wild and Cultivated Species of Rice Have Distinctive Proteomic Responses to Drought. International Journal of Molecular Sciences, 2020, 21, 5980.	1.8	14
115	Proteomic Analysis of Shade-Avoidance Response in Tomato Leaves. Journal of Agricultural and Food Chemistry, 2007, 55, 8310-8318.	2.4	13
116	Engineered Rings of Mixed Yeast Lsm Proteins Show Differential Interactions with Translation Factors and U-Rich RNA. Biochemistry, 2010, 49, 2335-2345.	1.2	13
117	Analysis of Rice Proteins Using SDS-PAGE Shotgun Proteomics. Methods in Molecular Biology, 2014, 1072, 289-302.	0.4	13
118	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
119	A Proteomic View of Cellular and Molecular Effects of Cannabis. Biomolecules, 2021, 11, 1411.	1.8	11
120	Multiple Abiotic Stresses Applied Simultaneously Elicit Distinct Responses in Two Contrasting Rice Cultivars. International Journal of Molecular Sciences, 2022, 23, 1739.	1.8	11
121	Plant Proteomics. Proteomics, 2011, 11, 1557-1558.	1.3	10
122	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. Proteomics, 2016, 16, 657-673.	1.3	10
123	Biomarkers of Winter Mortality resistance in selectively bred Sydney rock oysters (Saccostrea) Tj ETQq1 1 0.7843	14.rgBT /O	verlock 10
124	The biology of environmental stress: molecular biomarkers in Sydney rock oysters (Saccostrea) Tj ETQq0 0 0 rgBT	/Qyerlock	10 Tf 50 14
125	Potential protein biomarkers of QX disease resistance in selectively bred Sydney Rock Oysters. Aquaculture, 2018, 495, 144-152.	1.7	10
126	Current perspectives in proteomic analysis of abiotic stress in Grapevines. Frontiers in Plant Science, 2014, 5, 686.	1.7	9

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127	Proteomes of Leafâ€Growing Zones in Rice Genotypes with Contrasting Drought Tolerance. Proteomics, 2019, 19, 1800310.	1.3	9
128	Evidence from the proteome for local adaptation to extreme heat in a widespread tree species. Functional Ecology, 2019, 33, 436-446.	1.7	9
129	The Hsp90 inhibitor SNX-7081 is synergistic with fludarabine nucleoside via DNA damage and repair mechanisms in human, p53-negative chronic lymphocytic leukemia. Oncotarget, 2015, 6, 40981-40997.	0.8	9
130	Proteomics study reveals the molecular mechanisms underlying cryotolerance induced by mild sublethal stress in human sperm. Cell and Tissue Research, 2022, 387, 143-157.	1.5	9
131	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
132	Surface markers of human embryonic stem cells: a meta analysis of membrane proteomics reports. Expert Review of Proteomics, 2018, 15, 911-922.	1.3	8
133	The Quest for Missing Proteins in Rice. Molecular Plant, 2019, 12, 4-6.	3.9	8
134	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. Neural Regeneration Research, 2020, 15, 2131.	1.6	8
135	Development of a novel minimally invasive sampling and analysis technique using skin sampling tape strips for bioarchaeological proteomics. Journal of Archaeological Science, 2022, 139, 105548.	1.2	8
136	Two-Dimensional Differential In-Gel Electrophoresis (DIGE) of Leaf and Roots of <i>Lycopersicon esculentum</i> ., 2007, 355, 157-174.		7
137	Proteomic analysis of a filamentous fungal endophyte using EST datasets. Proteomics, 2009, 9, 2295-2300.	1.3	7
138	Differential glycosylation of epitope-tagged glycoprotein Gp72 during the Trypanosoma cruzi life cycle. Molecular and Biochemical Parasitology, 1996, 83, 253-256.	0.5	6
139	Data from a proteomic baseline study of Assemblage A in Giardia duodenalis. Data in Brief, 2015, 5, 23-27.	0.5	6
140	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
141	Two-Dimensional Nanoflow Liquid Chromatography-Tandem Mass Spectrometry of Proteins Extracted from Rice Leaves and Roots., 2007, 355, 249-266.		5
142	Applications of Quantitative Proteomics in Plant Research. , 2016, , 1-29.		5
143	Label-free and isobaric tandem mass tag (TMT) multiplexed quantitative proteomic data of two contrasting rice cultivars exposed to drought stress and recovery. Data in Brief, 2019, 22, 697-702.	0.5	5
144	The phosphoproteome of rice leaves responds to water and nitrogen supply. Molecular Omics, 2021, 17, 706-718.	1.4	5

