Stefanie Wienkoop

List of Publications by Year
in descending order

92 papers	4,867 citations	71061 41 h-index	95218 68 g-index
98 all docs	98 docs citations	98 times ranked	5699 citing authors

#	Article	IF	Citations
1	Hypoxia-Induced Aquaporins and Regulation of Redox Homeostasis by a Trans-Plasma Membrane Electron Transport System in Maize Roots. Antioxidants, 2022, 11, 836.	2.2	1
2	Phloem Sap Proteins Are Part of a Core Stress Responsive Proteome Involved in Drought Stress Adjustment. Frontiers in Plant Science, 2021, 12, 625224.	1.7	4
3	Altered Plant and Nodule Development and Protein S-Nitrosylation in Lotus japonicus Mutants Deficient in S-Nitrosoglutathione Reductases. Plant and Cell Physiology, 2020, 61, 105-117.	1.5	25
4	Hypoxia-Responsive Class III Peroxidases in Maize Roots: Soluble and Membrane-Bound Isoenzymes. International Journal of Molecular Sciences, 2020, 21, 8872.	1.8	8
5	Seed Metabolism and Pathogen Resistance Enhancement in Pisum sativum During Colonization of Arbuscular Mycorrhizal Fungi: An Integrative Metabolomics-Proteomics Approach. Frontiers in Plant Science, 2020, 11, 872.	1.7	9
6	Phellem Cell-Wall Components Are Discriminants of Cork Quality in Quercus suber. Frontiers in Plant Science, 2019, 10, 944.	1.7	10
7	Subcellular Phenotyping: Using Proteomics to Quantitatively Link Subcellular Leaf Protein and Organelle Distribution Analyses of Pisum sativum Cultivars. Frontiers in Plant Science, 2019, 10, 638.	1.7	4
8	Molecular Mechanisms of Tungsten Toxicity Differ for Glycine max Depending on Nitrogen Regime. Frontiers in Plant Science, 2019, 10, 367.	1.7	8
9	A Protein-Linger Strategy Keeps the Plant On-Hold After Rehydration of Drought-Stressed Beta vulgaris. Frontiers in Plant Science, 2019, 10, 381.	1.7	10
10	Didymella pinodes Affects N and P Uptakes and Their Efficiencies in a Tripartite Mutualism of Pea. Agronomy, 2019, 9, 52.	1.3	1
11	Sulfate is transported at significant rates through the symbiosome membrane and is crucial for nitrogenase biosynthesis. Plant, Cell and Environment, 2019, 42, 1180-1189.	2.8	29
12	Sulfur Transport and Metabolism in Legume Root Nodules. Frontiers in Plant Science, 2018, 9, 1434.	1.7	49
13	Key metabolic traits of Pisum sativum maintain cell vitality during Didymella pinodes infection: cultivar resistance and the microsymbionts' influence. Journal of Proteomics, 2017, 169, 189-201.	1.2	31
14	Changes in plastid proteome and structure in arbuscular mycorrhizal roots display a nutrient starvation signature. Physiologia Plantarum, 2017, 159, 13-29.	2.6	9
15	A Proteomic View on the Role of Legume Symbiotic Interactions. Frontiers in Plant Science, 2017, 8, 1267.	1.7	42
16	Rhizobium Impacts on Seed Productivity, Quality, and Protection of Pisum sativum upon Disease Stress Caused by Didymella pinodes: Phenotypic, Proteomic, and Metabolomic Traits. Frontiers in Plant Science, 2017, 8, 1961.	1.7	55
17	Proteomic Profiling of the Microsomal Root Fraction: Discrimination of Pisum sativum L. Cultivars and Identification of Putative Root Growth Markers. Proteomes, 2017, 5, 8.	1.7	6
18	Comparison between Proteome and Transcriptome Response in Potato (Solanum tuberosum L.) Leaves Following Potato Virus Y (PVY) Infection. Proteomes, 2017, 5, 14.	1.7	38

