

Yves Van de Peer

List of Publications by Year in descending order

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463
papers

75,605
citations

735

120
h-index

662

255
g-index

522
all docs

522
docs citations

522
times ranked

59221
citing authors

#	ARTICLE	IF	CITATIONS
1	PlantCARE, a database of plant cis-acting regulatory elements and a portal to tools for in silico analysis of promoter sequences. <i>Nucleic Acids Research</i> , 2002, 30, 325-327.	14.5	4,875
2	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 2006, 313, 1596-1604.	12.6	3,945
3	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	27.8	2,860
4	The genome of the domesticated apple (<i>Malus domestica</i> Borkh.). <i>Nature Genetics</i> , 2010, 42, 833-839.	21.4	1,891
5	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. <i>Science</i> , 2008, 319, 64-69.	12.6	1,712
6	The <i>Phaeodactylum</i> genome reveals the evolutionary history of diatom genomes. <i>Nature</i> , 2008, 456, 239-244.	27.8	1,458
7	The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013, 497, 579-584.	27.8	1,303
8	The evolutionary significance of polyploidy. <i>Nature Reviews Genetics</i> , 2017, 18, 411-424.	16.3	1,288
9	The <i>Medicago</i> genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	27.8	1,166
10	TREECON for Windows: a software package for the construction and drawing of evolutionary trees for the Microsoft Windows environment. <i>Bioinformatics</i> , 1994, 10, 569-570.	4.1	1,150
11	Re-evaluating prokaryotic species. <i>Nature Reviews Microbiology</i> , 2005, 3, 733-739.	28.6	1,019
12	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008, 452, 88-92.	27.8	1,003
13	A High Quality Draft Consensus Sequence of the Genome of a Heterozygous Grapevine Variety. <i>PLoS ONE</i> , 2007, 2, e1326.	2.5	945
14	From 2R to 3R: evidence for a fish-specific genome duplication (FSGD). <i>BioEssays</i> , 2005, 27, 937-945.	2.5	929
15	The evolutionary significance of ancient genome duplications. <i>Nature Reviews Genetics</i> , 2009, 10, 725-732.	16.3	919
16	The genome of <i>Tetranychus urticae</i> reveals herbivorous pest adaptations. <i>Nature</i> , 2011, 479, 487-492.	27.8	897
17	Modeling gene and genome duplications in eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5454-5459.	7.1	850
18	The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , 2011, 43, 476-481.	21.4	814

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19	Genome analysis of the smallest free-living eukaryote <i>Ostreococcus tauri</i> unveils many unique features. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11647-11652.	7.1	809
20	Genome Duplication, a Trait Shared by 22,000 Species of Ray-Finned Fish. <i>Genome Research</i> , 2003, 13, 382-390.	5.5	787
21	The <i>Ectocarpus</i> genome and the independent evolution of multicellularity in brown algae. <i>Nature</i> , 2010, 465, 617-621.	27.8	774
22	Draft Genome Sequence of the Sexually Transmitted Pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , 2007, 315, 207-212.	12.6	731
23	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	27.8	725
24	z : A Software Tool for Simple and Partial Mantel Tests. <i>Journal of Statistical Software</i> , 2002, 7, 1.	3.7	698
25	Genome-Wide Characterization of the Lignification Toolbox in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2003, 133, 1051-1071.	4.8	689
26	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9166-9171.	7.1	640
27	Estimating the total number of phosphoproteins and phosphorylation sites in eukaryotic proteomes. <i>GigaScience</i> , 2017, 6, 1-11.	6.4	602
28	Green Evolution and Dynamic Adaptations Revealed by Genomes of the Marine Picoeukaryotes <i>Micromonas</i> . <i>Science</i> , 2009, 324, 268-272.	12.6	591
29	Polyploidy and genome evolution in plants. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 119-125.	3.3	578
30	The tiny eukaryote <i>Ostreococcus</i> provides genomic insights into the paradox of plankton speciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7705-7710.	7.1	563
31	Plants with double genomes might have had a better chance to survive the Cretaceous-Tertiary extinction event. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5737-5742.	7.1	552
32	Compilation of small ribosomal subunit RNA sequences. <i>Nucleic Acids Research</i> , 1992, 20, 2075-2089.	14.5	545
33	Compilation of small ribosomal subunit RNA structures. <i>Nucleic Acids Research</i> , 1993, 21, 3025-3049.	14.5	497
34	Robust biomarker identification for cancer diagnosis with ensemble feature selection methods. <i>Bioinformatics</i> , 2010, 26, 392-398.	4.1	494
35	Major events in the genome evolution of vertebrates: Paraneome 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, 1638-1643.	7.1	489
36	Genome duplication and the origin of angiosperms. <i>Trends in Ecology and Evolution</i> , 2005, 20, 591-597.	8.7	483

