

# Joachim Selbig

## List of Publications by Year in descending order

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87  
papers

12,274  
citations

61687

45  
h-index

64407

83  
g-index

90  
all docs

90  
docs citations

90  
times ranked

18459  
citing authors

#	ARTICLE	IF	CITATIONS
1	Phenomic prediction of maize hybrids. <i>BioSystems</i> , 2016, 146, 102-109.	0.9	11
2	More effort " more results: recent advances in integrative "omics" data analysis. <i>Current Opinion in Plant Biology</i> , 2016, 30, 57-61.	3.5	56
3	Glucocorticoid (dexamethasone)-induced metabolome changes in healthy males suggest prediction of response and side effects. <i>Scientific Reports</i> , 2015, 5, 15954.	1.6	76
4	Refined elasticity sampling for Monte Carlo-based identification of stabilizing network patterns. <i>Bioinformatics</i> , 2015, 31, i214-i220.	1.8	4
5	BioMiner: Paving the Way for Personalized Medicine. <i>Cancer Informatics</i> , 2015, 14, CIN.S20910.	0.9	9
6	Towards a Graph-Theoretic Approach to Hybrid Performance Prediction from Large-Scale Phenotypic Data. <i>Lecture Notes in Computer Science</i> , 2015, , 173-184.	1.0	0
7	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.	1.1	19
8	Understanding the Relationship between Cotton Fiber Properties and Non-Cellulosic Cell Wall Polysaccharides. <i>PLoS ONE</i> , 2014, 9, e112168.	1.1	15
9	Co-ordination and divergence of cell-specific transcription and translation of genes in arabidopsis root cells. <i>Annals of Botany</i> , 2014, 114, 1109-1123.	1.4	10
10	Biological Cluster Evaluation for Gene Function Prediction. <i>Journal of Computational Biology</i> , 2014, 21, 428-445.	0.8	13
11	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.	1.2	19
12	Analysis of phylogenetic signal in protostomial intron patterns using Mutual Information. <i>Theory in Biosciences</i> , 2013, 132, 93-104.	0.6	1
13	Principal Components Analysis. <i>Methods in Molecular Biology</i> , 2013, 930, 527-547.	0.4	96
14	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.	2.3	87
15	Evolutionary significance of metabolic network properties. <i>Journal of the Royal Society Interface</i> , 2012, 9, 1168-1176.	1.5	19
16	A MATLAB toolbox for structural kinetic modeling. <i>Bioinformatics</i> , 2012, 28, 2546-2547.	1.8	7
17	A "Crossomics" Study Analysing Variability of Different Components in Peripheral Blood of Healthy Caucasoid Individuals. <i>PLoS ONE</i> , 2012, 7, e28761.	1.1	19
18	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.	2.0	49

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19	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.	2.8	117
20	A distinct metabolic signature predicts development of fasting plasma glucose. <i>Journal of Clinical Bioinformatics</i> , 2012, 2, 3.	1.2	6
21	Systematic Analysis of Stability Patterns in Plant Primary Metabolism. <i>PLoS ONE</i> , 2012, 7, e34686.	1.1	11
22	Integration of a Systems Biological Network Analysis and QTL Results for Biomass Heterosis in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2012, 7, e49951.	1.1	6
23	Isolation and characterization of bone marrow-derived progenitor cells from malignant gliomas. <i>Anticancer Research</i> , 2012, 32, 4971-82.	0.5	10
24	MAPA Distinguishes Genotype-Specific Variability of Highly Similar Regulatory Protein Isoforms in Potato Tuber. <i>Journal of Proteome Research</i> , 2011, 10, 2979-2991.	1.8	42
25	SLocX: predicting subcellular localization of Arabidopsis proteins leveraging gene expression data. <i>Frontiers in Plant Science</i> , 2011, 2, 43.	1.7	32
26	Corn hybrids display lower metabolite variability and complex metabolite inheritance patterns. <i>Plant Journal</i> , 2011, 68, 326-336.	2.8	75
27	Metabolic profiling reveals key metabolic features of renal cell carcinoma. <i>Journal of Cellular and Molecular Medicine</i> , 2011, 15, 109-118.	1.6	102
28	Complexity of automated gene annotation. <i>BioSystems</i> , 2011, 104, 1-8.	0.9	2
29	Comparison of metabolite profiles in U87 glioma cells and mesenchymal stem cells. <i>BioSystems</i> , 2011, 105, 130-139.	0.9	7
30	Spatiotemporal dynamics of the Calvin cycle: Multistationarity and symmetry breaking instabilities. <i>BioSystems</i> , 2011, 103, 212-223.	0.9	22
31	Mass-balanced randomization of metabolic networks. <i>Bioinformatics</i> , 2011, 27, 1397-1403.	1.8	25
32	QTL analysis of early stage heterosis for biomass in Arabidopsis. <i>Theoretical and Applied Genetics</i> , 2010, 120, 227-237.	1.8	90
33	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.	1.8	46
34	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.	1.8	26
35	Discovering plant metabolic biomarkers for phenotype prediction using an untargeted approach. <i>Plant Biotechnology Journal</i> , 2010, 8, 900-911.	4.1	113
36	Predicting Arabidopsis Freezing Tolerance and Heterosis in Freezing Tolerance from Metabolite Composition. <i>Molecular Plant</i> , 2010, 3, 224-235.	3.9	120

