

# Gane Ka-Shu Wong

## 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.

184 papers	27,472 citations	65 h-index	165 g-index
198 ext. papers	33,328 ext. citations	11.8 avg, IF	7.06 L-index

#	Paper	IF	Citations
184	Complete genome sequence of <i>Pseudomonas aeruginosa</i> PAO1, an opportunistic pathogen. <i>Nature</i> , <b>2000</b> , 406, 959-64	50.4	3373
183	A draft sequence of the rice genome ( <i>Oryza sativa</i> L. ssp. indica). <i>Science</i> , <b>2002</b> , 296, 79-92	33.3	2356
182	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , <b>2004</b> , 432, 695-716	50.4	2143
181	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , <b>2007</b> , 450, 203-18	50.4	1586
180	Independent optical excitation of distinct neural populations. <i>Nature Methods</i> , <b>2014</b> , 11, 338-46	21.6	1214
179	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , <b>2010</b> , 463, 311-7	50.4	864
178	A draft sequence for the genome of the domesticated silkworm ( <i>Bombyx mori</i> ). <i>Science</i> , <b>2004</b> , 306, 1937-40	33.3	859
177	Phylotranscriptomic analysis of the origin and early diversification of land plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E4859-68	11.5	835
176	The diploid genome sequence of an Asian individual. <i>Nature</i> , <b>2008</b> , 456, 60-5	50.4	744
175	The Genomes of <i>Oryza sativa</i> : a history of duplications. <i>PLoS Biology</i> , <b>2005</b> , 3, e38	9.7	695
174	KaKs_Calculator: calculating Ka and Ks through model selection and model averaging. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2006</b> , 4, 259-63	6.5	657
173	SOAPdenovo-Trans: de novo transcriptome assembly with short RNA-Seq reads. <i>Bioinformatics</i> , <b>2014</b> , 30, 1660-6	7.2	621
172	One thousand plant transcriptomes and the phylogenomics of green plants. <i>Nature</i> , <b>2019</b> , 574, 679-685	50.4	529
171	All-optical electrophysiology in mammalian neurons using engineered microbial rhodopsins. <i>Nature Methods</i> , <b>2014</b> , 11, 825-33	21.6	487
170	Characterization of the Gut Microbiome Using 16S or Shotgun Metagenomics. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 459	5.7	436
169	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , <b>2014</b> , 3, 17	7.6	403
168	TreeFam: a curated database of phylogenetic trees of animal gene families. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D572-80	20.1	383

167	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , <b>2004</b> , 432, 717-22	50.4	341
166	The genome of flax ( <i>Linum usitatissimum</i> ) assembled de novo from short shotgun sequence reads. <i>Plant Journal</i> , <b>2012</b> , 72, 461-73	6.9	315
165	Effect of Oral Capsule- vs Colonoscopy-Delivered Fecal Microbiota Transplantation on Recurrent <i>Clostridium difficile</i> Infection: A Randomized Clinical Trial. <i>JAMA - Journal of the American Medical Association</i> , <b>2017</b> , 318, 1985-1993	27.4	303
164	A genome triplication associated with early diversification of the core eudicots. <i>Genome Biology</i> , <b>2012</b> , 13, R3	18.3	266
163	Disorder and the superfluid transition in liquid 4He. <i>Physical Review Letters</i> , <b>1988</b> , 61, 1950-1953	7.4	260
162	Pigs in sequence space: a 0.66X coverage pig genome survey based on shotgun sequencing. <i>BMC Genomics</i> , <b>2005</b> , 6, 70	4.5	221
161	A high-density SNP-based linkage map of the chicken genome reveals sequence features correlated with recombination rate. <i>Genome Research</i> , <b>2009</b> , 19, 510-9	9.7	208
160	Algal ancestor of land plants was preadapted for symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 13390-5	11.5	197
159	High rate of chimeric gene origination by retroposition in plant genomes. <i>Plant Cell</i> , <b>2006</b> , 18, 1791-802	11.6	183
158	Genome-wide assessment of worldwide chicken SNP genetic diversity indicates significant absence of rare alleles in commercial breeds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 17312-7	11.5	180
157	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , <b>2018</b> , 93, 515-533	6.9	176
156	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , <b>2018</b> , 4, 460-475	11.5	176
155	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , <b>2018</b> , 361,	33.3	167
154	Occurrence, structure, and evolution of nitric oxide synthase-like proteins in the plant kingdom. <i>Science Signaling</i> , <b>2016</b> , 9, re2	8.8	155
153	Multiple polyploidy events in the early radiation of nodulating and nonnodulating legumes. <i>Molecular Biology and Evolution</i> , <b>2015</b> , 32, 193-210	8.3	154
152	Genomes of Subaerial Zygnematophyceae Provide Insights into Land Plant Evolution. <i>Cell</i> , <b>2019</b> , 179, 1057-1067.e14	56.2	151
151	Dissecting Molecular Evolution in the Highly Diverse Plant Clade Caryophyllales Using Transcriptome Sequencing. <i>Molecular Biology and Evolution</i> , <b>2015</b> , 32, 2001-14	8.3	149
150	SilkDB: a knowledgebase for silkworm biology and genomics. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D399-402	20.1	145

