

Stefanie Wienkoop

List of Publications by Year in descending order

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92
papers

4,867
citations

71102

41
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95266

68
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98
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docs citations

98
times ranked

5699
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteome Analysis of <i>Arabidopsis</i> Leaf Peroxisomes Reveals Novel Targeting Peptides, Metabolic Pathways, and Defense Mechanisms. <i>Plant Cell</i> , 2007, 19, 3170-3193.	6.6	324
2	Enrichment of phosphorylated proteins and peptides from complex mixtures using metal oxide/hydroxide affinity chromatography (MOAC). <i>Proteomics</i> , 2005, 5, 4389-4397.	2.2	272
3	Proteome Analysis. Novel Proteins Identified at the Peribacteroid Membrane from <i>Lotus japonicus</i> Root Nodules. <i>Plant Physiology</i> , 2003, 131, 1080-1090.	4.8	193
4	A Cytosolic Pathway for the Conversion of Hydroxypyruvate to Glycerate during Photorespiration in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2008, 20, 2848-2859.	6.6	193
5	<i>Medicago truncatula</i> Root Nodule Proteome Analysis Reveals Differential Plant and Bacteroid Responses to Drought Stress. <i>Plant Physiology</i> , 2007, 144, 1495-1507.	4.8	178
6	Integration of Metabolomic and Proteomic Phenotypes. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1725-1736.	3.8	155
7	Metabolomics- and Proteomics-Assisted Genome Annotation and Analysis of the Draft Metabolic Network of <i>Chlamydomonas reinhardtii</i> . <i>Genetics</i> , 2008, 179, 157-166.	2.9	141
8	Evidence for a rhizobia-induced drought stress response strategy in <i>Medicago truncatula</i> . <i>Journal of Proteomics</i> , 2016, 136, 202-213.	2.4	138
9	d-GLYCERATE 3-KINASE, the Last Unknown Enzyme in the Photorespiratory Cycle in <i>Arabidopsis</i> , Belongs to a Novel Kinase Family. <i>Plant Cell</i> , 2005, 17, 2413-2420.	6.6	126
10	Characterisation by proteomics of peribacteroid space and peribacteroid membrane preparations from pea (<i>Pisum sativum</i>) symbiosomes. <i>Proteomics</i> , 2002, 2, 325.	2.2	114
11	Carbon Metabolism and Bacteroid Functioning Are Involved in the Regulation of Nitrogen Fixation in <i>Medicago truncatula</i> Under Drought and Recovery. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1565-1576.	2.6	114
12	System-level network analysis of nitrogen starvation and recovery in <i>Chlamydomonas reinhardtii</i> reveals potential new targets for increased lipid accumulation. <i>Biotechnology for Biofuels</i> , 2014, 7, 171.	6.2	103
13	Local inhibition of nitrogen fixation and nodule metabolism in drought-stressed soybean. <i>Journal of Experimental Botany</i> , 2013, 64, 2171-2182.	4.8	101
14	Correlative GC-TOF-MS-based metabolite profiling and LC-MS-based protein profiling reveal time-related systemic regulation of metabolite-protein networks and improve pattern recognition for multiple biomarker selection. <i>Metabolomics</i> , 2005, 1, 109-121.	3.0	97
15	ProMEX: a mass spectral reference database for proteins and protein phosphorylation sites. <i>BMC Bioinformatics</i> , 2007, 8, 216.	2.6	96
16	Targeted proteomics for <i>Chlamydomonas reinhardtii</i> combined with rapid subcellular protein fractionation, metabolomics and metabolic flux analyses. <i>Molecular BioSystems</i> , 2010, 6, 1018.	2.9	94
17	MASCP Gator: An Aggregation Portal for the Visualization of <i>Arabidopsis</i> Proteomics Data. <i>Plant Physiology</i> , 2011, 155, 259-270.	4.8	94
18	Cell-specific protein profiling in <i>Arabidopsis thaliana</i> trichomes: identification of trichome-located proteins involved in sulfur metabolism and detoxification. <i>Phytochemistry</i> , 2004, 65, 1641-1649.	2.9	90

