

Klaas Vandepoele

List of Publications by Year in descending order

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Version: 2024-02-01

141
papers

20,243
citations

17440

63
h-index

12272

133
g-index

167
all docs

167
docs citations

167
times ranked

26824
citing authors

#	ARTICLE	IF	CITATIONS
1	ROS signaling: the new wave?. Trends in Plant Science, 2011, 16, 300-309.	8.8	1,911
2	The Phaeodactylum genome reveals the evolutionary history of diatom genomes. Nature, 2008, 456, 239-244.	27.8	1,458
3	JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. Nucleic Acids Research, 2018, 46, D260-D266.	14.5	1,232
4	A High Quality Draft Consensus Sequence of the Genome of a Heterozygous Grapevine Variety. PLoS ONE, 2007, 2, e1326.	2.5	945
5	JASPAR 2022: the 9th release of the open-access database of transcription factor binding profiles. Nucleic Acids Research, 2022, 50, D165-D173.	14.5	902
6	Structural and functional partitioning of bread wheat chromosome 3B. Science, 2014, 345, 1249721.	12.6	542
7	Genome-Wide Analysis of Core Cell Cycle Genes in Arabidopsis. Plant Cell, 2002, 14, 903-916.	6.6	523
8	Major events in the genome evolution of vertebrates: Paraneome age and size differ considerably between ray-finned fishes and land vertebrates. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1638-1643.	7.1	489
9	The hidden duplication past of Arabidopsis thaliana. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13627-13632.	7.1	463
10	PLAZA 4.0: an integrative resource for functional, evolutionary and comparative plant genomics. Nucleic Acids Research, 2018, 46, D1190-D1196.	14.5	460
11	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. Plant Journal, 2018, 93, 515-533.	5.7	406
12	Convergent gene loss following gene and genome duplications creates single-copy families in flowering plants. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2898-2903.	7.1	351
13	The gain and loss of genes during 600 million years of vertebrate evolution. Genome Biology, 2006, 7, R43.	9.6	332
14	PLAZA 3.0: an access point for plant comparative genomics. Nucleic Acids Research, 2015, 43, D974-D981.	14.5	329
15	Type II Metacaspases Atmc4 and Atmc9 of Arabidopsis thaliana Cleave Substrates after Arginine and Lysine. Journal of Biological Chemistry, 2004, 279, 45329-45336.	3.4	304
16	An update on LNCipedia: a database for annotated human lncRNA sequences. Nucleic Acids Research, 2015, 43, D174-D180.	14.5	298
17	The Membrane-Bound NAC Transcription Factor ANAC013 Functions in Mitochondrial Retrograde Regulation of the Oxidative Stress Response in <i>Arabidopsis</i> . Plant Cell, 2013, 25, 3472-3490.	6.6	293
18	The flowering world: a tale of duplications. Trends in Plant Science, 2009, 14, 680-688.	8.8	277

