

Joshua L Heazlewood

List of Publications by Year in descending order

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121
papers

9,177
citations

41344

49
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42399

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125
all docs

125
docs citations

125
times ranked

9691
citing authors

#	ARTICLE	IF	CITATIONS
1	Organellar Proteomic Profiling to Analyze Membrane Trafficking Pathways. Trends in Plant Science, 2021, 26, 299-300.	8.8	4
2	<i>BRITTLE PLANT1</i> is required for normal cell wall composition and mechanical strength in rice. Journal of Integrative Plant Biology, 2021, 63, 865-877.	8.5	10
3	A Pipeline towards the Biochemical Characterization of the Arabidopsis GT14 Family. International Journal of Molecular Sciences, 2021, 22, 1360.	4.1	7
4	Regulation of carbon metabolism in two maize sister lines contrasted for chilling tolerance. Journal of Experimental Botany, 2020, 71, 356-369.	4.8	22
5	UDP-GlcNAc/UDP-Xyl synthases affect plant development by controlling the content of UDP-GlcNAc to regulate the RG-β-D-GlcNAc complex. Plant Journal, 2020, 104, 252-267.	5.7	12
6	Plant Mitochondrial Carriers: Molecular Gatekeepers That Help to Regulate Plant Central Carbon Metabolism. Plants, 2020, 9, 117.	3.5	23
7	Enrichment of N-Linked Glycopeptides and Their Identification by Complementary Fragmentation Techniques. Methods in Molecular Biology, 2020, 2139, 225-240.	0.9	3
8	Profiling Cell Wall Monosaccharides and Nucleotide-Sugars from Plants. Current Protocols in Plant Biology, 2019, 4, e20092.	2.8	5
9	Separating Golgi Proteins from <i>Cis</i> to <i>Trans</i> Reveals Underlying Properties of Cisternal Localization. Plant Cell, 2019, 31, 2010-2034.	6.6	40
10	A hypomorphic allele of SLC35D1 results in Schneckbecken-like dysplasia. Human Molecular Genetics, 2019, 28, 3543-3551.	2.9	9
11	Differential distributions of trafficking and signaling proteins of the maize ER-Golgi apparatus. Plant Signaling and Behavior, 2019, 14, 1672513.	2.4	2
12	Glycome and Proteome Components of Golgi Membranes Are Common between Two Angiosperms with Distinct Cell-Wall Structures. Plant Cell, 2019, 31, 1094-1112.	6.6	35
13	The companion of cellulose synthase 1 confers salt tolerance through a Tau-like mechanism in plants. Nature Communications, 2019, 10, 857.	12.8	71
14	The Scope, Functions, and Dynamics of Posttranslational Protein Modifications. Annual Review of Plant Biology, 2019, 70, 119-151.	18.7	158
15	Overexpression of bifunctional fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase leads to enhanced photosynthesis and global reprogramming of carbon metabolism in Synechococcus sp. PCC 7002. Metabolic Engineering, 2018, 47, 170-183.	7.0	76
16	UDP-Glucuronic Acid Transport Is Required for Virulence of <i>Cryptococcus neoformans</i> . MBio, 2018, 9, .	4.1	15
17	N-linked Glycan Micro-heterogeneity in Glycoproteins of Arabidopsis. Molecular and Cellular Proteomics, 2018, 17, 413-421.	3.8	37
18	Three UDP-xylose transporters participate in xylan biosynthesis by conveying cytosolic UDP-xylose into the Golgi lumen in Arabidopsis. Journal of Experimental Botany, 2018, 69, 1125-1134.	4.8	22

