

Klaas Vandepoele

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

149
papers

14,230
citations

58
h-index

118
g-index

167
ext. papers

17,872
ext. citations

10
avg, IF

6.23
L-index

#	Paper	IF	Citations
149	ROS signaling: the new wave?. <i>Trends in Plant Science</i> , 2011 , 16, 300-9	13.1	1529
148	The Phaeodactylum genome reveals the evolutionary history of diatom genomes. <i>Nature</i> , 2008 , 456, 239-44	50.4	1200
147	A high quality draft consensus sequence of the genome of a heterozygous grapevine variety. <i>PLoS ONE</i> , 2007 , 2, e1326	3.7	779
146	JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. <i>Nucleic Acids Research</i> , 2018 , 46, D260-D266	20.1	761
145	Genome-wide analysis of core cell cycle genes in Arabidopsis. <i>Plant Cell</i> , 2002 , 14, 903-16	11.6	450
144	Major events in the genome evolution of vertebrates: paranome age and size differ considerably between ray-finned fishes and land vertebrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 1638-43	11.5	444
143	The hidden duplication past of Arabidopsis thaliana. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 13627-32	11.5	422
142	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014 , 345, 1249721	33.3	397
141	The gain and loss of genes during 600 million years of vertebrate evolution. <i>Genome Biology</i> , 2006 , 7, R43	18.3	270
140	Type II metacaspases Atmc4 and Atmc9 of Arabidopsis thaliana cleave substrates after arginine and lysine. <i>Journal of Biological Chemistry</i> , 2004 , 279, 45329-36	5.4	252
139	PLAZA 3.0: an access point for plant comparative genomics. <i>Nucleic Acids Research</i> , 2015 , 43, D974-81	20.1	248
138	PLAZA 4.0: an integrative resource for functional, evolutionary and comparative plant genomics. <i>Nucleic Acids Research</i> , 2018 , 46, D1190-D1196	20.1	247
137	The flowering world: a tale of duplications. <i>Trends in Plant Science</i> , 2009 , 14, 680-8	13.1	232
136	Convergent gene loss following gene and genome duplications creates single-copy families in flowering plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 2898-903	11.5	231
135	PLAZA: a comparative genomics resource to study gene and genome evolution in plants. <i>Plant Cell</i> , 2009 , 21, 3718-31	11.6	220
134	The membrane-bound NAC transcription factor ANAC013 functions in mitochondrial retrograde regulation of the oxidative stress response in Arabidopsis. <i>Plant Cell</i> , 2013 , 25, 3472-90	11.6	214
133	An update on LNCipedia: a database for annotated human lncRNA sequences. <i>Nucleic Acids Research</i> , 2015 , 43, D174-80	20.1	212

132	Dissecting plant genomes with the PLAZA comparative genomics platform. <i>Plant Physiology</i> , 2012 , 158, 590-600	6.6	212
131	ERF115 controls root quiescent center cell division and stem cell replenishment. <i>Science</i> , 2013 , 342, 860-3	3.3	193
130	Genome-wide identification of potential plant E2F target genes. <i>Plant Physiology</i> , 2005 , 139, 316-28	6.6	187
129	Evidence that rice and other cereals are ancient aneuploids. <i>Plant Cell</i> , 2003 , 15, 2192-202	11.6	184
128	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018 , 93, 515-533	6.9	176
127	Unraveling transcriptional control in <i>Arabidopsis</i> using cis-regulatory elements and coexpression networks. <i>Plant Physiology</i> , 2009 , 150, 535-46	6.6	173
126	Cold nights impair leaf growth and cell cycle progression in maize through transcriptional changes of cell cycle genes. <i>Plant Physiology</i> , 2007 , 143, 1429-38	6.6	143
125	ANGUSTIFOLIA3 binds to SWI/SNF chromatin remodeling complexes to regulate transcription during <i>Arabidopsis</i> leaf development. <i>Plant Cell</i> , 2014 , 26, 210-29	11.6	138
124	Gene duplication and biased functional retention of paralogs in bacterial genomes. <i>Trends in Microbiology</i> , 2004 , 12, 148-54	12.4	136
123	i-ADHoRe 3.0—fast and sensitive detection of genomic homology in extremely large data sets. <i>Nucleic Acids Research</i> , 2012 , 40, e11	20.1	131
122	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	3.7	120
121	Transcriptome analysis during cell division in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 14825-30	11.5	120
120	Novel plant-specific cyclin-dependent kinase inhibitors induced by biotic and abiotic stresses. <i>Journal of Biological Chemistry</i> , 2007 , 282, 25588-96	5.4	113
119	Hydrogen peroxide-induced gene expression across kingdoms: a comparative analysis. <i>Molecular Biology and Evolution</i> , 2008 , 25, 507-16	8.3	112
118	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, 6674-9	11.5	110
117	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	18.3	107
116	The automatic detection of homologous regions (ADHoRe) and its application to microcolinearity between <i>Arabidopsis</i> and rice. <i>Genome Research</i> , 2002 , 12, 1792-801	9.7	105
115	A small CDC25 dual-specificity tyrosine-phosphatase isoform in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 13380-5	11.5	103

