

Kris Laukens

List of Publications by Year in descending order

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Version: 2024-02-01

141
papers

5,435
citations

101384

36
h-index

102304

66
g-index

165
all docs

165
docs citations

165
times ranked

8602
citing authors

#	ARTICLE	IF	CITATIONS
1	MoMAC: Multi-objective optimization to combine multiple association rules into an interpretable classification. <i>Applied Intelligence</i> , 2022, 52, 3090-3102.	3.3	10
2	Preexisting memory CD4 T cells in naïve individuals confer robust immunity upon hepatitis B vaccination. <i>ELife</i> , 2022, 11, .	2.8	11
3	Recent advances in T-cell receptor repertoire analysis: Bridging the gap with multimodal single-cell RNA sequencing. <i>Immuninformatics</i> , 2022, 5, 100009.	1.2	27
4	A treatment recommender clinical decision support system for personalized medicine: method development and proof-of-concept for drug resistant tuberculosis. <i>BMC Medical Informatics and Decision Making</i> , 2022, 22, 56.	1.5	7
5	Viral Evolution and Immunology of SARS-CoV-2 in a Persistent Infection after Treatment with Rituximab. <i>Viruses</i> , 2022, 14, 752.	1.5	10
6	The effect of local non-thermal plasma therapy on the cancer-immunity cycle in a melanoma mouse model. <i>Bioengineering and Translational Medicine</i> , 2022, 7, .	3.9	15
7	Fractionated irradiation of MCF7 breast cancer cells rewires a gene regulatory circuit towards a treatment-resistant stemness phenotype. <i>Molecular Oncology</i> , 2022, 16, 3410-3435.	2.1	2
8	Variants in Bedaquiline-Candidate-Resistance Genes: Prevalence in Bedaquiline-Naive Patients, Effect on MIC, and Association with Mycobacterium tuberculosis Lineage. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	1.4	5
9	Current challenges for unseen-epitope TCR interaction prediction and a new perspective derived from image classification. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	78
10	Preparing students for the data-driven life science era through a real-world viral infection case. <i>Journal of Biological Education</i> , 2021, 55, 178-187.	0.8	2
11	Characterization of acquired nutlin-3 resistant non-small cell lung cancer cells. , 2021, 4, 233-243.		6
12	Open Science Resources for the Mass Spectrometry-Based Analysis of SARS-CoV-2. <i>Journal of Proteome Research</i> , 2021, 20, 1464-1475.	1.8	11
13	CONSTAND: An Efficient Normalization Method for Relative Quantification in Small- and Large-Scale Omics Experiments in R BioConductor and Python. <i>Journal of Proteome Research</i> , 2021, 20, 2151-2156.	1.8	5
14	Covalent Cysteine Targeting of Bruton's Tyrosine Kinase (BTK) Family by Withaferin-A Reduces Survival of Glucocorticoid-Resistant Multiple Myeloma MM1 Cells. <i>Cancers</i> , 2021, 13, 1618.	1.7	10
15	HLA-DRB1 Alleles Associated with Lower Leishmaniasis Susceptibility Share Common Amino Acid Polymorphisms and Epitope Binding Repertoires. <i>Vaccines</i> , 2021, 9, 270.	2.1	5
16	Sorted B cell transcriptomes point towards actively regulated B cell responses during ongoing chronic hepatitis B infections. <i>Cellular Immunology</i> , 2021, 362, 104283.	1.4	9
17	Constrained Standardization of Count Data from Massive Parallel Sequencing. <i>Journal of Molecular Biology</i> , 2021, 433, 166966.	2.0	1
18	Current and future deep learning algorithms for tandem mass spectrometry (MS/MS)-based small molecule structure elucidation. <i>Rapid Communications in Mass Spectrometry</i> , 2021, , e9120.	0.7	16

