Laurence V Bindschedler

List of Publications by Year
in descending order

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42 papers	4,480 citations	159585 30 h-index	302126 39 g-index
43 all docs	43 docs citations	43 times ranked	4962 citing authors

#	Article	IF	Citations
1	Genome Expansion and Gene Loss in Powdery Mildew Fungi Reveal Tradeoffs in Extreme Parasitism. Science, 2010, 330, 1543-1546.	12.6	725
2	Peroxidase-dependent apoplastic oxidative burst in Arabidopsis required for pathogen resistance. Plant Journal, 2006, 47, 851-863.	5.7	520
3	The apoplastic oxidative burst in response to biotic stress in plants: a threeâ€€component system. Journal of Experimental Botany, 2002, 53, 1367-1376.	4.8	484
4	The apoplastic oxidative burst in response to biotic stress in plants: a three-component system. Journal of Experimental Botany, 2002, 53, 1367-1376.	4.8	342
5	The apoplastic oxidative burst in response to biotic stress in plants: a three-component system. Journal of Experimental Botany, 2002, 53, 1367-76.	4.8	284
6	Structure and evolution of barley powdery mildew effector candidates. BMC Genomics, 2012, 13, 694.	2.8	238
7	Host-Induced Gene Silencing in Barley Powdery Mildew Reveals a Class of Ribonuclease-Like Effectors. Molecular Plant-Microbe Interactions, 2013, 26, 633-642.	2.6	190
8	Early signalling events in the apoplastic oxidative burst in suspension cultured French bean cells involve cAMP and Ca 2+. New Phytologist, 2001, 151, 185-194.	7.3	142
9	Hydroponic isotope labelling of entire plants (HILEP) for quantitative plant proteomics; an oxidative stress case study. Phytochemistry, 2008, 69, 1962-1972.	2.9	103
10	Production of reactive oxygen species in Arabidopsis thaliana cell suspension cultures in response to an elicitor from Fusarium oxysporum: implications for basal resistance. Journal of Experimental Botany, 2006, 57, 1817-1827.	4.8	87
11	Interactions between the Powdery Mildew Effector BEC1054 and Barley Proteins Identify Candidate Host Targets. Journal of Proteome Research, 2016, 15, 826-839.	3.7	85
12	Structure, expression and localization of a germin-like protein in barley (Hordeum vulgare L.) that is insolubilized in stressed leaves. Plant Molecular Biology, 1998, 37, 297-308.	3.9	83
13	Mildew-Omics: How Global Analyses Aid the Understanding of Life and Evolution of Powdery Mildews. Frontiers in Plant Science, 2016, 7, 123.	3.6	77
14	In Planta Proteomics and Proteogenomics of the Biotrophic Barley Fungal Pathogen Blumeria graminis f. sp. hordei>. Molecular and Cellular Proteomics, 2009, 8, 2368-2381.	3.8	75
15	Characterization of SNP1, a Cell Wall-Degrading Trypsin, Produced During Infection by Stagonospora nodorum. Molecular Plant-Microbe Interactions, 2000, 13, 538-550.	2.6	71
16	Heat-induced resistance in barley to powdery mildew (Blumeria graminisf.sp.hordei) is associated with a burst of active oxygen species. Physiological and Molecular Plant Pathology, 1998, 52, 185-199.	2.5	70
17	Quantitative plant proteomics. Proteomics, 2011, 11, 756-775.	2.2	70
18	A decade of plant proteomics and mass spectrometry: Translation of technical advancements to food security and safety issues. Mass Spectrometry Reviews, 2013, 32, 335-365.	5.4	70

