Aalt-Jan van Dijk

List of Publications by Year
in descending order

79 papers	5,526 citations	101496 36 h-index	85498 71 g-index
90 all docs	90 docs citations	90 times ranked	8364 citing authors

#	Article	IF	Citations
1	Domestication Shapes Recombination Patterns in Tomato. Molecular Biology and Evolution, 2022, 39, .	3.5	14
2	Machine learning in plant science and plant breeding. IScience, 2021, 24, 101890.	1.9	127
3	Integrating structure-based machine learning and co-evolution to investigate specificity in plant sesquiterpene synthases. PLoS Computational Biology, 2021, 17, e1008197.	1.5	11
4	Chasing breeding footprints through structural variations in Cucumis melo and wild relatives. G3: Genes, Genomes, Genetics, 2021, 11, 1-12.	0.8	7
5	Designing Eukaryotic Gene Expression Regulation Using Machine Learning. Trends in Biotechnology, 2020, 38, 191-201.	4.9	30
6	Meiotic recombination profiling of interspecific hybrid F1 tomato pollen by linked read sequencing. Plant Journal, 2020, 102, 480-492.	2.8	14
7	CAPICE: a computational method for Consequence-Agnostic Pathogenicity Interpretation of Clinical Exome variations. Genome Medicine, 2020, 12, 75.	3.6	30
8	The santalene synthase from Cinnamomum camphora: Reconstruction of a sesquiterpene synthase from a monoterpene synthase. Archives of Biochemistry and Biophysics, 2020, 695, 108647.	1.4	10
9	Caretta â€“ A multiple protein structure alignment and feature extraction suite. Computational and Structural Biotechnology Journal, 2020, 18, 981-992.	1.9	19
10	Coevolution-based prediction of proteinâ€“protein interactions in polyketide biosynthetic assembly lines. Bioinformatics, 2020, 36, 4846-4853.	1.8	9
11	Novel routes towards bioplastics from plants: elucidation of the methylperillate biosynthesis pathway from Salvia dorisiana trichomes. Journal of Experimental Botany, 2020, 71, 3052-3065.	2.4	13
12	A THP-1 Cell Line-Based Exploration of Immune Responses Toward Heat-Treated BLG. Frontiers in Nutrition, 2020, 7, 612397.	1.6	8
13	Prior Biological Knowledge Improves Genomic Prediction of Growth-Related Traits in Arabidopsis thaliana. Frontiers in Genetics, 2020, 11, 609117.	1.1	4
14	Geometricus represents protein structures as shape-mers derived from moment invariants. Bioinformatics, 2020, 36, i718-i725.	1.8	24
15	Comprehensive phenotyping reveals interactions and functions of <i>Arabidopsis thaliana</i> TCP genes in yield determination. Plant Journal, 2019, 99, 316-328.	2.8	19
16	Improved inference of intermolecular contacts through proteinâ€“protein interaction prediction using coevolutionary analysis. Bioinformatics, 2019, 35, 2036-2042.	1.8	9
17	An analysis of characterized plant sesquiterpene synthases. Phytochemistry, 2019, 158, 157-165.	1.4	67
18	Tulipa gesneriana and Lilium longiflorum PEBP Genes and Their Putative Roles in Flowering Time Control. Plant and Cell Physiology, 2018, 59, 90-106.	1.5	39