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19	Auranofin reveals therapeutic anticancer potential by triggering distinct molecular cell death mechanisms and innate immunity in mutant p53 non-small cell lung cancer. <i>Redox Biology</i> , 2021, 42, 101949.	3.9	63
20	ClusTCR: a python interface for rapid clustering of large sets of CDR3 sequences with unknown antigen specificity. <i>Bioinformatics</i> , 2021, 37, 4865-4867.	1.8	30
21	Large-scale tandem mass spectrum clustering using fast nearest neighbor searching. <i>Rapid Communications in Mass Spectrometry</i> , 2021, , e9153.	0.7	16
22	Ferroptosis Induction in Multiple Myeloma Cells Triggers DNA Methylation and Histone Modification Changes Associated with Cellular Senescence. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12234.	1.8	20
23	The use of plasma donor-derived, cell-free DNA to monitor acute rejection after kidney transplantation. <i>Nephrology Dialysis Transplantation</i> , 2020, 35, 714-721.	0.4	61
24	Visualizing the agreement of peptide assignments between different search engines. <i>Journal of Mass Spectrometry</i> , 2020, 55, e4471.	0.7	5
25	PRiSM: A prototype for exhaustive, restriction-free database searching for mass spectrometry-based identification. <i>Rapid Communications in Mass Spectrometry</i> , 2020, , e8962.	0.7	0
26	The Absence of C-5 DNA Methylation in <i>Leishmania donovani</i> Allows DNA Enrichment from Complex Samples. <i>Microorganisms</i> , 2020, 8, 1252.	1.6	9
27	Compound Characterization and Metabolic Profile Elucidation after In Vitro Gastrointestinal and Hepatic Biotransformation of an <i>Herniaria hirsuta</i> Extract Using Unbiased Dynamic Metabolomic Data Analysis. <i>Metabolites</i> , 2020, 10, 111.	1.3	16
28	Transcriptomic profiling of different responder types in adults after a Priorix [®] vaccination. <i>Vaccine</i> , 2020, 38, 3218-3226.	1.7	1
29	Machine Learning to Support Hemodynamic Intervention in the Neonatal Intensive Care Unit. <i>Clinics in Perinatology</i> , 2020, 47, 435-448.	0.8	10
30	Clustering association rules to build beliefs and discover unexpected patterns. <i>Applied Intelligence</i> , 2020, 50, 1943-1954.	3.3	10
31	Oocyte maturation under lipotoxic conditions induces carryover transcriptomic and functional alterations during post-hatching development of good-quality blastocysts: novel insights from a bovine embryo-transfer model. <i>Human Reproduction</i> , 2020, 35, 293-307.	0.4	17
32	Osmotic stress inhibits leaf growth of <i>Arabidopsis thaliana</i> by enhancing ARF-mediated auxin responses. <i>New Phytologist</i> , 2020, 226, 1766-1780.	3.5	31
33	MESSAR: Automated recommendation of metabolite substructures from tandem mass spectra. <i>PLoS ONE</i> , 2020, 15, e0226770.	1.1	24
34	Identification of Epitope-Specific T Cells in T-Cell Receptor Repertoires. <i>Methods in Molecular Biology</i> , 2020, 2120, 183-195.	0.4	3
35	Memory CD4+ T cell receptor repertoire data mining as a tool for identifying cytomegalovirus serostatus. <i>Genes and Immunity</i> , 2019, 20, 255-260.	2.2	19
36	Untargeted liquid chromatography-mass spectrometry metabolomics to assess drug-induced cholestatic features in HepaRG [®] cells. <i>Toxicology and Applied Pharmacology</i> , 2019, 379, 114666.	1.3	9

