

Dirk Walther

List of Publications by Year in descending order

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Version: 2024-02-01

111
papers

8,332
citations

76031

42
h-index

56606

87
g-index

124
all docs

124
docs citations

124
times ranked

14665
citing authors

#	ARTICLE	IF	CITATIONS
1	Biclique extension as an effective approach to identify missing links in metabolic compound-protein interaction networks. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	5
2	Graph-based models of the <i>Oenothera</i> mitochondrial genome capture the enormous complexity of higher plant mitochondrial DNA organization. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac027.	1.5	15
3	PRI: Re-Analysis of a Public Mass Cytometry Dataset Reveals Patterns of Effective Tumor Treatments. <i>Frontiers in Immunology</i> , 2022, 13, 849329.	2.2	0
4	Deciphering transcriptional regulators of banana fruit ripening by regulatory network analysis. <i>Plant Biotechnology Journal</i> , 2021, 19, 477-489.	4.1	59
5	Identification of cis-regulatory motifs in first introns and the prediction of intron-mediated enhancement of gene expression in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2021, 22, 390.	1.2	7
6	Tyr-Asp inhibition of glyceraldehyde 3-phosphate dehydrogenase affects plant redox metabolism. <i>EMBO Journal</i> , 2021, 40, e106800.	3.5	29
7	Genome-Wide Approach to Identify Quantitative Trait Loci for Drought Tolerance in Tetraploid Potato (<i>Solanum tuberosum</i> L.). <i>International Journal of Molecular Sciences</i> , 2021, 22, 6123.	1.8	9
8	Spatially Enriched Paralog Rearrangements Argue Functionally Diverse Ribosomes Arise during Cold Acclimation in <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 6160.	1.8	10
9	COSNet : Complexome-Structural Network Interpreter used to study spatial enrichment in metazoan ribosomes. <i>BMC Bioinformatics</i> , 2021, 22, 605.	1.2	2
10	A novel seed plants gene regulates oxidative stress tolerance in <i>Arabidopsis thaliana</i> . <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 705-718.	2.4	11
11	Can Metabolite- and Transcript-Based Selection for Drought Tolerance in <i>Solanum tuberosum</i> Replace Selection on Yield in Arid Environments?. <i>Frontiers in Plant Science</i> , 2020, 11, 1071.	1.7	8
12	Determinants of correlated expression of transcription factors and their target genes. <i>Nucleic Acids Research</i> , 2020, 48, 11347-11369.	6.5	15
13	Metabolomic markers and physiological adaptations for high phosphate utilization efficiency in rice. <i>Plant, Cell and Environment</i> , 2020, 43, 2066-2079.	2.8	19
14	Polymorphisms in miRNA binding sites involved in metabolic diseases in mice and humans. <i>Scientific Reports</i> , 2020, 10, 7202.	1.6	8
15	Photorespiration Enhances Acidification of the Thylakoid Lumen, Reduces the Plastoquinone Pool, and Contributes to the Oxidation of P700 at a Lower Partial Pressure of CO ₂ in Wheat Leaves. <i>Plants</i> , 2020, 9, 319.	1.6	19
16	Growth under Fluctuating Light Reveals Large Trait Variation in a Panel of <i>Arabidopsis</i> Accessions. <i>Plants</i> , 2020, 9, 316.	1.6	14
17	Similar Yet Different-Structural and Functional Diversity among <i>Arabidopsis thaliana</i> LEA_4 Proteins. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2794.	1.8	12
18	Effect of Senescence Phenotypes and Nitrate Availability on Wheat Leaf Metabolome during Grain Filling. <i>Agronomy</i> , 2019, 9, 305.	1.3	6

