

Kjell Sergeant

List of Publications by Year in descending order

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91
papers

4,037
citations

117625

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h-index

133252

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93
all docs

93
docs citations

93
times ranked

5571
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular insights into plant desiccation tolerance: transcriptomics, proteomics and targeted metabolite profiling in <i>Craterostigma plantagineum</i> . <i>Plant Journal</i> , 2021, 107, 377-398.	5.7	40
2	Molecular and Biochemical Insights Into Early Responses of Hemp to Cd and Zn Exposure and the Potential Effect of Si on Stress Response. <i>Frontiers in Plant Science</i> , 2021, 12, 711853.	3.6	8
3	The Cell Wall Proteome of <i>Craterostigma plantagineum</i> Cell Cultures Habituated to Dichlobenil and Isoxaben. <i>Cells</i> , 2021, 10, 2295.	4.1	4
4	Gene expression and metabolite analysis in barley inoculated with net blotch fungus and plant growth-promoting rhizobacteria. <i>Plant Physiology and Biochemistry</i> , 2021, 168, 488-500.	5.8	5
5	The Roots of Plant Frost Hardiness and Tolerance. <i>Plant and Cell Physiology</i> , 2020, 61, 3-20.	3.1	67
6	Long-Term Cd Exposure Alters the Metabolite Profile in Stem Tissue of <i>Medicago sativa</i> . <i>Cells</i> , 2020, 9, 2707.	4.1	14
7	Repair of sub-lethal freezing damage in leaves of <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2020, 20, 35.	3.6	8
8	Systems Biology of Metal Tolerance in Plants: A Case Study on the Effects of Cd Exposure on Two Model Plants. , 2019, , 23-37.		4
9	The Dynamics of the Cell Wall Proteome of Developing Alfalfa Stems. <i>Biology</i> , 2019, 8, 60.	2.8	16
10	Selection of Appropriate Reference Genes for Gene Expression Analysis under Abiotic Stresses in <i>Salix viminalis</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 4210.	4.1	12
11	Does long-term cadmium exposure influence the composition of pectic polysaccharides in the cell wall of <i>Medicago sativa</i> stems?. <i>BMC Plant Biology</i> , 2019, 19, 271.	3.6	56
12	Identification of the aquaporin gene family in <i>Cannabis sativa</i> and evidence for the accumulation of silicon in its tissues. <i>Plant Science</i> , 2019, 287, 110167.	3.6	41
13	Pollen development and function under heat stress: from effects to responses. <i>Acta Physiologiae Plantarum</i> , 2019, 41, 1.	2.1	45
14	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	15
15	De novo transcriptome assembly of textile hemp from datasets on hypocotyls and adult plants. <i>Data in Brief</i> , 2019, 27, 104790.	1.0	5
16	Reactive oxygen species and heavy metal stress in plants: Impact on the cell wall and secondary metabolism. <i>Environmental and Experimental Botany</i> , 2019, 161, 98-106.	4.2	302
17	Changes in the Proteome of <i>Medicago sativa</i> Leaves in Response to Long-Term Cadmium Exposure Using a Cell-Wall Targeted Approach. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2498.	4.1	41
18	Novel Insights from Comparative In Silico Analysis of Green Microalgal Cellulases. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1782.	4.1	12