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37	MIND: A Double-Linear Model To Accurately Determine Monoisotopic Precursor Mass in High-Resolution Top-Down Proteomics. <i>Analytical Chemistry</i> , 2019, 91, 10310-10319.	3.2	3
38	Mass spectrometry-based structure elucidation of small molecule impurities and degradation products in pharmaceutical development. <i>TrAC - Trends in Analytical Chemistry</i> , 2019, 121, 115686.	5.8	18
39	Exposure of HepaRG Cells to Sodium Saccharin Underpins the Importance of Including Non-Hepatotoxic Compounds When Investigating Toxicological Modes of Action Using Metabolomics. <i>Metabolites</i> , 2019, 9, 265.	1.3	1
40	Detection of Enriched T Cell Epitope Specificity in Full T Cell Receptor Sequence Repertoires. <i>Frontiers in Immunology</i> , 2019, 10, 2820.	2.2	108
41	Extremely Fast and Accurate Open Modification Spectral Library Searching of High-Resolution Mass Spectra Using Feature Hashing and Graphics Processing Units. <i>Journal of Proteome Research</i> , 2019, 18, 3792-3799.	1.8	39
42	Diagnosing enterovirus meningitis via blood transcriptomics: an alternative for lumbar puncture?. <i>Journal of Translational Medicine</i> , 2019, 17, 282.	1.8	10
43	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> : current standards and open issues. <i>Nature Reviews Microbiology</i> , 2019, 17, 533-545.	13.6	237
44	Using Expert Driven Machine Learning to Enhance Dynamic Metabolomics Data Analysis. <i>Metabolites</i> , 2019, 9, 54.	1.3	15
45	QCQuan: A Web Tool for the Automated Assessment of Protein Expression and Data Quality of Labeled Mass Spectrometry Experiments. <i>Journal of Proteome Research</i> , 2019, 18, 2221-2227.	1.8	9
46	Revelation of the metabolic pathway of hederacoside C using an innovative data analysis strategy for dynamic multiclass biotransformation experiments. <i>Journal of Chromatography A</i> , 2019, 1595, 240-247.	1.8	17
47	On the viability of unsupervised T-cell receptor sequence clustering for epitope preference. <i>Bioinformatics</i> , 2019, 35, 1461-1468.	1.8	52
48	Mining the Enriched Subgraphs for Specific Vertices in a Biological Graph. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1496-1507.	1.9	5
49	Integrated genomic and metabolomic profiling of ISC1, an emerging <i>Leishmania donovani</i> population in the Indian subcontinent. <i>Infection, Genetics and Evolution</i> , 2018, 62, 170-178.	1.0	32
50	pBRIT: gene prioritization by correlating functional and phenotypic annotations through integrative data fusion. <i>Bioinformatics</i> , 2018, 34, 2254-2262.	1.8	24
51	Transcriptome profiling of HepG2 cells exposed to the flame retardant 9,10-dihydro-9-oxa-10-phosphaphenanthrene 10-oxide (DOPO). <i>Toxicology Research</i> , 2018, 7, 492-502.	0.9	4
52	Toxicogenomics of the flame retardant tris (2-butoxyethyl) phosphate in HepG2 cells using RNA-seq. <i>Toxicology in Vitro</i> , 2018, 46, 178-188.	1.1	21
53	Increased herpes zoster risk associated with poor HLA-A immediate early 62 protein (IE62) affinity. <i>Immunogenetics</i> , 2018, 70, 363-372.	1.2	8
54	A tutorial in small molecule identification via electrospray ionization-mass spectrometry: The practical art of structural elucidation. <i>Mass Spectrometry Reviews</i> , 2018, 37, 607-629.	2.8	154

