

# Dirk Walther

## List of Publications by Year in descending order

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111  
papers

8,332  
citations

66343

42  
h-index

49909

87  
g-index

124  
all docs

124  
docs citations

124  
times ranked

13110  
citing authors

#	ARTICLE	IF	CITATIONS
1	pcaMethods a bioconductor package providing PCA methods for incomplete data. <i>Bioinformatics</i> , 2007, 23, 1164-1167.	4.1	944
2	Noninvasive Discrimination of Rejection in Cardiac Allograft Recipients Using Gene Expression Profiling. <i>American Journal of Transplantation</i> , 2006, 6, 150-160.	4.7	482
3	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.	4.8	414
4	Co-evolution of proteins with their interaction partners 1 Edited by B. Honig. <i>Journal of Molecular Biology</i> , 2000, 299, 283-293.	4.2	409
5	Endogenous Arabidopsis messenger RNAs transported to distant tissues. <i>Nature Plants</i> , 2015, 1, 15025.	9.3	331
6	The sucrose-trehalose 6-phosphate (Tre6P) nexus: specificity and mechanisms of sucrose signalling by Tre6P. <i>Journal of Experimental Botany</i> , 2014, 65, 1051-1068.	4.8	326
7	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
8	The Roles of Post-translational Modifications in the Context of Protein Interaction Networks. <i>PLoS Computational Biology</i> , 2015, 11, e1004049.	3.2	299
9	Decision tree supported substructure prediction of metabolites from GC-MS profiles. <i>Metabolomics</i> , 2010, 6, 322-333.	3.0	296
10	Expression profiling of rice cultivars differing in their tolerance to long-term drought stress. <i>Plant Molecular Biology</i> , 2009, 69, 133-153.	3.9	207
11	Closing the Folding Chamber of the Eukaryotic Chaperonin Requires the Transition State of ATP Hydrolysis. <i>Cell</i> , 2003, 113, 369-381.	28.9	195
12	Meta-Analysis of Arabidopsis thaliana Phospho-Proteomics Data Reveals Compartmentalization of Phosphorylation Motifs. <i>Plant Cell</i> , 2014, 26, 2367-2389.	6.6	158
13	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.	4.5	154
14	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.	7.1	145
15	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.	3.5	143
16	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.	4.2	143
17	tRNA-Related Sequences Trigger Systemic mRNA Transport in Plants. <i>Plant Cell</i> , 2016, 28, 1237-1249.	6.6	143
18	Metabolomics- and Proteomics-Assisted Genome Annotation and Analysis of the Draft Metabolic Network of Chlamydomonas reinhardtii. <i>Genetics</i> , 2008, 179, 157-166.	2.9	141