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19	Microbial symbionts affect Pisum sativum proteome and metabolome under Didymella pinodes infection. Journal of Proteomics, 2016, 143, 173-187.	1.2	42
20	Long-term iron deficiency: Tracing changes in the proteome of different pea (Pisum sativum L.) cultivars. Journal of Proteomics, 2016, 140, 13-23.	1.2	9
21	Authentication of Cereal Flours by Multivariate Analysis of GC–MS Data. Chromatographia, 2016, 79, 1387-1393.	0.7	16
22	Label–free quantitative proteomic analysis of tolerance to drought in *Pisum sativum*. Proteomics, 2016, 16, 2776-2787.	1.3	12
23	Drought and Recovery: Independently Regulated Processes Highlighting the Importance of Protein Turnover Dynamics and Translational Regulation in Medicago truncatula. Molecular and Cellular Proteomics, 2016, 15, 1921-1937.	2.5	50
24	Evidence for a rhizobia-induced drought stress response strategy in Medicago truncatula. Journal of Proteomics, 2016, 136, 202-213.	1.2	138
25	A Proteomic Workflow Using High-Throughput De Novo Sequencing Towards Complementation of Genome Information for Improved Comparative Crop Science. Methods in Molecular Biology, 2016, 1394, 233-243.	0.4	18
26	Differential CO_2 effect on primary carbon metabolism of flag leaves in durum wheat (*Triticum durum* Desf.). Plant, Cell and Environment, 2015, 38, 2780-2794.	2.8	29
27	The quest for tolerant varieties: the importance of integrating "omics" techniques to phenotyping. Frontiers in Plant Science, 2015, 6, 448.	1.7	67
28	Bimodal dynamics of primary metabolism-related responses in tolerant potato-Potato virus Y interaction. BMC Genomics, 2015, 16, 716.	1.2	73
29	Leghemoglobin is nitrated in functional legume nodules in a tyrosine residue within the heme cavity by a nitrite/peroxide–dependent mechanism. Plant Journal, 2015, 81, 723-735.	2.8	70
30	An improved protocol to study the plant cell wall proteome. Frontiers in Plant Science, 2015, 6, 237.	1.7	33
31	Physiological Responses of N2-Fixing Legumes to Water Limitation. , 2015, , 5-33.		10
32	Heat-Treatment-Responsive Proteins in Different Developmental Stages of Tomato Pollen Detected by Targeted Mass Accuracy Precursor Alignment (tMAPA). Journal of Proteome Research, 2015, 14, 4463-4471.	1.8	56
33	*Medicago truncatula* and *Glycine max*: Different Drought Tolerance and Similar Local Response of the Root Nodule Proteome. Journal of Proteome Research, 2015, 14, 5240-5251.	1.8	24
34	Targeted quantitative analysis of a diurnal RuBisCO subunit expression and translation profile in Chlamydomonas reinhardtii introducing a novel Mass Western approach. Journal of Proteomics, 2015, 113, 143-153.	1.2	34
35	System-level network analysis of nitrogen starvation and recovery in Chlamydomonas reinhardtii reveals potential new targets for increased lipid accumulation. Biotechnology for Biofuels, 2014, 7, 171.	6.2	103
36	Medicago truncatula Proteomics for Systems Biology: Novel Rapid Shotgun LC-MS Approach for Relative Quantification Based on Full-Scan Selective Peptide Extraction (Selpex). Methods in Molecular Biology, 2014, 1072, 303-313.	0.4	16