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19	Insights into the molecular regulation of monolignol-derived product biosynthesis in the growing hemp hypocotyl. BMC Plant Biology, 2018, 18, 1.	3.6	368
20	Long-term cadmium exposure influences the abundance of proteins that impact the cell wall structure in <i>Medicago sativa</i> stems. Plant Biology, 2018, 20, 1023-1035.	3.8	54
21	Pathogenic Leptospire Modulate Protein Expression and Post-translational Modifications in Response to Mammalian Host Signals. Frontiers in Cellular and Infection Microbiology, 2017, 7, 362.	3.9	36
22	Didehydrophenylalanine, an abundant modification in the beta subunit of plant polygalacturonases. PLoS ONE, 2017, 12, e0171990.	2.5	7
23	Copper Trafficking in Plants and Its Implication on Cell Wall Dynamics. Frontiers in Plant Science, 2016, 7, 601.	3.6	254
24	Combining -Omics to Unravel the Impact of Copper Nutrition on Alfalfa (<i>Medicago sativa</i>) Stem Metabolism. Plant and Cell Physiology, 2016, 57, 407-422.	3.1	23
25	Ups and downs in alfalfa: Proteomic and metabolic changes occurring in the growing stem. Plant Science, 2015, 238, 13-25.	3.6	10
26	Target or barrier? The cell wall of early- and later-diverging plants vs cadmium toxicity: differences in the response mechanisms. Frontiers in Plant Science, 2015, 6, 133.	3.6	286
27	An improved protocol to study the plant cell wall proteome. Frontiers in Plant Science, 2015, 6, 237.	3.6	33
28	Comparative proteomic analysis of lung tissue from guinea pigs with leptospiral pulmonary haemorrhage syndrome (LPHS) reveals a decrease in abundance of host proteins involved in cytoskeletal and cellular organization. Journal of Proteomics, 2015, 122, 55-72.	2.4	15
29	Unravelling the effect of sucrose and cold pretreatment on cryopreservation of potato through sugar analysis and proteomics. Cryobiology, 2015, 71, 432-441.	0.7	43
30	A 2-D guinea pig lung proteome map. Data in Brief, 2015, 4, 140-145.	1.0	2
31	Physiological and Proteomic Responses of Different Willow Clones (<i>Salix fragilis</i> X <i>Salix alba</i>) Exposed to Dredged Sediment Contaminated by Heavy Metals. International Journal of Phytoremediation, 2014, 16, 1148-1169.	3.1	22
32	Comparative analysis of Salmonella susceptibility and tolerance to the biocide chlorhexidine identifies a complex cellular defense network. Frontiers in Microbiology, 2014, 5, 373.	3.5	20
33	Proteomic changes in leaves of poplar exposed to both cadmium and low-temperature. Environmental and Experimental Botany, 2014, 106, 112-123.	4.2	40
34	Description of the mechanisms underlying geosmin production in <i>Penicillium expansum</i> using proteomics. Journal of Proteomics, 2014, 96, 13-28.	2.4	7
35	Changes in sugar content and proteome of potato in response to cold and dehydration stress and their implications for cryopreservation. Journal of Proteomics, 2014, 98, 99-111.	2.4	46
36	Wood biosynthesis and typologies: a molecular rhapsody. Tree Physiology, 2014, 34, 839-855.	3.1	44

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37	Abiotic Stress Tolerance in Plants. , 2014, , 23-68.		14
38	Changes in the proteome and water state in bark and xylem of <i>Hydrangea paniculata</i> during loss of freezing tolerance. <i>Environmental and Experimental Botany</i> , 2014, 106, 99-111.	4.2	15
39	Automation of C-terminal sequence analysis of 2D-PAGE separated proteins. <i>EuPA Open Proteomics</i> , 2014, 3, 250-261.	2.5	2
40	A multiple-level study of metal tolerance in <i>Salix fragilis</i> and <i>Salix aurita</i> clones. <i>Journal of Proteomics</i> , 2014, 101, 113-129.	2.4	20
41	Exploring chloroplastic changes related to chilling and freezing tolerance during cold acclimation of pea (<i>Pisum sativum</i> L.). <i>Journal of Proteomics</i> , 2013, 80, 145-159.	2.4	48
42	Differential Protein Expression in Response to Abiotic Stress in Two Potato Species: <i>Solanum commersonii</i> Dun and <i>Solanum tuberosum</i> L.. <i>International Journal of Molecular Sciences</i> , 2013, 14, 4912-4933.	4.1	39
43	Proteomic and phenotypic analysis of triclosan tolerant verocytotoxigenic <i>Escherichia coli</i> O157:H19. <i>Journal of Proteomics</i> , 2013, 80, 78-90.	2.4	23
44	Two Traditional Maize Inbred Lines of Contrasting Technological Abilities Are Discriminated by the Seed Flour Proteome. <i>Journal of Proteome Research</i> , 2013, 12, 3152-3165.	3.7	22
45	Physiological and proteome study of sunflowers exposed to a polymetallic constraint. <i>Proteomics</i> , 2013, 13, 1993-2015.	2.2	15
46	From Tolerance to Acute Metabolic Deregulation: Contribution of Proteomics To Dig into the Molecular Response of Alder Species under a Polymetallic Exposure. <i>Journal of Proteome Research</i> , 2013, 12, 5160-5179.	3.7	17
47	Proteomic changes associated with freeze-thaw injury and post-thaw recovery in onion (<i>Allium</i>) Tj ETQq1 1 0.784314 ggBT /Overl	3.7	34
48	Integrated -Omics: A Powerful Approach to Understanding the Heterogeneous Lignification of Fibre Crops. <i>International Journal of Molecular Sciences</i> , 2013, 14, 10958-10978.	4.1	47
49	A physiological and proteomic study of poplar leaves during ozone exposure combined with mild drought. <i>Proteomics</i> , 2013, 13, 1737-1754.	2.2	27
50	Gel-Based and Gel-Free Quantitative Proteomics Approaches at a Glance. <i>International Journal of Plant Genomics</i> , 2012, 2012, 1-17.	2.2	148
51	Screening for changes in leaf and cambial proteome of <i>Populus tremula</i> — <i>P. alba</i> under different heat constraints. <i>Journal of Plant Physiology</i> , 2012, 169, 1698-1718.	3.5	15
52	Comparative proteomic analysis of <i>Salmonella</i> tolerance to the biocide active agent triclosan. <i>Journal of Proteomics</i> , 2012, 75, 4505-4519.	2.4	35
53	Optimization of iTRAQ labelling coupled to OFFGEL fractionation as a proteomic workflow to the analysis of microsomal proteins of <i>Medicago truncatula</i> roots. <i>Proteome Science</i> , 2012, 10, 37.	1.7	34
54	Proteomics as a Toolbox to Study the Metabolic Adjustment of Trees During Exposure to Metal Trace Elements. , 2012, , 143-164.		2