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37	Evidence that microRNA precursors, unlike other non-coding RNAs, have lower folding free energies than random sequences. <i>Bioinformatics</i> , 2004, 20, 2911-2917.	4.1	480
38	The hidden duplication past of <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13627-13632.	7.1	463
39	The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. <i>Nature</i> , 2016, 530, 331-335.	27.8	460
40	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
41	Comparative genomics provides evidence for an ancient genome duplication event in fish. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2001, 356, 1661-1679.	4.0	450
42	Pan genome of the phytoplankton <i>Emiliania huxleyi</i> underpins its global distribution. <i>Nature</i> , 2013, 499, 209-213.	27.8	448
43	Detection of 91 potential conserved plant microRNAs in <i>Arabidopsis thaliana</i> and <i>Oryza sativa</i> identifies important target genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11511-11516.	7.1	427
44	Genome sequence of the recombinant protein production host <i>Pichia pastoris</i> . <i>Nature Biotechnology</i> , 2009, 27, 561-566.	17.5	422
45	Genome dynamics of the human embryonic kidney 293 lineage in response to cell biology manipulations. <i>Nature Communications</i> , 2014, 5, 4767.	12.8	421
46	The Chara Genome: Secondary Complexity and Implications for Plant Terrestrialization. <i>Cell</i> , 2018, 174, 448-464.e24.	28.9	420
47	The <i>Mycobacterium tuberculosis</i> regulatory network and hypoxia. <i>Nature</i> , 2013, 499, 178-183.	27.8	416
48	The genome sequence of the orchid <i>Phalaenopsis equestris</i> . <i>Nature Genetics</i> , 2015, 47, 65-72.	21.4	413
49	Robust Feature Selection Using Ensemble Feature Selection Techniques. <i>Lecture Notes in Computer Science</i> , 2008, , 313-325.	1.3	411
50	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	9.3	391
51	Analysis of 41 plant genomes supports a wave of successful genome duplications in association with the Cretaceous–Paleogene boundary. <i>Genome Research</i> , 2014, 24, 1334-1347.	5.5	381
52	TAPIR, a web server for the prediction of plant microRNA targets, including target mimics. <i>Bioinformatics</i> , 2010, 26, 1566-1568.	4.1	361
53	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, 2898-2903.	7.1	351
54	The gain and loss of genes during 600 million years of vertebrate evolution. <i>Genome Biology</i> , 2006, 7, R43.	9.6	332

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55	PLAZA 3.0: an access point for plant comparative genomics. <i>Nucleic Acids Research</i> , 2015, 43, D974-D981.	14.5	329
56	Polyploidy: an evolutionary and ecological force in stressful times. <i>Plant Cell</i> , 2021, 33, 11-26.	6.6	325
57	Targeted interactomics reveals a complex core cell cycle machinery in <i>Arabidopsis thaliana</i> . <i>Molecular Systems Biology</i> , 2010, 6, 397.	7.2	315
58	The <i>Apostasia</i> genome and the evolution of orchids. <i>Nature</i> , 2017, 549, 379-383.	27.8	305
59	The Membrane-Bound NAC Transcription Factor ANAC013 Functions in Mitochondrial Retrograde Regulation of the Oxidative Stress Response in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2013, 25, 3472-3490.	6.6	293
60	Legume genome evolution viewed through the <i>Medicago truncatula</i> and <i>Lotus japonicus</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14959-14964.	7.1	286
61	The Plant Genome Integrative Explorer Resource: PlantGenIE.org. <i>New Phytologist</i> , 2015, 208, 1149-1156.	7.3	282
62	The flowering world: a tale of duplications. <i>Trends in Plant Science</i> , 2009, 14, 680-688.	8.8	277
63	The Determination and Comparison of the 16S rRNA Gene Sequences of Species of the Genus		

