

# Gane Ka-Shu Wong

## List of Publications by Year in descending order

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178  
papers

37,561  
citations

10389

72  
h-index

3830

178  
g-index

198  
all docs

198  
docs citations

198  
times ranked

42987  
citing authors

#	ARTICLE	IF	CITATIONS
1	Metagenomics Versus Metatranscriptomics of the Murine Gut Microbiome for Assessing Microbial Metabolism During Inflammation. <i>Frontiers in Microbiology</i> , 2022, 13, 829378.	3.5	15
2	Origin and early evolution of the plant terpene synthase family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2100361119.	7.1	48
3	Isolation of a Human Betaretrovirus from Patients with Primary Biliary Cholangitis. <i>Viruses</i> , 2022, 14, 886.	3.3	7
4	Chromosome-level genome of <i>Pedinomonas minor</i> (Chlorophyta) unveils adaptations to abiotic stress in a rapidly fluctuating environment. <i>New Phytologist</i> , 2022, , .	7.3	2
5	P307â€¦FMT-associated alterations in the TCR repertoire of patients with severe or fulminant clostridioides difficile infection. , 2021, , .		0
6	Giant DNA viruses make big strides in eukaryote evolution. <i>Cell Host and Microbe</i> , 2021, 29, 152-154.	11.0	7
7	Rare versus common diseases: a false dichotomy in precision medicine. <i>Npj Genomic Medicine</i> , 2021, 6, 19.	3.8	14
8	Enrichment of low abundance DNA/RNA by oligonucleotide-clicked iron oxide nanoparticles. <i>Scientific Reports</i> , 2021, 11, 13053.	3.3	7
9	The coordination of major events in C4 photosynthesis evolution in the genus <i>Flaveria</i> . <i>Scientific Reports</i> , 2021, 11, 15618.	3.3	12
10	Cation and Anion Channelrhodopsins: Sequence Motifs and Taxonomic Distribution. <i>MBio</i> , 2021, 12, e0165621.	4.1	21
11	Genome profiles of pathologist-defined cell clusters by multiregional LCM and G&T-seq in one triple-negative breast cancer patient. <i>Cell Reports Medicine</i> , 2021, 2, 100404.	6.5	5
12	A Multi-Factorial Observational Study on Sequential Fecal Microbiota Transplant in Patients with Medically Refractory <i>Clostridioides difficile</i> Infection. <i>Cells</i> , 2021, 10, 3234.	4.1	14
13	Sequencing and Analyzing the Transcriptomes of a Thousand Species Across the Tree of Life for Green Plants. <i>Annual Review of Plant Biology</i> , 2020, 71, 741-765.	18.7	41
14	Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. <i>Nature Plants</i> , 2020, 6, 95-106.	9.3	146
15	Organelomic data sets confirm a cryptic consensus on (unrooted) landâ€plant relationships and provide new insights into bryophyte molecular evolution. <i>American Journal of Botany</i> , 2020, 107, 91-115.	1.7	38
16	The trans-kingdom battle between donor and recipient gut microbiome influences fecal microbiota transplantation outcome. <i>Scientific Reports</i> , 2020, 10, 18349.	3.3	25
17	Independent evolution of cutaneous lymphoma subclones in different microenvironments of the skin. <i>Scientific Reports</i> , 2020, 10, 15483.	3.3	3
18	Genetic insights into the evolution of genera with the eastern Asiaâ€eastern North America floristic disjunction: a transcriptomics analysis. <i>American Journal of Botany</i> , 2020, 107, 1736-1748.	1.7	6