114	Capturing the phosphorylation and protein interaction landscape of the plant TOR kinase. <i>Nature Plants</i> , 2019 , 5, 316-327	11.5	100
113	Systematic identification of functional plant modules through the integration of complementary data sources. <i>Plant Physiology</i> , 2012 , 159, 884-901	6.6	100
112	How many genes are there in plants (... and why are they there)?. <i>Current Opinion in Plant Biology</i> , 2007 , 10, 199-203	9.9	98
111	An improved toolbox to unravel the plant cellular machinery by tandem affinity purification of Arabidopsis protein complexes. <i>Nature Protocols</i> , 2015 , 10, 169-87	18.8	90
110	TRAPID: an efficient online tool for the functional and comparative analysis of de novo RNA-Seq transcriptomes. <i>Genome Biology</i> , 2013 , 14, R134	18.3	89
109	Dynamic Changes in ANGUSTIFOLIA3 Complex Composition Reveal a Growth Regulatory Mechanism in the Maize Leaf. <i>Plant Cell</i> , 2015 , 27, 1605-19	11.6	86
108	Predicting protein-protein interactions in Arabidopsis thaliana through integration of orthology, gene ontology and co-expression. <i>BMC Genomics</i> , 2009 , 10, 288	4.5	84
107	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, 1316-30	6.6	79
106	Molecular and physiological analysis of growth-limiting drought stress in Brachypodium distachyon leaves. <i>Molecular Plant</i> , 2013 , 6, 311-22	14.4	76
105	Insights into the Evolution of Multicellularity from the Sea Lettuce Genome. <i>Current Biology</i> , 2018 , 28, 2921-2933.e5	6.3	75
104	PhyD3: a phylogenetic tree viewer with extended phyloXML support for functional genomics data visualization. <i>Bioinformatics</i> , 2017 , 33, 2946-2947	7.2	74
103	A functional and evolutionary perspective on transcription factor binding in Arabidopsis thaliana. <i>Plant Cell</i> , 2014 , 26, 3894-910	11.6	73
102	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	18.3	72
101	A Repressor Protein Complex Regulates Leaf Growth in Arabidopsis. <i>Plant Cell</i> , 2015 , 27, 2273-87	11.6	71
100	Comparative co-expression analysis in plant biology. <i>Plant, Cell and Environment</i> , 2012 , 35, 1787-98	8.4	66
99	CoExpNetViz: Comparative Co-Expression Networks Construction and Visualization Tool. <i>Frontiers in Plant Science</i> , 2015 , 6, 1194	6.2	63
98	Phylogenomic analysis of gene co-expression networks reveals the evolution of functional modules. <i>Plant Journal</i> , 2017 , 90, 447-465	6.9	61
97	A DNA-binding-site landscape and regulatory network analysis for NAC transcription factors in Arabidopsis thaliana. <i>Nucleic Acids Research</i> , 2014 , 42, 7681-93	20.1	61

