

Yves Van de Peer

List of Publications by Year in descending order

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Version: 2024-02-01

463
papers

75,605
citations

735

120
h-index

663

255
g-index

522
all docs

522
docs citations

522
times ranked

59221
citing authors

#	ARTICLE	IF	CITATIONS
1	Mitochondrial genes from 18 angiosperms fill sampling gaps for phylogenomic inferences of the early diversification of flowering plants. <i>Journal of Systematics and Evolution</i> , 2022, 60, 773-788.	3.1	16
2	The Neighborhood of the Spike Gene Is a Hotspot for Modular Intertypic Homologous and Nonhomologous Recombination in Coronavirus Genomes. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	30
3	Application of second-generation sequencing (SGS) and third generation sequencing (TGS) in aquaculture breeding program. <i>Aquaculture</i> , 2022, 548, 737633.	3.5	12
4	Nearby transposable elements impact plant stress gene regulatory networks: a meta-analysis in <i>A. thaliana</i> and <i>S. lycopersicum</i> . <i>BMC Genomics</i> , 2022, 23, 18.	2.8	19
5	Genomes shed light on the evolution of <i>Begonia</i> , a mega-diverse genus. <i>New Phytologist</i> , 2022, 234, 295-310.	7.3	18
6	Divergence of active site motifs among different classes of <i>Populus</i> glutaredoxins results in substrate switches. <i>Plant Journal</i> , 2022, 110, 129-146.	5.7	3
7	The genome of <i>Hibiscus hamabo</i> reveals its adaptation to saline and waterlogged habitat. <i>Horticulture Research</i> , 2022, 9, uhac067.	6.3	12
8	MicroRNA-mediated post-transcriptional regulation of <i>Pinus pinaster</i> response and resistance to pinewood nematode. <i>Scientific Reports</i> , 2022, 12, 5160.	3.3	7
9	Reshuffling of the ancestral core-eudicot genome shaped chromatin topology and epigenetic modification in <i>Panax</i> . <i>Nature Communications</i> , 2022, 13, 1902.	12.8	30
10	Genomic and Metabolomic Analyses of the Marine Fungus <i>Emericellopsis cladophorae</i> : Insights into Saltwater Adaptability Mechanisms and Its Biosynthetic Potential. <i>Journal of Fungi (Basel)</i> , 2022, 8, 1011.	10.1	15
11	The <i>Cycas</i> genome and the early evolution of seed plants. <i>Nature Plants</i> , 2022, 8, 389-401.	9.3	80
12	The <i>Larix kaempferi</i> genome reveals new insights into wood properties. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 1364-1373.	8.5	17
13	Genomes of leafy and leafless <i>Platanthera</i> orchids illuminate the evolution of mycoheterotrophy. <i>Nature Plants</i> , 2022, 8, 373-388.	9.3	36
14	The genome of <i>Corydalis</i> reveals the evolution of benzylisoquinoline alkaloid biosynthesis in Ranunculales. <i>Plant Journal</i> , 2022, 111, 217-230.	5.7	19
15	A functionally conserved STORR gene fusion in <i>Papaver</i> species that diverged 16.8 million years ago. <i>Nature Communications</i> , 2022, 13, .	12.8	7
16	Cultivated hawthorn (<i>Crataegus pinnatifida</i> var. <i>major</i>) genome sheds light on the evolution of Maleae (apple tribe). <i>Journal of Integrative Plant Biology</i> , 2022, 64, 1487-1501.	8.5	12
17	SNP Detection in <i>Pinus pinaster</i> Transcriptome and Association with Resistance to Pinewood Nematode. <i>Forests</i> , 2022, 13, 946.	2.1	0
18	The emergence and evolution of intron-poor and intronless genes in intron-rich plant gene families. <i>Plant Journal</i> , 2021, 105, 1072-1082.	5.7	60