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19	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
20	Branched evolution and genomic intratumor heterogeneity in the pathogenesis of cutaneous T-cell lymphoma. <i>Blood Advances</i> , 2020, 4, 2489-2500.	5.2	45
21	<i>Anthoceros</i> genomes illuminate the origin of land plants and the unique biology of hornworts. <i>Nature Plants</i> , 2020, 6, 259-272.	9.3	225
22	An ancestral signalling pathway is conserved in intracellular symbioses-forming plant lineages. <i>Nature Plants</i> , 2020, 6, 280-289.	9.3	150
23	Conductance Mechanisms of Rapidly Desensitizing Cation Channelrhodopsins from Cryptophyte Algae. <i>MBio</i> , 2020, 11, .	4.1	20
24	Gains and losses of metabolic function inferred from a phylotranscriptomic analysis of algae. <i>Scientific Reports</i> , 2019, 9, 10482.	3.3	7
25	Impact of sequencing depth and technology on de novo RNA-Seq assembly. <i>BMC Genomics</i> , 2019, 20, 604.	2.8	40
26	Genomes of Subaerial Zygnematophyceae Provide Insights into Land Plant Evolution. <i>Cell</i> , 2019, 179, 1057-1067.e14.	28.9	320
27	Access to RNA-sequencing data from 1,173 plant species: The 1000 Plant transcriptomes initiative (1KP). <i>GigaScience</i> , 2019, 8, .	6.4	118
28	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> , 2019, 116, 5015-5020.	7.1	138
29	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> , 2019, 106, 280-291.	1.7	30
30	Fibroblast Growth Factor 2 Enhances Zika Virus Infection in Human Fetal Brain. <i>Journal of Infectious Diseases</i> , 2019, 220, 1377-1387.	4.0	23
31	Skin colonization by circulating neoplastic clones in cutaneous T-cell lymphoma. <i>Blood</i> , 2019, 134, 1517-1527.	1.4	44
32	Clonotypic heterogeneity in cutaneous T-cell lymphoma (mycosis fungoides) revealed by comprehensive whole-exome sequencing. <i>Blood Advances</i> , 2019, 3, 1175-1184.	5.2	39
33	One thousand plant transcriptomes and the phylogenomics of green plants. <i>Nature</i> , 2019, 574, 679-685.	27.8	1,162
34	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> , 2019, 10, 142-148.	9.8	44
35	Terpene Biosynthesis in Red Algae Is Catalyzed by Microbial Type But Not Typical Plant Terpene Synthases. <i>Plant Physiology</i> , 2019, 179, 382-390.	4.8	40
36	A Universal Probe Set for Targeted Sequencing of 353 Nuclear Genes from Any Flowering Plant Designed Using k-Medoids Clustering. <i>Systematic Biology</i> , 2019, 68, 594-606.	5.6	371

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37	Host immunoglobulin G selectively identifies pathobionts in pediatric inflammatory bowel diseases. <i>Microbiome</i> , 2019, 7, 1.	11.1	404
38	Natural selection and repeated patterns of molecular evolution following allopatric divergence. <i>ELife</i> , 2019, 8, .	6.0	18
39	10KP: A phylodiverse genome sequencing plan. <i>GigaScience</i> , 2018, 7, 1-9.	6.4	169
40	Identification of an algal xylan synthase indicates that there is functional orthology between algal and plant cell wall biosynthesis. <i>New Phytologist</i> , 2018, 218, 1049-1060.	7.3	67
41	Plastid phylogenomic analysis of green plants: A billion years of evolutionary history. <i>American Journal of Botany</i> , 2018, 105, 291-301.	1.7	220
42	Phylogenomic analysis of Ranunculales resolves branching events across the order. <i>Botanical Journal of the Linnean Society</i> , 2018, 187, 157-166.	1.6	20
43	Is there foul play in the leaf pocket? The metagenome of floating fern <i>Azolla</i> reveals endophytes that do not fix N <sub>2</sub> but may denitrify. <i>New Phytologist</i> , 2018, 217, 453-466.	7.3	42
44	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018, 93, 515-533.	5.7	406
45	Human Fetal Astrocytes Infected with Zika Virus Exhibit Delayed Apoptosis and Resistance to Interferon: Implications for Persistence. <i>Viruses</i> , 2018, 10, 646.	3.3	47
46	Extending the Time Domain of Neuronal Silencing with Cryptophyte Anion Channelrhodopsins. <i>ENeuro</i> , 2018, 5, ENEURO.0174-18.2018.	1.9	27
47	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , 2018, 361, .	12.6	339
48	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	9.3	391
49	Origin and evolution of the nuclear auxin response system. <i>ELife</i> , 2018, 7, .	6.0	195
50	A Survey of Molecular Heterogeneity in Hepatocellular Carcinoma. <i>Hepatology Communications</i> , 2018, 2, 945-959.	4.3	10
51	Quantitative in vivo whole genome motility screen reveals novel therapeutic targets to block cancer metastasis. <i>Nature Communications</i> , 2018, 9, 2343.	12.8	21
52	Concomitant loss of <i>NDH</i> complex-related genes within chloroplast and nuclear genomes in some orchids. <i>Plant Journal</i> , 2017, 90, 994-1006.	5.7	99
53	Insights into the Evolution of Hydroxyproline-Rich Glycoproteins from 1000 Plant Transcriptomes. <i>Plant Physiology</i> , 2017, 174, 904-921.	4.8	62
54	The Expanding Family of Natural Anion Channelrhodopsins Reveals Large Variations in Kinetics, Conductance, and Spectral Sensitivity. <i>Scientific Reports</i> , 2017, 7, 43358.	3.3	90