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19	Absolute Quantitation of In Vitro Expressed Plant Membrane Proteins by Targeted Proteomics (MRM) for the Determination of Kinetic Parameters. <i>Methods in Molecular Biology</i> , 2018, 1696, 217-234.	0.9	0
20	The Three Members of the Arabidopsis Glycosyltransferase Family 92 are Functional β -1,4-Galactan Synthases. <i>Plant and Cell Physiology</i> , 2018, 59, 2624-2636.	3.1	35
21	A Golgi UDP-GlcNAc transporter delivers substrates for N-linked glycans and sphingolipids. <i>Nature Plants</i> , 2018, 4, 792-801.	9.3	27
22	Xylose donor transport is critical for fungal virulence. <i>PLoS Pathogens</i> , 2018, 14, e1006765.	4.7	21
23	<i>Defective Pollen Wall 2 (DPW2)</i> Encodes an Acyl Transferase Required for Rice Pollen Development. <i>Plant Physiology</i> , 2017, 173, 240-255.	4.8	92
24	UUAT1 Is a Golgi-Localized UDP-Uronic Acid Transporter That Modulates the Polysaccharide Composition of Arabidopsis Seed Mucilage. <i>Plant Cell</i> , 2017, 29, 129-143.	6.6	60
25	The elaborate route for UDP-arabinose delivery into the Golgi of plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4261-4266.	7.1	52
26	Multiple marker abundance profiling: combining selected reaction monitoring and data-independent acquisition for rapid estimation of organelle abundance in subcellular samples. <i>Plant Journal</i> , 2017, 92, 1202-1217.	5.7	42
27	We Are Not Alone: The iMOP Initiative and Its Roles in a Biology- and Disease-Driven Human Proteome Project. <i>Journal of Proteome Research</i> , 2017, 16, 4273-4280.	3.7	8
28	Influence of light and nitrogen on the photosynthetic efficiency in the C4 plant <i>Miscanthus giganteus</i> . <i>Photosynthesis Research</i> , 2017, 131, 1-13.	2.9	20
29	GDP-L-fucose transport in plants: The missing piece. <i>Channels</i> , 2017, 11, 8-10.	2.8	4
30	Enrichment of Golgi Membranes from <i>Triticum aestivum</i> (Wheat) Seedlings. <i>Methods in Molecular Biology</i> , 2017, 1511, 131-150.	0.9	3
31	Enrichment of the Plant Cytosolic Fraction. <i>Methods in Molecular Biology</i> , 2017, 1511, 213-232.	0.9	0
32	Editorial: International Plant Proteomics Organization (INPPO) World Congress 2014. <i>Frontiers in Plant Science</i> , 2016, 7, 1190.	3.6	2
33	Role of UDP-Glucuronic Acid Decarboxylase in Xylan Biosynthesis in Arabidopsis. <i>Molecular Plant</i> , 2016, 9, 1119-1131.	8.3	57
34	Exploiting members of the BAHD acyltransferase family to synthesize multiple hydroxycinnamate and benzoate conjugates in yeast. <i>Microbial Cell Factories</i> , 2016, 15, 198.	4.0	32
35	Proteomic Characterization of Golgi Membranes Enriched from Arabidopsis Suspension Cell Cultures. <i>Methods in Molecular Biology</i> , 2016, 1496, 91-109.	0.9	1
36	The Arabidopsis Golgi-localized GDP-L-fucose transporter is required for plant development. <i>Nature Communications</i> , 2016, 7, 12119.	12.8	53