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73	Evolutionary Relationships Among the Eukaryotic Crown Taxa Taking into Account Site-to-Site Rate Variation in 18S rRNA. <i>Journal of Molecular Evolution</i> , 1997, 45, 619-630.	1.8	231
74	The European database on small subunit ribosomal RNA. <i>Nucleic Acids Research</i> , 2002, 30, 183-185.	14.5	230
75	Genome-Wide Identification of Potential Plant E2F Target Genes. <i>Plant Physiology</i> , 2005, 139, 316-328.	4.8	229
76	Choose your partners: dimerization in eukaryotic transcription factors. <i>Trends in Biochemical Sciences</i> , 2008, 33, 220-229.	7.5	229
77	Structural diversification and neo-functionalization during floral MADS-box gene evolution by C-terminal frameshift mutations. <i>Nucleic Acids Research</i> , 2003, 31, 4401-4409.	14.5	219
78	The European Small Subunit Ribosomal RNA database. <i>Nucleic Acids Research</i> , 2000, 28, 175-176.	14.5	215
79	Evidence That Rice and Other Cereals Are Ancient Aneuploids. <i>Plant Cell</i> , 2003, 15, 2192-2202.	6.6	212
80	Microsporidia: accumulating molecular evidence that a group of amitochondriate and suspectedly primitive eukaryotes are just curious fungi. <i>Gene</i> , 2000, 246, 1-8.	2.2	204
81	The hornwort genome and early land plant evolution. <i>Nature Plants</i> , 2020, 6, 107-118.	9.3	203
82	Gene Duplicability of Core Genes Is Highly Consistent across All Angiosperms. <i>Plant Cell</i> , 2016, 28, 326-344.	6.6	202
83	Unraveling Transcriptional Control in Arabidopsis Using cis-Regulatory Elements and Coexpression Networks. <i>Plant Physiology</i> , 2009, 150, 535-546.	4.8	197
84	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
85	Comparative analysis of more than 3000 sequences reveals the existence of two pseudoknots in area V4 of eukaryotic small subunit ribosomal RNA. <i>Nucleic Acids Research</i> , 2000, 28, 4698-4708.	14.5	190
86	GOLVEN Secretory Peptides Regulate Auxin Carrier Turnover during Plant Gravitropic Responses. <i>Developmental Cell</i> , 2012, 22, 678-685.	7.0	182
87	Generic eukaryotic core promoter prediction using structural features of DNA. <i>Genome Research</i> , 2008, 18, 310-323.	5.5	181
88	And then there were many: MADS goes genomic. <i>Trends in Plant Science</i> , 2003, 8, 475-483.	8.8	179
89	TREECON: A software package for the construction and drawing of evolutionary trees. <i>Bioinformatics</i> , 1993, 9, 177-182.	4.1	177
90	ORCAE: online resource for community annotation of eukaryotes. <i>Nature Methods</i> , 2012, 9, 1041-1041.	19.0	176