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55	Novel mutations involving $\hat{\gamma}2I$ , $\hat{\gamma}2IIA$ , or $\hat{\gamma}2IVB$ -tubulin isotypes with functional resemblance to $\hat{\gamma}2III$ -tubulin in breast cancer. <i>Protoplasma</i> , 2017, 254, 1163-1173.	2.1	22
56	CYP79 P450 monooxygenases in gymnosperms: CYP79A118 is associated with the formation of taxiphyllin in <i>Taxus baccata</i> . <i>Plant Molecular Biology</i> , 2017, 95, 169-180.	3.9	31
57	Effect of Oral Capsule vs Colonoscopy-Delivered Fecal Microbiota Transplantation on Recurrent <i>Clostridium difficile</i> Infection. <i>JAMA - Journal of the American Medical Association</i> , 2017, 318, 1985.	7.4	446
58	Evolution of strigolactone receptors by gradual neo-functionalization of KAI2 paralogues. <i>BMC Biology</i> , 2017, 15, 52.	3.8	99
59	Enhanced Detection of Cancer Biomarkers in Blood-Borne Extracellular Vesicles Using Nanodroplets and Focused Ultrasound. <i>Cancer Research</i> , 2017, 77, 3-13.	0.9	51
60	G $\alpha$ and regulator of G $\alpha$ 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> , 2017, 216, 562-575.	7.3	46
61	Evolutionary Analysis of the LAFL Genes Involved in the Land Plant Seed Maturation Program. <i>Frontiers in Plant Science</i> , 2017, 8, 439.	3.6	22
62	Modeling the <i>Colchicum autumnale</i> Tubulin and a Comparison of Its Interaction with Colchicine to Human Tubulin. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1676.	4.1	16
63	Whole-genome duplication and molecular evolution in <i>Cornus L.</i> (Cornaceae) Insights from transcriptome sequences. <i>PLoS ONE</i> , 2017, 12, e0171361.	2.5	17
64	Characterization of the Gut Microbiome Using 16S or Shotgun Metagenomics. <i>Frontiers in Microbiology</i> , 2016, 7, 459.	3.5	659
65	Evolution of RLSB, a nuclear-encoded S1 domain RNA binding protein associated with post-transcriptional regulation of plastid-encoded <i>rbcL</i> mRNA in vascular plants. <i>BMC Evolutionary Biology</i> , 2016, 16, 141.	3.2	9
66	Gamma-Retrovirus Integration Marks Cell Type-Specific Cancer Genes: A Novel Profiling Tool in Cancer Genomics. <i>PLoS ONE</i> , 2016, 11, e0154070.	2.5	8
67	Functional and topological diversity of LOV domain photoreceptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1442-51.	7.1	125
68	Diversity of ABC transporter genes across the plant kingdom and their potential utility in biotechnology. <i>BMC Biotechnology</i> , 2016, 16, 47.	3.3	91
69	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> , 2016, 113, 12328-12333.	7.1	70
70	Challenging the paradigms of leaf evolution: Class III HD-Zip1s in ferns and lycophytes. <i>New Phytologist</i> , 2016, 212, 745-758.	7.3	55
71	The Evolution of HD2 Proteins in Green Plants. <i>Trends in Plant Science</i> , 2016, 21, 1008-1016.	8.8	40
72	Occurrence, structure, and evolution of nitric oxide synthase-like proteins in the plant kingdom. <i>Science Signaling</i> , 2016, 9, re2.	3.6	213