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19	Salicylic Acid Accumulation in Barley Is Pathogen Specific but Not Required for Defense-Gene Activation. Molecular Plant-Microbe Interactions, 1998, 11, 702-705.	2.6	69
20	Heat-Shock Response in Arabidopsis thaliana Explored by Multiplexed Quantitative Proteomics Using Differential Metabolic Labeling. Journal of Proteome Research, 2008, 7, 780-785.	3.7	66
21	Translational plant proteomics: A perspective. Journal of Proteomics, 2012, 75, 4588-4601.	2.4	63
22	Combinatorial peptide ligand libraries and plant proteomics: A winning strategy at a price. Journal of Chromatography A, 2009, 1216, 1215-1222.	3.7	59
23	Proteogenomics and in silico structural and functional annotation of the barley powdery mildew Blumeria graminis f. sp. hordei. Methods, 2011, 54, 432-441.	3.8	57
24	Heat-induced resistance in barley to the powdery mildew fungus Erysiphe graminis f.sp. hordei. Physiological and Molecular Plant Pathology, 1995, 47, 51-66.	2.5	43
25	Chromatographic alignment of LC-MS and LC-MS/MS datasets by genetic algorithm feature extraction. Journal of the American Society for Mass Spectrometry, 2007, 18, 1835-1843.	2.8	42
26	Modification of hemicellulose content by antisense down-regulation of UDP-glucuronate decarboxylase in tobacco and its consequences for cellulose extractability. Phytochemistry, 2007, 68, 2635-2648.	2.9	41
27	Quantitative proteomics using uniform ¹⁵Nâ€labeling, MASCOT, and the transâ€proteomic pipeline. Proteomics, 2007, 7, 3462-3469.	2.2	41
28	A two component chitin-binding protein from French bean - association of a proline-rich protein with a cysteine-rich polypeptide. FEBS Letters, 2006, 580, 1541-1546.	2.8	40
29	The cell wall and secretory proteome of a tobacco cell line synthesising secondary wall. Proteomics, 2009, 9, 2355-2372.	2.2	37
30	Evolution of the EKA family of powdery mildew avirulence-effector genes from the ORF 1 of a LINE retrotransposon. BMC Genomics, 2015, 16, 917.	2.8	33
31	Broadly Conserved Fungal Effector BEC1019 Suppresses Host Cell Death and Enhances Pathogen Virulence in Powdery Mildew of Barley (Hordeum vulgare L.) (Retracted). Molecular Plant-Microbe Interactions, 2015, 28, 968-983.	2.6	33
32	Characterisation and expression of the pathway from UDP-glucose to UDP-xylose in differentiating tobacco tissue. Plant Molecular Biology, 2005, 57, 285-301.	3.9	32
33	Deletion of the SNP1 trypsin protease from Stagonospora nodorum reveals another major protease expressed during infection. Fungal Genetics and Biology, 2003, 38, 43-53.	2.1	27
34	Analysis of Barley Leaf Epidermis and Extrahaustorial Proteomes During Powdery Mildew Infection Reveals That the PR5 Thaumatin-Like Protein TLP5 Is Required for Susceptibility Towards Blumeria graminis f. sp. hordei. Frontiers in Plant Science, 2019, 10, 1138.	3.6	19
35	Transcriptional changes related to secondary wall formation in xylem of transgenic lines of tobacco altered for lignin or xylan content which show improved saccharification. Phytochemistry, 2012, 74, 79-89.	2.9	17
36	Automatic internal calibration in liquid chromatography/Fourier transform ion cyclotron resonance mass spectrometry of protein digests. Rapid Communications in Mass Spectrometry, 2006, 20, 3076-3080.	1.5	16

#	Article	IF	Citations
37	Fully automated software solution for protein quantitation by global metabolic labeling with stable isotopes. Rapid Communications in Mass Spectrometry, 2011, 25, 1461-1471.	1.5	11
38	Plant proteomics. , 2019, , 45-67.		7
39	Plant Proteomics in Crop Improvement. Proteomics, 2013, 13, 1771-1771.	2.2	5
40	Hydroponic Isotope Labeling of Entire Plants and High-Performance Mass Spectrometry for Quantitative Plant Proteomics. Methods in Molecular Biology, 2012, 893, 155-173.	0.9	3
41	Quantitative proteomics of Arabidopsis plants submitted to oxidative stress. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2007, 146, S256-S257.	1.8	0
42	Quantitative Plant Proteomics Using Hydroponic Isotope Labeling of Entire Plants (HILEP). , 2011, , 363-380.		0