

Joachim Selbig

List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

12,274
citations

53794

45
h-index

56724

83
g-index

90
all docs

90
docs citations

90
times ranked

16495
citing authors

#	ARTICLE	IF	CITATIONS
1	mapman: a user-driven tool to display genomics data sets onto diagrams of metabolic pathways and other biological processes. <i>Plant Journal</i> , 2004, 37, 914-939.	5.7	3,184
2	pcaMethods a bioconductor package providing PCA methods for incomplete data. <i>Bioinformatics</i> , 2007, 23, 1164-1167.	4.1	944
3	Extension of the Visualization Tool MapMan to Allow Statistical Analysis of Arrays, Display of Corresponding Genes, and Comparison with Known Responses. <i>Plant Physiology</i> , 2005, 138, 1195-1204.	4.8	576
4	A Robot-Based Platform to Measure Multiple Enzyme Activities in Arabidopsis Using a Set of Cycling Assays: Comparison of Changes of Enzyme Activities and Transcript Levels during Diurnal Cycles and in Prolonged Darkness[W]. <i>Plant Cell</i> , 2004, 16, 3304-3325.	6.6	489
5	Starch as a major integrator in the regulation of plant growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10348-10353.	7.1	467
6	Metabolomic and transcriptomic stress response of <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2010, 6, 364.	7.2	451
7	Metabolomics of temperature stress. <i>Physiologia Plantarum</i> , 2008, 132, 220-235.	5.2	439
8	The metabolic signature related to high plant growth rate in Arabidopsis thaliana. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 4759-4764.	7.1	377
9	Diversity and complexity of HIV-1 drug resistance: A bioinformatics approach to predicting phenotype from genotype. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 8271-8276.	7.1	310
10	Parallel analysis of transcript and metabolic profiles: a new approach in systems biology. <i>EMBO Reports</i> , 2003, 4, 989-993.	4.5	308
11	PhosPhAt: a database of phosphorylation sites in Arabidopsis thaliana and a plant-specific phosphorylation site predictor. <i>Nucleic Acids Research</i> , 2007, 36, D1015-D1021.	14.5	302
12	The Metabolic Response of Heterotrophic Arabidopsis Cells to Oxidative Stress. <i>Plant Physiology</i> , 2007, 143, 312-325.	4.8	234
13	Structural kinetic modeling of metabolic networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11868-11873.	7.1	229
14	Geno2pheno: estimating phenotypic drug resistance from HIV-1 genotypes. <i>Nucleic Acids Research</i> , 2003, 31, 3850-3855.	14.5	213
15	Identification of metabolic and biomass QTL in <i>Arabidopsis thaliana</i> in a parallel analysis of RIL and IL populations. <i>Plant Journal</i> , 2008, 53, 960-972.	5.7	211
16	Mode of Inheritance of Primary Metabolic Traits in Tomato. <i>Plant Cell</i> , 2008, 20, 509-523.	6.6	208
17	Non-linear PCA: a missing data approach. <i>Bioinformatics</i> , 2005, 21, 3887-3895.	4.1	167
18	Integration of Metabolomic and Proteomic Phenotypes. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1725-1736.	3.8	155

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19	Predicting Arabidopsis Freezing Tolerance and Heterosis in Freezing Tolerance from Metabolite Composition. <i>Molecular Plant</i> , 2010, 3, 224-235.	8.3	120
20	Heterosis manifestation during early Arabidopsis seedling development is characterized by intermediate gene expression and enhanced metabolic activity in the hybrids. <i>Plant Journal</i> , 2012, 71, 669-683.	5.7	117
21	Discovering plant metabolic biomarkers for phenotype prediction using an untargeted approach. <i>Plant Biotechnology Journal</i> , 2010, 8, 900-911.	8.3	113
22	Learning Multiple Evolutionary Pathways from Cross-Sectional Data. <i>Journal of Computational Biology</i> , 2005, 12, 584-598.	1.6	105
23	Computational methods for the design of effective therapies against drug resistant HIV strains. <i>Bioinformatics</i> , 2005, 21, 3943-3950.	4.1	103
24	Metabolic profiling reveals key metabolic features of renal cell carcinoma. <i>Journal of Cellular and Molecular Medicine</i> , 2011, 15, 109-118.	3.6	102
25	Correlative GC-TOF-MS-based metabolite profiling and LC-MS-based protein profiling reveal time-related systemic regulation of metabolite-protein networks and improve pattern recognition for multiple biomarker selection. <i>Metabolomics</i> , 2005, 1, 109-121.	3.0	97
26	The stability and robustness of metabolic states: identifying stabilizing sites in metabolic networks. <i>Molecular Systems Biology</i> , 2007, 3, 146.	7.2	97
27	ProMEX: a mass spectral reference database for proteins and protein phosphorylation sites. <i>BMC Bioinformatics</i> , 2007, 8, 216.	2.6	96
28	Robin: An Intuitive Wizard Application for R-Based Expression Microarray Quality Assessment and Analysis. <i>Plant Physiology</i> , 2010, 153, 642-651.	4.8	96
29	Principal Components Analysis. <i>Methods in Molecular Biology</i> , 2013, 930, 527-547.	0.9	96
30	Identification of heterotic metabolite QTL in <i>Arabidopsis thaliana</i> RIL and IL populations. <i>Plant Journal</i> , 2009, 59, 777-788.	5.7	95
31	QTL analysis of early stage heterosis for biomass in Arabidopsis. <i>Theoretical and Applied Genetics</i> , 2010, 120, 227-237.	3.6	90
32	Impact of the Carbon and Nitrogen Supply on Relationships and Connectivity between Metabolism and Biomass in a Broad Panel of Arabidopsis Accessions. <i>Plant Physiology</i> , 2013, 162, 347-363.	4.8	87
33	The Golm Metabolome Database: a database for GC-MS based metabolite profiling. <i>Topics in Current Genetics</i> , 2007, , 75-95.	0.7	79
34	Tenofovir Resistance and Resensitization. <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 3478-3484.	3.2	77
35	Estimating HIV Evolutionary Pathways and the Genetic Barrier to Drug Resistance. <i>Journal of Infectious Diseases</i> , 2005, 191, 1953-1960.	4.0	76
36	Glucocorticoid (dexamethasone)-induced metabolome changes in healthy males suggest prediction of response and side effects. <i>Scientific Reports</i> , 2015, 5, 15954.	3.3	76