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91	Database on the structure of small ribosomal subunit RNA. <i>Nucleic Acids Research</i> , 1994, 22, 3488-3494.	14.5	175
92	wgdâ€”simple command line tools for the analysis of ancient whole-genome duplications. <i>Bioinformatics</i> , 2019, 35, 2153-2155.	4.1	174
93	The Ghost of Selection Past: Rates of Evolution and Functional Divergence of Anciently Duplicated Genes. <i>Journal of Molecular Evolution</i> , 2001, 53, 436-446.	1.8	172
94	An ancient genome duplication contributed to the abundance of metabolic genes in the moss <i>Physcomitrella patens</i> . <i>BMC Evolutionary Biology</i> , 2007, 7, 130.	3.2	171
95	Reannotation and extended community resources for the genome of the non-seed plant <i>Physcomitrella patens</i> provide insights into the evolution of plant gene structures and functions. <i>BMC Genomics</i> , 2013, 14, 498.	2.8	170
96	Construction of evolutionary distance trees with TREECON for Windows: accounting for variation in nucleotide substitution rate among sites. <i>Bioinformatics</i> , 1997, 13, 227-230.	4.1	169
97	Substitution rate calibration of small subunit ribosomal RNA identifies chlorarachniophyte endosymbionts as remnants of green algae.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 7732-7736.	7.1	165
98	Contrasting Rates of Molecular Evolution and Patterns of Selection among Gymnosperms and Flowering Plants. <i>Molecular Biology and Evolution</i> , 2017, 34, 1363-1377.	8.9	164
99	Nonrandom divergence of gene expression following gene and genome duplications in the flowering plant <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2006, 7, R13.	9.6	163
100	The European Large Subunit Ribosomal RNA Database. <i>Nucleic Acids Research</i> , 2001, 29, 175-177.	14.5	160
101	Computational Approaches to Identify Promoters and cis-Regulatory Elements in Plant Genomes. <i>Plant Physiology</i> , 2003, 132, 1162-1176.	4.8	158
102	Genome duplication, divergent resolution and speciation. <i>Trends in Genetics</i> , 2001, 17, 299-301.	6.7	157
103	Globins in nonvertebrate species: dispersal by horizontal gene transfer and evolution of the structure-function relationships. <i>Molecular Biology and Evolution</i> , 1996, 13, 324-333.	8.9	154
104	Towards a prokaryotic genomic taxonomy. <i>FEMS Microbiology Reviews</i> , 2005, 29, 147-167.	8.6	152
105	The evolution of stramenopiles and alveolates as derived by â€œsubstitution rate calibrationâ€ of small ribosomal subunit RNA. <i>Journal of Molecular Evolution</i> , 1996, 42, 201-210.	1.8	151
106	Reciprocal Responses in the Interaction between <i>Arabidopsis</i> and the Cell-Content-Feeding Chelicerate Herbivore Spider Mite <i>Tetranychus</i> . <i>Plant Physiology</i> , 2014, 164, 384-399.	4.8	151
107	A genome for gnetophytes and early evolution of seed plants. <i>Nature Plants</i> , 2018, 4, 82-89.	9.3	151
108	Gene duplication and biased functional retention of paralogs in bacterial genomes. <i>Trends in Microbiology</i> , 2004, 12, 148-154.	7.7	150

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109	A Comprehensive Analysis of Genes Encoding Small Secreted Proteins Identifies Candidate Effectors in <i>Melampsora larici-populina</i> (Poplar Leaf Rust). <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 279-293.	2.6	150
110	Computational approaches to unveiling ancient genome duplications. <i>Nature Reviews Genetics</i> , 2004, 5, 752-763.	16.3	146
111	Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. <i>Nature Plants</i> , 2020, 6, 95-106.	9.3	146
112	Inference of Genome Duplications from Age Distributions Revisited. <i>Molecular Biology and Evolution</i> , 2013, 30, 177-190.	8.9	145
113	Gene functionalities and genome structure in <i>Bathycoccus prasinus</i> reflect cellular specializations at the base of the green lineage. <i>Genome Biology</i> , 2012, 13, R74.	9.6	143
114	Tangled up in two: a burst of genome duplications at the end of the Cretaceous and the consequences for plant evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130353.	4.0	141
115	Global expression analysis of the brown alga <i>Ectocarpus siliculosus</i> (Phaeophyceae) reveals large-scale reprogramming of the transcriptome in response to abiotic stress. <i>Genome Biology</i> , 2009, 10, R66.	9.6	138
116	An Updated and Comprehensive rRNA Phylogeny of (Crown) Eukaryotes Based on Rate-Calibrated Evolutionary Distances. <i>Journal of Molecular Evolution</i> , 2000, 51, 565-576.	1.8	136
117	The small RNA world of plants. <i>New Phytologist</i> , 2006, 171, 451-468.	7.3	136
118	Polyploidy: A Biological Force From Cells to Ecosystems. <i>Trends in Cell Biology</i> , 2020, 30, 688-694.	7.9	136
119	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
120	Insights into the Evolution of Multicellularity from the Sea Lettuce Genome. <i>Current Biology</i> , 2018, 28, 2921-2933.e5.	3.9	134
121	Distribution of substitution rates and location of insertion sites in the tertiary structure of ribosomal RNA. <i>Nucleic Acids Research</i> , 2001, 29, 5017-5028.	14.5	133
122	A Haploid System of Sex Determination in the Brown Alga <i>Ectocarpus</i> sp.. <i>Current Biology</i> , 2014, 24, 1945-1957.	3.9	131
123	EST data suggest that poplar is an ancient polyploid. <i>New Phytologist</i> , 2005, 167, 165-170.	7.3	128
124	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
125	Gamma Paleohexaploidy in the Stem Lineage of Core Eudicots: Significance for MADS-Box Gene and Species Diversification. <i>Molecular Biology and Evolution</i> , 2012, 29, 3793-3806.	8.9	127
126	Reconstructing evolution from eukaryotic small-ribosomal-subunit RNA sequences: Calibration of the molecular clock. <i>Journal of Molecular Evolution</i> , 1993, 37, 221-232.	1.8	126