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55	A Difference Gel Electrophoresis Study on Thylakoids Isolated from Poplar Leaves Reveals a Negative Impact of Ozone Exposure on Membrane Proteins. <i>Journal of Proteome Research</i> , 2011, 10, 3003-3011.	3.7	20
56	The use of 2D-electrophoresis and de novo sequencing to characterize inter- and intra-cultivar protein polymorphisms in an allopolyploid crop. <i>Phytochemistry</i> , 2011, 72, 1243-1250.	2.9	33
57	Alteration of plasma membrane-bound redox systems of iron deficient pea roots by chitosan. <i>Journal of Proteomics</i> , 2011, 74, 1437-1449.	2.4	35
58	Proteins associated with cork formation in <i>Quercus suber</i> L. stem tissues. <i>Journal of Proteomics</i> , 2011, 74, 1266-1278.	2.4	35
59	One dry summer: A leaf proteome study on the response of oak to drought exposure. <i>Journal of Proteomics</i> , 2011, 74, 1385-1395.	2.4	49
60	Poplar under drought: Comparison of leaf and cambial proteomic responses. <i>Journal of Proteomics</i> , 2011, 74, 1396-1410.	2.4	46
61	Human Muscle Proteome Modifications after Acute or Repeated Eccentric Exercises. <i>Medicine and Science in Sports and Exercise</i> , 2011, 43, 2281-2296.	0.4	52
62	A new chemical approach to differentiate carboxy terminal peptide fragments in cyanogen bromide digests of proteins. <i>Journal of Proteomics</i> , 2010, 73, 1454-1460.	2.4	11
63	A proteome map of the pituitary melanotrope cell activated by blackâ€œbackground adaptation of <i>Xenopus laevis</i> . <i>Proteomics</i> , 2010, 10, 574-580.	2.2	4
64	Acute metal stress in <i>Populus tremula</i> – <i>P. alba</i> (717â€œB4 genotype): Leaf and cambial proteome changes induced by cadmium ²⁺ . <i>Proteomics</i> , 2010, 10, 349-368.	2.2	94
65	Identification of a gene coding for a deglycosylating enzyme in <i>Hypocrea jecorina</i> . <i>FEMS Microbiology Letters</i> , 2010, 303, 9-17.	1.8	57
66	Differential impact of chronic ozone exposure on expanding and fully expanded poplar leaves. <i>Tree Physiology</i> , 2010, 30, 1415-1432.	3.1	30
67	Plant Biotic Stress and Proteomics. <i>Current Proteomics</i> , 2010, 7, 275-297.	0.3	24
68	Potato (<i>Solanum tuberosum</i> L.) tuber ageing induces changes in the proteome and antioxidants associated with the sprouting pattern. <i>Journal of Experimental Botany</i> , 2009, 60, 1273-1288.	4.8	47
69	Transglutaminase-mediated Intramolecular Cross-linking of Membrane-bound α -Synuclein Promotes Amyloid Formation in Lewy Bodies. <i>Journal of Biological Chemistry</i> , 2009, 284, 27252-27264.	3.4	32
70	The impact of atmospheric composition on plants: A case study of ozone and poplar. <i>Mass Spectrometry Reviews</i> , 2009, 28, 495-516.	5.4	64
71	Multiplicity of aspartic proteinases from <i>Cynara cardunculus</i> L.. <i>Planta</i> , 2009, 230, 429-439.	3.2	54
72	Proteomic evaluation of woundâ€œhealing processes in potato (<i>Solanum tuberosum</i> L.) tuber tissue. <i>Proteomics</i> , 2009, 9, 4154-4175.	2.2	39