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37	Isolation of cellular membranes from lignin–producing tissues of Norway spruce and analysis of redox enzymes. Physiologia Plantarum, 2014, 152, 599-616.	2.6	9
38	Drought stress provokes the down–regulation of methionine and ethylene biosynthesis pathways in <scp><i>M</i></scp><i>edicago truncatula</i> roots and nodules. Plant, Cell and Environment, 2014, 37, 2051-2063.	2.8	57
39	Mass Western for Absolute Quantification of Target Proteins and Considerations About the Instrument of Choice. Methods in Molecular Biology, 2014, 1072, 199-208.	0.4	12
40	From Proteomics to Systems Biology: MAPA, MASS WESTERN, PROMEX, and COVAIN as a User-Oriented Platform. Methods in Molecular Biology, 2014, 1072, 15-27.	0.4	10
41	Automated Protein Turnover Calculations from 15N Partial Metabolic Labeling LC/MS Shotgun Proteomics Data. PLoS ONE, 2014, 9, e94692.	1.1	8
42	Local inhibition of nitrogen fixation and nodule metabolism in drought-stressed soybean. Journal of Experimental Botany, 2013, 64, 2171-2182.	2.4	101
43	Mitochondria are an early target of oxidative modifications in senescing legume nodules. New Phytologist, 2013, 197, 873-885.	3.5	46
44	The plasma membrane proteome of maize roots grown under low and high iron conditions. Journal of Proteomics, 2013, 91, 605-618.	1.2	45
45	Using ProtMAX to create high-mass-accuracy precursor alignments from label-free quantitative mass spectrometry data generated in shotgun proteomics experiments. Nature Protocols, 2013, 8, 595-601.	5.5	44
46	Phytochemical composition of Potentilla anserina L. analyzed by an integrative GC-MS and LC-MS metabolomics platform. Metabolomics, 2013, 9, 599-607.	1.4	70
47	INPPO Actions and Recognition as a Driving Force for Progress in Plant Proteomics: Change of Guard, INPPO Update, and Upcoming Activities. Proteomics, 2013, 13, 3093-3100.	1.3	0
48	Spectral Count. , 2013, , 1967-1967.		0
49	Mass Spectrometry, Proteomics, and Metabolomics. , 2013, , 1179-1180.		0
50	Plant Systems Biology. , 2013, , 1716-1717.		0
51	MAPA. , 2013, , 1174-1175.		0
52	Proteomics, Quantification-Unbiased and Target Approach. , 2013, , 1799-1800.		0
53	Possible Role of Nutritional Priming for Early Salt and Drought Stress Responses in Medicago truncatula. Frontiers in Plant Science, 2012, 3, 285.	1.7	28
54	ProMEX â€" a mass spectral reference database for plant proteomics. Frontiers in Plant Science, 2012, 3, 125.	1.7	36

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55	The different proteomes of Chlamydomonas reinhardtii. Journal of Proteomics, 2012, 75, 5883-5887.	1.2	16
56	Neurotoxin localization to ectodermal gland cells uncovers an alternative mechanism of venom delivery in sea anemones. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 1351-1358.	1.2	90
57	Boosting the Globalization of Plant Proteomics through INPPO: Current Developments and Future Prospects. Proteomics, 2012, 12, 359-368.	1.3	10
58	Oxidative stress is a consequence, not a cause, of aluminum toxicity in the forage legume *Lotus corniculatus*. New Phytologist, 2012, 193, 625-636.	3.5	66
59	MAPA Distinguishes Genotype-Specific Variability of Highly Similar Regulatory Protein Isoforms in Potato Tuber. Journal of Proteome Research, 2011, 10, 2979-2991.	1.8	42
60	AN OPTIMIZED METHOD FOR THE ISOLATION OF NUCLEI FROM CHLAMYDOMONAS REINHARDTII (CHLOROPHYCEAE)1. Journal of Phycology, 2011, 47, 333-340.	1.0	13
61	Functional analysis of proteins and protein species using shotgun proteomics and linear mathematics. Amino Acids, 2011, 41, 329-341.	1.2	10
62	MASCP Gator: An Aggregation Portal for the Visualization of Arabidopsis Proteomics Data. Plant Physiology, 2011, 155, 259-270.	2.3	94
63	Arabidopsis thaliana as a model organism for plant proteome research. Journal of Proteomics, 2010, 73, 2239-2248.	1.2	65
64	Spectral counting robust on high mass accuracy mass spectrometers. Rapid Communications in Mass Spectrometry, 2010, 24, 3609-3614.	0.7	38
65	Targeted proteomics for Chlamydomonas reinhardtii combined with rapid subcellular protein fractionation, metabolomics and metabolic flux analyses. Molecular BioSystems, 2010, 6, 1018.	2.9	94
66	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 *Chlamydomonas reinhardtii* cells. Journal of Basic Microbiology, 2009, 49, 82-91.	1.8	62
67	Carbon Metabolism and Bacteroid Functioning Are Involved in the Regulation of Nitrogen Fixation in *Medicago truncatula* Under Drought and Recovery. Molecular Plant-Microbe Interactions, 2009, 22, 1565-1576.	1.4	114
68	Evidence for Novel Tomato Seed Allergens: IgE-Reactive Legumin and Vicilin Proteins Identified by Multidimensional Protein Fractionation–Mass Spectrometry and in Silico Epitope Modeling. Journal of Proteome Research, 2009, 8, 1111-1122.	1.8	45
69	A rapid approach for phenotype–screening and database independent detection of cSNP/protein polymorphism using mass accuracy precursor alignment. Proteomics, 2008, 8, 4214-4225.	1.3	78
70	If the antibody fails – a mass Western approach. Plant Journal, 2008, 55, 1039-1046.	2.8	77
71	Absolute quantification of Medicago truncatula sucrose synthase isoforms and N-metabolism enzymes in symbiotic root nodules and the detection of novel nodule phosphoproteins by mass spectrometry. Journal of Experimental Botany, 2008, 59, 3307-3315.	2.4	40
72	Integration of Metabolomic and Proteomic Phenotypes. Molecular and Cellular Proteomics, 2008, 7, 1725-1736.	2.5	155