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19	ERF115 Controls Root Quiescent Center Cell Division and Stem Cell Replenishment. <i>Science</i> , 2013, 342, 860-863.	12.6	263
20	PLAZA: A Comparative Genomics Resource to Study Gene and Genome Evolution in Plants. <i>Plant Cell</i> , 2010, 21, 3718-3731.	6.6	243
21	Dissecting Plant Genomes with the PLAZA Comparative Genomics Platform. <i>Plant Physiology</i> , 2012, 158, 590-600.	4.8	238
22	Genome-Wide Identification of Potential Plant E2F Target Genes. <i>Plant Physiology</i> , 2005, 139, 316-328.	4.8	229
23	ANGUSTIFOLIA3 Binds to SWI/SNF Chromatin Remodeling Complexes to Regulate Transcription during <i>Arabidopsis</i> Leaf Development. <i>Plant Cell</i> , 2014, 26, 210-229.	6.6	219
24	Evidence That Rice and Other Cereals Are Ancient Aneuploids. <i>Plant Cell</i> , 2003, 15, 2192-2202.	6.6	212
25	Capturing the phosphorylation and protein interaction landscape of the plant TOR kinase. <i>Nature Plants</i> , 2019, 5, 316-327.	9.3	205
26	Unraveling Transcriptional Control in <i>Arabidopsis</i> Using cis-Regulatory Elements and Coexpression Networks. <i>Plant Physiology</i> , 2009, 150, 535-546.	4.8	197
27	Cold Nights Impair Leaf Growth and Cell Cycle Progression in Maize through Transcriptional Changes of Cell Cycle Genes. <i>Plant Physiology</i> , 2007, 143, 1429-1438.	4.8	193
28	i-ADHoRe 3.0 – fast and sensitive detection of genomic homology in extremely large data sets. <i>Nucleic Acids Research</i> , 2012, 40, e11-e11.	14.5	192
29	Drought Tolerance Conferred to Sugarcane by Association with <i>Gluconacetobacter diazotrophicus</i> : A Transcriptomic View of Hormone Pathways. <i>PLoS ONE</i> , 2014, 9, e114744.	2.5	187
30	An improved toolbox to unravel the plant cellular machinery by tandem affinity purification of <i>Arabidopsis</i> protein complexes. <i>Nature Protocols</i> , 2015, 10, 169-187.	12.0	160
31	Dynamic Changes in ANGUSTIFOLIA3 Complex Composition Reveal a Growth Regulatory Mechanism in the Maize Leaf. <i>Plant Cell</i> , 2015, 27, 1605-1619.	6.6	154
32	Gene duplication and biased functional retention of paralogs in bacterial genomes. <i>Trends in Microbiology</i> , 2004, 12, 148-154.	7.7	150
33	Gene functionalities and genome structure in <i>Bathycoccus prasinos</i> reflect cellular specializations at the base of the green lineage. <i>Genome Biology</i> , 2012, 13, R74.	9.6	143
34	PhyD3: a phylogenetic tree viewer with extended phyloXML support for functional genomics data visualization. <i>Bioinformatics</i> , 2017, 33, 2946-2947.	4.1	142
35	Transcriptome analysis during cell division in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14825-14830.	7.1	140
36	Novel Plant-specific Cyclin-dependent Kinase Inhibitors Induced by Biotic and Abiotic Stresses. <i>Journal of Biological Chemistry</i> , 2007, 282, 25588-25596.	3.4	139

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37	Plastid gene expression and plant development require a plastidic protein of the mitochondrial transcription termination factor family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6674-6679.	7.1	134
38	Insights into the Evolution of Multicellularity from the Sea Lettuce Genome. <i>Current Biology</i> , 2018, 28, 2921-2933.e5.	3.9	134
39	The Automatic Detection of Homologous Regions (ADHoRe) and Its Application to Microcolinearity Between Arabidopsis and Rice. <i>Genome Research</i> , 2002, 12, 1792-1801.	5.5	127
40	Hydrogen Peroxide-Induced Gene Expression across Kingdoms: A Comparative Analysis. <i>Molecular Biology and Evolution</i> , 2008, 25, 507-516.	8.9	122
41	Predicting protein-protein interactions in Arabidopsis thaliana through integration of orthology, gene ontology and co-expression. <i>BMC Genomics</i> , 2009, 10, 288.	2.8	120
42	A Repressor Protein Complex Regulates Leaf Growth in Arabidopsis. <i>Plant Cell</i> , 2015, 27, 2273-2287.	6.6	118
43	How many genes are there in plants (and why are they there)? <i>Current Opinion in Plant Biology</i> , 2007, 10, 199-203.	7.1	115
44	Systematic Identification of Functional Plant Modules through the Integration of Complementary Data Sources. <i>Plant Physiology</i> , 2012, 159, 884-901.	4.8	108
45	TRAPID: an efficient online tool for the functional and comparative analysis of de novo RNA-Seq transcriptomes. <i>Genome Biology</i> , 2013, 14, R134.	9.6	108
46	TF2Network: predicting transcription factor regulators and gene regulatory networks in Arabidopsis using publicly available binding site information. <i>Nucleic Acids Research</i> , 2018, 46, e31-e31.	14.5	107
47	A small CDC25 dual-specificity tyrosine-phosphatase isoform in Arabidopsis thaliana. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13380-13385.	7.1	105
48	A Functional and Evolutionary Perspective on Transcription Factor Binding in Arabidopsis thaliana. <i>Plant Cell</i> , 2014, 26, 3894-3910.	6.6	102
49	Comparative Network Analysis Reveals That Tissue Specificity and Gene Function Are Important Factors Influencing the Mode of Expression Evolution in Arabidopsis and Rice. <i>Plant Physiology</i> , 2011, 156, 1316-1330.	4.8	100
50	Phylogenomic analysis of gene co-expression networks reveals the evolution of functional modules. <i>Plant Journal</i> , 2017, 90, 447-465.	5.7	97
51	PLAZA 5.0: extending the scope and power of comparative and functional genomics in plants. <i>Nucleic Acids Research</i> , 2022, 50, D1468-D1474.	14.5	95
52	Molecular and Physiological Analysis of Growth-Limiting Drought Stress in Brachypodium distachyon Leaves. <i>Molecular Plant</i> , 2013, 6, 311-322.	8.3	94
53	CoExpNetViz: Comparative Co-Expression Networks Construction and Visualization Tool. <i>Frontiers in Plant Science</i> , 2015, 6, 1194.	3.6	93
54	Genome-wide analysis of the diatom cell cycle unveils a novel type of cyclins involved in environmental signaling. <i>Genome Biology</i> , 2010, 11, R17.	9.6	91