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19	Transcription Factor-Mediated Control of Anthocyanin Biosynthesis in Vegetative Tissues. Plant Physiology, 2018, 176, 1862-1878.	2.3	41
20	<scp>DNA</scp> sequence and shape are predictive for meiotic crossovers throughout the plant kingdom. Plant Journal, 2018, 95, 686-699.	2.8	24
21	Effect of ambient temperature fluctuation on the timing of the transition to the generative stage in cauliflower. Environmental and Experimental Botany, 2018, 155, 742-750.	2.0	9
22	Comparative analysis of binding patterns of MADS-domain proteins in Arabidopsis thaliana. BMC Plant Biology, 2018, 18, 131.	1.6	37
23	Sequence-based analysis of protein degradation rates. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1593-1601.	1.5	14
24	Cross-Family Transcription Factor Interactions: An Additional Layer of Gene Regulation. Trends in Plant Science, 2017, 22, 66-80.	4.3	87
25	Distribution, position and genomic characteristics of crossovers in tomato recombinant inbred lines derived from an interspecific cross between <i>Solanum lycopersicum</i> and <i>Solanum pimpinellifolium</i>. Plant Journal, 2017, 89, 554-564.	2.8	46
26	Divergent regulation of Arabidopsis SAUR genes: a focus on the SAUR10-clade. BMC Plant Biology, 2017, 17, 245.	1.6	60
27	Floral pathway integrator gene expression mediates gradual transmission of environmental and endogenous cues to flowering time. PeerJ, 2017, 5, e3197.	0.9	14
28	Similarities between plant traits based on their connection to underlying gene functions. PLoS ONE, 2017, 12, e0182097.	1.1	0
29	An interactomics overview of the human and bovine milk proteome over lactation. Proteome Science, 2016, 15, 1.	0.7	37
30	Selected proceedings of Machine Learning in Systems Biology: MLSB 2016. BMC Bioinformatics, 2016, 17, 437.	1.2	3
31	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
32	Towards recommendations for metadata and data handling in plant phenotyping. Journal of Experimental Botany, 2015, 66, 5417-5427.	2.4	116
33	The KnownLeaf literature curation system captures knowledge about Arabidopsis leaf growth and development and facilitates integrated data mining. Current Plant Biology, 2015, 2, 1-11.	2.3	7
34	A Quantitative and Dynamic Model of the Arabidopsis Flowering Time Gene Regulatory Network. PLoS ONE, 2015, 10, e0116973.	1.1	40
35	Biological process annotation of proteins across the plant kingdom. Current Plant Biology, 2014, 1, 73-82.	2.3	7
36	Prioritization of candidate genes in QTL regions based on associations between traits and biological processes. BMC Plant Biology, 2014, 14, 330.	1.6	40

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37	Structural determinants of DNA recognition by plant MADS-domain transcription factors. Nucleic Acids Research, 2014, 42, 2138-2146.	6.5	39
38	Rice cytochrome P450 MAX1 homologs catalyze distinct steps in strigolactone biosynthesis. Nature Chemical Biology, 2014, 10, 1028-1033.	3.9	340
39	Valencene synthase from the heartwood of <scp>N</scp>ootka cypress (<i><scp>C</scp>allitropsis) Tj ETQq1 1 0.784314 rgBT /Overl 12, 174-182.	4.1	115
40	The (r)evolution of gene regulatory networks controlling Arabidopsis plant reproduction: a two-decade history. Journal of Experimental Botany, 2014, 65, 4731-4745.	2.4	106
41	Inferring the Gene Network Underlying the Branching of Tomato Inflorescence. PLoS ONE, 2014, 9, e89689.	1.1	4
42	Gene Ontology consistent protein function prediction: the FALCON algorithm applied to six eukaryotic genomes. Algorithms for Molecular Biology, 2013, 8, 10.	0.3	9
43	Mining Minimal Motif Pair Sets Maximally Covering Interactions in a Protein-Protein Interaction Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 73-86.	1.9	2
44	N-glycan occupancy of Arabidopsis N-glycoproteins. Journal of Proteomics, 2013, 93, 343-355.	1.2	68
45	Solvated proteinâ€“protein docking using Kyteâ€Doolittleâ€based water preferences. Proteins: Structure, Function and Bioinformatics, 2013, 81, 510-518.	1.5	26
46	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	9.0	789
47	Analysis of functional redundancies within the Arabidopsis TCP transcription factor family. Journal of Experimental Botany, 2013, 64, 5673-5685.	2.4	124
48	Integrating two patterning processes in the flower. Plant Signaling and Behavior, 2012, 7, 682-684.	1.2	0
49	Arabidopsis Class I and Class II TCP Transcription Factors Regulate Jasmonic Acid Metabolism and Leaf Development Antagonistically Â Â. Plant Physiology, 2012, 159, 1511-1523.	2.3	279
50	Characterization of SOC1â€™s Central Role in Flowering by the Identification of Its Upstream and Downstream Regulators Â Â. Plant Physiology, 2012, 160, 433-449.	2.3	169
51	Explicit Treatment of Water Molecules in Data-Driven Proteinâ€“Protein Docking: The Solvated HADDOCKing Approach. Methods in Molecular Biology, 2012, 819, 355-374.	0.4	20
52	Simulation of Organ Patterning on the Floral Meristem Using a Polar Auxin Transport Model. PLoS ONE, 2012, 7, e28762.	1.1	41
53	Mutational Robustness of Gene Regulatory Networks. PLoS ONE, 2012, 7, e30591.	1.1	11
54	Interactome-Wide Prediction of Protein-Protein Binding Sites Reveals Effects of Protein Sequence Variation in Arabidopsis thaliana. PLoS ONE, 2012, 7, e47022.	1.1	1