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73	A Cytosolic Pathway for the Conversion of Hydroxypyruvate to Glycerate during Photorespiration in *Arabidopsis*. Plant Cell, 2008, 20, 2848-2859.	3.1	193
74	Metabolomics- and Proteomics-Assisted Genome Annotation and Analysis of the Draft Metabolic Network of *Chlamydomonas reinhardtii*. Genetics, 2008, 179, 157-166.	1.2	141
75	Proteome Analysis of *Arabidopsis* Leaf Peroxisomes Reveals Novel Targeting Peptides, Metabolic Pathways, and Defense Mechanisms. Plant Cell, 2007, 19, 3170-3193.	3.1	324
76	Medicago truncatula Root Nodule Proteome Analysis Reveals Differential Plant and Bacteroid Responses to Drought Stress. Plant Physiology, 2007, 144, 1495-1507.	2.3	178
77	ProMEX: a mass spectral reference database for proteins and protein phosphorylation sites. BMC Bioinformatics, 2007, 8, 216.	1.2	96
78	Integrative Profiling of Metabolites and Proteins. Methods in Molecular Biology, 2007, 358, 57-75.	0.4	33
79	Relative and absolute quantitative shotgun proteomics: targeting low-abundance proteins in Arabidopsis thaliana. Journal of Experimental Botany, 2006, 57, 1529-1535.	2.4	81
80	Stable isotope-free quantitative shotgun proteomics combined with sample pattern recognition for rapid diagnostics. Journal of Separation Science, 2006, 29, 2793-2801.	1.3	48
81	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. Metabolomics, 2005, 1, 109-121.	1.4	97
82	Enrichment of phosphorylated proteins and peptides from complex mixtures using metal oxide/hydroxide affinity chromatography (MOAC). Proteomics, 2005, 5, 4389-4397.	1.3	272
83	d-GLYCERATE 3-KINASE, the Last Unknown Enzyme in the Photorespiratory Cycle in Arabidopsis, Belongs to a Novel Kinase Family. Plant Cell, 2005, 17, 2413-2420.	3.1	126
84	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. Rapid Communications in Mass Spectrometry, 2004, 18, 643-650.	0.7	80
85	Cell-specific protein profiling in Arabidopsis thaliana trichomes: identification of trichome-located proteins involved in sulfur metabolism and detoxification. Phytochemistry, 2004, 65, 1641-1649.	1.4	90
86	Stable isotope labeling of phosphopeptides for multiparallel kinase target analysis and identification of phosphorylation sites. Rapid Communications in Mass Spectrometry, 2003, 17, 1579-1584.	0.7	45
87	Proteome Analysis. Novel Proteins Identified at the Peribacteroid Membrane from Lotus japonicus Root Nodules. Plant Physiology, 2003, 131, 1080-1090.	2.3	193
88	Characterisation by proteomics of peribacteroid space and peribacteroid membrane preparations from pea (Pisum sativum) symbiosomes. Proteomics, 2002, 2, 325.	1.3	114
89	Differentiation of Plant Cells During Symbiotic Nitrogen Fixation. Comparative and Functional Genomics, 2002, 3, 151-157.	2.0	17
90	Different diurnal cycles of expression of two nitrate reductase transcripts in tobacco roots. Protoplasma, 2001, 217, 15-19.	1.0	4

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91	Nitrate reductase in roots: Succinate- and NADH-dependent plasma membrane-bound forms. , 2001, , 119-122.		4
92	Kinetic characterization of succinate-dependent plasma membrane-bound nitrate reductase in tobacco roots 1. Physiologia Plantarum, 1999, 105, 609-614.	2.6	8