149	Evaluating methods for isolating total RNA and predicting the success of sequencing phylogenetically diverse plant transcriptomes. <i>PLoS ONE</i> , <b>2012</b> , 7, e50226	3.7	142
148	Compositional gradients in Gramineae genes. <i>Genome Research</i> , <b>2002</b> , 12, 851-6	9.7	139
147	A Universal Probe Set for Targeted Sequencing of 353 Nuclear Genes from Any Flowering Plant Designed Using k-Medoids Clustering. <i>Systematic Biology</i> , <b>2019</b> , 68, 594-606	8.4	139
146	Host immunoglobulin G selectively identifies pathobionts in pediatric inflammatory bowel diseases. <i>Microbiome</i> , <b>2019</b> , 7, 1	16.6	139
145	Plastid phylogenomic analysis of green plants: A billion years of evolutionary history. <i>American Journal of Botany</i> , <b>2018</b> , 105, 291-301	2.7	129
144	Mucosal Barrier Depletion and Loss of Bacterial Diversity are Primary Abnormalities in Paediatric Ulcerative Colitis. <i>Journal of Crohn's and Colitis</i> , <b>2016</b> , 10, 462-71	1.5	123
143	Horizontal transfer of an adaptive chimeric photoreceptor from bryophytes to ferns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 6672-7	11.5	121
142	The evolutionary history of ferns inferred from 25 low-copy nuclear genes. <i>American Journal of Botany</i> , <b>2015</b> , 102, 1089-107	2.7	114
141	10KP: A phylodiverse genome sequencing plan. <i>GigaScience</i> , <b>2018</b> , 7, 1-9	7.6	108
140	Lineage-specific gene radiations underlie the evolution of novel betalain pigmentation in Caryophyllales. <i>New Phytologist</i> , <b>2015</b> , 207, 1170-80	9.8	104
139	A microarray analysis of the rice transcriptome and its comparison to Arabidopsis. <i>Genome Research</i> , <b>2005</b> , 15, 1274-83	9.7	103
138	Phytochrome diversity in green plants and the origin of canonical plant phytochromes. <i>Nature Communications</i> , <b>2015</b> , 6, 7852	17.4	100
137	Origin and evolution of the nuclear auxin response system. <i>ELife</i> , <b>2018</b> , 7,	8.9	99
136	BGI-RIS: an integrated information resource and comparative analysis workbench for rice genomics. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D377-82	20.1	97
135	A promiscuous intermediate underlies the evolution of LEAFY DNA binding specificity. <i>Science</i> , <b>2014</b> , 343, 645-8	33.3	94
134	Neutral evolution of non-coding complementary DNAs. <i>Nature</i> , <b>2004</b> , 431, 1-2	50.4	93
133	The location and translocation of ndh genes of chloroplast origin in the Orchidaceae family. <i>Scientific Reports</i> , <b>2015</b> , 5, 9040	4.9	90
132	Functional and topological diversity of LOV domain photoreceptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E1442-51	11.5	86