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55	On the feasibility of mining CD8+ T cell receptor patterns underlying immunogenic peptide recognition. <i>Immunogenetics</i> , 2018, 70, 159-168.	1.2	64
56	Quality control in mass spectrometry-based proteomics. <i>Mass Spectrometry Reviews</i> , 2018, 37, 697-711.	2.8	82
57	Plasma donor-derived cell-free DNA kinetics after kidney transplantation using a single tube multiplex PCR assay. <i>PLoS ONE</i> , 2018, 13, e0208207.	1.1	50
58	Proteomic analysis of posterior capsular plaques in congenital unilateral cataract. <i>Acta Ophthalmologica</i> , 2018, 96, e963-e969.	0.6	5
59	Fast Open Modification Spectral Library Searching through Approximate Nearest Neighbor Indexing. <i>Journal of Proteome Research</i> , 2018, 17, 3463-3474.	1.8	69
60	Grasping frequent subgraph mining for bioinformatics applications. <i>BioData Mining</i> , 2018, 11, 20.	2.2	30
61	Transcriptome profiling in blood before and after hepatitis B vaccination shows significant differences in gene expression between responders and non-responders. <i>Vaccine</i> , 2018, 36, 6282-6289.	1.7	47
62	In vitro assessment of hepatotoxicity by metabolomics: a review. <i>Archives of Toxicology</i> , 2018, 92, 3007-3029.	1.9	55
63	speaq 2.0: A complete workflow for high-throughput 1D NMR spectra processing and quantification. <i>PLoS Computational Biology</i> , 2018, 14, e1006018.	1.5	42
64	Protein complex analysis: From raw protein lists to protein interaction networks. <i>Mass Spectrometry Reviews</i> , 2017, 36, 600-614.	2.8	22
65	Tailored liquid chromatography-mass spectrometry analysis improves the coverage of the intracellular metabolome of HepaRG cells. <i>Journal of Chromatography A</i> , 2017, 1487, 168-178.	1.8	20
66	sfinx: an R package for the elimination of false positives from affinity purification-mass spectrometry datasets. <i>Bioinformatics</i> , 2017, 33, 1902-1904.	1.8	3
67	Multiplexed Spliced-Leader Sequencing: A high-throughput, selective method for RNA-seq in Trypanosomatids. <i>Scientific Reports</i> , 2017, 7, 3725.	1.6	24
68	Genome-Wide SNP Analysis Reveals Distinct Origins of <i>Trypanosoma evansi</i> and <i>Trypanosoma equiperdum</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1990-1997.	1.1	33
69	InSourcerer: a high-throughput method to search for unknown metabolite modifications by mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2017, 31, 1396-1404.	0.7	5
70	Computational quality control tools for mass spectrometry proteomics. <i>Proteomics</i> , 2017, 17, 1600159.	1.3	34
71	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , 2017, 6, 875.	0.8	13
72	Designing biomedical proteomics experiments: state-of-the-art and future perspectives. <i>Expert Review of Proteomics</i> , 2016, 13, 495-511.	1.3	13