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19	Control of retrograde signalling by protein import and cytosolic folding stress. <i>Nature Plants</i> , 2019, 5, 525-538.	4.7	109
20	Chloroplast competition is controlled by lipid biosynthesis in evening primroses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5665-5674.	3.3	39
21	Highly Resolved Systems Biology to Dissect the Etioplast-to-Chloroplast Transition in Tobacco Leaves. <i>Plant Physiology</i> , 2019, 180, 654-681.	2.3	51
22	Plant Temperature Acclimation and Growth Rely on Cytosolic Ribosome Biogenesis Factor Homologs. <i>Plant Physiology</i> , 2018, 176, 2251-2276.	2.3	39
23	Metabolite and transcript markers for the prediction of potato drought tolerance. <i>Plant Biotechnology Journal</i> , 2018, 16, 939-950.	4.1	68
24	Promising Metabolite Profiles in the Plasma and CSF of Early Clinical Parkinson's Disease. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 51.	1.7	74
25	Metabolomic Profiles for Primary Progressive Multiple Sclerosis Stratification and Disease Course Monitoring. <i>Frontiers in Human Neuroscience</i> , 2018, 12, 226.	1.0	47
26	A genome-wide scan for correlated mutations detects macromolecular and chromatin interactions in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2018, 46, 8114-8132.	6.5	5
27	Chlorosis caused by two recessively interacting genes reveals a role of <i>RNA</i> helicase in hybrid breakdown in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2017, 91, 251-262.	2.8	24
28	Towards understanding the crosstalk between protein post-translational modifications: Homotypic and heterotypic PTM pair distances on protein surfaces are not random. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 78-92.	1.5	17
29	Metabolic Pathway Assignment of Plant Genes based on Phylogenetic Profiling – A Feasibility Study. <i>Frontiers in Plant Science</i> , 2017, 8, 1831.	1.7	7
30	Characterization of the Wheat Leaf Metabolome during Grain Filling and under Varied N-Supply. <i>Frontiers in Plant Science</i> , 2017, 8, 2048.	1.7	42
31	Editorial: Metabolome Informatics and Statistics: Current State and Emerging Trends. <i>Frontiers in Bioengineering and Biotechnology</i> , 2016, 4, 63.	2.0	3
32	Spatial proximity statistics suggest a regulatory role of protein phosphorylation on compound binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 565-579.	1.5	6
33	The drought response of potato reference cultivars with contrasting tolerance. <i>Plant, Cell and Environment</i> , 2016, 39, 2370-2389.	2.8	66
34	The Identification of Cis-Regulatory Sequence Motifs in Gene Promoters Based on SNP Information. <i>Methods in Molecular Biology</i> , 2016, 1482, 31-47.	0.4	3
35	Limited Phosphate: Mobile RNAs convey the message. <i>Nature Plants</i> , 2016, 2, 16040.	4.7	8
36	tRNA-Related Sequences Trigger Systemic mRNA Transport in Plants. <i>Plant Cell</i> , 2016, 28, 1237-1249.	3.1	143

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37	The orientation of transcription factor binding site motifs in gene promoter regions: does it matter?. BMC Genomics, 2016, 17, 185.	1.2	40
38	Physicochemical characteristics of structurally determined metabolite-protein and drug-protein binding events with respect to binding specificity. Frontiers in Molecular Biosciences, 2015, 2, 51.	1.6	9
39	Multiple RNA Processing Defects and Impaired Chloroplast Function in Plants Deficient in the Organellar Protein-Only RNase P Enzyme. PLoS ONE, 2015, 10, e0120533.	1.1	19
40	COordination of Standards in MetabOLOmics (COSMOS): facilitating integrated metabolomics data access. Metabolomics, 2015, 11, 1587-1597.	1.4	140
41	The Roles of Post-translational Modifications in the Context of Protein Interaction Networks. PLoS Computational Biology, 2015, 11, e1004049.	1.5	299
42	Assessment of drought tolerance and its potential yield penalty in potato. Functional Plant Biology, 2015, 42, 655.	1.1	26
43	Substantial reprogramming of the <i>Eutrema salsugineum</i> (<i>Thellungiella salsuginea</i>) transcriptome in response to UV and silver nitrate challenge. BMC Plant Biology, 2015, 15, 137.	1.6	18
44	Computational Phosphorylation Network Reconstruction: Methods and Resources. Methods in Molecular Biology, 2015, 1306, 177-194.	0.4	2
45	Endogenous Arabidopsis messenger RNAs transported to distant tissues. Nature Plants, 2015, 1, 15025.	4.7	331
46	Characterization and Identification of cis-Regulatory Elements in Arabidopsis Based on Single-Nucleotide Polymorphism Information Å. Plant Physiology, 2014, 164, 181-200.	2.3	66
47	The sucroseâ€“trehalose 6-phosphate (Tre6P) nexus: specificity and mechanisms of sucrose signalling by Tre6P. Journal of Experimental Botany, 2014, 65, 1051-1068.	2.4	326
48	Meta-Analysis of <i>Arabidopsis thaliana</i> Phospho-Proteomics Data Reveals Compartmentalization of Phosphorylation Motifs. Plant Cell, 2014, 26, 2367-2389.	3.1	158
49	Reconstruction and analysis of nutrient-induced phosphorylation networks in <i>Arabidopsis thaliana</i> . Frontiers in Plant Science, 2013, 4, 540.	1.7	21
50	The Metabolic Interplay between Plants and Phytopathogens. Metabolites, 2013, 3, 1-23.	1.3	47
51	The Combinatorics Of Cis-Regulatory Elements: From Cooperatively Acting Motifs To Gene Regulatory Networks. , 2013, , 176-188.		1
52	Give It AGO: The Search for miRNA-Argonaute Sorting Signals in <i>Arabidopsis thaliana</i> Indicates a Relevance of Sequence Positions Other than the 5â€“2-Position Alone. Frontiers in Plant Science, 2012, 3, 272.	1.7	25
53	Characterization and Prediction of Protein Phosphorylation Hotspots in <i>Arabidopsis thaliana</i> . Frontiers in Plant Science, 2012, 3, 207.	1.7	22
54	Data management pipeline for plant phenotyping in a multisite project. Functional Plant Biology, 2012, 39, 948.	1.1	23