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19	COordination of Standards in MetabOlomicS (COSMOS): facilitating integrated metabolomics data access. <i>Metabolomics</i> , 2015, 11, 1587-1597.	3.0	140
20	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.	3.5	138
21	Principles of Helix-Helix Packing in Proteins: The Helical Lattice Superposition Model. <i>Journal of Molecular Biology</i> , 1996, 255, 536-553.	4.2	113
22	Local Absence of Secondary Structure Permits Translation of mRNAs that Lack Ribosome-Binding Sites. <i>PLoS Genetics</i> , 2011, 7, e1002155.	3.5	109
23	Control of retrograde signalling by protein import and cytosolic folding stress. <i>Nature Plants</i> , 2019, 5, 525-538.	9.3	109
24	Plant phosphoproteomics: An update. <i>Proteomics</i> , 2009, 9, 964-988.	2.2	107
25	ProMEX: a mass spectral reference database for proteins and protein phosphorylation sites. <i>BMC Bioinformatics</i> , 2007, 8, 216.	2.6	96
26	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
27	Comparison of atomic solvation parametric sets: Applicability and limitations in protein folding and binding. <i>Protein Science</i> , 1995, 4, 2499-2509.	7.6	84
28	The Golm Metabolome Database: a database for GC-MS based metabolite profiling. <i>Topics in Current Genetics</i> , 2007, , 75-95.	0.7	79
29	Promising Metabolite Profiles in the Plasma and CSF of Early Clinical Parkinson's Disease. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 51.	3.4	74
30	ChlamyCyc: an integrative systems biology database and web-portal for <i>Chlamydomonas reinhardtii</i> . <i>BMC Genomics</i> , 2009, 10, 209.	2.8	73
31	WebMol—a Java-based PDB viewer. <i>Trends in Biochemical Sciences</i> , 1997, 22, 274-275.	7.5	68
32	Metabolite and transcript markers for the prediction of potato drought tolerance. <i>Plant Biotechnology Journal</i> , 2018, 16, 939-950.	8.3	68
33	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
34	Characterization and Identification of cis-Regulatory Elements in Arabidopsis Based on Single-Nucleotide Polymorphism Information. <i>Plant Physiology</i> , 2014, 164, 181-200.	4.8	66
35	The drought response of potato reference cultivars with contrasting tolerance. <i>Plant, Cell and Environment</i> , 2016, 39, 2370-2389.	5.7	66
36	Deciphering transcriptional regulators of banana fruit ripening by regulatory network analysis. <i>Plant Biotechnology Journal</i> , 2021, 19, 477-489.	8.3	59

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37	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
38	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
39	Dynamic Transcriptional and Metabolic Responses in Yeast Adapting to Temperature Stress. <i>OMICS A Journal of Integrative Biology</i> , 2010, 14, 249-259.	2.0	53
40	Highly Resolved Systems Biology to Dissect the Etioplast-to-Chloroplast Transition in Tobacco Leaves. <i>Plant Physiology</i> , 2019, 180, 654-681.	4.8	51
41	The Metabolic Interplay between Plants and Phytopathogens. <i>Metabolites</i> , 2013, 3, 1-23.	2.9	47
42	Metabolomic Profiles for Primary Progressive Multiple Sclerosis Stratification and Disease Course Monitoring. <i>Frontiers in Human Neuroscience</i> , 2018, 12, 226.	2.0	47
43	MolSurfer: a macromolecular interface navigator. <i>Nucleic Acids Research</i> , 2003, 31, 3349-3351.	14.5	44
44	Identification and classification of ncRNA molecules using graph properties. <i>Nucleic Acids Research</i> , 2009, 37, e66-e66.	14.5	44
45	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.	2.0	42
46	Characterization of the Wheat Leaf Metabolome during Grain Filling and under Varied N-Supply. <i>Frontiers in Plant Science</i> , 2017, 8, 2048.	3.6	42
47	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.	4.2	40
48	The orientation of transcription factor binding site motifs in gene promoter regions: does it matter?. <i>BMC Genomics</i> , 2016, 17, 185.	2.8	40
49	Plant Temperature Acclimation and Growth Rely on Cytosolic Ribosome Biogenesis Factor Homologs. <i>Plant Physiology</i> , 2018, 176, 2251-2276.	4.8	39
50	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.	7.1	39
51	Ratio-dependent significance thresholds in reciprocal <sup>15</sup> N-labeling experiments as a robust tool in detection of candidate proteins responding to biological treatment. <i>Proteomics</i> , 2009, 9, 1916-1924.	2.2	33
52	The complexity of gene expression dynamics revealed by permutation entropy. <i>BMC Bioinformatics</i> , 2010, 11, 607.	2.6	33
53	Sequence-structure relationships in RNA loops: establishing the basis for loop homology modeling. <i>Nucleic Acids Research</i> , 2010, 38, 970-980.	14.5	31
54	Tyr <sup>Asp</sup> inhibition of glyceraldehyde 3-phosphate dehydrogenase affects plant redox metabolism. <i>EMBO Journal</i> , 2021, 40, e106800.	7.8	29