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55	Are We There Yet? Reliably Estimating the Completeness of Plant Genome Sequences. <i>Plant Cell</i> , 2016, 28, 1759-1768.	6.6	89
56	KIRA1 and ORESARA1 terminate flower receptivity by promoting cell death in the stigma of <i>Arabidopsis</i> . <i>Nature Plants</i> , 2018, 4, 365-375.	9.3	88
57	picoâ€œscp>PLAZA</scp>, a genome database of microbial photosynthetic eukaryotes. <i>Environmental Microbiology</i> , 2013, 15, 2147-2153.	3.8	87
58	Neoproterozoic origin and multiple transitions to macroscopic growth in green seaweeds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2551-2559.	7.1	85
59	A DNA-binding-site landscape and regulatory network analysis for NAC transcription factors in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2014, 42, 7681-7693.	14.5	84
60	Comparative coâ€œexpression analysis in plant biology. <i>Plant, Cell and Environment</i> , 2012, 35, 1787-1798.	5.7	83
61	Functional characterization of the <i>Arabidopsis</i> transcription factor bZIP29 reveals its role in leaf and root development. <i>Journal of Experimental Botany</i> , 2016, 67, 5825-5840.	4.8	78
62	Small-scale gene duplications played a major role in the recent evolution of wheat chromosome 3B. <i>Genome Biology</i> , 2015, 16, 188.	8.8	76
63	Quantitative RNA expression analysis with Affymetrix Tiling 1.0R arrays identifies new E2F target genes. <i>Plant Journal</i> , 2009, 57, 184-194.	5.7	65
64	A widespread alternative squalene epoxidase participates in eukaryote steroid biosynthesis. <i>Nature Microbiology</i> , 2019, 4, 226-233.	13.3	64
65	The <i>PRA1</i> Gene Family in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2008, 147, 1735-1749.	4.8	63
66	Building Genomic Profiles for Uncovering Segmental Homology in the Twilight Zone. <i>Genome Research</i> , 2004, 14, 1095-1106.	5.5	62
67	The MCM-Binding Protein ETG1 Aids Sister Chromatid Cohesion Required for Postreplicative Homologous Recombination Repair. <i>PLoS Genetics</i> , 2010, 6, e1000817.	3.5	58
68	Metagenomes of the Picoalga <i>Bathycoccus</i> from the Chile Coastal Upwelling. <i>PLoS ONE</i> , 2012, 7, e39648.	2.5	58
69	Inference of Transcriptional Networks in <i>Arabidopsis</i> through Conserved Noncoding Sequence Analysis. <i>Plant Cell</i> , 2014, 26, 2729-2745.	6.6	57
70	Identification of novel regulatory modules in dicotyledonous plants using expression data and comparative genomics. <i>Genome Biology</i> , 2006, 7, R103.	9.6	55
71	The <i>Seminavis robusta</i> genome provides insights into the evolutionary adaptations of benthic diatoms. <i>Nature Communications</i> , 2020, 11, 3320.	12.8	55
72	The transcriptional repressor complex FRS7-FRS12 regulates flowering time and growth in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2017, 8, 15235.	12.8	54