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37	Metabolomic and transcriptomic stress response of <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2010, 6, 364.	3.2	451
38	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.	1.9	14
39	Robin: An Intuitive Wizard Application for R-Based Expression Microarray Quality Assessment and Analysis. <i>Plant Physiology</i> , 2010, 153, 642-651.	2.3	96
40	Stability of Metabolic Correlations under Changing Environmental Conditions in <i>Escherichia coli</i> – A Systems Approach. <i>PLoS ONE</i> , 2009, 4, e7441.	1.1	39
41	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.	3.3	467
42	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.	1.2	66
43	Identification of heterotic metabolite QTL in <i>Arabidopsis thaliana</i> RIL and IL populations. <i>Plant Journal</i> , 2009, 59, 777-788.	2.8	95
44	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.	2.2	42
45	Improved Heterosis Prediction by Combining Information on DNA- and Metabolic Markers. <i>PLoS ONE</i> , 2009, 4, e5220.	1.1	57
46	HIV-1 Drug Resistance Prediction and Therapy Optimization: A Case Study for the Application of Classification and Clustering Methods. <i>Lecture Notes in Computer Science</i> , 2009, , 185-201.	1.0	0
47	Metabolomics of temperature stress. <i>Physiologia Plantarum</i> , 2008, 132, 220-235.	2.6	439
48	Metabolite profile analysis: from raw data to regression and classification. <i>Physiologia Plantarum</i> , 2008, 132, 150-161.	2.6	64
49	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.	2.8	211
50	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.	1.9	20
51	Mode of Inheritance of Primary Metabolic Traits in Tomato. <i>Plant Cell</i> , 2008, 20, 509-523.	3.1	208
52	Integration of Metabolomic and Proteomic Phenotypes. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1725-1736.	2.5	155
53	The metabolic signature related to high plant growth rate in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 4759-4764.	3.3	377
54	PhosPhAt: a database of phosphorylation sites in <i>Arabidopsis thaliana</i> and a plant-specific phosphorylation site predictor. <i>Nucleic Acids Research</i> , 2007, 36, D1015-D1021.	6.5	302

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55	The Metabolic Response of Heterotrophic Arabidopsis Cells to Oxidative Stress. <i>Plant Physiology</i> , 2007, 143, 312-325.	2.3	234
56	From structure to dynamics of metabolic pathways: application to the plant mitochondrial TCA cycle. <i>Bioinformatics</i> , 2007, 23, 1378-1385.	1.8	65
57	The stability and robustness of metabolic states: identifying stabilizing sites in metabolic networks. <i>Molecular Systems Biology</i> , 2007, 3, 146.	3.2	97
58	pcaMethods a bioconductor package providing PCA methods for incomplete data. <i>Bioinformatics</i> , 2007, 23, 1164-1167.	1.8	944
59	The Golm Metabolome Database: a database for GC-MS based metabolite profiling. <i>Topics in Current Genetics</i> , 2007, , 75-95.	0.7	79
60	ProMEX: a mass spectral reference database for proteins and protein phosphorylation sites. <i>BMC Bioinformatics</i> , 2007, 8, 216.	1.2	96
61	Transcription factor target prediction using multiple short expression time series from <i>Arabidopsis thaliana</i> . <i>BMC Bioinformatics</i> , 2007, 8, 454.	1.2	28
62	Visualization and Analysis of Molecular Data. <i>Methods in Molecular Biology</i> , 2007, 358, 87-104.	0.4	25
63	Integrated data analysis for genome-wide research. , 2007, 97, 309-329.		24
64	Validation and functional annotation of expression-based clusters based on gene ontology. <i>BMC Bioinformatics</i> , 2006, 7, 380.	1.2	14
65	Bioinformatics approach to predicting HIV drug resistance. <i>Expert Review of Molecular Diagnostics</i> , 2006, 6, 207-215.	1.5	13
66	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.	3.3	229
67	Arevir: A Secure Platform for Designing Personalized Antiretroviral Therapies Against HIV. <i>Lecture Notes in Computer Science</i> , 2006, , 185-194.	1.0	11
68	Species-specific analysis of protein sequence motifs using mutual information. <i>BMC Bioinformatics</i> , 2005, 6, 164.	1.2	8
69	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.	1.4	97
70	Non-linear PCA: a missing data approach. <i>Bioinformatics</i> , 2005, 21, 3887-3895.	1.8	167
71	Estimating HIV Evolutionary Pathways and the Genetic Barrier to Drug Resistance. <i>Journal of Infectious Diseases</i> , 2005, 191, 1953-1960.	1.9	76
72	Learning Multiple Evolutionary Pathways from Cross-Sectional Data. <i>Journal of Computational Biology</i> , 2005, 12, 584-598.	0.8	105

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73	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.	2.3	576
74	Computational methods for the design of effective therapies against drug resistant HIV strains. <i>Bioinformatics</i> , 2005, 21, 3943-3950.	1.8	103
75	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.	1.6	20
76	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.	3.1	489
77	PaVESy: Pathway Visualization and Editing System. <i>Bioinformatics</i> , 2004, 20, 2841-2844.	1.8	39
78	Learning multiple evolutionary pathways from cross-sectional data. , 2004, , .		3
79	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.	2.8	3,184
80	Parallel analysis of transcript and metabolic profiles: a new approach in systems biology. <i>EMBO Reports</i> , 2003, 4, 989-993.	2.0	308
81	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.	1.0	13
82	Geno2pheno: estimating phenotypic drug resistance from HIV-1 genotypes. <i>Nucleic Acids Research</i> , 2003, 31, 3850-3855.	6.5	213
83	Tenofovir Resistance and Resensitization. <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 3478-3484.	1.4	77
84	Methods for optimizing antiviral combination therapies. <i>Bioinformatics</i> , 2003, 19, i16-i25.	1.8	39
85	MetaGeneAllyse: analysis of integrated transcriptional and metabolite data. <i>Bioinformatics</i> , 2003, 19, 2332-2333.	1.8	60
86	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.	3.3	310
87	Decision tree-based formation of consensus protein secondary structure prediction. <i>Bioinformatics</i> , 1999, 15, 1039-1046.	1.8	52