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19	Genome sequence and genetic diversity analysis of an under-domesticated orphan crop, white fonio (<i>Digitaria exilis</i>). <i>GigaScience</i> , 2021, 10, .	6.4	23
20	Improved chromosome-level genome assembly and annotation of the seagrass, <i>Zostera marina</i> (eelgrass). <i>F1000Research</i> , 2021, 10, 289.	1.6	26
21	Transcriptomic analysis of the poultry red mite, <i>Dermanyssus gallinae</i> , across all stages of the lifecycle. <i>BMC Genomics</i> , 2021, 22, 248.	2.8	9
22	Divergence of a genomic island leads to the evolution of melanization in a halophyte root fungus. <i>ISME Journal</i> , 2021, 15, 3468-3479.	9.8	9
23	Wolfberry genomes and the evolution of <i>Lycium</i> (Solanaceae). <i>Communications Biology</i> , 2021, 4, 671.	4.4	40
24	A chromosome-level <i>Amaranthus cruentus</i> genome assembly highlights gene family evolution and biosynthetic gene clusters that may underpin the nutritional value of this traditional crop. <i>Plant Journal</i> , 2021, 107, 613-628.	5.7	30
25	Insights Into the Mechanisms Implicated in <i>Pinus pinaster</i> Resistance to Pinewood Nematode. <i>Frontiers in Plant Science</i> , 2021, 12, 690857.	3.6	15
26	Whole-genome microsynteny-based phylogeny of angiosperms. <i>Nature Communications</i> , 2021, 12, 3498.	12.8	53
27	The <i>Welwitschia</i> genome reveals a unique biology underpinning extreme longevity in deserts. <i>Nature Communications</i> , 2021, 12, 4247.	12.8	51
28	Genome-wide analysis of butterfly bush (<i>Buddleja alternifolia</i>) in three uplands provides insights into biogeography, demography and speciation. <i>New Phytologist</i> , 2021, 232, 1463-1476.	7.3	21
29	Haplotype-resolved genome assembly and allele-specific gene expression in cultivated ginger. <i>Horticulture Research</i> , 2021, 8, 188.	6.3	31
30	The genome of the extremophile <i>Artemia</i> provides insight into strategies to cope with extreme environments. <i>BMC Genomics</i> , 2021, 22, 635.	2.8	20
31	Chromosome-scale assembly and evolution of the tetraploid <i>Salvia splendens</i> (Lamiaceae) genome. <i>Horticulture Research</i> , 2021, 8, 177.	6.3	27
32	The <i>Euscaphis japonica</i> genome and the evolution of malvids. <i>Plant Journal</i> , 2021, 108, 1382-1399.	5.7	6
33	A non-duplicated magnoliid genome. <i>Nature Plants</i> , 2021, 7, 1162-1163.	9.3	3
34	Genomic Resources to Guide Improvement of the Shea Tree. <i>Frontiers in Plant Science</i> , 2021, 12, 720670.	3.6	11
35	Rapid protein evolution, organellar reductions, and invasive intronic elements in the marine aerobic parasite dinoflagellate <i>Amoebophrya</i> spp. <i>BMC Biology</i> , 2021, 19, 1.	3.8	135
36	Polyploidy: an evolutionary and ecological force in stressful times. <i>Plant Cell</i> , 2021, 33, 11-26.	6.6	325