131	Paralogous radiations of PIN proteins with multiple origins of noncanonical PIN structure. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 2042-60	8.3	83
130	Mouse transcriptome: neutral evolution of 'non-coding' complementary DNAs. <i>Nature</i> , <b>2004</b> , 431, 1 p following 757; discussion following 757	50.4	82
129	ReAS: Recovery of ancestral sequences for transposable elements from the unassembled reads of a whole genome shotgun. <i>PLoS Computational Biology</i> , <b>2005</b> , 1, e43	5	81
128	Origin and evolution of new exons in rodents. <i>Genome Research</i> , <b>2005</b> , 15, 1258-64	9.7	79
127	Superfluid critical behavior in 4He-filled porous media. <i>Physical Review Letters</i> , <b>1990</b> , 65, 2410-2413	7.4	78
126	Anthoceros genomes illuminate the origin of land plants and the unique biology of hornworts. <i>Nature Plants</i> , <b>2020</b> , 6, 259-272	11.5	77
125	Evolution of chloroplast retrograde signaling facilitates green plant adaptation to land. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 5015-5020	11.5	74
124	Metagenomic analysis of microbiome in colon tissue from subjects with inflammatory bowel diseases reveals interplay of viruses and bacteria. <i>Inflammatory Bowel Diseases</i> , <b>2015</b> , 21, 1419-27	4.5	74
123	Genetic Analysis of <i>Physcomitrella patens</i> Identifies ABSCISIC ACID NON-RESPONSIVE, a Regulator of ABA Responses Unique to Basal Land Plants and Required for Desiccation Tolerance. <i>Plant Cell</i> , <b>2016</b> , 28, 1310-27	11.6	73
122	Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. <i>Nature Plants</i> , <b>2020</b> , 6, 95-106	11.5	73
121	Cyclotide discovery in Gentianales revisited--identification and characterization of cyclic cystine-knot peptides and their phylogenetic distribution in Rubiaceae plants. <i>Biopolymers</i> , <b>2013</b> , 100, 438-52	2.2	72
120	Minimal introns are not "junk". <i>Genome Research</i> , <b>2002</b> , 12, 1185-9	9.7	65
119	Peptidomics of Circular Cysteine-Rich Plant Peptides: Analysis of the Diversity of Cyclotides from <i>Viola tricolor</i> by Transcriptome and Proteome Mining. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 4851-62	5.6	62
118	Shared origins of a key enzyme during the evolution of C4 and CAM metabolism. <i>Journal of Experimental Botany</i> , <b>2014</b> , 65, 3609-21	7	59
117	Recurrent loss of sex is associated with accumulation of deleterious mutations in <i>Oenothera</i> . <i>Molecular Biology and Evolution</i> , <b>2015</b> , 32, 896-905	8.3	59
116	A complete sequence and comparative analysis of a SARS-associated virus (Isolate BJ01). <i>Science Bulletin</i> , <b>2003</b> , 48, 941-948		59
115	The Expanding Family of Natural Anion Channelrhodopsins Reveals Large Variations in Kinetics, Conductance, and Spectral Sensitivity. <i>Scientific Reports</i> , <b>2017</b> , 7, 43358	4.9	58
114	Evolution of strigolactone receptors by gradual neo-functionalization of KAI2 paralogues. <i>BMC Biology</i> , <b>2017</b> , 15, 52	7.3	58

