

# Kjell Sergeant

## List of Publications by Year in descending order

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91  
papers

4,037  
citations

117625

34  
h-index

133252

59  
g-index

93  
all docs

93  
docs citations

93  
times ranked

5571  
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into the molecular regulation of monolignol-derived product biosynthesis in the growing hemp hypocotyl. <i>BMC Plant Biology</i> , 2018, 18, 1.	3.6	368
2	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
3	Target or barrier? The cell wall of early- and later-diverging plants vs cadmium toxicity: differences in the response mechanisms. <i>Frontiers in Plant Science</i> , 2015, 6, 133.	3.6	286
4	Copper Trafficking in Plants and Its Implication on Cell Wall Dynamics. <i>Frontiers in Plant Science</i> , 2016, 7, 601.	3.6	254
5	Proteome analysis of non-model plants: A challenging but powerful approach. <i>Mass Spectrometry Reviews</i> , 2008, 27, 354-377.	5.4	180
6	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
7	Acute metal stress in <i>Populus tremula</i> — <i>P. alba</i> (717B4 genotype): Leaf and cambial proteome changes induced by cadmium <sup>2+</sup> . <i>Proteomics</i> , 2010, 10, 349-368.	2.2	94
8	Matrix-assisted laser desorption ionisation-time-of-flight mass spectrometry of intact cells allows rapid identification of <i>Burkholderia cepacia</i> complex. <i>Journal of Microbiological Methods</i> , 2008, 75, 279-286.	1.6	92
9	Prolyl oligopeptidase stimulates the aggregation of $\hat{\pm}$ -synuclein. <i>Peptides</i> , 2008, 29, 1472-1478.	2.4	76
10	The Roots of Plant Frost Hardiness and Tolerance. <i>Plant and Cell Physiology</i> , 2020, 61, 3-20.	3.1	67
11	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
12	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
13	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
14	Multiplicity of aspartic proteinases from <i>Cynara cardunculus</i> L.. <i>Planta</i> , 2009, 230, 429-439.	3.2	54
15	Long-term cadmium exposure influences the abundance of proteins that impact the cell wall structure in <i>Medicago sativa</i> stems. <i>Plant Biology</i> , 2018, 20, 1023-1035.	3.8	54
16	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
17	Functional Proteome Analysis of the Banana Plant ( <i>Musa</i> spp.) Using de Novo Sequence Analysis of Derivatized Peptides. <i>Journal of Proteome Research</i> , 2007, 6, 70-80.	3.7	49
18	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

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19	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
20	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
21	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
22	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
23	Poplar under drought: Comparison of leaf and cambial proteomic responses. <i>Journal of Proteomics</i> , 2011, 74, 1396-1410.	2.4	46
24	Changes in sugar content and proteome of potato in response to cold and dehydration stress and their implications for cryopreservation. <i>Journal of Proteomics</i> , 2014, 98, 99-111.	2.4	46
25	A new method for C-terminal sequence analysis in the proteomic era. <i>Nature Methods</i> , 2005, 2, 193-200.	19.0	45
26	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
27	Pollen development and function under heat stress: from effects to responses. <i>Acta Physiologiae Plantarum</i> , 2019, 41, 1.	2.1	45
28	Wood biosynthesis and typologies: a molecular rhapsody. <i>Tree Physiology</i> , 2014, 34, 839-855.	3.1	44
29	Unravelling the effect of sucrose and cold pretreatment on cryopreservation of potato through sugar analysis and proteomics. <i>Cryobiology</i> , 2015, 71, 432-441.	0.7	43
30	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
31	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
32	Proteomic changes in leaves of poplar exposed to both cadmium and low-temperature. <i>Environmental and Experimental Botany</i> , 2014, 106, 112-123.	4.2	40
33	Molecular insights into plant desiccation tolerance: transcriptomics, proteomics and targeted metabolite profiling in <i>Cratogeomys plantagineum</i> . <i>Plant Journal</i> , 2021, 107, 377-398.	5.7	40
34	Activation, Proteolytic Processing, and Peptide Specificity of Recombinant Cardosin A. <i>Journal of Biological Chemistry</i> , 2005, 280, 13047-13054.	3.4	39
35	Proteomic evaluation of woundâ€healing processes in potato ( <i>Solanum tuberosum</i> L.) tuber tissue. <i>Proteomics</i> , 2009, 9, 4154-4175.	2.2	39
36	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

