

# Gane Ka-Shu Wong

## List of Publications by Year in Descending Order

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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	Metagenomics Versus Metatranscriptomics of the Murine Gut Microbiome for Assessing Microbial Metabolism During Inflammation.. <i>Frontiers in Microbiology</i> , <b>2022</b> , 13, 829378	5.7	0
183	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> , <b>2022</b> , 119, e2100361119	11.5	0
182	Isolation of a Human Betaretrovirus from Patients with Primary Biliary Cholangitis. <i>Viruses</i> , <b>2022</b> , 14, 886	6.2	1
181	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> , <b>2021</b> , 2, 100404	18	0
180	A Multi-Factorial Observational Study on Sequential Fecal Microbiota Transplant in Patients with Medically Refractory Infection. <i>Cells</i> , <b>2021</b> , 10,	7.9	2
179	Enrichment of low abundance DNA/RNA by oligonucleotide-clicked iron oxide nanoparticles. <i>Scientific Reports</i> , <b>2021</b> , 11, 13053	4.9	0
178	Giant DNA viruses make big strides in eukaryote evolution. <i>Cell Host and Microbe</i> , <b>2021</b> , 29, 152-154	23.4	0
177	Rare versus common diseases: a false dichotomy in precision medicine. <i>Npj Genomic Medicine</i> , <b>2021</b> , 6, 19	6.2	1
176	The coordination of major events in C photosynthesis evolution in the genus <i>Flaveria</i> . <i>Scientific Reports</i> , <b>2021</b> , 11, 15618	4.9	2
175	Cation and Anion Channelrhodopsins: Sequence Motifs and Taxonomic Distribution. <i>MBio</i> , <b>2021</b> , 12, e0165621 8	6.5	1
174	Genetic insights into the evolution of genera with the eastern Asia-eastern North America floristic disjunction: a transcriptomics analysis. <i>American Journal of Botany</i> , <b>2020</b> , 107, 1736-1748	2.7	2
173	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
172	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
171	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
170	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
169	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
168	Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. <i>Nature Plants</i> , <b>2020</b> , 6, 95-106	11.5	73

167	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
166	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
165	Independent evolution of cutaneous lymphoma subclones in different microenvironments of the skin. <i>Scientific Reports</i> , <b>2020</b> , 10, 15483	4.9	1
164	Conductance Mechanisms of Rapidly Desensitizing Cation Channelrhodopsins from Cryptophyte Algae. <i>MBio</i> , <b>2020</b> , 11,	7.8	7
163	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
162	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
161	Gains and losses of metabolic function inferred from a phylotranscriptomic analysis of algae. <i>Scientific Reports</i> , <b>2019</b> , 9, 10482	4.9	3
160	Impact of sequencing depth and technology on de novo RNA-Seq assembly. <i>BMC Genomics</i> , <b>2019</b> , 20, 604	4.5	17
159	Genomes of Subaerial Zygnematophyceae Provide Insights into Land Plant Evolution. <i>Cell</i> , <b>2019</b> , 179, 1057-1067.e14	56.2	151
158	Natural selection and repeated patterns of molecular evolution following allopatric divergence. <i>ELife</i> , <b>2019</b> , 8,	8.9	7
157	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
156	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
155	Skin colonization by circulating neoplastic clones in cutaneous T-cell lymphoma. <i>Blood</i> , <b>2019</b> , 134, 1517-1527	15.2	20
154	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
153	One thousand plant transcriptomes and the phylogenomics of green plants. <i>Nature</i> , <b>2019</b> , 574, 679-685	50.4	529
152	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
151	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
150	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

149	Host immunoglobulin G selectively identifies pathobionts in pediatric inflammatory bowel diseases. <i>Microbiome</i> , <b>2019</b> , 7, 1	16.6	139
148	10KP: A phylodiverse genome sequencing plan. <i>GigaScience</i> , <b>2018</b> , 7, 1-9	7.6	108
147	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
146	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
145	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
144	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
143	A Survey of Molecular Heterogeneity in Hepatocellular Carcinoma. <i>Hepatology Communications</i> , <b>2018</b> , 2, 941-955	6	5
142	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
141	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
140	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
139	Extending the Time Domain of Neuronal Silencing with Cryptophyte Anion Channelrhodopsins. <i>ENeuro</i> , <b>2018</b> , 5,	3.9	16
138	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , <b>2018</b> , 361,	33.3	167
137	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , <b>2018</b> , 4, 460-475	11.5	176
136	Origin and evolution of the nuclear auxin response system. <i>ELife</i> , <b>2018</b> , 7,	8.9	99
135	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
134	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
133	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
132	Novel mutations involving $\beta$ , $\beta$ A-, or $\beta$ B-tubulin isotypes with functional resemblance to $\beta$ I-tubulin in breast cancer. <i>Protoplasma</i> , <b>2017</b> , 254, 1163-1173	3.4	11

131	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
130	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
129	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
128	Evolution of strigolactone receptors by gradual neo-functionalization of KAI2 paralogues. <i>BMC Biology</i> , <b>2017</b> , 15, 52	7.3	58
127	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
126	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
125	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
124	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> , <b>2017</b> , 18,	6.3	14
123	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
122	The Evolution of HD2 Proteins in Green Plants. <i>Trends in Plant Science</i> , <b>2016</b> , 21, 1008-1016	13.1	27
121	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
120	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
119	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
118	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
117	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
116	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> , <b>2016</b> , 6, 198	5.9	7
115	Characterization of the Gut Microbiome Using 16S or Shotgun Metagenomics. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 459	5.7	436
114	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> , <b>2016</b> , 16, 141	3	8