113	De novo assembly of a haplotype-resolved human genome. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 617-22	44.5	57
112	The origin and evolution of phototropins. <i>Frontiers in Plant Science</i> , <b>2015</b> , 6, 637	6.2	56
111	Diversity of ABC transporter genes across the plant kingdom and their potential utility in biotechnology. <i>BMC Biotechnology</i> , <b>2016</b> , 16, 47	3.5	55
110	The complete genomic sequence of 424,015 bp at the centromeric end of the HLA class I region: gene content and polymorphism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1998</b> , 95, 9494-9	11.5	54
109	Access to RNA-sequencing data from 1,173 plant species: The 1000 Plant transcriptomes initiative (1KP). <i>GigaScience</i> , <b>2019</b> , 8,	7.6	52
108	Multiple-complete-digest restriction fragment mapping: generating sequence-ready maps for large-scale DNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1997</b> , 94, 5225-30	11.5	51
107	An ancestral signalling pathway is conserved in intracellular symbioses-forming plant lineages. <i>Nature Plants</i> , <b>2020</b> , 6, 280-289	11.5	50
106	Concomitant loss of NDH complex-related genes within chloroplast and nuclear genomes in some orchids. <i>Plant Journal</i> , <b>2017</b> , 90, 994-1006	6.9	49
105	RePS: a sequence assembler that masks exact repeats identified from the shotgun data. <i>Genome Research</i> , <b>2002</b> , 12, 824-31	9.7	48
104	Microbial-type terpene synthase genes occur widely in nonseed land plants, but not in seed plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 12328-12333	11.5	48
103	Vertebrate gene predictions and the problem of large genes. <i>Nature Reviews Genetics</i> , <b>2003</b> , 4, 741-9	30.1	47
102	Most of the human genome is transcribed. <i>Genome Research</i> , <b>2001</b> , 11, 1975-7	9.7	45
101	Transcriptome-mining for single-copy nuclear markers in ferns. <i>PLoS ONE</i> , <b>2013</b> , 8, e76957	3.7	44
100	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , <b>2006</b> , 440, 1194-8	50.4	43
99	Challenging the paradigms of leaf evolution: Class III HD-Zips in ferns and lycophytes. <i>New Phytologist</i> , <b>2016</b> , 212, 745-758	9.8	42
98	Correlation between Ka/Ks and Ks is related to substitution model and evolutionary lineage. <i>Journal of Molecular Evolution</i> , <b>2009</b> , 68, 414-23	3.1	42
97	Evolution of fruit development genes in flowering plants. <i>Frontiers in Plant Science</i> , <b>2014</b> , 5, 300	6.2	41
96	Is "junk" DNA mostly intron DNA?. <i>Genome Research</i> , <b>2000</b> , 10, 1672-8	9.7	41

95	Gene conversion in the rice genome. <i>BMC Genomics</i> , <b>2008</b> , 9, 93	4.5	40
94	Identification of hepatotropic viruses from plasma using deep sequencing: a next generation diagnostic tool. <i>PLoS ONE</i> , <b>2013</b> , 8, e60595	3.7	40
93	Phylogenetic pinpointing of a paleopolyploidy event within the flax genus ( <i>Linum</i> ) using transcriptomics. <i>Annals of Botany</i> , <b>2014</b> , 113, 753-61	4.1	38
92	Positive correlation between recombination rate and nucleotide diversity is shown under domestication selection in the chicken genome. <i>Science Bulletin</i> , <b>2008</b> , 53, 746-750		37
91	Insights into the Evolution of Hydroxyproline-Rich Glycoproteins from 1000 Plant Transcriptomes. <i>Plant Physiology</i> , <b>2017</b> , 174, 904-921	6.6	36
90	Wild soybean roots depend on specific transcription factors and oxidation reduction related genes in response to alkaline stress. <i>Functional and Integrative Genomics</i> , <b>2015</b> , 15, 651-60	3.8	35
89	Identification of an algal xylan synthase indicates that there is functional orthology between algal and plant cell wall biosynthesis. <i>New Phytologist</i> , <b>2018</b> , 218, 1049-1060	9.8	35
88	Superfluid critical behavior in the presence of a dilute correlated impurity. <i>Physical Review B</i> , <b>1993</b> , 48, 3858-3880	3.3	35
87	Identification and characterization of insect-specific proteins by genome data analysis. <i>BMC Genomics</i> , <b>2007</b> , 8, 93	4.5	33
86	Human Fetal Astrocytes Infected with Zika Virus Exhibit Delayed Apoptosis and Resistance to Interferon: Implications for Persistence. <i>Viruses</i> , <b>2018</b> , 10,	6.2	33
85	Elucidating steroid alkaloid biosynthesis in <i>Veratrum californicum</i> : production of verazine in Sf9 cells. <i>Plant Journal</i> , <b>2015</b> , 82, 991-1003	6.9	32
84	A population threshold for functional polymorphisms. <i>Genome Research</i> , <b>2003</b> , 13, 1873-9	9.7	32
83	The genome of <i>Prasinoderma coloniale</i> unveils the existence of a third phylum within green plants. <i>Nature Ecology and Evolution</i> , <b>2020</b> , 4, 1220-1231	12.3	31
82	ChickVD: a sequence variation database for the chicken genome. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D438-41	10.1	31
81	Nucleomorph and plastid genome sequences of the chlorarachniophyte <i>Lotharella oceanica</i> : convergent reductive evolution and frequent recombination in nucleomorph-bearing algae. <i>BMC Genomics</i> , <b>2014</b> , 15, 374	4.5	29
80	RNA-Seq based phylogeny recapitulates previous phylogeny of the genus <i>Flaveria</i> (Asteraceae) with some modifications. <i>BMC Evolutionary Biology</i> , <b>2015</b> , 15, 116	3	28
79	The Evolution of HD2 Proteins in Green Plants. <i>Trends in Plant Science</i> , <b>2016</b> , 21, 1008-1016	13.1	27
78	G1 and regulator of G-protein signaling (RGS) protein pairs maintain functional compatibility and conserved interaction interfaces throughout evolution despite frequent loss of RGS proteins in plants. <i>New Phytologist</i> , <b>2017</b> , 216, 562-575	9.8	26