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37	Taxus yunnanensis genome offers insights into gymnosperm phylogeny and taxol production. Communications Biology, 2021, 4, 1203.	4.4	15
38	Evolutionary history and pan-genome dynamics of strawberry (<i>Fragaria</i> spp.). Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	43
39	The Cymbidium genome reveals the evolution of unique morphological traits. Horticulture Research, 2021, 8, 255.	6.3	33
40	Genome and Metabolome MS-Based Mining of a Marine Strain of Aspergillus affinis. Journal of Fungi (Basel, Switzerland), 2021, 7, 1091.	3.5	9
41	Evolution of NLR Resistance Genes in Magnoliids: Dramatic Expansions of CNLs and Multiple Losses of TNLs. Frontiers in Plant Science, 2021, 12, 777157.	3.6	11
42	Sequencing and Analyzing the Transcriptomes of a Thousand Species Across the Tree of Life for Green Plants. Annual Review of Plant Biology, 2020, 71, 741-765.	18.7	41
43	Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. Nature Plants, 2020, 6, 95-106.	9.3	146
44	The water lily genome and the early evolution of flowering plants. Nature, 2020, 577, 79-84.	27.8	238
45	“Winter Is Coming” How did Polyploid Plants Survive?. Molecular Plant, 2020, 13, 4-5.	8.3	4
46	Draft Genomes of Two Artocarpus Plants, Jackfruit (<i>A. heterophyllus</i>) and Breadfruit (<i>A. altilis</i>). Genes, 2020, 11, 27.	2.4	30
47	The Seagrass Methylome Is Associated With Variation in Photosynthetic Performance Among Clonal Shoots. Frontiers in Plant Science, 2020, 11, 571646.	3.6	21
48	Chromosome-level genome assembly of a parent species of widely cultivated azaleas. Nature Communications, 2020, 11, 5269.	12.8	90
49	Nymphaea colorata (Blue-Petal Water Lily). Trends in Genetics, 2020, 36, 718-719.	6.7	3
50	Current status of the multinational Arabidopsis community. Plant Direct, 2020, 4, e00248.	1.9	13
51	The evolutionary conundrum of whole-genome duplication. American Journal of Botany, 2020, 107, 1101-1105.	1.7	28
52	Model-Based Detection of Whole-Genome Duplications in a Phylogeny. Molecular Biology and Evolution, 2020, 37, 2734-2746.	8.9	9
53	Multi-proxy analyses of a mid-15th century Middle Iron Age Bantu-speaker palaeo-faecal specimen elucidates the configuration of the “ancestral” sub-Saharan African intestinal microbiome. Microbiome, 2020, 8, 62.	11.1	14
54	Polyploidy breaks speciation barriers in Australian burrowing frogs Neobatrachus. PLoS Genetics, 2020, 16, e1008769.	3.5	40

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55	Phages Actively Challenge Niche Communities in Antarctic Soils. <i>MSystems</i> , 2020, 5, .	3.8	17
56	Multi-faceted analysis provides little evidence for recurrent whole-genome duplications during hexapod evolution. <i>BMC Biology</i> , 2020, 18, 57.	3.8	19
57	The genome of <i>Prasinoderma coloniale</i> unveils the existence of a third phylum within green plants. <i>Nature Ecology and Evolution</i> , 2020, 4, 1220-1231.	7.8	84
58	The honeysuckle genome provides insight into the molecular mechanism of carotenoid metabolism underlying dynamic flower coloration. <i>New Phytologist</i> , 2020, 227, 930-943.	7.3	68
59	The <i>Litsea</i> genome and the evolution of the laurel family. <i>Nature Communications</i> , 2020, 11, 1675.	12.8	80
60	Polyploidy: A Biological Force From Cells to Ecosystems. <i>Trends in Cell Biology</i> , 2020, 30, 688-694.	7.9	136
61	The hornwort genome and early land plant evolution. <i>Nature Plants</i> , 2020, 6, 107-118.	9.3	203
62	Distinct Expression and Methylation Patterns for Genes with Different Fates following a Single Whole-Genome Duplication in Flowering Plants. <i>Molecular Biology and Evolution</i> , 2020, 37, 2394-2413.	8.9	75
63	Virus-host coexistence in phytoplankton through the genomic lens. <i>Science Advances</i> , 2020, 6, eaay2587.	10.3	30
64	De novo Assembly of Transcriptomes From a B73 Maize Line Introgressed With a QTL for Resistance to Gray Leaf Spot Disease Reveals a Candidate Allele of a Lectin Receptor-Like Kinase. <i>Frontiers in Plant Science</i> , 2020, 11, 191.	3.6	9
65	The evolutionary origin and domestication history of goldfish (<i>Carassius auratus</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 29775-29785.	7.1	47
66	First draft genome assembly of the desert locust, <i>Schistocerca gregaria</i> . <i>F1000Research</i> , 2020, 9, 775.	1.6	34
67	Genome streamlining in a minute herbivore that manipulates its host plant. <i>ELife</i> , 2020, 9, .	6.0	33
68	Small RNA profiling in <i>Pinus pinaster</i> reveals the transcriptome of developing seeds and highlights differences between zygotic and somatic embryos. <i>Scientific Reports</i> , 2019, 9, 11327.	3.3	28
69	The evolution of gene duplicates in angiosperms and the impact of protein-protein interactions and the mechanism of duplication. <i>Genome Biology and Evolution</i> , 2019, 11, 2292-2305.	2.5	48
70	Using digital organisms to study the evolutionary consequences of whole genome duplication and polyploidy. <i>PLoS ONE</i> , 2019, 14, e0220257.	2.5	30
71	A genomic analysis and transcriptomic atlas of gene expression in <i>Psoroptes ovis</i> reveals feeding- and stage-specific patterns of allergen expression. <i>BMC Genomics</i> , 2019, 20, 756.	2.8	14
72	A multi-omics analysis of the grapevine pathogen <i>Lasiodiplodia theobromae</i> reveals that temperature affects the expression of virulence- and pathogenicity-related genes. <i>Scientific Reports</i> , 2019, 9, 13144.	3.3	47