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55	Conducting Molecular Biomarker Discovery Studies in Plants. <i>Methods in Molecular Biology</i> , 2012, 918, 127-150.	0.4	6
56	Matapax: An Online High-Throughput Genome-Wide Association Study Pipeline. <i>Plant Physiology</i> , 2012, 158, 1534-1541.	2.3	15
57	Comparative analysis of miRNAs and their targets across four plant species. <i>BMC Research Notes</i> , 2011, 4, 483.	0.6	18
58	Local Absence of Secondary Structure Permits Translation of mRNAs that Lack Ribosome-Binding Sites. <i>PLoS Genetics</i> , 2011, 7, e1002155.	1.5	109
59	The influence of the local sequence environment on RNA loop structures. <i>Rna</i> , 2011, 17, 1247-1257.	1.6	1
60	Integration of Proteomic and Metabolomic Profiling as well as Metabolic Modeling for the Functional Analysis of Metabolic Networks. <i>Methods in Molecular Biology</i> , 2011, 694, 341-363.	0.4	10
61	Decision tree supported substructure prediction of metabolites from GC-MS profiles. <i>Metabolomics</i> , 2010, 6, 322-333.	1.4	296
62	The complexity of gene expression dynamics revealed by permutation entropy. <i>BMC Bioinformatics</i> , 2010, 11, 607.	1.2	33
63	Single feature polymorphism (SFP)-based selective sweep identification and association mapping of growth-related metabolic traits in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2010, 11, 188.	1.2	11
64	Proteome-wide survey of phosphorylation patterns affected by nuclear DNA polymorphisms in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2010, 11, 411.	1.2	21
65	Modeling RNA loops using sequence homology and geometric constraints. <i>Bioinformatics</i> , 2010, 26, 1671-1672.	1.8	6
66	Sequence-structure relationships in RNA loops: establishing the basis for loop homology modeling. <i>Nucleic Acids Research</i> , 2010, 38, 970-980.	6.5	31
67	Metabolic Pathway Relationships Revealed by an Integrative Analysis of the Transcriptional and Metabolic Temperature Stress-Response Dynamics in Yeast. <i>OMICS A Journal of Integrative Biology</i> , 2010, 14, 261-274.	1.0	42
68	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
69	Dynamic Transcriptional and Metabolic Responses in Yeast Adapting to Temperature Stress. <i>OMICS A Journal of Integrative Biology</i> , 2010, 14, 249-259.	1.0	53
70	ChlamyCyc - a comprehensive database and web-portal centered on <i>Chlamydomonas reinhardtii</i> . <i>Nature Precedings</i> , 2009, , .	0.1	0
71	Identification and classification of ncRNA molecules using graph properties. <i>Nucleic Acids Research</i> , 2009, 37, e66-e66.	6.5	44
72	Identification of Nutrient-Responsive Arabidopsis and Rapeseed MicroRNAs by Comprehensive Real-Time Polymerase Chain Reaction Profiling and Small RNA Sequencing. <i>Plant Physiology</i> , 2009, 150, 1541-1555.	2.3	414

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73	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
74	ChlamyCyc: an integrative systems biology database and web-portal for <i>Chlamydomonas reinhardtii</i> . <i>BMC Genomics</i> , 2009, 10, 209.	1.2	73
75	Expression profiling of rice cultivars differing in their tolerance to long-term drought stress. <i>Plant Molecular Biology</i> , 2009, 69, 133-153.	2.0	207
76	Ratio-dependent significance thresholds in reciprocal ^{15}N -labeling experiments as a robust tool in detection of candidate proteins responding to biological treatment. <i>Proteomics</i> , 2009, 9, 1916-1924.	1.3	33
77	Plant phosphoproteomics: An update. <i>Proteomics</i> , 2009, 9, 964-988.	1.3	107
78	Analysis of <i>Arabidopsis</i> natural variation in biomass accumulation and metabolism. <i>New Biotechnology</i> , 2009, 25, S307.	2.4	2
79	Chapter 7. Metabolic Engineering. , 2009, , 195-219.		0
80	The integrated analysis of metabolic and protein interaction networks reveals novel molecular organizing principles. <i>BMC Systems Biology</i> , 2008, 2, 100.	3.0	54
81	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
82	Metabolomics- and Proteomics-Assisted Genome Annotation and Analysis of the Draft Metabolic Network of <i>Chlamydomonas reinhardtii</i> . <i>Genetics</i> , 2008, 179, 157-166.	1.2	141
83	The Regulatory Code for Transcriptional Response Diversity and Its Relation to Genome Structural Properties in <i>A. thaliana</i> . <i>PLoS Genetics</i> , 2007, 3, e11.	1.5	138
84	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
85	pcaMethods a bioconductor package providing PCA methods for incomplete data. <i>Bioinformatics</i> , 2007, 23, 1164-1167.	1.8	944
86	The Golm Metabolome Database: a database for GC-MS based metabolite profiling. <i>Topics in Current Genetics</i> , 2007, , 75-95.	0.7	79
87	ProMEX: a mass spectral reference database for proteins and protein phosphorylation sites. <i>BMC Bioinformatics</i> , 2007, 8, 216.	1.2	96
88	Integrated data analysis for genome-wide research. , 2007, 97, 309-329.		24
89	Noninvasive Discrimination of Rejection in Cardiac Allograft Recipients Using Gene Expression Profiling. <i>American Journal of Transplantation</i> , 2006, 6, 150-160.	2.6	482
90	Gene Expression Profiles and B-Type Natriuretic Peptide Elevation in Heart Transplantation: More Than a Hemodynamic Marker. <i>Circulation</i> , 2006, 114, I-21-I-26.	1.6	53