77	Assembly of high-resolution restriction maps based on multiple complete digests of a redundant set of overlapping clones. <i>Genomics</i> , <b>1996</b> , 33, 389-408	4.3	26
76	Review of the initial validation and characterization of a 3K chicken SNP array. <i>World Poultry Science Journal</i> , <b>2008</b> , 64, 219-226	3	25
75	Sampling SNPs. <i>Nature Genetics</i> , <b>2000</b> , 26, 13-4	36.3	24
74	Effective fecal microbiota transplantation for recurrent <i>Clostridioides difficile</i> infection in humans is associated with increased signalling in the bile acid-farnesoid X receptor-fibroblast growth factor pathway. <i>Gut Microbes</i> , <b>2019</b> , 10, 142-148	8.8	24
73	Terpene Biosynthesis in Red Algae Is Catalyzed by Microbial Type But Not Typical Plant Terpene Synthases. <i>Plant Physiology</i> , <b>2019</b> , 179, 382-390	6.6	23
72	Large-insert genome analysis technology detects structural variation in <i>Pseudomonas aeruginosa</i> clinical strains from cystic fibrosis patients. <i>Genomics</i> , <b>2008</b> , 91, 530-7	4.3	22
71	Sequencing and Analyzing the Transcriptomes of a Thousand Species Across the Tree of Life for Green Plants. <i>Annual Review of Plant Biology</i> , <b>2020</b> , 71, 741-765	30.7	22
70	Frequent proviral integration of the human betaretrovirus in biliary epithelium of patients with autoimmune and idiopathic liver disease. <i>Alimentary Pharmacology and Therapeutics</i> , <b>2015</b> , 41, 393-405	6.1	21
69	Apparition of the NAC Transcription Factors Predates the Emergence of Land Plants. <i>Molecular Plant</i> , <b>2016</b> , 9, 1345-1348	14.4	20
68	Mesophyll Chloroplast Investment in C3, C4 and C2 Species of the Genus <i>Flaveria</i> . <i>Plant and Cell Physiology</i> , <b>2016</b> , 57, 904-18	4.9	20
67	Angiosperm Phylogeny Based on 18S/26S rDNA Sequence Data: Constructing a Large Data Set Using Next-Generation Sequence Data. <i>International Journal of Plant Sciences</i> , <b>2014</b> , 175, 613-650	2.6	20
66	CYP79 P450 monooxygenases in gymnosperms: CYP79A118 is associated with the formation of taxiphyllin in <i>Taxus baccata</i> . <i>Plant Molecular Biology</i> , <b>2017</b> , 95, 169-180	4.6	20
65	Skin colonization by circulating neoplastic clones in cutaneous T-cell lymphoma. <i>Blood</i> , <b>2019</b> , 134, 1517-1527	15.2	20
64	Branched evolution and genomic intratumor heterogeneity in the pathogenesis of cutaneous T-cell lymphoma. <i>Blood Advances</i> , <b>2020</b> , 4, 2489-2500	7.8	18
63	Intellectual property. Publication rights in the era of open data release policies. <i>Science</i> , <b>2000</b> , 289, 1881-1883	33.3	18
62	Organellomic data sets confirm a cryptic consensus on (unrooted) land-plant relationships and provide new insights into bryophyte molecular evolution. <i>American Journal of Botany</i> , <b>2020</b> , 107, 91-115	2.7	18
61	Is there foul play in the leaf pocket? The metagenome of floating fern <i>Azolla</i> reveals endophytes that do not fix N but may denitrify. <i>New Phytologist</i> , <b>2018</b> , 217, 453-466	9.8	17
60	Impact of sequencing depth and technology on de novo RNA-Seq assembly. <i>BMC Genomics</i> , <b>2019</b> , 20, 604	4.5	17