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73	Genome sequence of <i>Malania oleifera</i> , a tree with great value for nervonic acid production. <i>GigaScience</i> , 2019, 8, .	6.4	36
74	Multiple Independent Recruitment of Sodefrin Precursor-Like Factors in Anuran Sexually Dimorphic Glands. <i>Molecular Biology and Evolution</i> , 2019, 36, 1921-1930.	8.9	16
75	Illumina error correction near highly repetitive DNA regions improves de novo genome assembly. <i>BMC Bioinformatics</i> , 2019, 20, 298.	2.6	23
76	Loss of Wood Formation Genes in Monocot Genomes. <i>Genome Biology and Evolution</i> , 2019, 11, 1986-1996.	2.5	20
77	Inference of Ancient Whole-Genome Duplications and the Evolution of Gene Duplication and Loss Rates. <i>Molecular Biology and Evolution</i> , 2019, 36, 1384-1404.	8.9	65
78	Genome of <i>Crucihimalaya himalaica</i> , a close relative of <i>Arabidopsis</i> , shows ecological adaptation to high altitude. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7137-7146.	7.1	108
79	Draft Genome Assembly of the False Spider Mite <i>Brevipalpus yothersi</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	6
80	Pseudo-chromosome length genome assembly of a double haploid Bartlett pear (<i>Pyrus communis</i> L.). <i>GigaScience</i> , 2019, 8, .	6.4	76
81	ORCAE-AOCC: A Centralized Portal for the Annotation of African Orphan Crop Genomes. <i>Genes</i> , 2019, 10, 950.	2.4	10
82	Dual RNA Sequencing of <i>Vitis vinifera</i> during <i>Lasiodiplodia theobromae</i> Infection Unveils Host-Pathogen Interactions. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6083.	4.1	28
83	Applications of Next-Generation Sequencing Technologies and Computational Tools in Molecular Evolution and Aquatic Animals Conservation Studies: A Short Review. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431989228.	1.2	17
84	Finding Evidence for Whole Genome Duplications: A Reappraisal. <i>Molecular Plant</i> , 2019, 12, 133-136.	8.3	26
85	wgd simple command line tools for the analysis of ancient whole-genome duplications. <i>Bioinformatics</i> , 2019, 35, 2153-2155.	4.1	174
86	Optimising orbit counting of arbitrary order by equation selection. <i>BMC Bioinformatics</i> , 2019, 20, 27.	2.6	4
87	The draft genomes of five agriculturally important African orphan crops. <i>GigaScience</i> , 2019, 8, .	6.4	108
88	Mining the Enriched Subgraphs for Specific Vertices in a Biological Graph. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1496-1507.	3.0	5
89	Polyploid <i>Arabidopsis</i> species originated around recent glaciation maxima. <i>Current Opinion in Plant Biology</i> , 2018, 42, 8-15.	7.1	64
90	Draft Genome Assembly of the Sheep Scab Mite, <i>Psoroptes ovis</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	15