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73	Genetic analysis of <i>Physcomitrella patens</i> identifies ABSCISIC ACID NON-RESPONSIVE (ANR), a regulator of ABA responses unique to basal land plants and required for desiccation tolerance. <i>Plant Cell</i> , 2016, 28, tpc.00091.2016.	6.6	98
74	Apparition of the NAC Transcription Factors Predates the Emergence of Land Plants. <i>Molecular Plant</i> , 2016, 9, 1345-1348.	8.3	32
75	Mucosal Barrier Depletion and Loss of Bacterial Diversity are Primary Abnormalities in Paediatric Ulcerative Colitis. <i>Journal of Crohn's and Colitis</i> , 2016, 10, 462-471.	1.3	178
76	Mesophyll Chloroplast Investment in <i>C<sub>3</sub></i> , <i>C<sub>4</sub></i> and <i>C<sub>2</sub></i> Species of the Genus <i>Flaveria</i> . <i>Plant and Cell Physiology</i> , 2016, 57, 904-918.	3.1	32
77	Cerebrospinal Fluid in a Small Cohort of Patients with Multiple Sclerosis Was Generally Free of Microbial DNA. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 198.	3.9	9
78	Lineage-specific gene radiations underlie the evolution of novel betalain pigmentation in Caryophyllales. <i>New Phytologist</i> , 2015, 207, 1170-1180.	7.3	152
79	Metagenomic Analysis of Microbiome in Colon Tissue from Subjects with Inflammatory Bowel Diseases Reveals Interplay of Viruses and Bacteria. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 1.	1.9	100
80	Fecal Microbial Transplant After Ileocolic Resection Reduces Ileitis but Restores Colitis in IL-10 <sup>-/-</sup> Mice. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 1479-1490.	1.9	13
81	The origin and evolution of phototropins. <i>Frontiers in Plant Science</i> , 2015, 6, 637.	3.6	68
82	De novo assembly of a haplotype-resolved human genome. <i>Nature Biotechnology</i> , 2015, 33, 617-622.	17.5	73
83	The Origin and Evolution of the Plant Cell Surface: Algal Integrin-Associated Proteins and a New Family of Integrin-Like Cytoskeleton-ECM Linker Proteins. <i>Genome Biology and Evolution</i> , 2015, 7, 1580-1589.	2.5	4
84	Response to Comment on "A promiscuous intermediate underlies the evolution of LEAFY DNA binding specificity". <i>Science</i> , 2015, 347, 621-621.	12.6	4
85	Recurrent Loss of Sex Is Associated with Accumulation of Deleterious Mutations in <i>Oenothera</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 896-905.	8.9	82
86	Phytochrome diversity in green plants and the origin of canonical plant phytochromes. <i>Nature Communications</i> , 2015, 6, 7852.	12.8	139
87	The evolutionary history of ferns inferred from 25 low-copy nuclear genes. <i>American Journal of Botany</i> , 2015, 102, 1089-1107.	1.7	157
88	Wild soybean roots depend on specific transcription factors and oxidation reduction related genes in response to alkaline stress. <i>Functional and Integrative Genomics</i> , 2015, 15, 651-660.	3.5	51
89	The location and translocation of <i>ndh</i> genes of chloroplast origin in the Orchidaceae family. <i>Scientific Reports</i> , 2015, 5, 9040.	3.3	143
90	Dissecting Molecular Evolution in the Highly Diverse Plant Clade Caryophyllales Using Transcriptome Sequencing. <i>Molecular Biology and Evolution</i> , 2015, 32, 2001-2014.	8.9	198