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73	Withaferin A induces heme oxygenase (HO-1) expression in endothelial cells via activation of the Keap1/Nrf2 pathway. <i>Biochemical Pharmacology</i> , 2016, 109, 48-61.	2.0	55
74	Apolipoprotein L1 Variant Associated with Increased Susceptibility to Trypanosome Infection. <i>MBio</i> , 2016, 7, e02198-15.	1.8	18
75	Immunological evasion of immediate-early varicella zoster virus proteins. <i>Immunogenetics</i> , 2016, 68, 483-486.	1.2	8
76	Practical Approaches for Mining Frequent Patterns in Molecular Datasets. <i>Bioinformatics and Biology Insights</i> , 2016, 10, BBI.S38419.	1.0	2
77	Highlights from the 11th ISCB Student Council Symposium 2015. <i>BMC Bioinformatics</i> , 2016, 17, 95.	1.2	4
78	Unsupervised Quality Assessment of Mass Spectrometry Proteomics Experiments by Multivariate Quality Control Metrics. <i>Journal of Proteome Research</i> , 2016, 15, 1300-1307.	1.8	15
79	COLOMBOS v3.0: leveraging gene expression compendia for cross-species analyses: Table 1.. <i>Nucleic Acids Research</i> , 2016, 44, D620-D623.	6.5	69
80	SFINX: Straightforward Filtering Index for Affinity Purificationâ€“Mass Spectrometry Data Analysis. <i>Journal of Proteome Research</i> , 2016, 15, 332-338.	1.8	20
81	Mining the human proteome for conserved mechanisms. <i>BMC Bioinformatics</i> , 2015, 16, .	1.2	1
82	Varicella-Zoster Virus-Derived Major Histocompatibility Complex Class I-Restricted Peptide Affinity Is a Determining Factor in the HLA Risk Profile for the Development of Postherpetic Neuralgia. <i>Journal of Virology</i> , 2015, 89, 962-969.	1.5	20
83	Mining the entire Protein DataBank for frequent spatially cohesive amino acid patterns. <i>BioData Mining</i> , 2015, 8, 4.	2.2	12
84	iMonDB: Mass Spectrometry Quality Control through Instrument Monitoring. <i>Journal of Proteome Research</i> , 2015, 14, 2360-2366.	1.8	21
85	Mining Association Rules in Graphs Based on Frequent Cohesive Itemsets. <i>Lecture Notes in Computer Science</i> , 2015, , 637-648.	1.0	15
86	A primer to frequent itemset mining for bioinformatics. <i>Briefings in Bioinformatics</i> , 2015, 16, 216-231.	3.2	102
87	Open-Source, Platform-Independent Library and Online Scripting Environment for Accessing Thermo Scientific RAW Files. <i>Journal of Proteome Research</i> , 2015, 14, 4940-4943.	1.8	3
88	Metabolomics analysis of the toxicity pathways of triphenyl phosphate in HepaRG cells and comparison to oxidative stress mechanisms caused by acetaminophen. <i>Toxicology in Vitro</i> , 2015, 29, 2045-2054.	1.1	31
89	Bioinformatics approaches for the functional interpretation of protein lists: From ontology term enrichment to network analysis. <i>Proteomics</i> , 2015, 15, 981-996.	1.3	27
90	A generic approach for â€œshotgunâ€“analysis of the soluble proteome of plant cell suspension cultures. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2015, 974, 48-56.	1.2	1

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91	Comparative Analysis of Gene Expression: Uncovering Expression Conservation and Divergence Between <i>Salmonella enterica</i> Serovar Typhimurium Strains LT2 and 14028S. <i>Methods in Molecular Biology</i> , 2015, 1231, 125-135.	0.4	0
92	Structural Properties of Prokaryotic Promoter Regions Correlate with Functional Features. <i>PLoS ONE</i> , 2014, 9, e88717.	1.1	22
93	jqcML: An Open-Source Java API for Mass Spectrometry Quality Control Data in the qcML Format. <i>Journal of Proteome Research</i> , 2014, 13, 3484-3487.	1.8	9
94	Unravelling associations between unassigned mass spectrometry peaks with frequent itemset mining techniques. <i>Proteome Science</i> , 2014, 12, 54.	0.7	3
95	Machine learning applications in proteomics research: How the past can boost the future. <i>Proteomics</i> , 2014, 14, 353-366.	1.3	52
96	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	2.5	42
97	COLOMBOS v2.0: an ever expanding collection of bacterial expression compendia: Table 1.. <i>Nucleic Acids Research</i> , 2014, 42, D649-D653.	6.5	38
98	The role of monocytes in the development of Tuberculosis-associated Immune Reconstitution Inflammatory Syndrome. <i>Immunobiology</i> , 2014, 219, 37-44.	0.8	48
99	Discovery of Spatially Cohesive Itemsets in Three-Dimensional Protein Structures. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 814-825.	1.9	5
100	Efficient Reduction of Candidate Matches in Peptide Spectrum Library Searching Using the Top k Most Intense Peaks. <i>Journal of Proteome Research</i> , 2014, 13, 4175-4183.	1.8	6
101	The radiosensitising effect of gemcitabine and its main metabolite dFdU under low oxygen conditions is in vitro not dependent on functional HIF-1 protein. <i>BMC Cancer</i> , 2014, 14, 594.	1.1	6
102	The use of the isotopic distribution as a complementary quality metric to assess tandem mass spectra results. <i>Journal of Proteomics</i> , 2014, 98, 150-158.	1.2	8
103	Towards automated discrimination of lipids versus peptides from full scan mass spectra. <i>EuPA Open Proteomics</i> , 2014, 4, 87-100.	2.5	6
104	Dietary Flavanols Modulate the Transcription of Genes Associated with Cardiovascular Pathology without Changes in Their DNA Methylation State. <i>PLoS ONE</i> , 2014, 9, e95527.	1.1	49
105	Ectopic MicroRNA-150-5p Transcription Sensitizes Glucocorticoid Therapy Response in MM1S Multiple Myeloma Cells but Fails to Overcome Hormone Therapy Resistance in MM1R Cells. <i>PLoS ONE</i> , 2014, 9, e113842.	1.1	38
106	¹ H-NMR study of the metabolome of an exceptionally anoxia tolerant vertebrate, the crucian carp (<i>Carassius carassius</i>). <i>Metabolomics</i> , 2013, 9, 311-323.	1.4	25
107	¹ H-NMR study of the metabolome of a moderately hypoxia-tolerant fish, the common carp (<i>Cyprinus</i>) Tj ETQq1 1 0,784314 rgBT /Ov	1.4	37
108	Getting Your Peaks in Line: A Review of Alignment Methods for NMR Spectral Data. <i>Metabolites</i> , 2013, 3, 259-276.	1.3	101