96	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	20.1	59
95	Are We There Yet? Reliably Estimating the Completeness of Plant Genome Sequences. <i>Plant Cell</i> , 2016 , 28, 1759-68	11.6	59
94	pico-PLAZA, a genome database of microbial photosynthetic eukaryotes. <i>Environmental Microbiology</i> , 2013 , 15, 2147-53	5.2	58
93	JASPAR 2022: the 9th release of the open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2021 ,	20.1	58
92	Quantitative RNA expression analysis with Affymetrix Tiling 1.0R arrays identifies new E2F target genes. <i>Plant Journal</i> , 2009 , 57, 184-94	6.9	56
91	Small-scale gene duplications played a major role in the recent evolution of wheat chromosome 3B. <i>Genome Biology</i> , 2015 , 16, 188	18.3	53
90	Metagenomes of the picoalga Bathycoccus from the Chile coastal upwelling. <i>PLoS ONE</i> , 2012 , 7, e39648	3.7	51
89	Building genomic profiles for uncovering segmental homology in the twilight zone. <i>Genome Research</i> , 2004 , 14, 1095-106	9.7	51
88	Identification of novel regulatory modules in dicotyledonous plants using expression data and comparative genomics. <i>Genome Biology</i> , 2006 , 7, R103	18.3	50
87	The MCM-binding protein ETG1 aids sister chromatid cohesion required for postreplicative homologous recombination repair. <i>PLoS Genetics</i> , 2010 , 6, e1000817	6	49
86	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, 3427-32	11.5	49
85	Investigating ancient duplication events in the Arabidopsis genome. <i>Journal of Structural and Functional Genomics</i> , 2003 , 3, 117-129		49
84	Detecting the undetectable: uncovering duplicated segments in Arabidopsis by comparison with rice. <i>Trends in Genetics</i> , 2002 , 18, 606-8	8.5	48
83	Inference of transcriptional networks in Arabidopsis through conserved noncoding sequence analysis. <i>Plant Cell</i> , 2014 , 26, 2729-45	11.6	45
82	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	11.5	44
81	Ancient duplication of cereal genomes. <i>New Phytologist</i> , 2005 , 165, 658-61	9.8	40
80	Exploring the plant transcriptome through phylogenetic profiling. <i>Plant Physiology</i> , 2005 , 137, 31-42	6.6	39
79	A widespread alternative squalene epoxidase participates in eukaryote steroid biosynthesis. <i>Nature Microbiology</i> , 2019 , 4, 226-233	26.6	38

78	The Transcription Factor MYB29 Is a Regulator of. <i>Plant Physiology</i> , 2017 , 173, 1824-1843	6.6	36
77	The Plastid Genome in Cladophorales Green Algae Is Encoded by Hairpin Chromosomes. <i>Current Biology</i> , 2017 , 27, 3771-3782.e6	6.3	36
76	The PRA1 gene family in Arabidopsis. <i>Plant Physiology</i> , 2008 , 147, 1735-49	6.6	36
75	Functional characterization of the Arabidopsis transcription factor bZIP29 reveals its role in leaf and root development. <i>Journal of Experimental Botany</i> , 2016 , 67, 5825-5840	7	36
74	KIRA1 and ORESARA1 terminate flower receptivity by promoting cell death in the stigma of Arabidopsis. <i>Nature Plants</i> , 2018 , 4, 365-375	11.5	33
73	Investigating ancient duplication events in the Arabidopsis genome. <i>Journal of Structural and Functional Genomics</i> , 2003 , 3, 117-29		32
72	Selection for Improved Energy Use Efficiency and Drought Tolerance in Canola Results in Distinct Transcriptome and Epigenome Changes. <i>Plant Physiology</i> , 2015 , 168, 1338-50	6.6	30
71	Identification of cis-regulatory elements specific for different types of reactive oxygen species in Arabidopsis thaliana. <i>Gene</i> , 2012 , 499, 52-60	3.8	30
70	A Collection of Conserved Noncoding Sequences to Study Gene Regulation in Flowering Plants. <i>Plant Physiology</i> , 2016 , 171, 2586-98	6.6	28
69	SHUGOSHINS and PATRONUS protect meiotic centromere cohesion in Arabidopsis thaliana. <i>Plant Journal</i> , 2014 , 77, 782-94	6.9	26
68	The transcriptional repressor complex FRS7-FRS12 regulates flowering time and growth in Arabidopsis. <i>Nature Communications</i> , 2017 , 8, 15235	17.4	25
67	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018 , 34, 323-329		25
66	Tetraspanin genes in plants. <i>Plant Science</i> , 2012 , 190, 9-15	5.3	24
65	The <i>Seminavis robusta</i> genome provides insights into the evolutionary adaptations of benthic diatoms. <i>Nature Communications</i> , 2020 , 11, 3320	17.4	23
64	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, 1122-33	6.6	23
63	On the origin and evolution of vertebrate and viral profilins. <i>FEBS Letters</i> , 2007 , 581, 211-7	3.8	23
62	Recent developments in computational approaches for uncovering genomic homology. <i>BioEssays</i> , 2004 , 26, 1225-35	4.1	21
61	Functional Analysis of the Arabidopsis TETRASPANIN Gene Family in Plant Growth and Development. <i>Plant Physiology</i> , 2015 , 169, 2200-14	6.6	20