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127	GenomeView: a next-generation genome browser. <i>Nucleic Acids Research</i> , 2012, 40, e12-e12.	14.5	126
128	Genome-Wide Mapping of Structural Variations Reveals a Copy Number Variant That Determines Reproductive Morphology in Cucumber. <i>Plant Cell</i> , 2015, 27, 1595-1604.	6.6	125
129	Hydrogen Peroxide-Induced Gene Expression across Kingdoms: A Comparative Analysis. <i>Molecular Biology and Evolution</i> , 2008, 25, 507-516.	8.9	122
130	Towards a prokaryotic genomic taxonomy. <i>FEMS Microbiology Reviews</i> , 2005, 29, 147-167.	8.6	121
131	Database on the structure of large ribosomal subunit RNA. <i>Nucleic Acids Research</i> , 1996, 24, 92-97.	14.5	120
132	Predicting protein-protein interactions in <i>Arabidopsis thaliana</i> through integration of orthology, gene ontology and co-expression. <i>BMC Genomics</i> , 2009, 10, 288.	2.8	120
133	Redundancy and rewiring of genetic networks following genome-wide duplication events. <i>Current Opinion in Plant Biology</i> , 2012, 15, 168-176.	7.1	118
134	Deletions Involving Long-Range Conserved Nongenic Sequences Upstream and Downstream of FOXL2 as a Novel Disease-Causing Mechanism in Blepharophimosis Syndrome. <i>American Journal of Human Genetics</i> , 2005, 77, 205-218.	6.2	116
135	Systematic Structural Characterization of Metabolites in <i>Arabidopsis</i> via Candidate Substrate-Product Pair Networks. <i>Plant Cell</i> , 2014, 26, 929-945.	6.6	116
136	The evolutionary position of the rhodophyte <i>Porphyra umbilicalis</i> and the basidiomycete <i>Leucosporidium scottii</i> among other eukaryotes as deduced from complete sequences of small ribosomal subunit RNA. <i>Journal of Molecular Evolution</i> , 1991, 32, 167-177.	1.8	115
137	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
138	Genomewide Structural Annotation and Evolutionary Analysis of the Type I MADS-Box Genes in Plants. <i>Journal of Molecular Evolution</i> , 2003, 56, 573-586.	1.8	109
139	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
140	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
141	The draft genomes of five agriculturally important African orphan crops. <i>GigaScience</i> , 2019, 8, .	6.4	108
142	The Complete Chloroplast and Mitochondrial DNA Sequence of <i>Ostreococcus tauri</i> : Organelle Genomes of the Smallest Eukaryote Are Examples of Compaction. <i>Molecular Biology and Evolution</i> , 2007, 24, 956-968.	8.9	106
143	The (r)evolution of gene regulatory networks controlling <i>Arabidopsis</i> plant reproduction: a two-decade history. <i>Journal of Experimental Botany</i> , 2014, 65, 4731-4745.	4.8	106
144	Large-scale structural analysis of the core promoter in mammalian and plant genomes. <i>Nucleic Acids Research</i> , 2005, 33, 4255-4264.	14.5	103