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19	Neurotoxin localization to ectodermal gland cells uncovers an alternative mechanism of venom delivery in sea anemones. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 1351-1358.	2.6	90
20	Relative and absolute quantitative shotgun proteomics: targeting low-abundance proteins in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2006, 57, 1529-1535.	4.8	81
21	Linking protein fractionation with multidimensional monolithic reversed-phase peptide chromatography/mass spectrometry enhances protein identification from complex mixtures even in the presence of abundant proteins. <i>Rapid Communications in Mass Spectrometry</i> , 2004, 18, 643-650.	1.5	80
22	A rapid approach for phenotype screening and database independent detection of cSNP/protein polymorphism using mass accuracy precursor alignment. <i>Proteomics</i> , 2008, 8, 4214-4225.	2.2	78
23	If the antibody fails – a mass Western approach. <i>Plant Journal</i> , 2008, 55, 1039-1046.	5.7	77
24	Bimodal dynamics of primary metabolism-related responses in tolerant potato-Potato virus Y interaction. <i>BMC Genomics</i> , 2015, 16, 716.	2.8	73
25	Phytochemical composition of <i>Potentilla anserina</i> L. analyzed by an integrative GC-MS and LC-MS metabolomics platform. <i>Metabolomics</i> , 2013, 9, 599-607.	3.0	70
26	Leghemoglobin is nitrated in functional legume nodules in a tyrosine residue within the heme cavity by a nitrite/peroxide-dependent mechanism. <i>Plant Journal</i> , 2015, 81, 723-735.	5.7	70
27	The quest for tolerant varieties: the importance of integrating ‘omics-techniques to phenotyping. <i>Frontiers in Plant Science</i> , 2015, 6, 448.	3.6	67
28	Oxidative stress is a consequence, not a cause, of aluminum toxicity in the forage legume <i>Lotus corniculatus</i> . <i>New Phytologist</i> , 2012, 193, 625-636.	7.3	66
29	<i>Arabidopsis thaliana</i> as a model organism for plant proteome research. <i>Journal of Proteomics</i> , 2010, 73, 2239-2248.	2.4	65
30	An automated GCxGC-TOF-MS protocol for batch-wise extraction and alignment of mass isotopomer matrixes from differential ¹³ C labelling experiments: a case study for photoautotrophic-mixotrophic grown <i>Chlamydomonas reinhardtii</i> cells. <i>Journal of Basic Microbiology</i> , 2009, 49, 82-91.	3.3	62
31	Drought stress provokes the down-regulation of methionine and ethylene biosynthesis pathways in <i>Medicago truncatula</i> roots and nodules. <i>Plant, Cell and Environment</i> , 2014, 37, 2051-2063.	5.7	57
32	Heat-Treatment-Responsive Proteins in Different Developmental Stages of Tomato Pollen Detected by Targeted Mass Accuracy Precursor Alignment (tMAPA). <i>Journal of Proteome Research</i> , 2015, 14, 4463-4471.	3.7	56
33	Rhizobium Impacts on Seed Productivity, Quality, and Protection of <i>Pisum sativum</i> upon Disease Stress Caused by <i>Didymella pinodes</i> : Phenotypic, Proteomic, and Metabolomic Traits. <i>Frontiers in Plant Science</i> , 2017, 8, 1961.	3.6	55
34	Drought and Recovery: Independently Regulated Processes Highlighting the Importance of Protein Turnover Dynamics and Translational Regulation in <i>Medicago truncatula</i> . <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1921-1937.	3.8	50
35	Sulfur Transport and Metabolism in Legume Root Nodules. <i>Frontiers in Plant Science</i> , 2018, 9, 1434.	3.6	49
36	Stable isotope-free quantitative shotgun proteomics combined with sample pattern recognition for rapid diagnostics. <i>Journal of Separation Science</i> , 2006, 29, 2793-2801.	2.5	48