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55	Helix-helix packing angle preferences for finite helix axes. , 1998, 33, 457-459.		26
56	Assessment of drought tolerance and its potential yield penalty in potato. <i>Functional Plant Biology</i> , 2015, 42, 655.	2.1	26
57	Give It AGO: The Search for miRNA-Argonaute Sorting Signals in <i>Arabidopsis thaliana</i> Indicates a Relevance of Sequence Positions Other than the 5' Position Alone. <i>Frontiers in Plant Science</i> , 2012, 3, 272.	3.6	25
58	Chlorosis caused by two recessively interacting genes reveals a role of <i>scpRNA</i> helicase in hybrid breakdown in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2017, 91, 251-262.	5.7	24
59	Integrated data analysis for genome-wide research. , 2007, 97, 309-329.		24
60	Data management pipeline for plant phenotyping in a multisite project. <i>Functional Plant Biology</i> , 2012, 39, 948.	2.1	23
61	Conformational attractors on the Ramachandran map. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 506-517.	2.5	22
62	Characterization and Prediction of Protein Phosphorylation Hotspots in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2012, 3, 207.	3.6	22
63	MolSurfer: two-dimensional maps for navigating three-dimensional structures of proteins. <i>Trends in Biochemical Sciences</i> , 1999, 24, 285-287.	7.5	21
64	Proteome-wide survey of phosphorylation patterns affected by nuclear DNA polymorphisms in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2010, 11, 411.	2.8	21
65	Reconstruction and analysis of nutrient-induced phosphorylation networks in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 540.	3.6	21
66	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
67	Basecalling with LifeTrace. <i>Genome Research</i> , 2001, 11, 875-888.	5.5	19
68	Multiple RNA Processing Defects and Impaired Chloroplast Function in Plants Deficient in the Organellar Protein-Only RNase P Enzyme. <i>PLoS ONE</i> , 2015, 10, e0120533.	2.5	19
69	Metabolomic markers and physiological adaptations for high phosphate utilization efficiency in rice. <i>Plant, Cell and Environment</i> , 2020, 43, 2066-2079.	5.7	19
70	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 <sub>2</sub> in Wheat Leaves. <i>Plants</i> , 2020, 9, 319.	3.5	19
71	Comparative analysis of miRNAs and their targets across four plant species. <i>BMC Research Notes</i> , 2011, 4, 483.	1.4	18
72	Substantial reprogramming of the <i>Eutrema salsugineum</i> ( <i>Thellungiella salsuginea</i> ) transcriptome in response to UV and silver nitrate challenge. <i>BMC Plant Biology</i> , 2015, 15, 137.	3.6	18

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73	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.	2.1	17
74	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.	2.6	17
75	Matapax: An Online High-Throughput Genome-Wide Association Study Pipeline. <i>Plant Physiology</i> , 2012, 158, 1534-1541.	4.8	15
76	Determinants of correlated expression of transcription factors and their target genes. <i>Nucleic Acids Research</i> , 2020, 48, 11347-11369.	14.5	15
77	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.	3.2	15
78	Growth under Fluctuating Light Reveals Large Trait Variation in a Panel of Arabidopsis Accessions. <i>Plants</i> , 2020, 9, 316.	3.5	14
79	Similar Yet Different Structural and Functional Diversity among Arabidopsis thaliana LEA_4 Proteins. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2794.	4.1	12
80	Serine 171, a Conserved Residue in the $\beta$ -Aminobutyric Acid Type A (GABAA) Receptor $\beta$ 2 Subunit, Mediates Subunit Interaction and Cell Surface Localization. <i>Journal of Biological Chemistry</i> , 2004, 279, 14179-14183.	3.4	11
81	Single feature polymorphism (SFP)-based selective sweep identification and association mapping of growth-related metabolic traits in Arabidopsis thaliana. <i>BMC Genomics</i> , 2010, 11, 188.	2.8	11
82	A novel seed plants gene regulates oxidative stress tolerance in Arabidopsis thaliana. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 705-718.	5.4	11
83	Spatially Enriched Paralog Rearrangements Argue Functionally Diverse Ribosomes Arise during Cold Acclimation in Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6160.	4.1	10
84	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.	0.9	10
85	Physicochemical characteristics of structurally determined metabolite-protein and drug-protein binding events with respect to binding specificity. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 51.	3.5	9
86	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.	4.1	9
87	Limited Phosphate: Mobile RNAs convey the message. <i>Nature Plants</i> , 2016, 2, 16040.	9.3	8
88	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.	3.6	8
89	Polymorphisms in miRNA binding sites involved in metabolic diseases in mice and humans. <i>Scientific Reports</i> , 2020, 10, 7202.	3.3	8
90	Metabolic Pathway Assignment of Plant Genes based on Phylogenetic Profiling—A Feasibility Study. <i>Frontiers in Plant Science</i> , 2017, 8, 1831.	3.6	7