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109	AcoSeeD: An Ant Colony Optimization for Finding Optimal Spaced Seeds in Biological Sequence Search. Lecture Notes in Computer Science, 2012, , 204-211.	1.0	6
110	¹ H NMR based metabolomics of CSF and blood serum: A metabolic profile for a transgenic rat model of Huntington disease. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2011, 1812, 1371-1379.	1.8	73
111	An integrated workflow for robust alignment and simplified quantitative analysis of NMR spectrometry data. BMC Bioinformatics, 2011, 12, 405.	1.2	64
112	Unraveling tobacco BY-2 protein complexes with BN PAGE/LC-MS/MS and clustering methods. Journal of Proteomics, 2011, 74, 1201-1217.	1.2	15
113	Next generation functional proteomics in non-model plants: A survey on techniques and applications for the analysis of protein complexes and post-translational modifications. Phytochemistry, 2011, 72, 1192-1218.	1.4	28
114	Use of structural DNA properties for the prediction of transcription-factor binding sites in Escherichia coli. Nucleic Acids Research, 2011, 39, e6-e6.	6.5	42
115	Flexible network reconstruction from relational databases with Cytoscape and CytoSQL. BMC Bioinformatics, 2010, 11, 360.	1.2	0
116	2D-DIGE reveals changes in wheat xylanase inhibitor protein families due to <i>Fusarium graminearum</i> Tri5 infection and grain development. Proteomics, 2010, 10, 2303-2319.	1.3	28
117	Alternative Experimental Design with an Applied Normalization Scheme Can Improve Statistical Power in 2D-DIGE Experiments. Journal of Proteome Research, 2010, 9, 4919-4926.	1.8	6
118	Targeted interactomics reveals a complex core cell cycle machinery in <i>Arabidopsis thaliana</i> . Molecular Systems Biology, 2010, 6, 397.	3.2	315
119	A manually curated network of the PML nuclear body interactome reveals an important role for PML-NBs in SUMOylation dynamics. International Journal of Biological Sciences, 2010, 6, 51-67.	2.6	175
120	Best practices for hybridization design in two-colour microarray analysis. Trends in Biotechnology, 2009, 27, 406-414.	4.9	36
121	A bioanalytical method for the proteome wide display and analysis of protein complexes from whole plant cell lysates. Proteomics, 2009, 9, 598-609.	1.3	11
122	A quantitative portrait of three xylanase inhibiting protein families in different wheat cultivars using 2D-DIGE and multivariate statistical tools. Journal of Proteomics, 2009, 72, 484-500.	1.2	15
123	Conditional Random Fields Feature Subset Selection Based on Genetic Algorithms for Phosphorylation Site Prediction. , 2009, , .		0
124	Proteome analysis of non-model plants: A challenging but powerful approach. Mass Spectrometry Reviews, 2008, 27, 354-377.	2.8	180
125	Proteomic profiling of cellular targets of lipopolysaccharide-induced signalling in <i>Nicotiana tabacum</i> BY-2 cells. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 1750-1762.	1.1	34
126	Functional genomics in a non-model crop: transcriptomics or proteomics?. Physiologia Plantarum, 2008, 133, 117-130.	2.6	50