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37	Mitochondria are an early target of oxidative modifications in senescing legume nodules. <i>New Phytologist</i> , 2013, 197, 873-885.	7.3	46
38	Stable isotope labeling of phosphopeptides for multiparallel kinase target analysis and identification of phosphorylation sites. <i>Rapid Communications in Mass Spectrometry</i> , 2003, 17, 1579-1584.	1.5	45
39	Evidence for Novel Tomato Seed Allergens: IgE-Reactive Legumin and Vicilin Proteins Identified by Multidimensional Protein Fractionation ² Mass Spectrometry and in Silico Epitope Modeling. <i>Journal of Proteome Research</i> , 2009, 8, 1111-1122.	3.7	45
40	The plasma membrane proteome of maize roots grown under low and high iron conditions. <i>Journal of Proteomics</i> , 2013, 91, 605-618.	2.4	45
41	Using ProtMAX to create high-mass-accuracy precursor alignments from label-free quantitative mass spectrometry data generated in shotgun proteomics experiments. <i>Nature Protocols</i> , 2013, 8, 595-601.	12.0	44
42	MAPA Distinguishes Genotype-Specific Variability of Highly Similar Regulatory Protein Isoforms in Potato Tuber. <i>Journal of Proteome Research</i> , 2011, 10, 2979-2991.	3.7	42
43	Microbial symbionts affect <i>Pisum sativum</i> proteome and metabolome under <i>Didymella pinodes</i> infection. <i>Journal of Proteomics</i> , 2016, 143, 173-187.	2.4	42
44	A Proteomic View on the Role of Legume Symbiotic Interactions. <i>Frontiers in Plant Science</i> , 2017, 8, 1267.	3.6	42
45	Absolute quantification of <i>Medicago truncatula</i> sucrose synthase isoforms and N-metabolism enzymes in symbiotic root nodules and the detection of novel nodule phosphoproteins by mass spectrometry. <i>Journal of Experimental Botany</i> , 2008, 59, 3307-3315.	4.8	40
46	Spectral counting robust on high mass accuracy mass spectrometers. <i>Rapid Communications in Mass Spectrometry</i> , 2010, 24, 3609-3614.	1.5	38
47	Comparison between Proteome and Transcriptome Response in Potato (<i>Solanum tuberosum</i> L.) Leaves Following Potato Virus Y (PVY) Infection. <i>Proteomes</i> , 2017, 5, 14.	3.5	38
48	ProMEX – a mass spectral reference database for plant proteomics. <i>Frontiers in Plant Science</i> , 2012, 3, 125.	3.6	36
49	Targeted quantitative analysis of a diurnal RuBisCO subunit expression and translation profile in <i>Chlamydomonas reinhardtii</i> introducing a novel Mass Western approach. <i>Journal of Proteomics</i> , 2015, 113, 143-153.	2.4	34
50	Integrative Profiling of Metabolites and Proteins. <i>Methods in Molecular Biology</i> , 2007, 358, 57-75.	0.9	33
51	An improved protocol to study the plant cell wall proteome. <i>Frontiers in Plant Science</i> , 2015, 6, 237.	3.6	33
52	Key metabolic traits of <i>Pisum sativum</i> maintain cell vitality during <i>Didymella pinodes</i> infection: cultivar resistance and the microsymbionts' influence. <i>Journal of Proteomics</i> , 2017, 169, 189-201.	2.4	31
53	Differential ¹³ C ₂ effect on primary carbon metabolism of flag leaves in durum wheat (<i>Triticum durum</i> Desf.). <i>Plant, Cell and Environment</i> , 2015, 38, 2780-2794.	5.7	29
54	Sulfate is transported at significant rates through the symbiosome membrane and is crucial for nitrogenase biosynthesis. <i>Plant, Cell and Environment</i> , 2019, 42, 1180-1189.	5.7	29

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55	Possible Role of Nutritional Priming for Early Salt and Drought Stress Responses in <i>Medicago truncatula</i> . <i>Frontiers in Plant Science</i> , 2012, 3, 285.	3.6	28
56	Altered Plant and Nodule Development and Protein S-Nitrosylation in <i>Lotus japonicus</i> Mutants Deficient in S-Nitrosoglutathione Reductases. <i>Plant and Cell Physiology</i> , 2020, 61, 105-117.	3.1	25
57	<i>Medicago truncatula</i> and <i>Glycine max</i> : Different Drought Tolerance and Similar Local Response of the Root Nodule Proteome. <i>Journal of Proteome Research</i> , 2015, 14, 5240-5251.	3.7	24
58	A Proteomic Workflow Using High-Throughput De Novo Sequencing Towards Complementation of Genome Information for Improved Comparative Crop Science. <i>Methods in Molecular Biology</i> , 2016, 1394, 233-243.	0.9	18
59	Differentiation of Plant Cells During Symbiotic Nitrogen Fixation. <i>Comparative and Functional Genomics</i> , 2002, 3, 151-157.	2.0	17
60	The different proteomes of <i>Chlamydomonas reinhardtii</i> . <i>Journal of Proteomics</i> , 2012, 75, 5883-5887.	2.4	16
61	<i>Medicago truncatula</i> Proteomics for Systems Biology: Novel Rapid Shotgun LC-MS Approach for Relative Quantification Based on Full-Scan Selective Peptide Extraction (Selpex). <i>Methods in Molecular Biology</i> , 2014, 1072, 303-313.	0.9	16
62	Authentication of Cereal Flours by Multivariate Analysis of GC-MS Data. <i>Chromatographia</i> , 2016, 79, 1387-1393.	1.3	16
63	AN OPTIMIZED METHOD FOR THE ISOLATION OF NUCLEI FROM CHLAMYDOMONAS REINHARDTII (CHLOROPHYCEAE)1. <i>Journal of Phycology</i> , 2011, 47, 333-340.	2.3	13
64	Label-free quantitative proteomic analysis of tolerance to drought in <i>Pisum sativum</i> . <i>Proteomics</i> , 2016, 16, 2776-2787.	2.2	12
65	Mass Western for Absolute Quantification of Target Proteins and Considerations About the Instrument of Choice. <i>Methods in Molecular Biology</i> , 2014, 1072, 199-208.	0.9	12
66	Functional analysis of proteins and protein species using shotgun proteomics and linear mathematics. <i>Amino Acids</i> , 2011, 41, 329-341.	2.7	10
67	Boosting the Globalization of Plant Proteomics through INPPO: Current Developments and Future Prospects. <i>Proteomics</i> , 2012, 12, 359-368.	2.2	10
68	Physiological Responses of N ₂ -Fixing Legumes to Water Limitation. , 2015, , 5-33.		10
69	Phellem Cell-Wall Components Are Discriminants of Cork Quality in <i>Quercus suber</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 944.	3.6	10
70	A Protein-Linger Strategy Keeps the Plant On-Hold After Rehydration of Drought-Stressed <i>Beta vulgaris</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 381.	3.6	10
71	From Proteomics to Systems Biology: MAPA, MASS WESTERN, PROMEX, and COVAIN as a User-Oriented Platform. <i>Methods in Molecular Biology</i> , 2014, 1072, 15-27.	0.9	10
72	Isolation of cellular membranes from lignin-producing tissues of Norway spruce and analysis of redox enzymes. <i>Physiologia Plantarum</i> , 2014, 152, 599-616.	5.2	9