60	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	3.9	20
59	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	8.4	19
58	Genome-wide characterization of differential transcript usage in Arabidopsis thaliana. <i>Plant Journal</i> , 2017 , 92, 1218-1231	6.9	16
57	A greedy, graph-based algorithm for the alignment of multiple homologous gene lists. <i>Bioinformatics</i> , 2011 , 27, 749-56	7.2	16
56	Evolutionary trails of plant steroid genes. <i>Trends in Plant Science</i> , 2015 , 20, 301-308	13.1	15
55	Identification and evolution of gene regulatory networks: insights from comparative studies in plants. <i>Current Opinion in Plant Biology</i> , 2020 , 54, 42-48	9.9	14
54	Ensemble gene function prediction database reveals genes important for complex I formation in Arabidopsis thaliana. <i>New Phytologist</i> , 2018 , 217, 1521-1534	9.8	14
53	Evolutionary relationships and expression analysis of EUL domain proteins in rice (<i>Oryza sativa</i>). <i>Rice</i> , 2017 , 10, 26	5.8	13
52	Comprehensive and Functional Analysis of Horizontal Gene Transfer Events in Diatoms. <i>Molecular Biology and Evolution</i> , 2020 , 37, 3243-3257	8.3	13
51	Distinctive Growth and Transcriptional Changes of the Diatom in Response to Quorum Sensing Related Compounds. <i>Frontiers in Microbiology</i> , 2020 , 11, 1240	5.7	12
50	Virus-host coexistence in phytoplankton through the genomic lens. <i>Science Advances</i> , 2020 , 6, eaay2587	14.3	12
49	The mouse thymosin beta15 gene family displays unique complexity and encodes a functional thymosin repeat. <i>Journal of Molecular Biology</i> , 2009 , 387, 809-25	6.5	12
48	Integrative inference of transcriptional networks in Arabidopsis yields novel ROS signalling regulators. <i>Nature Plants</i> , 2021 , 7, 500-513	11.5	12
47	Gene space completeness in complex plant genomes. <i>Current Opinion in Plant Biology</i> , 2019 , 48, 9-17	9.9	11
46	Curse: building expression atlases and co-expression networks from public RNA-Seq data. <i>Bioinformatics</i> , 2019 , 35, 2880-2881	7.2	11
45	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	5.7	10
44	Neofunctionalization of Mitochondrial Proteins and Incorporation into Signaling Networks in Plants. <i>Molecular Biology and Evolution</i> , 2019 , 36, 974-989	8.3	10
43	GS, a Multifaceted Tag for Functional Protein Analysis in Monocot and Dicot Plants. <i>Plant Physiology</i> , 2018 , 177, 447-464	6.6	10

42	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, 249-59	3.1	10
41	The Quest for Genomic Homology. <i>Current Genomics</i> , 2004 , 5, 299-308	2.6	10
40	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	6	10
39	Enhanced Maps of Transcription Factor Binding Sites Improve Regulatory Networks Learned from Accessible Chromatin Data. <i>Plant Physiology</i> , 2019 , 181, 412-425	6.6	10
38	BLSSpeller: exhaustive comparative discovery of conserved cis-regulatory elements. <i>Bioinformatics</i> , 2015 , 31, 3758-66	7.2	9
37	Comparative transcriptomics enables the identification of functional orthologous genes involved in early leaf growth. <i>Plant Biotechnology Journal</i> , 2020 , 18, 553-567	11.6	9
36	Canonical correlations reveal adaptive loci and phenotypic responses to climate in perennial ryegrass. <i>Molecular Ecology Resources</i> , 2021 , 21, 849-870	8.4	9
35	Mating type specific transcriptomic response to sex inducing pheromone in the pennate diatom <i>Seminavis robusta</i> . <i>ISME Journal</i> , 2021 , 15, 562-576	11.9	9
34	Evolution of vascular plants through redeployment of ancient developmental regulators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 733-740	11.5	8
33	Light Regulation of LHCX Genes in the Benthic Diatom <i>Seminavis robusta</i> . <i>Frontiers in Marine Science</i> , 2020 , 7,	4.5	7
32	A new evolutionary model for the vertebrate actin family including two novel groups. <i>Molecular Phylogenetics and Evolution</i> , 2019 , 141, 106632	4.1	7
31	A Guide to the PLAZA 3.0 Plant Comparative Genomic Database. <i>Methods in Molecular Biology</i> , 2017 , 1533, 183-200	1.4	7
30	Mitotic recombination between homologous chromosomes drives genomic diversity in diatoms. <i>Current Biology</i> , 2021 , 31, 3221-3232.e9	6.3	7
29	Identification of putative cancer genes through data integration and comparative genomics between plants and humans. <i>Cellular and Molecular Life Sciences</i> , 2012 , 69, 2041-55	10.3	6
28	Gene expression during bacterivorous growth of a widespread marine heterotrophic flagellate. <i>ISME Journal</i> , 2021 , 15, 154-167	11.9	6
27	PLAZA 5.0: extending the scope and power of comparative and functional genomics in plants. <i>Nucleic Acids Research</i> , 2021 ,	20.1	5
26	Investigating ancient duplication events in the Arabidopsis genome 2003 , 117-129		5
25	Systematic and functional analysis of horizontal gene transfer events in diatoms		5