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91	A genome for gnetophytes and early evolution of seed plants. <i>Nature Plants</i> , 2018, 4, 82-89.	9.3	151
92	PLAZA 4.0: an integrative resource for functional, evolutionary and comparative plant genomics. <i>Nucleic Acids Research</i> , 2018, 46, D1190-D1196.	14.5	460
93	The sociobiology of genes: the gene's eye view as a unifying behavioural-ecological framework for biological evolution. <i>History and Philosophy of the Life Sciences</i> , 2018, 40, 6.	1.1	2
94	Draft Genome Assembly of the Poultry Red Mite, <i>Dermanyssus gallinae</i> . <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	26
95	BrownieAligner: accurate alignment of Illumina sequencing data to de Bruijn graphs. <i>BMC Bioinformatics</i> , 2018, 19, 311.	2.6	22
96	Size does matter. <i>Nature Plants</i> , 2018, 4, 859-860.	9.3	4
97	Functional and evolutionary genomic inferences in <i>Populus</i> through genome and population sequencing of American and European aspen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10970-E10978.	7.1	84
98	Insights into the Evolution of Multicellularity from the Sea Lettuce Genome. <i>Current Biology</i> , 2018, 28, 2921-2933.e5.	3.9	134
99	Gene cluster conservation provides insight into cercosporin biosynthesis and extends production to the genus <i>Colletotrichum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5459-E5466.	7.1	61
100	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	9.3	391
101	Network Modeling Unravels Mechanisms of Crosstalk between Ethylene and Salicylate Signaling in Potato. <i>Plant Physiology</i> , 2018, 178, 488-499.	4.8	28
102	Function, dynamics and evolution of network motif modules in integrated gene regulatory networks of worm and plant. <i>Nucleic Acids Research</i> , 2018, 46, 6480-6503.	14.5	33
103	MorphDB: Prioritizing Genes for Specialized Metabolism Pathways and Gene Ontology Categories in Plants. <i>Frontiers in Plant Science</i> , 2018, 9, 352.	3.6	7
104	Agulhas Current properties shape microbial community diversity and potential functionality. <i>Scientific Reports</i> , 2018, 8, 10542.	3.3	12
105	The TruSeq [™] 3 [™] sequencing method for high-throughput transcriptomics and gene space refinement in plant genomes. <i>Plant Journal</i> , 2018, 96, 223-232.	5.7	23
106	The Chara Genome: Secondary Complexity and Implications for Plant Terrestrialization. <i>Cell</i> , 2018, 174, 448-464.e24.	28.9	420
107	Editorial overview: Genome studies and molecular genetics: Treasure troves of evolution. <i>Current Opinion in Plant Biology</i> , 2018, 42, iii-v.	7.1	0
108	A reservoir of "historical" antibiotic resistance genes in remote pristine Antarctic soils. <i>Microbiome</i> , 2018, 6, 40.	11.1	244