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37	Corn hybrids display lower metabolite variability and complex metabolite inheritance patterns. <i>Plant Journal</i> , 2011, 68, 326-336.	5.7	75
38	Detection and characterization of 3D-signature phosphorylation site motifs and their contribution towards improved phosphorylation site prediction in proteins. <i>BMC Bioinformatics</i> , 2009, 10, 117.	2.6	66
39	From structure to dynamics of metabolic pathways: application to the plant mitochondrial TCA cycle. <i>Bioinformatics</i> , 2007, 23, 1378-1385.	4.1	65
40	Metabolite profile analysis: from raw data to regression and classification. <i>Physiologia Plantarum</i> , 2008, 132, 150-161.	5.2	64
41	MetaGeneAlyse: analysis of integrated transcriptional and metabolite data. <i>Bioinformatics</i> , 2003, 19, 2332-2333.	4.1	60
42	Improved Heterosis Prediction by Combining Information on DNA- and Metabolic Markers. <i>PLoS ONE</i> , 2009, 4, e5220.	2.5	57
43	More effort – more results: recent advances in integrative ‘omics’ data analysis. <i>Current Opinion in Plant Biology</i> , 2016, 30, 57-61.	7.1	56
44	Decision tree-based formation of consensus protein secondary structure prediction. <i>Bioinformatics</i> , 1999, 15, 1039-1046.	4.1	52
45	Mesenchymal stem cells and glioma cells form a structural as well as a functional syncytium in vitro. <i>Experimental Neurology</i> , 2012, 234, 208-219.	4.1	49
46	Prediction of hybrid biomass in <i>Arabidopsis thaliana</i> by selected parental SNP and metabolic markers. <i>Theoretical and Applied Genetics</i> , 2010, 120, 239-247.	3.6	46
47	Kinetic hybrid models composed of mechanistic and simplified enzymatic rate laws – a promising method for speeding up the kinetic modelling of complex metabolic networks. <i>FEBS Journal</i> , 2009, 276, 410-424.	4.7	42
48	MAPA Distinguishes Genotype-Specific Variability of Highly Similar Regulatory Protein Isoforms in Potato Tuber. <i>Journal of Proteome Research</i> , 2011, 10, 2979-2991.	3.7	42
49	Methods for optimizing antiviral combination therapies. <i>Bioinformatics</i> , 2003, 19, i16-i25.	4.1	39
50	PaVESy: Pathway Visualization and Editing System. <i>Bioinformatics</i> , 2004, 20, 2841-2844.	4.1	39
51	Stability of Metabolic Correlations under Changing Environmental Conditions in <i>Escherichia coli</i> – A Systems Approach. <i>PLoS ONE</i> , 2009, 4, e7441.	2.5	39
52	SLocX: predicting subcellular localization of <i>Arabidopsis</i> proteins leveraging gene expression data. <i>Frontiers in Plant Science</i> , 2011, 2, 43.	3.6	32
53	Transcription factor target prediction using multiple short expression time series from <i>Arabidopsis thaliana</i> . <i>BMC Bioinformatics</i> , 2007, 8, 454.	2.6	28
54	Enriched partial correlations in genome-wide gene expression profiles of hybrids (<i>A. thaliana</i>): a systems biological approach towards the molecular basis of heterosis. <i>Theoretical and Applied Genetics</i> , 2010, 120, 249-259.	3.6	26