24	Overcoming challenges in variant calling: exploring sequence diversity in candidate genes for plant development in perennial ryegrass (<i>Lolium perenne</i>). <i>DNA Research</i> , 2019 , 26, 1-12	4.5	5
23	Comparative genomics reveals new functional insights in uncultured MAST species. <i>ISME Journal</i> , 2021 , 15, 1767-1781	11.9	5
22	Chromatin accessibility landscapes activated by cell surface and intracellular immune receptors		4
21	Diurnal transcript profiling of the diatom <i>Seminavis robusta</i> reveals adaptations to a benthic lifestyle. <i>Plant Journal</i> , 2021 , 107, 315-336	6.9	4
20	TRAPID 2.0: a web application for taxonomic and functional analysis of de novo transcriptomes. <i>Nucleic Acids Research</i> , 2021 , 49, e101	20.1	4
19	Chromatin accessibility landscapes activated by cell-surface and intracellular immune receptors. <i>Journal of Experimental Botany</i> , 2021 , 72, 7927-7941	7	4
18	Multi-omics network-based functional annotation of unknown <i>Arabidopsis</i> genes. <i>Plant Journal</i> , 2021 , 108, 1193-1212	6.9	4
17	TF2Network: predicting transcription factor regulators and gene regulatory networks in <i>Arabidopsis</i> using publicly available binding site information		3
16	MAGIC: access portal to a cross-platform gene expression compendium for maize. <i>Bioinformatics</i> , 2014 , 30, 1316-8	7.2	2
15	TRAPID 2.0: a web application for taxonomic and functional analysis of de novo transcriptomes		2
14	Comment on Hayai-Annotation plants: an ultra-fast and comprehensive functional gene annotation system in plants The importance of taking the GO graph structure into account. <i>Bioinformatics</i> , 2020 ,	7.2	2
13	A network-based comparative framework to study conservation and divergence of proteomes in plant phylogenies. <i>Nucleic Acids Research</i> , 2021 , 49, e3	20.1	2
12	Subfunctionalization of Paralog Transcription Factors Contributes to Regulation of Alkaloid Pathway Branch Choice in. <i>Frontiers in Plant Science</i> , 2021 , 12, 687406	6.2	2
11	The mutation nrpb1-A325V in the largest subunit of RNA polymerase II suppresses compromised growth of <i>Arabidopsis</i> plants deficient in a function of the general transcription factor IIF. <i>Plant Journal</i> , 2017 , 89, 730-745	6.9	1
10	The <i>Seminavis robusta</i> genome provides insights into the evolutionary adaptations of benthic diatoms		1
9	A Parallel, Distributed-Memory Framework for Comparative Motif Discovery. <i>Lecture Notes in Computer Science</i> , 2014 , 268-277	0.9	1
8	Mating type specific transcriptomic response to sex inducing pheromone in the pennate diatom <i>Seminavis robusta</i>		1
7	Neoproterozoic origin and multiple transitions to macroscopic growth in green seaweeds		1

6	Genome-wide characterization of differential transcript usage in <i>Arabidopsis thaliana</i>		1
5	The plastid genome in Cladophorales green algae is encoded by hairpin plasmids		1
4	Evolutionary Genomics of Sex-Related Chromosomes at the Base of the Green Lineage. <i>Genome Biology and Evolution</i> , 2021 , 13,	3.9	1
3	Light intensity and spectral composition drive reproductive success in the marine benthic diatom <i>Seminavis robusta</i> . <i>Scientific Reports</i> , 2021 , 11, 17560	4.9	1
2	Spatiotemporal expression profile of novel and known small RNAs throughout rice plant development focussing on seed tissues.. <i>BMC Genomics</i> , 2022 , 23, 44	4.5	0
1	The medium-size noncoding RNA transcriptome of , 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	3.7	