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37	A DUF-246 family glycosyltransferase-like gene affects male fertility and the biosynthesis of pectic arabinogalactans. <i>BMC Plant Biology</i> , 2016, 16, 90.	3.6	32
38	Free-Flow Electrophoresis of Plasma Membrane Vesicles Enriched by Two-Phase Partitioning Enhances the Quality of the Proteome from <i>Arabidopsis</i> Seedlings. <i>Journal of Proteome Research</i> , 2016, 15, 900-913.	3.7	47
39	Biochemical characterization of <i>Arabidopsis</i> APYRASE family reveals their roles in regulating endomembrane NDP/NMP homeostasis. <i>Biochemical Journal</i> , 2015, 472, 43-54.	3.7	18
40	Multi-Organism Proteomes (iMOP): Advancing our Understanding of Human Biology. <i>Proteomics</i> , 2015, 15, 2885-2894.	2.2	2
41	Beyond the Western front: targeted proteomics and organelle abundance profiling. <i>Frontiers in Plant Science</i> , 2015, 6, 301.	3.6	18
42	Structural characterization of a mixed-linkage glucan deficient mutant reveals alteration in cellulose microfibril orientation in rice coleoptile mesophyll cell walls. <i>Frontiers in Plant Science</i> , 2015, 6, 628.	3.6	24
43	Characterization of protein N-glycosylation by tandem mass spectrometry using complementary fragmentation techniques. <i>Frontiers in Plant Science</i> , 2015, 6, 674.	3.6	26
44	Proteome profile of the endomembrane of developing coleoptiles from switchgrass (<i>Panicum</i>)	2.2	6
45	Engineering temporal accumulation of a low recalcitrance polysaccharide leads to increased C6 sugar content in plant cell walls. <i>Plant Biotechnology Journal</i> , 2015, 13, 903-914.	8.3	37
46	The rice immune receptor XA21 recognizes a tyrosine-sulfated protein from a Gram-negative bacterium. <i>Science Advances</i> , 2015, 1, e1500245.	10.3	209
47	Transgenic Expression of the Dicotyledonous Pattern Recognition Receptor EFR in Rice Leads to Ligand-Dependent Activation of Defense Responses. <i>PLoS Pathogens</i> , 2015, 11, e1004809.	4.7	103
48	Identification and Characterization of a Golgi-Localized UDP-Xylose Transporter Family from <i>Arabidopsis</i> . <i>Plant Cell</i> , 2015, 27, 1218-1227.	6.6	61
49	Standard Flow Liquid Chromatography for Shotgun Proteomics in Bioenergy Research. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 44.	4.1	44
50	The Golgi localized bifunctional UDP-rhamnose/UDP-galactose transporter family of <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11563-11568.	7.1	113
51	The <i>Arabidopsis</i> cytosolic proteome: the metabolic heart of the cell. <i>Frontiers in Plant Science</i> , 2014, 5, 21.	3.6	11
52	Separation of the Plant Golgi Apparatus and Endoplasmic Reticulum by Free-Flow Electrophoresis. <i>Methods in Molecular Biology</i> , 2014, 1072, 527-539.	0.9	19
53	An XA21-Associated Kinase (OsSERK2) Regulates Immunity Mediated by the XA21 and XA3 Immune Receptors. <i>Molecular Plant</i> , 2014, 7, 874-892.	8.3	129
54	Analysis of plant nucleotide sugars by hydrophilic interaction liquid chromatography and tandem mass spectrometry. <i>Analytical Biochemistry</i> , 2014, 448, 14-22.	2.4	49