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91	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> , 2015, 14, 4851-4862.	3.7	80
92	Algal ancestor of land plants was preadapted for symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13390-13395.	7.1	292
93	Frequent proviral integration of the human betaretrovirus in biliary epithelium of patients with autoimmune and idiopathic liver disease. <i>Alimentary Pharmacology and Therapeutics</i> , 2015, 41, 393-405.	3.7	31
94	Editorial: betaretrovirus in biliary epithelia of patients with autoimmune and cryptogenic liver disease – authors' reply. <i>Alimentary Pharmacology and Therapeutics</i> , 2015, 41, 491-491.	3.7	1
95	Elucidating steroid alkaloid biosynthesis in <i>Veratrum californicum</i> : production of verazine in Sf9 cells. <i>Plant Journal</i> , 2015, 82, 991-1003.	5.7	62
96	RNA-Seq based phylogeny recapitulates previous phylogeny of the genus <i>Flaveria</i> (Asteraceae) with some modifications. <i>BMC Evolutionary Biology</i> , 2015, 15, 116.	3.2	46
97	Multiple Polyploidy Events in the Early Radiation of Nodulating and Nonnodulating Legumes. <i>Molecular Biology and Evolution</i> , 2015, 32, 193-210.	8.9	223
98	Next-generation sequencing and bioinformatic approaches to detect and analyze influenza virus in ferrets. <i>Journal of Infection in Developing Countries</i> , 2014, 8, 498-509.	1.2	19
99	Evolution of fruit development genes in flowering plants. <i>Frontiers in Plant Science</i> , 2014, 5, 300.	3.6	74
100	Paralogous Radiations of PIN Proteins with Multiple Origins of Noncanonical PIN Structure. <i>Molecular Biology and Evolution</i> , 2014, 31, 2042-2060.	8.9	111
101	Addendum: Independent optical excitation of distinct neural populations. <i>Nature Methods</i> , 2014, 11, 972-972.	19.0	33
102	Origin of a novel regulatory module by duplication and degeneration of an ancient plant transcription factor. <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 159-173.	2.7	14
103	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , 2014, 3, 17.	6.4	582
104	Independent optical excitation of distinct neural populations. <i>Nature Methods</i> , 2014, 11, 338-346.	19.0	1,879
105	Phylogenetic pinpointing of a paleopolyploidy event within the flax genus ( <i>Linum</i> ) using transcriptomics. <i>Annals of Botany</i> , 2014, 113, 753-761.	2.9	47
106	A Promiscuous Intermediate Underlies the Evolution of LEAFY DNA Binding Specificity. <i>Science</i> , 2014, 343, 645-648.	12.6	117
107	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> , 2014, 111, E4859-68.	7.1	1,123
108	Shared origins of a key enzyme during the evolution of C4 and CAM metabolism. <i>Journal of Experimental Botany</i> , 2014, 65, 3609-3621.	4.8	90

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109	SOAPdenovo-Trans: <i>de novo</i> transcriptome assembly with short RNA-Seq reads. <i>Bioinformatics</i> , 2014, 30, 1660-1666.	4.1	826
110	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> , 2014, 15, 374.	2.8	32
111	All-optical electrophysiology in mammalian neurons using engineered microbial rhodopsins. <i>Nature Methods</i> , 2014, 11, 825-833.	19.0	666
112	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> , 2014, 175, 613-650.	1.3	24
113	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> , 2014, 111, 6672-6677.	7.1	146
114	Phylogeny and evolutionary history of glycogen synthase kinase 3/SHAGGY-like kinase genes in land plants. <i>BMC Evolutionary Biology</i> , 2013, 13, 143.	3.2	21
115	Cyclotide discovery in Gentianales revisited—identification and characterization of cyclic cystine-knot peptides and their phylogenetic distribution in Rubiaceae plants. <i>Biopolymers</i> , 2013, 100, 438-452.	2.4	86
116	Transcriptome-Mining for Single-Copy Nuclear Markers in Ferns. <i>PLoS ONE</i> , 2013, 8, e76957.	2.5	69
117	Identification of Hepatotropic Viruses from Plasma Using Deep Sequencing: A Next Generation Diagnostic Tool. <i>PLoS ONE</i> , 2013, 8, e60595.	2.5	53
118	The genome of flax ( <i>Linum usitatissimum</i> ) assembled <i>de novo</i> from short shotgun sequence reads. <i>Plant Journal</i> , 2012, 72, 461-473.	5.7	415
119	A genome triplication associated with early diversification of the core eudicots. <i>Genome Biology</i> , 2012, 13, R3.	9.6	389
120	Evaluating Methods for Isolating Total RNA and Predicting the Success of Sequencing Phylogenetically Diverse Plant Transcriptomes. <i>PLoS ONE</i> , 2012, 7, e50226.	2.5	172
121	Modeling the Yew Tree Tubulin and a Comparison of its Interaction with Paclitaxel to Human Tubulin. <i>Pharmaceutical Research</i> , 2012, 29, 3007-3021.	3.5	20
122	The sequence and <i>de novo</i> assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	27.8	1,058
123	Evolutionary Transients in the Rice Transcriptome. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 211-228.	6.9	9
124	A high-density SNP-based linkage map of the chicken genome reveals sequence features correlated with recombination rate. <i>Genome Research</i> , 2009, 19, 510-519.	5.5	261
125	Correlation Between Ka/Ks and Ks is Related to Substitution Model and Evolutionary Lineage. <i>Journal of Molecular Evolution</i> , 2009, 68, 414-423.	1.8	71
126	Positive correlation between recombination rate and nucleotide diversity is shown under domestication selection in the chicken genome. <i>Science Bulletin</i> , 2008, 53, 746-750.	1.7	40