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145	Moss transcriptome and beyond. Trends in Plant Science, 2002, 7, 535-538.	8.8	102
146	Genome Annotation in Plants and Fungi: EuGene as a Model Platform. Current Bioinformatics, 2008, 3, 87-97.	1.5	102
147	Comparative genomics of the pathogenic ciliate <i>Ichthyophthirius multifiliis</i> , its free-living relatives and a host species provide insights into adoption of a parasitic lifestyle and prospects for disease control. Genome Biology, 2011, 12, R100.	9.6	102
148	Comparative Network Analysis Reveals That Tissue Specificity and Gene Function Are Important Factors Influencing the Mode of Expression Evolution in Arabidopsis and Rice. Plant Physiology, 2011, 156, 1316-1330.	4.8	100
149	Molecular Genealogy of Some Nematode Taxa as Based on Cytochrome c and Globin Amino Acid Sequences. Molecular Phylogenetics and Evolution, 1994, 3, 92-101.	2.7	99
150	Database on the structure of large subunit ribosomal RNA. Nucleic Acids Research, 1999, 27, 174-178.	14.5	99
151	Canalization without flux sensors: a traveling-wave hypothesis. Trends in Plant Science, 2007, 12, 384-390.	8.8	98
152	The Global Invertebrate Genomics Alliance (GIGA): Developing Community Resources to Study Diverse Invertebrate Genomes. Journal of Heredity, 2014, 105, 1-18.	2.4	96
153	The biosynthetic gene cluster for sophorolipids: a biotechnological interesting biosurfactant produced by <i>Sarmerella bombicola</i> . Molecular Microbiology, 2013, 88, 501-509.	2.5	94
154	Feature subset selection for splice site prediction. Bioinformatics, 2002, 18, S75-S83.	4.1	93
155	CoExpNetViz: Comparative Co-Expression Networks Construction and Visualization Tool. Frontiers in Plant Science, 2015, 6, 1194.	3.6	93
156	Database on the structure of large ribosomal subunit RNA. Nucleic Acids Research, 1994, 22, 3495-3501.	14.5	92
157	SpliceMachine: predicting splice sites from high-dimensional local context representations. Bioinformatics, 2005, 21, 1332-1338.	4.1	92
158	Genome-wide analysis of the diatom cell cycle unveils a novel type of cyclins involved in environmental signaling. Genome Biology, 2010, 11, R17.	9.6	91
159	Journey through the past: 150 million years of plant genome evolution. Plant Journal, 2011, 66, 58-65.	5.7	91
160	The Nucleotide Sequence of the Small Ribosomal Subunit RNA of the Yeast <i>Candida albicans</i> and the Evolutionary Position of the Fungi among the Eukaryotes. Systematic and Applied Microbiology, 1989, 12, 223-229.	2.8	90
161	Overview of tomato (<i>Solanum lycopersicum</i>) candidate pathogen recognition genes reveals important <i>Solanum</i> R locus dynamics. New Phytologist, 2013, 197, 223-237.	7.3	90
162	An improved genome of the model marine alga <i>Ostreococcus tauri</i> unfolds by assessing Illumina de novo assemblies. BMC Genomics, 2014, 15, 1103.	2.8	90

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163	Chromosome-level genome assembly of a parent species of widely cultivated azaleas. <i>Nature Communications</i> , 2020, 11, 5269.	12.8	90
164	Evolutionary Relationships Among Higher Fungi Inferred from Small Ribosomal Subunit RNA Sequence Analysis. <i>Systematic and Applied Microbiology</i> , 1993, 16, 436-444.	2.8	87
165	picoâ€œscp>PLAZA</scp>, a genome database of microbial photosynthetic eukaryotes. <i>Environmental Microbiology</i> , 2013, 15, 2147-2153.	3.8	87
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