113	Gamma-Retrovirus Integration Marks Cell Type-Specific Cancer Genes: A Novel Profiling Tool in Cancer Genomics. <i>PLoS ONE</i> , <b>2016</b> , 11, e0154070	3.7	7
112	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
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	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
109	Phytochrome diversity in green plants and the origin of canonical plant phytochromes. <i>Nature Communications</i> , <b>2015</b> , 6, 7852	17.4	100
108	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
107	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
106	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
105	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
104	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
103	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
102	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
101	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
100	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
99	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
98	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
97	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
96	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

95	The origin and evolution of phototropins. <i>Frontiers in Plant Science</i> , <b>2015</b> , 6, 637	6.2	56
94	De novo assembly of a haplotype-resolved human genome. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 617-22	44.5	57
93	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> , <b>2015</b> , 7, 1580-93	9	4
92	Evolution. Response to Comment on "A promiscuous intermediate underlies the evolution of LEAFY DNA binding specificity". <i>Science</i> , <b>2015</b> , 347, 621	33.3	4
91	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
90	Independent optical excitation of distinct neural populations. <i>Nature Methods</i> , <b>2014</b> , 11, 338-46	21.6	1214
89	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
88	A promiscuous intermediate underlies the evolution of LEAFY DNA binding specificity. <i>Science</i> , <b>2014</b> , 343, 645-8	33.3	94
87	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
86	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
85	SOAPdenovo-Trans: de novo transcriptome assembly with short RNA-Seq reads. <i>Bioinformatics</i> , <b>2014</b> , 30, 1660-6	7.2	621
84	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
83	All-optical electrophysiology in mammalian neurons using engineered microbial rhodopsins. <i>Nature Methods</i> , <b>2014</b> , 11, 825-33	21.6	487
82	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
81	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
80	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
79	Evolution of fruit development genes in flowering plants. <i>Frontiers in Plant Science</i> , <b>2014</b> , 5, 300	6.2	41
78	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

77	Addendum: independent optical excitation of distinct neural populations. <i>Nature Methods</i> , <b>2014</b> , 11, 972	21.6	12
76	Origin of a novel regulatory module by duplication and degeneration of an ancient plant transcription factor. <i>Molecular Phylogenetics and Evolution</i> , <b>2014</b> , 81, 159-73	4.1	10
75	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , <b>2014</b> , 3, 17	7.6	403
74	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
73	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
72	Protein Coding <b>2013</b> ,		1
71	Transcriptome-mining for single-copy nuclear markers in ferns. <i>PLoS ONE</i> , <b>2013</b> , 8, e76957	3.7	44
70	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
69	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
68	A genome triplication associated with early diversification of the core eudicots. <i>Genome Biology</i> , <b>2012</b> , 13, R3	18.3	266
67	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
66	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
65	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , <b>2010</b> , 463, 311-7	50.4	864
64	Evolutionary transients in the rice transcriptome. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2010</b> , 8, 211-28	3.5	8
63	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
62	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
61	The diploid genome sequence of an Asian individual. <i>Nature</i> , <b>2008</b> , 456, 60-5	50.4	744
60	Gene conversion in the rice genome. <i>BMC Genomics</i> , <b>2008</b> , 9, 93	4.5	40

59	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
58	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
57	Review of the initial validation and characterization of a 3K chicken SNP array. <i>World's Poultry Science Journal</i> , <b>2008</b> , 64, 219-226	3	25
56	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
55	Metagenomics and the case of the deadly hamster. <i>Hepatology</i> , <b>2008</b> , 48, 679-83	11.2	2
54	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , <b>2007</b> , 450, 203-18	50.4	1586
53	Identification and characterization of insect-specific proteins by genome data analysis. <i>BMC Genomics</i> , <b>2007</b> , 8, 93	4.5	33
52	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> , <b>2007</b> , 36, 283-91	2.4	7
51	A comprehensive crop genome research project: the Superhybrid Rice Genome Project in China. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2007</b> , 362, 1023-34	5.8	10
50	A cross-species alignment tool (CAT). <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 349	3.6	2
49	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
48	High rate of chimeric gene origination by retroposition in plant genomes. <i>Plant Cell</i> , <b>2006</b> , 18, 1791-802	11.6	183
47	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
46	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
45	Shotgun Sequencing (SGS) <b>2006</b> ,		3
44	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , <b>2006</b> , 440, 1194-8	50.4	43
43	ChickVD: a sequence variation database for the chicken genome. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D438-40	10.1	31
42	SilkDB: a knowledgebase for silkworm biology and genomics. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D399-402	20.1	145

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36	Origin and evolution of new exons in rodents. <i>Genome Research</i> , <b>2005</b> , 15, 1258-64	9.7	79
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30	A draft sequence for the genome of the domesticated silkworm ( <i>Bombyx mori</i> ). <i>Science</i> , <b>2004</b> , 306, 1937-40	34.9	859
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7	Origin and evolution of the nuclear auxin response system		2
6	The complex origins of strigolactone signalling in land plants		2

5	A Universal Probe Set for Targeted Sequencing of 353 Nuclear Genes from Any Flowering Plant Designed Using k-medoids Clustering	7
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