## Dierk Wanke

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5785592/publications.pdf

Version: 2024-02-01

25 papers 3,158 citations

331670
21
h-index

24 g-index

26 all docs

26 docs citations

26 times ranked

4622 citing authors

#	Article	IF	CITATIONS
1	The AtGenExpress global stress expression data set: protocols, evaluation and model data analysis of UV-B light, drought and cold stress responses. Plant Journal, 2007, 50, 347-363.	5.7	1,322
2	Studies on DNA-binding selectivity of WRKY transcription factors lend structural clues into WRKY-domain function. Plant Molecular Biology, 2008, 68, 81-92.	3.9	395
3	Elucidating the evolutionary conserved DNA-binding specificities of WRKY transcription factors by molecular dynamics and in vitro binding assays. Nucleic Acids Research, 2013, 41, 9764-9778.	14.5	161
4	Transcriptome Analysis of High-Temperature Stress in Developing Barley Caryopses: Early Stress Responses and Effects on Storage Compound Biosynthesis. Molecular Plant, 2011, 4, 97-115.	8.3	141
5	The Arabidopsis GAGA-Binding Factor BASIC PENTACYSTEINE6 Recruits the POLYCOMB-REPRESSIVE COMPLEX1 Component LIKE HETEROCHROMATIN PROTEIN1 to GAGA DNA Motifs. Plant Physiology, 2015, 168, 1013-1024.	4.8	112
6	The GA octodinucleotide repeat binding factor BBR participates in the transcriptional regulation of the homeobox geneBkn3. Plant Journal, 2003, 34, 813-826.	5.7	109
7	DPI-ELISA: a fast and versatile method to specify the binding of plant transcription factors to DNA in vitro. Plant Methods, 2010, 6, 25.	4.3	99
8	Volatiles of two growthâ€inhibiting rhizobacteria commonly engage AtWRKY18 function. Plant Journal, 2012, 70, 445-459.	5.7	93
9	Family business: the multidrug-resistance related protein (MRP) ABC transporter genes in Arabidopsis thaliana. Planta, 2002, 216, 107-119.	3.2	76
10	Plant Core Environmental Stress Response Genes Are Systemically Coordinated during Abiotic Stresses. International Journal of Molecular Sciences, 2013, 14, 7617-7641.	4.1	73
11	The Enzyme-Like Domain of Arabidopsis Nuclear $\hat{l}^2$ -Amylases Is Critical for DNA Sequence Recognition and Transcriptional Activation $\hat{A}$ $\hat{A}$ . Plant Cell, 2014, 26, 1746-1763.	6.6	73
12	Cis-motifs upstream of the transcription and translation initiation sites are effectively revealed by their positional disequilibrium in eukaryote genomes using frequency distribution curves. BMC Bioinformatics, 2006, 7, 522.	2.6	64
13	The SCO2 protein disulphide isomerase is required for thylakoid biogenesis and interacts with LCHB1 chlorophyll a/b binding proteins which affects chlorophyll biosynthesis in Arabidopsis seedlings. Plant Journal, 2012, 69, 743-754.	5.7	64
14	Alanine Zipper-Like Coiled-Coil Domains Are Necessary for Homotypic Dimerization of Plant GAGA-Factors in the Nucleus and Nucleolus. PLoS ONE, 2011, 6, e16070.	2.5	53
15	Role of <i>BASIC PENTACYSTEINE</i> transcription factors in a subset of cytokinin signaling responses. Plant Journal, 2018, 95, 458-473.	5.7	52
16	Significance of Light, Sugar, and Amino Acid Supply for Diurnal Gene Regulation in Developing Barley Caryopses  Â. Plant Physiology, 2010, 153, 14-33.	4.8	45
17	The ABA-mediated switch between submersed and emersed life-styles in aquatic macrophytes. Journal of Plant Research, 2011, 124, 467-475.	2.4	38
18	Phylogenetic Analyses and GAGA-Motif Binding Studies of BBR/BPC Proteins Lend to Clues in GAGA-Motif Recognition and a Regulatory Role in Brassinosteroid Signaling. Frontiers in Plant Science, 2019, 10, 466.	3.6	37

#	Article	IF	CITATION
19	Arabidopsis AZG2 transports cytokinins <i>in vivo</i> and regulates lateral root emergence. New Phytologist, 2021, 229, 979-993.	7.3	36
20	Identification of the sex-determining factor in the liverwort Marchantia polymorpha reveals unique evolution of sex chromosomes in a haploid system. Current Biology, 2021, 31, 5522-5532.e7.	3.9	36
21	Quantitative Analysis of Protein–DNA Interaction by qDPI-ELISA. Methods in Molecular Biology, 2016, 1482, 49-66.	0.9	25
22	Screening for Protein-DNA Interactions by Automatable DNA-Protein Interaction ELISA. PLoS ONE, 2013, 8, e75177.	2.5	20
23	TFpredict and SABINE: Sequence-Based Prediction of Structural and Functional Characteristics of Transcription Factors. PLoS ONE, 2013, 8, e82238.	2.5	17
24	Application of FLIM-FIDSAM for the in vivo analysis of hormone competence of different cell types. Analytical and Bioanalytical Chemistry, 2010, 398, 1919-1925.	3.7	13
25	Inferring transcriptional regulators for sets of co-expressed genes by multi-objective evolutionary optimization. , 2011, , .		0