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91	The regulatory code for transcriptional response diversity and its relation to genome structural properties in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2005, preprint, e11.	1.5	1
92	Serine 171, a Conserved Residue in the $\hat{\Gamma}^3$ -Aminobutyric Acid Type A (GABAA) Receptor $\hat{\Gamma}^3_2$ Subunit, Mediates Subunit Interaction and Cell Surface Localization. <i>Journal of Biological Chemistry</i> , 2004, 279, 14179-14183.	1.6	11
93	Closing the Folding Chamber of the Eukaryotic Chaperonin Requires the Transition State of ATP Hydrolysis. <i>Cell</i> , 2003, 113, 369-381.	13.5	195
94	MolSurfer: a macromolecular interface navigator. <i>Nucleic Acids Research</i> , 2003, 31, 3349-3351.	6.5	44
95	Basecalling with LifeTrace. <i>Genome Research</i> , 2001, 11, 875-888.	2.4	19
96	Reconstruction of low-resolution three-dimensional density maps from one-dimensional small-angle X-ray solution scattering data for biomolecules. <i>Journal of Applied Crystallography</i> , 2000, 33, 350-363.	1.9	154
97	Co-evolution of proteins with their interaction partners 1 Edited by B. Honig. <i>Journal of Molecular Biology</i> , 2000, 299, 283-293.	2.0	409
98	Solution structural studies and low-resolution model of the <i>Schizosaccharomyces pombe</i> sap1 protein. <i>Journal of Molecular Biology</i> , 2000, 300, 563-574.	2.0	40
99	Conformational attractors on the Ramachandran map. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 506-517.	2.5	22
100	MolSurfer: two-dimensional maps for navigating three-dimensional structures of proteins. <i>Trends in Biochemical Sciences</i> , 1999, 24, 285-287.	3.7	21
101	Helix-helix packing angle preferences for finite helix axes. , 1998, 33, 457-459.		26
102	Identification of a prion protein epitope modulating transmission of bovine spongiform encephalopathy prions to transgenic mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 14279-14284.	3.3	145
103	Nonlinear Hairy Layer Theory of Electrophoretic Fingerprinting Applied to Consecutive Layer by Layer Polyelectrolyte Adsorption onto Charged Polystyrene Latex Particles. <i>Langmuir</i> , 1997, 13, 5294-5305.	1.6	143
104	Solution structure of the spectrin repeat: a left-handed antiparallel triple-helical coiled-coil 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1997, 273, 740-751.	2.0	143
105	WebMolâ€”a Java-based PDB viewer. <i>Trends in Biochemical Sciences</i> , 1997, 22, 274-275.	3.7	68
106	A New Relaxation Effect with Polymer Depletion Layers. <i>Langmuir</i> , 1996, 12, 6263-6269.	1.6	4
107	Principles of Helix-Helix Packing in Proteins: The Helical Lattice Superposition Model. <i>Journal of Molecular Biology</i> , 1996, 255, 536-553.	2.0	113
108	Brownian dynamics simulation of the lateral distribution of charged membrane components. <i>European Biophysics Journal</i> , 1996, 24, 125-35.	1.2	6

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109	Intrahelical side chain-side chain contacts: the consequences of restricted rotameric states and implications for helix engineering and design. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 471-478.	1.0	17
110	Comparison of atomic solvation parametric sets: Applicability and limitations in protein folding and binding. <i>Protein Science</i> , 1995, 4, 2499-2509.	3.1	84
111	Brownian Dynamics Simulation of Charged Membrane Components: Implications for their Lateral Distribution and Voltage Dependence of Ion Transport through Membranes. , 1993, , 71-76.		0