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109	First draft genome assembly of the Argane tree (Argania spinosa). F1000Research, 2018, 7, 1310.	1.6	7
110	First draft genome assembly of the Argane tree (Argania spinosa). F1000Research, 2018, 7, 1310.	1.6	8
111	A Cytoscape app for motif enumeration with ISMAGS. Bioinformatics, 2017, 33, 461-463.	4.1	22
112	Network-based integration of systems genetics data reveals pathways associated with lignocellulosic biomass accumulation and processing. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1195-1200.	7.1	55
113	The evolutionary significance of polyploidy. Nature Reviews Genetics, 2017, 18, 411-424.	16.3	1,288
114	OMSim: a simulator for optical map data. Bioinformatics, 2017, 33, 2740-2742.	4.1	14
115	Single-Copy Genes as Molecular Markers for Phylogenomic Studies in Seed Plants. Genome Biology and Evolution, 2017, 9, 1130-1147.	2.5	75
116	The gene expression landscape of pine seedling tissues. Plant Journal, 2017, 91, 1064-1087.	5.7	41
117	Coordinated Functional Divergence of Genes after Genome Duplication in <i>Arabidopsis thaliana</i> . Plant Cell, 2017, 29, 2786-2800.	6.6	46
118	Draft Genome Sequences of Two Unclassified Bacteria, Sphingomonas sp. Strains IBVSS1 and IBVSS2, Isolated from Environmental Samples. Genome Announcements, 2017, 5, .	0.8	1
119	Genome of wild olive and the evolution of oil biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9413-E9422.	7.1	233
120	Draft Genome Sequences of Two Unclassified Chitinophagaceae Bacteria, IBVUCB1 and IBVUCB2, Isolated from Environmental Samples. Genome Announcements, 2017, 5, .	0.8	1
121	Reciprocally Retained Genes in the Angiosperm Lineage Show the Hallmarks of Dosage Balance Sensitivity. Plant Cell, 2017, 29, 2766-2785.	6.6	81
122	Revisiting ancestral polyploidy in plants. Science Advances, 2017, 3, e1603195.	10.3	73
123	The Apostasia genome and the evolution of orchids. Nature, 2017, 549, 379-383.	27.8	305
124	Simulating Biological Complexity through Artificial Evolution. , 2017, , .		1
125	Conservation of Nonsense-Mediated mRNA Decay Complex Components Throughout Eukaryotic Evolution. Scientific Reports, 2017, 7, 16692.	3.3	34
126	Contrasting Rates of Molecular Evolution and Patterns of Selection among Gymnosperms and Flowering Plants. Molecular Biology and Evolution, 2017, 34, 1363-1377.	8.9	164

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127	Systems genetics reveals a transcriptional network associated with susceptibility in the maize "grey leaf spot pathosystem. <i>Plant Journal</i> , 2017, 89, 746-763.	5.7	49
128	Re-annotation, improved large-scale assembly and establishment of a catalogue of noncoding loci for the genome of the model brown alga <i>Ectocarpus</i> . <i>New Phytologist</i> , 2017, 214, 219-232.	7.3	65
129	Estimating the total number of phosphoproteins and phosphorylation sites in eukaryotic proteomes. <i>GigaScience</i> , 2017, 6, 1-11.	6.4	602
130	Draft Genome Sequences of Two Unclassified Bacteria, <i>Hydrogenophaga</i> sp. Strains IBVHS1 and IBVHS2, Isolated from Environmental Samples. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
131	Draft genome of <i>Cercospora zeina</i> , <i>Fusarium pininemorale</i> , <i>Hawksworthiomyces lignivorus</i> , <i>Huntia decipiens</i> and <i>Ophiostoma ips</i> . <i>IMA Fungus</i> , 2017, 8, 385-396.	3.8	37
132	Evaluation of the impact of Illumina error correction tools on de novo genome assembly. <i>BMC Bioinformatics</i> , 2017, 18, 374.	2.6	49
133	Evidence for an ancient whole genome duplication in the cycad lineage. <i>PLoS ONE</i> , 2017, 12, e0184454.	2.5	36
134	Cell line name recognition in support of the identification of synthetic lethality in cancer from text. <i>Bioinformatics</i> , 2016, 32, 276-282.	4.1	20
135	Lack of GLYCOLATE OXIDASE1, but Not GLYCOLATE OXIDASE2, Attenuates the Photorespiratory Phenotype of CATALASE2-Deficient Arabidopsis. <i>Plant Physiology</i> , 2016, 171, 1704-1719.	4.8	84
136	Complex Evolutionary Dynamics of Massively Expanded Chemosensory Receptor Families in an Extreme Generalist Chelicerate Herbivore. <i>Genome Biology and Evolution</i> , 2016, 8, 3323-3339.	2.5	42
137	Genomic resources and databases for plant research community. <i>Current Plant Biology</i> , 2016, 7-8, 1.	4.7	0
138	Editorial overview: Genome studies and molecular genetics: Of plant genes, genomes, and genomics. <i>Current Opinion in Plant Biology</i> , 2016, 30, iv-vi.	7.1	1
139	hfAIM: A reliable bioinformatics approach for in silico genome-wide identification of autophagy-associated Atg8-interacting motifs in various organisms. <i>Autophagy</i> , 2016, 12, 876-887.	9.1	68
140	Comparative Metagenomic Analysis Reveals Mechanisms for Stress Response in Hypoliths from Extreme Hyperarid Deserts. <i>Genome Biology and Evolution</i> , 2016, 8, 2737-2747.	2.5	61
141	The Challenges of Interpreting Phosphoproteomics Data: A Critical View Through the Bioinformatics Lens. <i>Lecture Notes in Computer Science</i> , 2016, , 196-204.	1.3	3
142	The <i>Dendrobium catenatum</i> Lindl. genome sequence provides insights into polysaccharide synthase, floral development and adaptive evolution. <i>Scientific Reports</i> , 2016, 6, 19029.	3.3	255
143	Transcriptomic responses of a simplified soil microcosm to a plant pathogen and its biocontrol agent reveal a complex reaction to harsh habitat. <i>BMC Genomics</i> , 2016, 17, 838.	2.8	13
144	RNA-sequencing of <i>Cercospora beticola</i> DMI-sensitive and -resistant isolates after treatment with tetraconazole identifies common and contrasting pathway induction. <i>Fungal Genetics and Biology</i> , 2016, 92, 1-13.	2.1	30