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127	Prediction of kinase-specific phosphorylation sites using conditional random fields. <i>Bioinformatics</i> , 2008, 24, 2857-2864.	1.8	63
128	Organization of Proteomics Data With YassDB. , 2007, 367, 271-288.		1
129	Gradual Soil Water Depletion Results in Reversible Changes of Gene Expression, Protein Profiles, Ecophysiology, and Growth Performance in <i>Populus euphratica</i> , a Poplar Growing in Arid Regions. <i>Plant Physiology</i> , 2007, 143, 876-892.	2.3	338
130	A Tandem Affinity Purification-based Technology Platform to Study the Cell Cycle Interactome in <i>Arabidopsis thaliana</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1226-1238.	2.5	196
131	Banana (<i>Musa spp.</i>) as a model to study the meristem proteome: Acclimation to osmotic stress. <i>Proteomics</i> , 2007, 7, 92-105.	1.3	110
132	A novel cell division factor from tobacco 2B-13 cells that induced cell division in auxin-starved tobacco BY-2 cells. <i>Die Naturwissenschaften</i> , 2006, 93, 278-285.	0.6	9
133	Lipopolysaccharide-responsive phosphoproteins in <i>Nicotiana glauca</i> cells. <i>Plant Physiology and Biochemistry</i> , 2006, 44, 369-379.	2.8	48
134	Integration of gel-based proteome data with pProRep. <i>Bioinformatics</i> , 2006, 22, 2838-2840.	1.8	5
135	A Hormone and Proteome Approach to Picturing the Initial Metabolic Events During <i>Plasmodiophora brassicae</i> Infection on <i>Arabidopsis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1431-1443.	1.4	133
136	Preparation of protein extracts from recalcitrant plant tissues: An evaluation of different methods for two-dimensional gel electrophoresis analysis. <i>Proteomics</i> , 2005, 5, 2497-2507.	1.3	447
137	Construction of a two-dimensional gel electrophoresis protein database for the <i>Nicotiana tabacum</i> cv. Bright Yellow-2 cell suspension culture. <i>Proteomics</i> , 2004, 4, 720-727.	1.3	29
138	Tobacco BY-2 Proteomics. <i>Biotechnology in Agriculture and Forestry</i> , 2004, , 332-343.	0.2	0
139	Fast liquid chromatography coupled to electrospray tandem mass spectrometry peptide sequencing for cross-species protein identification. <i>Rapid Communications in Mass Spectrometry</i> , 2003, 17, 2188-2194.	0.7	27
140	Cytokinin affinity purification and identification of a tobacco BY-2 adenosine kinase. <i>FEBS Letters</i> , 2003, 533, 63-66.	1.3	11
141	Cyclic AMP affinity purification and ESI-QTOF MS-MS identification of cytosolic glyceraldehyde 3-phosphate dehydrogenase and two nucleoside diphosphate kinase isoforms from tobacco BY-2 cells. <i>FEBS Letters</i> , 2001, 508, 75-79.	1.3	20