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73	Long-term iron deficiency: Tracing changes in the proteome of different pea (<i>Pisum sativum</i> L.) cultivars. <i>Journal of Proteomics</i> , 2016, 140, 13-23.	2.4	9
74	Changes in plastid proteome and structure in arbuscular mycorrhizal roots display a nutrient starvation signature. <i>Physiologia Plantarum</i> , 2017, 159, 13-29.	5.2	9
75	Seed Metabolism and Pathogen Resistance Enhancement in <i>Pisum sativum</i> During Colonization of Arbuscular Mycorrhizal Fungi: An Integrative Metabolomics-Proteomics Approach. <i>Frontiers in Plant Science</i> , 2020, 11, 872.	3.6	9
76	Kinetic characterization of succinate-dependent plasma membrane-bound nitrate reductase in tobacco roots 1. <i>Physiologia Plantarum</i> , 1999, 105, 609-614.	5.2	8
77	Molecular Mechanisms of Tungsten Toxicity Differ for <i>Glycine max</i> Depending on Nitrogen Regime. <i>Frontiers in Plant Science</i> , 2019, 10, 367.	3.6	8
78	Hypoxia-Responsive Class III Peroxidases in Maize Roots: Soluble and Membrane-Bound Isoenzymes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8872.	4.1	8
79	Automated Protein Turnover Calculations from 15N Partial Metabolic Labeling LC/MS Shotgun Proteomics Data. <i>PLoS ONE</i> , 2014, 9, e94692.	2.5	8
80	Proteomic Profiling of the Microsomal Root Fraction: Discrimination of <i>Pisum sativum</i> L. Cultivars and Identification of Putative Root Growth Markers. <i>Proteomes</i> , 2017, 5, 8.	3.5	6
81	Different diurnal cycles of expression of two nitrate reductase transcripts in tobacco roots. <i>Protoplasma</i> , 2001, 217, 15-19.	2.1	4
82	Subcellular Phenotyping: Using Proteomics to Quantitatively Link Subcellular Leaf Protein and Organelle Distribution Analyses of <i>Pisum sativum</i> Cultivars. <i>Frontiers in Plant Science</i> , 2019, 10, 638.	3.6	4
83	Phloem Sap Proteins Are Part of a Core Stress Responsive Proteome Involved in Drought Stress Adjustment. <i>Frontiers in Plant Science</i> , 2021, 12, 625224.	3.6	4
84	Nitrate reductase in roots: Succinate- and NADH-dependent plasma membrane-bound forms. , 2001, , 119-122.		4
85	<i>Didymella pinodes</i> Affects N and P Uptakes and Their Efficiencies in a Tripartite Mutualism of Pea. <i>Agronomy</i> , 2019, 9, 52.	3.0	1
86	Hypoxia-Induced Aquaporins and Regulation of Redox Homeostasis by a Trans-Plasma Membrane Electron Transport System in Maize Roots. <i>Antioxidants</i> , 2022, 11, 836.	5.1	1
87	INPPO Actions and Recognition as a Driving Force for Progress in Plant Proteomics: Change of Guard, INPPO Update, and Upcoming Activities. <i>Proteomics</i> , 2013, 13, 3093-3100.	2.2	0
88	Spectral Count. , 2013, , 1967-1967.		0
89	Mass Spectrometry, Proteomics, and Metabolomics. , 2013, , 1179-1180.		0
90	Plant Systems Biology. , 2013, , 1716-1717.		0

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91	MAPA., 2013,, 1174-1175.		0
92	Proteomics, Quantification-Unbiased and Target Approach., 2013,, 1799-1800.		0