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55	Secretome analysis of the thermophilic xylanase hyper-producer <i>Thermomyces lanuginosus</i> SSBP cultivated on corn cobs. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 1687-1696.	3.0	32
56	Identification of a Sphingolipid β -Glucuronosyltransferase That Is Essential for Pollen Function in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 3314-3325.	6.6	80
57	The plant glycosyltransferase clone collection for functional genomics. <i>Plant Journal</i> , 2014, 79, 517-529.	5.7	67
58	Isolation of the Plant Cytosolic Fraction for Proteomic Analysis. <i>Methods in Molecular Biology</i> , 2014, 1072, 453-467.	0.9	10
59	Proteome coverage of the model plant <i>Arabidopsis thaliana</i> : Implications for shotgun proteomic studies. <i>Journal of Proteomics</i> , 2013, 79, 195-199.	2.4	4
60	MASCP gator: an overview of the <i>Arabidopsis</i> proteomic aggregation portal. <i>Frontiers in Plant Science</i> , 2013, 4, 411.	3.6	14
61	Managing the green proteomes for the next decade of plant research. <i>Frontiers in Plant Science</i> , 2013, 4, 501.	3.6	2
62	Golgi Enrichment and Proteomic Analysis of Developing <i>Pinus radiata</i> Xylem by Free-Flow Electrophoresis. <i>PLoS ONE</i> , 2013, 8, e84669.	2.5	11
63	Isolation and Proteomic Characterization of the <i>Arabidopsis</i> Golgi Defines Functional and Novel Components Involved in Plant Cell Wall Biosynthesis. <i>Plant Physiology</i> , 2012, 159, 12-26.	4.8	164
64	1001 Proteomes: a functional proteomics portal for the analysis of <i>Arabidopsis thaliana</i> accessions. <i>Bioinformatics</i> , 2012, 28, 1303-1306.	4.1	21
65	Dependence of Plant Cell Wall Composition and Structure on Cellulose Synthase-Like Knock Out Mutant. <i>Biophysical Journal</i> , 2012, 102, 590a-591a.	0.5	0
66	AtAPY1 and AtAPY2 Function as Golgi-Localized Nucleoside Diphosphatases in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2012, 53, 1913-1925.	3.1	30
67	Structural and Chemical Characterization of Hardwood from Tree Species with Applications as Bioenergy Feedstocks. <i>PLoS ONE</i> , 2012, 7, e52820.	2.5	32
68	The HUPO initiative on Model Organism Proteomes, iMOP. <i>Proteomics</i> , 2012, 12, 340-345.	2.2	9
69	Boosting the Globalization of Plant Proteomics through INPPO: Current Developments and Future Prospects. <i>Proteomics</i> , 2012, 12, 359-368.	2.2	10
70	Proteomic dissection of the <i>Arabidopsis</i> Golgi and trans-Golgi network. <i>Frontiers in Plant Science</i> , 2012, 3, 298.	3.6	21
71	Analysis of the <i>Arabidopsis</i> Cytosolic Proteome Highlights Subcellular Partitioning of Central Plant Metabolism. <i>Journal of Proteome Research</i> , 2011, 10, 1571-1582.	3.7	113
72	The Green Proteome: Challenges in Plant Proteomics. <i>Frontiers in Plant Science</i> , 2011, 2, 6.	3.6	26