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37	Proteomic changes in rat hippocampus and adrenals following short-term sleep deprivation. <i>Proteome Science</i> , 2008, 6, 14.	1.7	38
38	Pathogenic Leptospire Modulate Protein Expression and Post-translational Modifications in Response to Mammalian Host Signals. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 362.	3.9	36
39	MALDI-TOF/TOF de novo sequence analysis of 2-D PAGE-separated proteins from <i>Halorhodospira halophila</i> , a bacterium with unsequenced genome. <i>Electrophoresis</i> , 2006, 27, 2702-2711.	2.4	35
40	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
41	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
42	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
43	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
44	Proteomic changes associated with freeze-thaw injury and post-thaw recovery in onion ( <i>Allium</i> ) Tj ETQq0 0 Q rgBT /Overlock 10 T	3.7	34
45	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
46	An improved protocol to study the plant cell wall proteome. <i>Frontiers in Plant Science</i> , 2015, 6, 237.	3.6	33
47	Transglutaminase-mediated Intramolecular Cross-linking of Membrane-bound $\alpha$ -Synuclein Promotes Amyloid Formation in Lewy Bodies. <i>Journal of Biological Chemistry</i> , 2009, 284, 27252-27264.	3.4	32
48	Differential impact of chronic ozone exposure on expanding and fully expanded poplar leaves. <i>Tree Physiology</i> , 2010, 30, 1415-1432.	3.1	30
49	De novo sequence analysis of N-terminal sulfonated peptides after in-gel guanidination. <i>Proteomics</i> , 2005, 5, 2369-2380.	2.2	28
50	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
51	Plant Biotic Stress and Proteomics. <i>Current Proteomics</i> , 2010, 7, 275-297.	0.3	24
52	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
53	Combining -Omics to Unravel the Impact of Copper Nutrition on Alfalfa ( <i>Medicago sativa</i> ) Stem Metabolism. <i>Plant and Cell Physiology</i> , 2016, 57, 407-422.	3.1	23
54	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

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55	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. <i>International Journal of Phytoremediation</i> , 2014, 16, 1148-1169.	3.1	22
56	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
57	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
58	Comparative analysis of Salmonella susceptibility and tolerance to the biocide chlorhexidine identifies a complex cellular defense network. <i>Frontiers in Microbiology</i> , 2014, 5, 373.	3.5	20
59	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
60	A method for C-terminal sequence analysis in the proteomic era (proteins cleaved with cyanogen bromide) <i>Journal of Proteome Research</i> , 2007, 6, 120-128.	12.0	18
61	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
62	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
63	The Dynamics of the Cell Wall Proteome of Developing Alfalfa Stems. <i>Biology</i> , 2019, 8, 60.	2.8	16
64	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
65	Physiological and proteome study of sunflowers exposed to a polymetallic constraint. <i>Proteomics</i> , 2013, 13, 1993-2015.	2.2	15
66	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
67	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. <i>Journal of Proteomics</i> , 2015, 122, 55-72.	2.4	15
68	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
69	Abiotic Stress Tolerance in Plants. , 2014, , 23-68.		14
70	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
71	Novel Insights from Comparative In Silico Analysis of Green Microalgal Cellulases. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1782.	4.1	12
72	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

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73	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
74	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
75	Ups and downs in alfalfa: Proteomic and metabolic changes occurring in the growing stem. <i>Plant Science</i> , 2015, 238, 13-25.	3.6	10
76	Repair of sub-lethal freezing damage in leaves of <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2020, 20, 35.	3.6	8
77	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
78	Description of the mechanisms underlying geosmin production in <i>Penicillium expansum</i> using proteomics. <i>Journal of Proteomics</i> , 2014, 96, 13-28.	2.4	7
79	Didehydrophenylalanine, an abundant modification in the beta subunit of plant polygalacturonases. <i>PLoS ONE</i> , 2017, 12, e0171990.	2.5	7
80	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
81	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
82	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
83	Systems Biology of Metal Tolerance in Plants: A Case Study on the Effects of Cd Exposure on Two Model Plants. , 2019, , 23-37.		4
84	The Cell Wall Proteome of <i>Cratogeomys plantagineum</i> Cell Cultures Habituated to Dichlobenil and Isoxaben. <i>Cells</i> , 2021, 10, 2295.	4.1	4
85	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
86	151 Identification of <i>Burkholderia cepacia</i> complex using MALDI-TOF mass spectrometry. <i>Journal of Cystic Fibrosis</i> , 2006, 5, S34.	0.7	2
87	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
88	Proteomics as a Toolbox to Study the Metabolic Adjustment of Trees During Exposure to Metal Trace Elements. , 2012, , 143-164.		2
89	Automation of C-terminal sequence analysis of 2D-PAGE separated proteins. <i>EuPA Open Proteomics</i> , 2014, 3, 250-261.	2.5	2
90	A 2-D guinea pig lung proteome map. <i>Data in Brief</i> , 2015, 4, 140-145.	1.0	2

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91	C-Terminal Sequence Analysis of 2DE-Separated Proteins. Methods in Molecular Biology, 2009, 519, 469-482.	0.9	0