Christof Rampitsch

List of Publications by Year
in descending order

37	1,241	394421	361022
papers	citations	19 h-index	35 g-index

37	37	37	1651
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Analysis of the wheat andPuccinia triticina (leaf rust) proteomes during a susceptible host-pathogen interaction. Proteomics, 2006, 6, 1897-1907.	2.2	117
2	A review of wheat leaf rust research and the development of resistant cultivars in Canada. Canadian Journal of Plant Pathology, 2016, 38, 1-18.	1.4	107
3	Advances in plant proteomics toward improvement of crop productivity and stress resistancex. Frontiers in Plant Science, 2015, 6, 209.	3.6	98
4	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
5	Proteomic analysis of the phytopathogenic soilborne fungusVerticillium dahliaereveals differential protein expression in isolates that differ in aggressiveness. Proteomics, 2010, 10, 289-303.	2.2	69
6	Proteome analysis of wheat leaf rust fungus, Puccinia triticina, infection structures enriched for haustoria. Proteomics, 2011, 11, 944-963.	2.2	62
7	Determination and Characterization of Site-Specific N-Glycosylation Using MALDI-Qq-TOF Tandem Mass Spectrometry:Â Case Study with a Plant Protease. Analytical Chemistry, 2006, 78, 1093-1103.	6.5	59
8	Redoxâ€sensitive proteome and antioxidant strategies in wheat seed dormancy control. Proteomics, 2011, 11, 865-882.	2.2	59
9	Integrated analysis of seed proteome and <scp>mRNA</scp> oxidation reveals distinct postâ€transcriptional features regulating dormancy in wheat (Triticum aestivum L.). Plant Biotechnology Journal, 2013, 11, 921-932.	8.3	59
10	Proteomics and plant disease: Advances in combating a major threat to the global food supply. Proteomics, 2012, 12, 673-690.	2.2	55
11	Developmental and seed aging mediated regulation of antioxidative genes and differential expression of proteins during pre- and post-germinative phases in pea. Journal of Plant Physiology, 2012, 169, 1477-1488.	3.5	47
12	Genomic analysis of MAP kinase cascades inArabidopsis defense responses. Plant Molecular Biology Reporter, 2005, 23, 331-343.	1.8	43
13	The beginnings of crop phosphoproteomics: exploring early warning systems of stress. Frontiers in Plant Science, 2012, 3, 144.	3.6	39
14	Thiol redox-sensitive seed proteome in dormant and non-dormant hybrid genotypes of wheat. Phytochemistry, 2011, 72, 1162-1172.	2.9	35
15	Modulating protein function through reversible oxidation: Redoxâ€mediated processes in plants revealed through proteomics. Proteomics, 2013, 13, 579-596.	2.2	35
16	Proteome of monoclonal antibody-purified haustoria fromPuccinia triticinaRace-1. Proteomics, 2015, 15, 1307-1315.	2.2	29
17	Proteomic analyses of the cyanobacterium Arthrospira (Spirulina) platensis under iron and salinity stress. Environmental and Experimental Botany, 2018, 147, 63-74.	4.2	29
18	The phosphoproteome of Fusarium graminearum at the onset of nitrogen starvation. Proteomics, 2010, 10, 124-140.	2.2	28

#	Article	IF	Citations
19	Comparative secretome analysis ofFusarium graminearumand two of its non-pathogenic mutants upon deoxynivalenol induction in vitro. Proteomics, 2013, 13, 1913-1921.	2.2	28
20	Development of a Monoclonal Antibody-Based Enzyme-Linked Immunosorbent Assay To Quantify Soluble Î²-Glucans in Oats and Barley. Journal of Agricultural and Food Chemistry, 2003, 51, 5882-5887.	5.2	18
21	Prenatal alcohol exposure alters phosphorylation and glycosylation of proteins in rat offspring liver. Proteomics, 2010, 10, 417-434.	2.2	18
22	The application of proteomics to plant biology: a review. Canadian Journal of Botany, 2006, 84, 883-892.	1.1	14
23	Methods for Functional Proteomic Analyses. Methods in Molecular Biology, 2009, 513, 93-110.	0.9	13
24	Redox signalling from NADPH oxidase targets metabolic enzymes and developmental proteins in Fusarium graminearum. Molecular Plant Pathology, 2019, 20, 92-106.	4.2	13
25	TAB2, a nucleoside diphosphate protein kinase, is a component of the tMEK2 disease resistance pathway in tomato. Physiological and Molecular Plant Pathology, 2008, 73, 33-39.	2.5	12
26	Proteomic profiling reveals insights into Triticeae stigma development and function. Journal of Experimental Botany, 2014, 65, 6069-6080.	4.8	10
27	Phosphoproteomic profiling of wheat callus labelled in vivo. Plant Science, 2006, 171, 488-496.	3.6	9
28	Towards Systems Biology of Mycotoxin Regulation. Toxins, 2013, 5, 675-682.	3.4	9
29	Secretome Analysis of Clavibacter nebraskensis Strains Treated with Natural Xylem Sap In Vitro Predicts Involvement of Glycosyl Hydrolases and Proteases in Bacterial Aggressiveness. Proteomes, 2021, 9, 1.	3.5	9
30	Identification and characterization of a serine protease from wheat leaves. European Journal of Plant Pathology, 2016, 146, 293-304.	1.7	7
31	Temporal Quantitative Changes in the Resistant and Susceptible Wheat Leaf Apoplastic Proteome During Infection by Wheat Leaf Rust (Puccinia triticina). Frontiers in Plant Science, 2019, 10, 1291.	3.6	7
32	The role of reactive oxygen species in the virulence of wheat leaf rust fungus Puccinia triticina. Environmental Microbiology, 2020, 22, 2956-2967.	3.8	7
33	Misoprostol treatment prevents hypoxia-induced cardiac dysfunction through a 14-3-3 and PKA regulatory motif on Bnip3. Cell Death and Disease, 2021, 12, 1105.	6.3	7
34	Early Generation Î²-Glucan Selection in Oat Using a Monoclonal Antibody-Based Enzyme-Linked Immunosorbent Assay. Cereal Chemistry, 2006, 83, 510-512.	2.2	6
35	Functional genomic approaches in cereal rusts. Canadian Journal of Plant Pathology, 2012, 34, 3-12.	1.4	5
36	Wheat seed proteins regulated by imbibition independent of dormancy status. Plant Signaling and Behavior, 2013, 8, e26601.	2.4	5

#	Article	IF	Citations
37	Phosphoproteomics Analysis for Probing Plant Stress Tolerance. Methods in Molecular Biology, 2017, 1631, 181-193.	0.9	4