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145	Diffany: an ontology-driven framework to infer, visualise and analyse differential molecular networks. BMC Bioinformatics, 2016, 17, 18.	2.6	30
146	Jabba: hybrid error correction for long sequencing reads. Algorithms for Molecular Biology, 2016, 11, 10.	1.2	67
147	The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. Nature, 2016, 530, 331-335.	27.8	460
148	Of dups and dinos: evolution at the K/Pg boundary. Current Opinion in Plant Biology, 2016, 30, 62-69.	7.1	64
149	Gene Duplicability of Core Genes Is Highly Consistent across All Angiosperms. Plant Cell, 2016, 28, 326-344.	6.6	202
150	Complete mitochondrial genome of the Verticillium-wilt causing plant pathogen <i>Verticillium nonalfalfae</i> . PLoS ONE, 2016, 11, e0148525.	2.5	19
151	Emergent adaptive behaviour of GRN-controlled simulated robots in a changing environment. PeerJ, 2016, 4, e2812.	2.0	4
152	Application of the EVEX resource to event extraction and network construction: Shared Task entry and result analysis. BMC Bioinformatics, 2015, 16, S3.	2.6	7
153	Exploration of alternative splicing events in ten different grapevine cultivars. BMC Genomics, 2015, 16, 706.	2.8	21
154	Comparative in silico analysis of SSRs in coding regions of high confidence predicted genes in Norway spruce (<i>Picea abies</i>) and Loblolly pine (<i>Pinus taeda</i>). BMC Genetics, 2015, 16, 149.	2.7	3
155	Serendipitous Meta-Transcriptomics: The Fungal Community of Norway Spruce (<i>Picea abies</i>). PLoS ONE, 2015, 10, e0139080.	2.5	27
156	Genome-Wide Mapping of Structural Variations Reveals a Copy Number Variant That Determines Reproductive Morphology in Cucumber. Plant Cell, 2015, 27, 1595-1604.	6.6	125
157	Horsetails Are Ancient Polyploids: Evidence from <i>Equisetum giganteum</i> . Plant Cell, 2015, 27, 1567-1578.	6.6	78
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