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55	Mass-balanced randomization of metabolic networks. <i>Bioinformatics</i> , 2011, 27, 1397-1403.	4.1	25
56	Visualization and Analysis of Molecular Data. <i>Methods in Molecular Biology</i> , 2007, 358, 87-104.	0.9	25
57	Integrated data analysis for genome-wide research. , 2007, 97, 309-329.		24
58	Spatiotemporal dynamics of the Calvin cycle: Multistationarity and symmetry breaking instabilities. <i>BioSystems</i> , 2011, 103, 212-223.	2.0	22
59	Evolution of HIV resistance during treatment interruption in experienced patients and after restarting a new therapy. <i>Journal of Clinical Virology</i> , 2005, 34, 277-287.	3.1	20
60	A plant resource and experiment management system based on the Golm Plant Database as a basic tool for omics research. <i>Plant Methods</i> , 2008, 4, 11.	4.3	20
61	Evolutionary significance of metabolic network properties. <i>Journal of the Royal Society Interface</i> , 2012, 9, 1168-1176.	3.4	19
62	A "Crossomics" Study Analysing Variability of Different Components in Peripheral Blood of Healthy Caucasoid Individuals. <i>PLoS ONE</i> , 2012, 7, e28761.	2.5	19
63	Deducing Hybrid Performance from Parental Metabolic Profiles of Young Primary Roots of Maize by Using a Multivariate Diallel Approach. <i>PLoS ONE</i> , 2014, 9, e85435.	2.5	19
64	The expression of Wnt-inhibitor DKK1 (Dickkopf 1) is determined by intercellular crosstalk and hypoxia in human malignant gliomas. <i>Journal of Cancer Research and Clinical Oncology</i> , 2014, 140, 1261-1270.	2.5	19
65	Understanding the Relationship between Cotton Fiber Properties and Non-Cellulosic Cell Wall Polysaccharides. <i>PLoS ONE</i> , 2014, 9, e112168.	2.5	15
66	Validation and functional annotation of expression-based clusters based on gene ontology. <i>BMC Bioinformatics</i> , 2006, 7, 380.	2.6	14
67	Decision trees as a simple-to-use and reliable tool to identify individuals with impaired glucose metabolism or type 2 diabetes mellitus. <i>European Journal of Endocrinology</i> , 2010, 163, 565-571.	3.7	14
68	Scoring and identifying organism-specific functional patterns and putative phosphorylation sites in protein sequences using mutual information. <i>Biochemical and Biophysical Research Communications</i> , 2003, 307, 516-521.	2.1	13
69	Bioinformatics approach to predicting HIV drug resistance. <i>Expert Review of Molecular Diagnostics</i> , 2006, 6, 207-215.	3.1	13
70	Biological Cluster Evaluation for Gene Function Prediction. <i>Journal of Computational Biology</i> , 2014, 21, 428-445.	1.6	13
71	Phenomic prediction of maize hybrids. <i>BioSystems</i> , 2016, 146, 102-109.	2.0	11
72	Arevir: A Secure Platform for Designing Personalized Antiretroviral Therapies Against HIV. <i>Lecture Notes in Computer Science</i> , 2006, , 185-194.	1.3	11

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73	Systematic Analysis of Stability Patterns in Plant Primary Metabolism. PLoS ONE, 2012, 7, e34686.	2.5	11
74	Co-ordination and divergence of cell-specific transcription and translation of genes in arabidopsis root cells. Annals of Botany, 2014, 114, 1109-1123.	2.9	10
75	Isolation and characterization of bone marrow-derived progenitor cells from malignant gliomas. Anticancer Research, 2012, 32, 4971-82.	1.1	10
76	BioMiner: Paving the Way for Personalized Medicine. Cancer Informatics, 2015, 14, CIN.S20910.	1.9	9
77	Species-specific analysis of protein sequence motifs using mutual information. BMC Bioinformatics, 2005, 6, 164.	2.6	8
78	Comparison of metabolite profiles in U87 glioma cells and mesenchymal stem cells. BioSystems, 2011, 105, 130-139.	2.0	7
79	A MATLAB toolbox for structural kinetic modeling. Bioinformatics, 2012, 28, 2546-2547.	4.1	7
80	A distinct metabolic signature predicts development of fasting plasma glucose. Journal of Clinical Bioinformatics, 2012, 2, 3.	1.2	6
81	Integration of a Systems Biological Network Analysis and QTL Results for Biomass Heterosis in Arabidopsis thaliana. PLoS ONE, 2012, 7, e49951.	2.5	6
82	Refined elasticity sampling for Monte Carlo-based identification of stabilizing network patterns. Bioinformatics, 2015, 31, i214-i220.	4.1	4
83	Learning multiple evolutionary pathways from cross-sectional data. , 2004, , .		3
84	Complexity of automated gene annotation. BioSystems, 2011, 104, 1-8.	2.0	2
85	Analysis of phylogenetic signal in protostomial intron patterns using Mutual Information. Theory in Biosciences, 2013, 132, 93-104.	1.4	1
86	Towards a Graph-Theoretic Approach to Hybrid Performance Prediction from Large-Scale Phenotypic Data. Lecture Notes in Computer Science, 2015, , 173-184.	1.3	0
87	HIV-1 Drug Resistance Prediction and Therapy Optimization: A Case Study for the Application of Classification and Clustering Methods. Lecture Notes in Computer Science, 2009, , 185-201.	1.3	0