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127	Metagenomics and the case of the deadly hamster. <i>Hepatology</i> , 2008, 48, 679-683.	7.3	2
128	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008, 456, 60-65.	27.8	834
129	Gene conversion in the rice genome. <i>BMC Genomics</i> , 2008, 9, 93.	2.8	42
130	Large-insert genome analysis technology detects structural variation in <i>Pseudomonas aeruginosa</i> clinical strains from cystic fibrosis patients. <i>Genomics</i> , 2008, 91, 530-537.	2.9	22
131	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> , 2008, 105, 17312-17317.	7.1	230
132	Review of the initial validation and characterization of a 3K chicken SNP array. <i>World's Poultry Science Journal</i> , 2008, 64, 219-226.	3.0	30
133	Genetic variation at the tumour virus B locus in commercial and laboratory chicken populations assessed by a medium-throughput or a high-throughput assay. <i>Avian Pathology</i> , 2007, 36, 283-291.	2.0	11
134	A comprehensive crop genome research project: the Superhybrid Rice Genome Project in China. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2007, 362, 1023-1034.	4.0	10
135	A cross-species alignment tool (CAT). <i>BMC Bioinformatics</i> , 2007, 8, 349.	2.6	4
136	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
137	Identification and characterization of insect-specific proteins by genome data analysis. <i>BMC Genomics</i> , 2007, 8, 93.	2.8	38
138	High Rate of Chimeric Gene Origination by Retroposition in Plant Genomes. <i>Plant Cell</i> , 2006, 18, 1791-1802.	6.6	207
139	KaKs_Calculator: Calculating Ka and Ks Through Model Selection and Model Averaging. <i>Genomics, Proteomics and Bioinformatics</i> , 2006, 4, 259-263.	6.9	940
140	Comparing the whole-genome-shotgun and map-based sequences of the rice genome. <i>Trends in Plant Science</i> , 2006, 11, 387-391.	8.8	14
141	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , 2006, 440, 1194-1198.	27.8	53
142	TreeFam: a curated database of phylogenetic trees of animal gene families. <i>Nucleic Acids Research</i> , 2006, 34, D572-D580.	14.5	465
143	Genome Biology: The Second Modern Synthesis. <i>Genomics, Proteomics and Bioinformatics</i> , 2005, 3, 3-4.	6.9	5
144	Pigs in sequence space: A 0.66X coverage pig genome survey based on shotgun sequencing. <i>BMC Genomics</i> , 2005, 6, 70.	2.8	283

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145	The Genomes of <i>Oryza sativa</i> : A History of Duplications. <i>PLoS Biology</i> , 2005, 3, e38.	5.6	808
146	ReAS: Recovery of Ancestral Sequences for Transposable Elements from the Unassembled Reads of a Whole Genome Shotgun. <i>PLoS Computational Biology</i> , 2005, 1, e43.	3.2	93
147	A microarray analysis of the rice transcriptome and its comparison to <i>Arabidopsis</i> . <i>Genome Research</i> , 2005, 15, 1274-1283.	5.5	112
148	Origin and evolution of new exons in rodents. <i>Genome Research</i> , 2005, 15, 1258-1264.	5.5	91
149	ReAS: Recovery of ancestral sequences for transposable elements from the unassembled reads of a whole genome shotgun. <i>PLoS Computational Biology</i> , 2005, preprint, e43.	3.2	1
150	BGI-RIS: an integrated information resource and comparative analysis workbench for rice genomics. <i>Nucleic Acids Research</i> , 2004, 32, 377D-382.	14.5	108
151	ChickVD: a sequence variation database for the chicken genome. <i>Nucleic Acids Research</i> , 2004, 33, D438-D441.	14.5	33
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