

# Wolfgang Hoehenwarter

## List of Publications by Year in descending order

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54  
papers

2,074  
citations

236925

25  
h-index

254184

43  
g-index

66  
all docs

66  
docs citations

66  
times ranked

3334  
citing authors

#	ARTICLE	IF	CITATIONS
1	Endocytosis is a significant contributor to uranium(VI) uptake in tobacco ( <i>Nicotiana tabacum</i> ) BY-2 cells in phosphate-deficient culture. <i>Science of the Total Environment</i> , 2022, 823, 153700.	8.0	9
2	Bacterial-type ferroxidase tunes iron-dependent phosphate sensing during <i>Arabidopsis</i> root development. <i>Current Biology</i> , 2022, 32, 2189-2205.e6.	3.9	16
3	A modular two yeast species secretion system for the production and preparative application of unspecific peroxygenases. <i>Communications Biology</i> , 2021, 4, 562.	4.4	38
4	Exocyst subunit Exo70B2 is linked to immune signaling and autophagy. <i>Plant Cell</i> , 2021, 33, 404-419.	6.6	31
5	LC-MS Based Draft Map of the <i>Arabidopsis thaliana</i> Nuclear Proteome and Protein Import in Pattern Triggered Immunity. <i>Frontiers in Plant Science</i> , 2021, 12, 744103.	3.6	8
6	Phosphorylation-dependent control of an RNA granule-localized protein that fine-tunes defence gene expression at a post-transcriptional level. <i>Plant Journal</i> , 2020, 101, 1023-1039.	5.7	26
7	Bringing New Methods to the Seed Proteomics Platform: Challenges and Perspectives. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9162.	4.1	19
8	Phosphorylation of the CAMTA3 Transcription Factor Triggers Its Destabilization and Nuclear Export. <i>Plant Physiology</i> , 2020, 184, 1056-1071.	4.8	29
9	Working day and night: plastid casein kinase 2 catalyses phosphorylation of proteins with diverse functions in light- and dark-adapted plastids. <i>Plant Journal</i> , 2020, 104, 546-558.	5.7	4
10	Reshaping of the <i>Arabidopsis thaliana</i> Proteome Landscape and Co-regulation of Proteins in Development and Immunity. <i>Molecular Plant</i> , 2020, 13, 1709-1732.	8.3	26
11	Flexibility of intrinsically disordered degrons in AUX/IAA proteins reinforces auxin co-receptor assemblies. <i>Nature Communications</i> , 2020, 11, 2277.	12.8	38
12	Expression of elastolytic cathepsins in human skin and their involvement in age-dependent elastin degradation. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129544.	2.4	21
13	A comprehensive map of human elastin cross-linking during elastogenesis. <i>FEBS Journal</i> , 2019, 286, 3594-3610.	4.7	26
14	Multiple Glycation Sites in Blood Plasma Proteins as an Integrated Biomarker of Type 2 Diabetes Mellitus. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2329.	4.1	28
15	Rapid and reproducible phosphopeptide enrichment by tandem metal oxide affinity chromatography : application to boron deficiency induced phosphoproteomics. <i>Plant Journal</i> , 2019, 98, 370-384.	5.7	14
16	UbiGate: a synthetic biology toolbox to analyse ubiquitination. <i>New Phytologist</i> , 2018, 217, 1749-1763.	7.3	23
17	Degradation of tropoelastin and skin elastin by neprilysin. <i>Biochimie</i> , 2018, 146, 73-78.	2.6	21
18	Proteome Map of Pea ( <i>Pisum sativum</i> L.) Embryos Containing Different Amounts of Residual Chlorophylls. <i>International Journal of Molecular Sciences</i> , 2018, 19, 4066.	4.1	15