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91	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.	2.8	7
92	Brownian dynamics simulation of the lateral distribution of charged membrane components. <i>European Biophysics Journal</i> , 1996, 24, 125-35.	2.2	6
93	Modeling RNA loops using sequence homology and geometric constraints. <i>Bioinformatics</i> , 2010, 26, 1671-1672.	4.1	6
94	Conducting Molecular Biomarker Discovery Studies in Plants. <i>Methods in Molecular Biology</i> , 2012, 918, 127-150.	0.9	6
95	Spatial proximity statistics suggest a regulatory role of protein phosphorylation on compound binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 565-579.	2.6	6
96	Effect of Senescence Phenotypes and Nitrate Availability on Wheat Leaf Metabolome during Grain Filling. <i>Agronomy</i> , 2019, 9, 305.	3.0	6
97	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.	14.5	5
98	Biclique extension as an effective approach to identify missing links in metabolic compound–protein interaction networks. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	5
99	A New Relaxation Effect with Polymer Depletion Layers. <i>Langmuir</i> , 1996, 12, 6263-6269.	3.5	4
100	Editorial: Metabolome Informatics and Statistics: Current State and Emerging Trends. <i>Frontiers in Bioengineering and Biotechnology</i> , 2016, 4, 63.	4.1	3
101	The Identification of Cis-Regulatory Sequence Motifs in Gene Promoters Based on SNP Information. <i>Methods in Molecular Biology</i> , 2016, 1482, 31-47.	0.9	3
102	Analysis of <i>Arabidopsis</i> natural variation in biomass accumulation and metabolism. <i>New Biotechnology</i> , 2009, 25, S307.	4.4	2
103	Computational Phosphorylation Network Reconstruction: Methods and Resources. <i>Methods in Molecular Biology</i> , 2015, 1306, 177-194.	0.9	2
104	$\text{COSNet}_i$ : ComplexOme-Structural Network Interpreter used to study spatial enrichment in metazoan ribosomes. <i>BMC Bioinformatics</i> , 2021, 22, 605.	2.6	2
105	The influence of the local sequence environment on RNA loop structures. <i>Rna</i> , 2011, 17, 1247-1257.	3.5	1
106	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.	3.5	1
107	The Combinatorics Of Cis-Regulatory Elements: From Cooperatively Acting Motifs To Gene Regulatory Networks. , 2013, , 176-188.		1
108	ChlamyCyc - a comprehensive database and web-portal centered on <i>Chlamydomonas reinhardtii</i> . <i>Nature Precedings</i> , 2009, , .	0.1	0

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109	Chapter 7. Metabolic Engineering. , 2009, , 195-219.		0
110	Brownian Dynamics Simulation of Charged Membrane Components: Implications for their Lateral Distribution and Voltage Dependence of Ion Transport through Membranes. , 1993, , 71-76.		0
111	PRI: Re-Analysis of a Public Mass Cytometry Dataset Reveals Patterns of Effective Tumor Treatments. Frontiers in Immunology, 2022, 13, 849329.	4.8	0