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73	Whole-genome analysis reveals molecular innovations and evolutionary transitions in chromalveolate species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3427-3432.	7.1	53
74	Investigating ancient duplication events in the Arabidopsis genome. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 117-129.	1.2	52
75	Detecting the undetectable: uncovering duplicated segments in Arabidopsis by comparison with rice. <i>Trends in Genetics</i> , 2002, 18, 606-608.	6.7	50
76	Selection for Improved Energy Use Efficiency and Drought Tolerance in Canola Results in Distinct Transcriptome and Epigenome Changes. <i>Plant Physiology</i> , 2015, 168, 1338-1350.	4.8	49
77	The Transcription Factor MYB29 Is a Regulator of <i>ALTERNATIVE OXIDASE1a</i> . <i>Plant Physiology</i> , 2017, 173, 1824-1843.	4.8	46
78	The Plastid Genome in Cladophorales Green Algae Is Encoded by Hairpin Chromosomes. <i>Current Biology</i> , 2017, 27, 3771-3782.e6.	3.9	45
79	Ancient duplication of cereal genomes. <i>New Phytologist</i> , 2005, 165, 658-661.	7.3	43
80	A Generic Tool for Transcription Factor Target Gene Discovery in Arabidopsis Cell Suspension Cultures Based on Tandem Chromatin Affinity Purification. <i>Plant Physiology</i> , 2014, 164, 1122-1133.	4.8	43
81	Identification and evolution of gene regulatory networks: insights from comparative studies in plants. <i>Current Opinion in Plant Biology</i> , 2020, 54, 42-48.	7.1	43
82	Integrative inference of transcriptional networks in Arabidopsis yields novel ROS signalling regulators. <i>Nature Plants</i> , 2021, 7, 500-513.	9.3	43
83	Exploring the Plant Transcriptome through Phylogenetic Profiling. <i>Plant Physiology</i> , 2005, 137, 31-42.	4.8	41
84	A Collection of Conserved Noncoding Sequences to Study Gene Regulation in Flowering Plants. <i>Plant Physiology</i> , 2016, 171, 2586-2598.	4.8	39
85	Multi-omics network-based functional annotation of unknown Arabidopsis genes. <i>Plant Journal</i> , 2021, 108, 1193-1212.	5.7	39
86	Identification of cis-regulatory elements specific for different types of reactive oxygen species in Arabidopsis thaliana. <i>Gene</i> , 2012, 499, 52-60.	2.2	36
87	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	4.1	36
88	Genome Analyses of the Microalga Picochlorum Provide Insights into the Evolution of Thermotolerance in the Green Lineage. <i>Genome Biology and Evolution</i> , 2018, 10, 2347-2365.	2.5	36
89	Understanding genetic control of root system architecture in soybean: Insights into the genetic basis of lateral root number. <i>Plant, Cell and Environment</i> , 2019, 42, 212-229.	5.7	36
90	<i>SHUGOSHIN</i> s and <i>PATRONUS</i> protect meiotic centromere cohesion in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2014, 77, 782-794.	5.7	34