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73	Combining multivariate analysis and monosaccharide composition modeling to identify plant cell wall variations by Fourier Transform Near Infrared spectroscopy. <i>Plant Methods</i> , 2011, 7, 26.	4.3	23
74	The <i>Arabidopsis thaliana</i> 2D gel mitochondrial proteome: Refining the value of reference maps for assessing protein abundance, contaminants and post-translational modifications. <i>Proteomics</i> , 2011, 11, 1720-1733.	2.2	63
75	MASCP Gator: An Aggregation Portal for the Visualization of Arabidopsis Proteomics Data. <i>Plant Physiology</i> , 2011, 155, 259-270.	4.8	94
76	An Integrative Approach to the Identification of Arabidopsis and Rice Genes Involved in Xylan and Secondary Wall Development. <i>PLoS ONE</i> , 2010, 5, e15481.	2.5	82
77	Analysis of the Rice Mitochondrial Carrier Family Reveals Anaerobic Accumulation of a Basic Amino Acid Carrier Involved in Arginine Metabolism during Seed Germination. <i>Plant Physiology</i> , 2010, 154, 691-704.	4.8	67
78	The Role of Proteomics in the Development of Cellulosic Biofuels. <i>Current Proteomics</i> , 2010, 7, 121-134.	0.3	5
79	PhosPhAt: the Arabidopsis thaliana phosphorylation site database. An update. <i>Nucleic Acids Research</i> , 2010, 38, D828-D834.	14.5	346
80	Proteomic identification of extracellular proteins regulated by the Gna1 G α subunit in <i>Stagonospora nodorum</i> . <i>Mycological Research</i> , 2009, 113, 523-531.	2.5	24
81	The seminal fluid proteome of the honeybee <i>Apis mellifera</i> . <i>Proteomics</i> , 2009, 9, 2085-2097.	2.2	152
82	A survey of the <i>Arabidopsis thaliana</i> mitochondrial phosphoproteome. <i>Proteomics</i> , 2009, 9, 4229-4240.	2.2	78
83	The Multinational Arabidopsis Steering Subcommittee for Proteomics Assembles the Largest Proteome Database Resource for Plant Systems Biology. <i>Journal of Proteome Research</i> , 2008, 7, 4209-4210.	3.7	29
84	A Signaling-Regulated, Short-Chain Dehydrogenase of <i>Stagonospora nodorum</i> Regulates Asexual Development. <i>Eukaryotic Cell</i> , 2008, 7, 1916-1929.	3.4	45
85	Analysis of the Arabidopsis Cytosolic Ribosome Proteome Provides Detailed Insights into Its Components and Their Post-translational Modification. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 347-369.	3.8	175
86	Novel Proteins, Putative Membrane Transporters, and an Integrated Metabolic Network Are Revealed by Quantitative Proteomic Analysis of Arabidopsis Cell Culture Peroxisomes. <i>Plant Physiology</i> , 2008, 148, 1809-1829.	4.8	169
87	Isolation and Subfractionation of Plant Mitochondria for Proteomic Analysis. <i>Journal of Proteome Research</i> , 2007, 355, 49-62.		24
88	The Cytotoxic Lipid Peroxidation Product 4-Hydroxy-2-nonenal Covalently Modifies a Selective Range of Proteins Linked to Respiratory Function in Plant Mitochondria. <i>Journal of Biological Chemistry</i> , 2007, 282, 37436-37447.	3.4	76
89	SUBA: the Arabidopsis Subcellular Database. <i>Nucleic Acids Research</i> , 2007, 35, D213-D218.	14.5	394
90	PhosPhAt: a database of phosphorylation sites in Arabidopsis thaliana and a plant-specific phosphorylation site predictor. <i>Nucleic Acids Research</i> , 2007, 36, D1015-D1021.	14.5	302