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145	Mouse model of Alzheimer's disease demonstrates differential effects of early disease pathology on various brain regions. Proteomics, 2021, 21, e2000213.	1.3	5
146	Partial Characterization of a Vicilin-Like Glycoprotein from Seeds of Flowering Tobacco ( <i>Nicotiana) Tj ETQ</i>	q0 0 0 rgBT /0	Overlock 10 T
147	Statistics in Proteomics: A Meta-analysis of 100 Proteomics Papers Published in 2019. Journal of the American Society for Mass Spectrometry, 2020, 31, 1337-1343.	1.2	4
148	Comparison of protein and peptide fractionation approaches in protein identification and quantification from Saccharomyces cerevisiae. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2021, 1162, 122453.	1.2	4
149	Patterns of gene expression in pollen of cotton ( <i>Gossypium hirsutum</i> ) indicate downregulation as a feature of thermotolerance. Plant Journal, 2022, 109, 965-979.	2.8	4
150	Genome survey sequencing of wild cotton ( $\langle i \rangle$ Gossypium robinsonii $\langle i \rangle$ ) reveals insights into proteomic responses of pollen to extreme heat. Plant, Cell and Environment, 2022, 45, 1242-1256.	2.8	4
151	Comparative Pistacia vera leaf proteomics in response to herbivory of the common pistachio psylla (Agonoscena pistaciae). Arthropod-Plant Interactions, 2022, 16, 215-226.	0.5	4
152	PeptideWitchâ€"A Software Package to Produce High-Stringency Proteomics Data Visualizations from Label-Free Shotgun Proteomics Data. Proteomes, 2020, 8, 21.	1.7	3
153	Comparative Leaf Proteomics of Brassica napus Genotypes with Distinctive Levels of Early Cold Acclimation. Plant Molecular Biology Reporter, 2020, 39, 317.	1.0	3
154	Quantitative proteomics analysis of high and low polyphenol expressing recombinant inbred lines (RILs) of peanut (Arachis hypogaea L.). Food Chemistry, 2021, 334, 127517.	4.2	3
155	Towards an Integrated Analytical Technology for the Generation of Multidimensional Protein Expression Maps., 2000,, 143-162.		3
156	Extended exposure to sugar and/or caffeine produces distinct behavioral and neurochemical profiles in the orbitofrontal cortex of rats: Implications for neural function. Proteomics, 2016, 16, 2894-2910.	1.3	2
157	Data quality issues in proteomics - there are many paths to enlightenment. Proteomics, 2016, 16, 2433-2434.	1.3	2
158	Proteomics of Riceâ€"Our Most Valuable Food Crop. , 2017, , 17-33.		2
159	Promoting Agriculture Proteome Research Activities in the Asia and Oceania Region. Journal of Proteome Research, 2012, 11, 1461-1461.	1.8	1
160	Realizing the Potential of Agricultural and Environmental Proteomics. Journal of Proteome Research, 2013, 12, 4651-4651.	1.8	1
161	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
162	Proteomic Analysis of Disease in Sydney Rock Oysters. , 2017, , 343-357.		1

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163	Front Cover: Plant–Microbe Symbiosis: What Has Proteomics Taught Us?. Proteomics, 2019, 19, 1970141.	1.3	1
164	Front Cover: Proteomes of Leafâ€Growing Zones in Rice Genotypes with Contrasting Drought Tolerance. Proteomics, 2019, 19, 1970071.	1.3	1
165	5.26 Hsp90 Inhibitor Restores P53-Mutated MEC1 Chronic Lymphocytic Leukemia Cell Sensitivity to Fludarabine by Downregulating DNA Repair and Endoplasmic Reticulum Chaperone Proteins. Clinical Lymphoma, Myeloma and Leukemia, 2011, 11, S260-S261.	0.2	0
166	PeptideMind â€" Applying machine learning algorithms to assess replicate quality in shotgun proteomic data. SoftwareX, 2021, 13, 100644.	1.2	O