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19	The effect of simulated microgravity on the Brassica napus seedling proteome. <i>Functional Plant Biology</i> , 2018, 45, 440.	2.1	12
20	Mining seed proteome: from protein dynamics to modification profiles. <i>Biological Communications</i> , 2018, 63, 43-58.	0.8	15
21	Assessment of Label-Free Quantification in Discovery Proteomics and Impact of Technological Factors and Natural Variability of Protein Abundance. <i>Journal of Proteome Research</i> , 2017, 16, 1410-1424.	3.7	91
22	Changes in PUB22 Ubiquitination Modes Triggered by MITOGEN-ACTIVATED PROTEIN KINASE3 Dampen the Immune Response. <i>Plant Cell</i> , 2017, 29, 726-745.	6.6	63
23	Multi-Omics of Tomato Glandular Trichomes Reveals Distinct Features of Central Carbon Metabolism Supporting High Productivity of Specialized Metabolites. <i>Plant Cell</i> , 2017, 29, 960-983.	6.6	143
24	Identification of STN7/STN8 kinase targets reveals connections between electron transport, metabolism and gene expression. <i>Plant Journal</i> , 2017, 90, 1176-1186.	5.7	50
25	MAPKs Influence Pollen Tube Growth by Controlling the Formation of Phosphatidylinositol 4,5-Bisphosphate in an Apical Plasma Membrane Domain. <i>Plant Cell</i> , 2017, 29, 3030-3050.	6.6	34
26	Variation in auxin sensing guides AUX/IAA transcriptional repressor ubiquitylation and destruction. <i>Nature Communications</i> , 2017, 8, 15706.	12.8	56
27	Stress-Related Mitogen-Activated Protein Kinases Stimulate the Accumulation of Small Molecules and Proteins in Arabidopsis thaliana Root Exudates. <i>Frontiers in Plant Science</i> , 2017, 8, 1292.	3.6	15
28	Combined <sup>15</sup> N-Labeling and TandemMOAC Quantifies Phosphorylation of MAP Kinase Substrates Downstream of MKK7 in Arabidopsis. <i>Frontiers in Plant Science</i> , 2017, 8, 2050.	3.6	19
29	Regulation of WRKY46 Transcription Factor Function by Mitogen-Activated Protein Kinases in Arabidopsis thaliana. <i>Frontiers in Plant Science</i> , 2016, 7, 61.	3.6	54
30	Phenotypes on demand via switchable target protein degradation in multicellular organisms. <i>Nature Communications</i> , 2016, 7, 12202.	12.8	50
31	Comparative expression profiling reveals a role of the root apoplast in local phosphate response. <i>BMC Plant Biology</i> , 2016, 16, 106.	3.6	70
32	Molecular-level insights into aging processes of skin elastin. <i>Biochimie</i> , 2016, 128-129, 163-173.	2.6	87
33	Immobilized metal affinity chromatography on collapsed Langmuir-Blodgett iron(III) stearate films and iron(III) oxide nanoparticles for bottom-up phosphoproteomics. <i>Journal of Chromatography A</i> , 2016, 1443, 181-190.	3.7	18
34	Phosphoprotein Enrichment Combined with Phosphopeptide Enrichment to Identify Putative Phosphoproteins During Defense Response in Arabidopsis thaliana. <i>Methods in Molecular Biology</i> , 2016, 1398, 373-383.	0.9	3
35	Identification of protein N-termini in Cyanophora paradoxa cyanelles: transit peptide composition and sequence determinants for precursor maturation. <i>Frontiers in Plant Science</i> , 2015, 6, 559.	3.6	17
36	Changes in the Phosphoproteome and Metabolome Link Early Signaling Events to Rearrangement of Photosynthesis and Central Metabolism in Salinity and Oxidative Stress Response in Arabidopsis. <i>Plant Physiology</i> , 2015, 169, 3021-3033.	4.8	53

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37	Combining Metabolic <sup>15</sup> N Labeling with Improved Tandem MOAC for Enhanced Probing of the Phosphoproteome. <i>Methods in Molecular Biology</i> , 2015, 1306, 81-96.	0.9	9
38	The RNA-binding protein RNP29 is an unusual Toc159 transport substrate. <i>Frontiers in Plant Science</i> , 2014, 5, 258.	3.6	9
39	Targeted Proteomics Analysis of Protein Degradation in Plant Signaling on an LTQ-Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2014, 13, 4246-4258.	3.7	44
40	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
41	Tandem Metal-Oxide Affinity Chromatography for Enhanced Depth of Phosphoproteome Analysis. <i>Methods in Molecular Biology</i> , 2014, 1072, 621-632.	0.9	10
42	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
43	Identification of Novel in vivo MAP Kinase Substrates in <i>Arabidopsis thaliana</i> Through Use of Tandem Metal Oxide Affinity Chromatography. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 369-380.	3.8	122
44	Proteome and metabolome profiling of cytokinin action in <i>Arabidopsis</i> identifying both distinct and similar responses to cytokinin down- and up-regulation. <i>Journal of Experimental Botany</i> , 2013, 64, 4193-4206.	4.8	58
45	ProMEX – a mass spectral reference database for plant proteomics. <i>Frontiers in Plant Science</i> , 2012, 3, 125.	3.6	36
46	Proteomic and Phosphoproteomic Analysis of <i>Picea wilsonii</i> Pollen Development under Nutrient Limitation. <i>Journal of Proteome Research</i> , 2012, 11, 4180-4190.	3.7	19
47	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
48	Functional analysis of proteins and protein species using shotgun proteomics and linear mathematics. <i>Amino Acids</i> , 2011, 41, 329-341.	2.7	10
49	Spectral counting robust on high mass accuracy mass spectrometers. <i>Rapid Communications in Mass Spectrometry</i> , 2010, 24, 3609-3614.	1.5	38
50	Comparative analysis of phytohormone-responsive phosphoproteins in <i>Arabidopsis thaliana</i> using TiO <sub>2</sub> -phosphopeptide enrichment and mass accuracy precursor alignment. <i>Plant Journal</i> , 2010, 63, no-no.	5.7	190
51	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
52	Identification of proteins that modify cataract of mouse eye lens. <i>Proteomics</i> , 2008, 8, 5011-5024.	2.2	21
53	Eye lens proteomics. <i>Amino Acids</i> , 2006, 30, 369-389.	2.7	60
54	Eye lens proteomics: from global approach to detailed information about phakinin and gamma E and F crystallin genes. <i>Proteomics</i> , 2005, 5, 245-257.	2.2	9