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55	Predicting the Impact of Alternative Splicing on Plant MADS Domain Protein Function. PLoS ONE, 2012, 7, e30524.	1.1	80
56	SLIDER: A Generic Metaheuristic for the Discovery of Correlated Motifs in Protein-Protein Interaction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1344-1357.	1.9	8
57	Genome-Wide Computational Function Prediction of Arabidopsis Proteins by Integration of Multiple Data Sources Â Â Â. Plant Physiology, 2011, 155, 271-281.	2.3	29
58	Assessing the contribution of alternative splicing to proteome diversity in Arabidopsis thaliana using proteomics data. BMC Plant Biology, 2011, 11, 82.	1.6	37
59	Correlated mutations via regularized multinomial regression. BMC Bioinformatics, 2011, 12, 444.	1.2	9
60	N-glycoproteomics in plants: Perspectives and challenges. Journal of Proteomics, 2011, 74, 1463-1474.	1.2	50
61	PRI-CAT: a web-tool for the analysis, storage and visualization of plant ChIP-seq experiments. Nucleic Acids Research, 2011, 39, W524-W527.	6.5	14
62	Conserved and variable correlated mutations in the plant MADS protein network. BMC Genomics, 2010, 11, 607.	1.2	2
63	Continuous-time modeling of cell fate determination in Arabidopsis flowers. BMC Systems Biology, 2010, 4, 101.	3.0	18
64	Bayesian Markov Random Field Analysis for Protein Function Prediction Based on Network Data. PLoS ONE, 2010, 5, e9293.	1.1	81
65	Sequence Motifs in MADS Transcription Factors Responsible for Specificity and Diversification of Protein-Protein Interaction. PLoS Computational Biology, 2010, 6, e1001017.	1.5	61
66	SLIDER: Mining Correlated Motifs in Protein-Protein Interaction Networks. , 2009, , .		5
67	Comparative analysis indicates that alternative splicing in plants has a limited role in functional expansion of the proteome. BMC Genomics, 2009, 10, 154.	1.2	50
68	SEPALLATA3: the 'glue' for MADS box transcription factor complex formation. Genome Biology, 2009, 10, R24.	13.9	250
69	Nuclear Magnetic Resonance-Based Modeling and Refinement of Protein Three-Dimensional Structures and Their Complexes. Methods in Molecular Biology, 2008, 443, 229-255.	0.4	2
70	Impaired Peroxisome Proliferator-Activated Receptor Î³ Function through Mutation of a Conserved Salt Bridge (R425C) in Familial Partial Lipodystrophy. Molecular Endocrinology, 2007, 21, 1049-1065.	3.7	42
71	Modeling Proteinâ˜'Protein Complexes Involved in the CytochromecOxidase Copper-Delivery Pathway. Journal of Proteome Research, 2007, 6, 1530-1539.	1.8	27
72	HADDOCK versus HADDOCK: New features and performance of HADDOCK2.0 on the CAPRI targets. Proteins: Structure, Function and Bioinformatics, 2007, 69, 726-733.	1.5	504

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73	Information-driven protein-DNA docking using HADDOCK: it is a matter of flexibility. Nucleic Acids Research, 2006, 34, 3317-3325.	6.5	169
74	Solvated docking: introducing water into the modelling of biomolecular complexes. Bioinformatics, 2006, 22, 2340-2347.	1.8	143
75	WHISCY: What information does surface conservation yield? Application to data-driven docking. Proteins: Structure, Function and Bioinformatics, 2006, 63, 479-489.	1.5	128
76	Combining NMR Relaxation with Chemical Shift Perturbation Data to Drive Proteinâ€“protein Docking. Journal of Biomolecular NMR, 2006, 34, 237-244.	1.6	39
77	Data-driven docking for the study of biomolecular complexes. FEBS Journal, 2005, 272, 293-312.	2.2	125
78	Various strategies of using residual dipolar couplings in NMR-driven protein docking: Application to Lys48-linked di-ubiquitin and validation against 15N-relaxation data. Proteins: Structure, Function and Bioinformatics, 2005, 60, 367-381.	1.5	78
79	Data-driven docking: HADDOCK's adventures in CAPRI. Proteins: Structure, Function and Bioinformatics, 2005, 60, 232-238.	1.5	74