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73	Taking Advantage of Nonspecific Trypsin Cleavages for the Identification of Seed Storage Proteins in Cereals. <i>Journal of Proteome Research</i> , 2009, 8, 3182-3190.	3.7	16
74	de Novo Sequence Analysis of N-Terminal Sulfonated Peptides After in-Gel Guanidination. <i>Methods in Molecular Biology</i> , 2009, 519, 495-506.	0.9	3
75	C-Terminal Sequence Analysis of 2DE-Separated Proteins. <i>Methods in Molecular Biology</i> , 2009, 519, 469-482.	0.9	0
76	The mTOR target 4Eâ€BP1 contributes to differential protein expression during normoxia and hypoxia through changes in mRNA translation efficiency. <i>Proteomics</i> , 2008, 8, 1019-1028.	2.2	45
77	Proteome analysis of nonâ€model plants: A challenging but powerful approach. <i>Mass Spectrometry Reviews</i> , 2008, 27, 354-377.	5.4	180
78	Proteomic changes in rat hippocampus and adrenals following short-term sleep deprivation. <i>Proteome Science</i> , 2008, 6, 14.	1.7	38
79	Matrix-assisted laser desorption ionisation-time-of-flight mass spectrometry of intact cells allows rapid identification of Burkholderia cepacia complex. <i>Journal of Microbiological Methods</i> , 2008, 75, 279-286.	1.6	92
80	Prolyl oligopeptidase stimulates the aggregation of Î±-synuclein. <i>Peptides</i> , 2008, 29, 1472-1478.	2.4	76
81	Physiological manipulation of cellular activity tunes protein and ultrastructural profiles in a neuroendocrine cell. <i>Journal of Endocrinology</i> , 2008, 198, 607-616.	2.6	2
82	Proteomic analysis of gene expression following hypoxia and reoxygenation reveals proteins involved in the recovery from endoplasmic reticulum and oxidative stress. <i>Radiotherapy and Oncology</i> , 2007, 83, 340-345.	0.6	21
83	Functional Proteome Analysis of the Banana Plant (Musa spp.) Using de Novo Sequence Analysis of Derivatized Peptides. <i>Journal of Proteome Research</i> , 2007, 6, 70-80.	3.7	49
84	151 Identification of Burkholderia cepacia complex using MALDI-TOF mass spectrometry. <i>Journal of Cystic Fibrosis</i> , 2006, 5, S34.	0.7	2
85	A method for C-terminal sequence analysis in the proteomic era (proteins cleaved with cyanogen) Tj ETQq1 1 0.784314 rgBT /Overloc 12.0 18		
86	MALDI-TOF/TOFde novo sequence analysis of 2-D PAGE-separated proteins fromHalorhodospira halophila, a bacterium with unsequenced genome. <i>Electrophoresis</i> , 2006, 27, 2702-2711.	2.4	35
87	A new method for C-terminal sequence analysis in the proteomic era. <i>Nature Methods</i> , 2005, 2, 193-200.	19.0	45
88	De novo sequence analysis ofN-terminal sulfonated peptides after in-gel guanidination. <i>Proteomics</i> , 2005, 5, 2369-2380.	2.2	28
89	Activation, Proteolytic Processing, and Peptide Specificity of Recombinant Cardosin A. <i>Journal of Biological Chemistry</i> , 2005, 280, 13047-13054.	3.4	39
90	A case study of de novo sequence analysis of N-sulfonated peptides by MALDI TOF/TOF mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2004, 15, 1838-1852.	2.8	48

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91	Genomic and phenotypic comparison of <i>Bacillus fumarioli</i> isolates from geothermal Antarctic soil and gelatine. <i>Research in Microbiology</i> , 2004, 155, 483-490.	2.1	10