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91	Identification of intra- and intermolecular disulphide bonding in the plant mitochondrial proteome by diagonal gel electrophoresis. <i>Proteomics</i> , 2007, 7, 4158-4170.	2.2	51
92	The plant mitochondrial proteome and the challenge of defining the posttranslational modifications responsible for signalling and stress effects on respiratory functions. <i>Physiologia Plantarum</i> , 2007, 129, 207-224.	5.2	14
93	Mitochondrial acyl carrier proteins in <i>Arabidopsis thaliana</i> are predominantly soluble matrix proteins and none can be confirmed as subunits of respiratory Complex I. <i>Plant Molecular Biology</i> , 2007, 64, 319-327.	3.9	59
94	<i>Arabidopsis</i> Mitochondrial Proteomics. <i>Methods in Molecular Biology</i> , 2007, 372, 559-571.	0.9	7
95	Analysis of the Soluble ATP-Binding Proteome of Plant Mitochondria Identifies New Proteins and Nucleotide Triphosphate Interactions within the Matrix. <i>Journal of Proteome Research</i> , 2006, 5, 3459-3469.	3.7	60
96	Differential Impact of Environmental Stresses on the Pea Mitochondrial Proteome. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1122-1133.	3.8	231
97	Combining Experimental and Predicted Datasets for Determination of the Subcellular Location of Proteins in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2005, 139, 598-609.	4.8	120
98	The plant mitochondrial proteome. <i>Trends in Plant Science</i> , 2005, 10, 36-43.	8.8	188
99	Lipoic Acid-Dependent Oxidative Catabolism of β -Keto Acids in Mitochondria Provides Evidence for Branched-Chain Amino Acid Catabolism in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2004, 134, 838-848.	4.8	176
100	A Transcriptomic and Proteomic Characterization of the <i>Arabidopsis</i> Mitochondrial Protein Import Apparatus and Its Response to Mitochondrial Dysfunction. <i>Plant Physiology</i> , 2004, 134, 777-789.	4.8	148
101	Changes in the Mitochondrial Proteome during the Anoxia to Air Transition in Rice Focus around Cytochrome-containing Respiratory Complexes. <i>Journal of Biological Chemistry</i> , 2004, 279, 39471-39478.	3.4	71
102	AtMYB32 is required for normal pollen development in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2004, 40, 979-995.	5.7	289
103	Mitochondrial cytochrome c oxidase and succinate dehydrogenase complexes contain plant specific subunits. <i>Plant Molecular Biology</i> , 2004, 56, 77-90.	3.9	184
104	Untangling Multi-gene Families in Plants by Integrating Proteomics into Functional Genomics. <i>ChemInform</i> , 2004, 35, no.	0.0	0
105	Untangling multi-gene families in plants by integrating proteomics into functional genomics. <i>Phytochemistry</i> , 2004, 65, 1517-1530.	2.9	36
106	Experimental Analysis of the <i>Arabidopsis</i> Mitochondrial Proteome Highlights Signaling and Regulatory Components, Provides Assessment of Targeting Prediction Programs, and Indicates Plant-Specific Mitochondrial Proteins [W]. <i>Plant Cell</i> , 2004, 16, 241-256.	6.6	550
107	AMPDB: the <i>Arabidopsis</i> Mitochondrial Protein Database. <i>Nucleic Acids Research</i> , 2004, 33, D605-D610.	14.5	59
108	Untangling multi-gene families in plants by integrating proteomics into functional genomics. <i>Phytochemistry</i> , 2004, 65, 1517-1517.	2.9	3

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109	A plant outer mitochondrial membrane protein with high amino acid sequence identity to a chloroplast protein import receptor. <i>FEBS Letters</i> , 2004, 557, 109-114.	2.8	126
110	Proteomic identification of divalent metal cation binding proteins in plant mitochondria. <i>FEBS Letters</i> , 2003, 537, 96-100.	2.8	56
111	The products of the mitochondrial <i>orf25</i> and <i>orfB</i> genes are FO components in the plant F1 FO ATP synthase. <i>FEBS Letters</i> , 2003, 540, 201-205.	2.8	114
112	Mitochondrial complex I from Arabidopsis and rice: orthologs of mammalian and fungal components coupled with plant-specific subunits. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2003, 1604, 159-169.	1.0	180
113	Integrated plant proteomics " putting the green genomes to work. <i>Functional Plant Biology</i> , 2003, 30, 471.	2.1	44
114	What makes a mitochondrion?. <i>Genome Biology</i> , 2003, 4, 218.	9.6	13
115	Towards an Analysis of the Rice Mitochondrial Proteome. <i>Plant Physiology</i> , 2003, 132, 230-242.	4.8	194
116	Control of Ascorbate Synthesis by Respiration and Its Implications for Stress Responses. <i>Plant Physiology</i> , 2003, 133, 443-447.	4.8	328
117	Enzymes of Glycolysis Are Functionally Associated with the Mitochondrion in Arabidopsis Cells. <i>Plant Cell</i> , 2003, 15, 2140-2151.	6.6	345
118	Genomic and Proteomic Analysis of Mitochondrial Carrier Proteins in Arabidopsis. <i>Plant Physiology</i> , 2003, 131, 443-453.	4.8	185
119	Expansin-Like Molecules: Novel Functions Derived from Common Domains. <i>Journal of Molecular Evolution</i> , 2002, 54, 587-594.	1.8	48
120	The impact of oxidative stress on Arabidopsis mitochondria. <i>Plant Journal</i> , 2002, 32, 891-904.	5.7	478
121	Plant Proteomics: Challenges and Resources. , 0, , 1-31.		2