59	Quantitative in vivo whole genome motility screen reveals novel therapeutic targets to block cancer metastasis. <i>Nature Communications</i> , <b>2018</b> , 9, 2343	17.4	16
58	Modeling the yew tree tubulin and a comparison of its interaction with paclitaxel to human tubulin. <i>Pharmaceutical Research</i> , <b>2012</b> , 29, 3007-21	4.5	16
57	A complete sequence and comparative analysis of a SARS-associated virus (Isolate BJ01). <i>Science Bulletin</i> , <b>2003</b> , 48, 941		16
56	Fibroblast Growth Factor 2 Enhances Zika Virus Infection in Human Fetal Brain. <i>Journal of Infectious Diseases</i> , <b>2019</b> , 220, 1377-1387	7	16
55	Clonotypic heterogeneity in cutaneous T-cell lymphoma (mycosis fungoides) revealed by comprehensive whole-exome sequencing. <i>Blood Advances</i> , <b>2019</b> , 3, 1175-1184	7.8	16
54	Extending the Time Domain of Neuronal Silencing with Cryptophyte Anion Channelrhodopsins. <i>ENeuro</i> , <b>2018</b> , 5,	3.9	16
53	Phylogeny and evolutionary history of glycogen synthase kinase 3/SHAGGY-like kinase genes in land plants. <i>BMC Evolutionary Biology</i> , <b>2013</b> , 13, 143	3	15
52	Enhanced Detection of Cancer Biomarkers in Blood-Borne Extracellular Vesicles Using Nanodroplets and Focused Ultrasound. <i>Cancer Research</i> , <b>2017</b> , 77, 3-13	10.1	15
51	Phylogenomic analysis of Ranunculales resolves branching events across the order. <i>Botanical Journal of the Linnean Society</i> , <b>2018</b> , 187, 157-166	2.2	14
50	Modeling the Colchicum autumnale Tubulin and a Comparison of Its Interaction with Colchicine to Human Tubulin. <i>International Journal of Molecular Sciences</i> , <b>2017</b> , 18,	6.3	14
49	Evolutionary Analysis of the Genes Involved in the Land Plant Seed Maturation Program. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 439	6.2	13
48	A genome sequence of novel SARS-CoV isolates: the genotype, GD-Ins29, leads to a hypothesis of viral transmission in South China. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2003</b> , 1, 101-7	6.5	13
47	Divergent gene expression levels between diploid and autotetraploid <i>Tolmiea</i> relative to the total transcriptome, the cell, and biomass. <i>American Journal of Botany</i> , <b>2019</b> , 106, 280-291	2.7	13
46	Addendum: independent optical excitation of distinct neural populations. <i>Nature Methods</i> , <b>2014</b> , 11, 972	21.6	12
45	The trans-kingdom battle between donor and recipient gut microbiome influences fecal microbiota transplantation outcome. <i>Scientific Reports</i> , <b>2020</b> , 10, 18349	4.9	12
44	Novel mutations involving $\beta$ , $\beta$ A-, or $\beta$ B-tubulin isotypes with functional resemblance to $\beta$ II-tubulin in breast cancer. <i>Protoplasma</i> , <b>2017</b> , 254, 1163-1173	3.4	11
43	Comparing the whole-genome-shotgun and map-based sequences of the rice genome. <i>Trends in Plant Science</i> , <b>2006</b> , 11, 387-91	13.1	11
42	Whole-genome duplication and molecular evolution in <i>Cornus</i> L. (Cornaceae) - Insights from transcriptome sequences. <i>PLoS ONE</i> , <b>2017</b> , 12, e0171361	3.7	10

41	Fecal Microbial Transplant After Ileocolic Resection Reduces Ileitis but Restores Colitis in IL-10-/- Mice. <i>Inflammatory Bowel Diseases</i> , <b>2015</b> , 21, 1479-90	4.5	10
40	Next-generation sequencing and bioinformatic approaches to detect and analyze influenza virus in ferrets. <i>Journal of Infection in Developing Countries</i> , <b>2014</b> , 8, 498-509	2.3	10
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