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91	Investigating ancient duplication events in the Arabidopsis genome. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 117-29.	1.2	32
92	Evolutionary relationships and expression analysis of EUL domain proteins in rice (<i>Oryza sativa</i>). <i>Rice</i> , 2017, 10, 26.	4.0	31
93	Genome-wide characterization of differential transcript usage in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2017, 92, 1218-1231.	5.7	31
94	Tetraspanin genes in plants. <i>Plant Science</i> , 2012, 190, 9-15.	3.6	30
95	Virus-host coexistence in phytoplankton through the genomic lens. <i>Science Advances</i> , 2020, 6, eaay2587.	10.3	30
96	Functional Analysis of Arabidopsis TETRASPANIN Gene Family in Plant Growth and Development. <i>Plant Physiology</i> , 2015, 169, pp.01310.2015.	4.8	29
97	Mitotic recombination between homologous chromosomes drives genomic diversity in diatoms. <i>Current Biology</i> , 2021, 31, 3221-3232.e9.	3.9	29
98	Inference of plant gene regulatory networks using data-driven methods: A practical overview. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194447.	1.9	28
99	Comprehensive and Functional Analysis of Horizontal Gene Transfer Events in Diatoms. <i>Molecular Biology and Evolution</i> , 2020, 37, 3243-3257.	8.9	28
100	Ensemble gene function prediction database reveals genes important for complex I formation in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2018, 217, 1521-1534.	7.3	27
101	Investigating ancient duplication events in the Arabidopsis genome. , 2003, , 117-129.		27
102	Curse: building expression atlases and co-expression networks from public RNA-Seq data. <i>Bioinformatics</i> , 2019, 35, 2880-2881.	4.1	25
103	A greedy, graph-based algorithm for the alignment of multiple homologous gene lists. <i>Bioinformatics</i> , 2011, 27, 749-756.	4.1	24
104	Enhanced Maps of Transcription Factor Binding Sites Improve Regulatory Networks Learned from Accessible Chromatin Data. <i>Plant Physiology</i> , 2019, 181, 412-425.	4.8	24
105	Comparative transcriptomics enables the identification of functional orthologous genes involved in early leaf growth. <i>Plant Biotechnology Journal</i> , 2020, 18, 553-567.	8.3	24
106	On the origin and evolution of vertebrate and viral profilins. <i>FEBS Letters</i> , 2007, 581, 211-217.	2.8	23
107	Recent developments in computational approaches for uncovering genomic homology. <i>BioEssays</i> , 2004, 26, 1225-1235.	2.5	22
108	Associated Bacteria Affect Sexual Reproduction by Altering Gene Expression and Metabolic Processes in a Biofilm Inhabiting Diatom. <i>Frontiers in Microbiology</i> , 2019, 10, 1790.	3.5	21

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109	Evolution of vascular plants through redeployment of ancient developmental regulators. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 733-740.	7.1	21
110	Distinctive Growth and Transcriptional Changes of the Diatom <i>Seminavis robusta</i> in Response to Quorum Sensing Related Compounds. Frontiers in Microbiology, 2020, 11, 1240.	3.5	21
111	TRAPID 2.0: a web application for taxonomic and functional analysis of <i>de novo</i> transcriptomes. Nucleic Acids Research, 2021, 49, e101-e101.	14.5	21
112	Canonical correlations reveal adaptive loci and phenotypic responses to climate in perennial ryegrass. Molecular Ecology Resources, 2021, 21, 849-870.	4.8	20
113	Evolutionary trails of plant steroid genes. Trends in Plant Science, 2015, 20, 301-308.	8.8	19
114	GS ^{yellow} , a Multifaceted Tag for Functional Protein Analysis in Monocot and Dicot Plants. Plant Physiology, 2018, 177, 447-464.	4.8	19
115	Comparative genomics reveals new functional insights in uncultured MAST species. ISME Journal, 2021, 15, 1767-1781.	9.8	18
116	Neofunctionalization of Mitochondrial Proteins and Incorporation into Signaling Networks in Plants. Molecular Biology and Evolution, 2019, 36, 974-989.	8.9	17
117	Mating type specific transcriptomic response to sex inducing pheromone in the pennate diatom <i>Seminavis robusta</i> . ISME Journal, 2021, 15, 562-576.	9.8	17
118	Chromosome-scale assembly and annotation of the perennial ryegrass genome. BMC Genomics, 2022, 23, .	2.8	17
119	Gene space completeness in complex plant genomes. Current Opinion in Plant Biology, 2019, 48, 9-17.	7.1	16
120	Diurnal transcript profiling of the diatom <i>Seminavis robusta</i> reveals adaptations to a benthic lifestyle. Plant Journal, 2021, 107, 315-336.	5.7	15
121	The Mouse Thymosin Beta15 Gene Family Displays Unique Complexity and Encodes A Functional Thymosin Repeat. Journal of Molecular Biology, 2009, 387, 809-825.	4.2	14
122	BLSSpeller: exhaustive comparative discovery of conserved <i>cis</i> -regulatory elements. Bioinformatics, 2015, 31, 3758-3766.	4.1	14
123	Overcoming challenges in variant calling: exploring sequence diversity in candidate genes for plant development in perennial ryegrass (<i>Lolium perenne</i>). DNA Research, 2019, 26, 1-12.	3.4	14
124	Chromatin accessibility landscapes activated by cell-surface and intracellular immune receptors. Journal of Experimental Botany, 2021, 72, 7927-7941.	4.8	14
125	Gene expression during bacterivorous growth of a widespread marine heterotrophic flagellate. ISME Journal, 2021, 15, 154-167.	9.8	13
126	Light Regulation of LHCX Genes in the Benthic Diatom <i>Seminavis robusta</i> . Frontiers in Marine Science, 2020, 7, .	2.5	12

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127	A Guide to the PLAZA 3.0 Plant Comparative Genomic Database. <i>Methods in Molecular Biology</i> , 2017, 1533, 183-200.	0.9	11
128	Unravelling cis-Regulatory Elements in the Genome of the Smallest Photosynthetic Eukaryote: Phylogenetic Footprinting in <i>Ostreococcus</i> . <i>Journal of Molecular Evolution</i> , 2009, 69, 249-259.	1.8	10
129	Identification of putative cancer genes through data integration and comparative genomics between plants and humans. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 2041-2055.	5.4	10
130	A new evolutionary model for the vertebrate actin family including two novel groups. <i>Molecular Phylogenetics and Evolution</i> , 2019, 141, 106632.	2.7	10
131	Subfunctionalization of Paralog Transcription Factors Contributes to Regulation of Alkaloid Pathway Branch Choice in <i>Catharanthus roseus</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 687406.	3.6	10
132	The Quest for Genomic Homology. <i>Current Genomics</i> , 2004, 5, 299-308.	1.6	10
133	Evolutionary Genomics of Sex-Related Chromosomes at the Base of the Green Lineage. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	5
134	A network-based comparative framework to study conservation and divergence of proteomes in plant phylogenies. <i>Nucleic Acids Research</i> , 2021, 49, e3-e3.	14.5	5
135	Light intensity and spectral composition drive reproductive success in the marine benthic diatom <i>Seminavis robusta</i> . <i>Scientific Reports</i> , 2021, 11, 17560.	3.3	4
136	Spatiotemporal expression profile of novel and known small RNAs throughout rice plant development focussing on seed tissues. <i>BMC Genomics</i> , 2022, 23, 44.	2.8	4
137	MAGIC: access portal to a cross-platform gene expression compendium for maize. <i>Bioinformatics</i> , 2014, 30, 1316-1318.	4.1	2
138	The mutation <i>nrpb1A325V</i> in the largest subunit of <i>RNA</i> polymerase <i>II</i> suppresses compromised growth of <i>Arabidopsis</i> plants deficient in a function of the general transcription factor <i>IIF</i> . <i>Plant Journal</i> , 2017, 89, 730-745.	5.7	2
139	Comment on "Hayai-Annotation Plants: an ultrafast and comprehensive functional gene annotation system in plants": the importance of taking the GO graph structure into account. <i>Bioinformatics</i> , 2021, 36, 5558-5560.	4.1	2
140	The medium-size noncoding RNA transcriptome of <i>Ostreococcus tauri</i> , the smallest living eukaryote, reveals a large family of small nucleolar RNAs displaying multiple genomic expression strategies. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa080.	3.2	1
141	A Parallel, Distributed-Memory Framework for Comparative Motif Discovery. <i>Lecture Notes in Computer Science</i> , 2014, , 268-277.	1.3	1