Hong-Zhi Kong

List of Publications by Year
in descending order

66 papers	6,044 citations	159585 30 h-index	98798 67 g-index
68 all docs	68 docs citations	68 times ranked	7269 citing authors

#	Article	IF	Citations
1	Loss of innovative traits underlies multiple origins of <i>Aquilegia ecalcarata</i>. Journal of Systematics and Evolution, 2022, 60, 1291-1302.	3.1	1
2	Petal development and elaboration. Journal of Experimental Botany, 2022, 73, 3308-3318.	4.8	9
3	The genome of Ginkgo biloba refined. Nature Plants, 2021, 7, 714-715.	9.3	1
4	Insights into angiosperm evolution, floral development and chemical biosynthesis from the Aristolochia fimbriata genome. Nature Plants, 2021, 7, 1239-1253.	9.3	51
5	Evolution of the grass leaf by primordium extension and petiole-lamina remodeling. Science, 2021, 374, 1377-1381.	12.6	18
6	The water lily genome and the early evolution of flowering plants. Nature, 2020, 577, 79-84.	27.8	238
7	The Tetracentron genome provides insight into the early evolution of eudicots and the formation of vessel elements. Genome Biology, 2020, 21, 291.	8.8	23
8	Identification of the Key Regulatory Genes Involved in Elaborate Petal Development and Specialized Character Formation in <i>Nigella</i><i>damascena</i> (Ranunculaceae). Plant Cell, 2020, 32, 3095-3112.	6.6	27
9	Parallel evolution of apetalous lineages within the buttercup family (Ranunculaceae): outward expansion of <i>AGAMOUS1</i>, rather than disruption of <i>APETALA3â€3</i>. Plant Journal, 2020, 104, 1169-1181.	5.7	4
10	A chromosome-scale reference genome of Aquilegia oxysepala var. kansuensis. Horticulture Research, 2020, 7, 113.	6.3	20
11	The hornwort genome and early land plant evolution. Nature Plants, 2020, 6, 107-118.	9.3	203
12	A role for the Auxin Response Factors <i>ARF6</i> and <i>ARF8</i> homologs in petal spur elongation and nectary maturation in <i>Aquilegia</i>. New Phytologist, 2020, 227, 1392-1405.	7.3	21
13	Identification of the target genes of AqAPETALA3â€3 (AqAP3â€3) in <i>Aquilegia coerulea</i> (Ranunculaceae) helps understand the molecular bases of the conserved and nonconserved features of petals. New Phytologist, 2020, 227, 1235-1248.	7.3	7
14	The morphology, molecular development and ecological function of pseudonectaries on Nigella damascena (Ranunculaceae) petals. Nature Communications, 2020, 11, 1777.	12.8	18
15	Developmental mechanisms involved in the diversification of flowers. Nature Plants, 2019, 5, 917-923.	9.3	46
16	The making of elaborate petals in <i>Nigella</i> through developmental repatterning. New Phytologist, 2019, 223, 385-396.	7.3	21
17	Chloroplast genomic data provide new and robust insights into the phylogeny and evolution of the Ranunculaceae. Molecular Phylogenetics and Evolution, 2019, 135, 12-21.	2.7	123
18	Diversity of flowers in basic structure and its underlying molecular mechanisms. Scientia Sinica Vitae, 2019, 49, 292-300.	0.3	4

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19	Phylogenomic detection and functional prediction of genes potentially important for plant meiosis. Gene, 2018, 643, 83-97.	2.2	4
20	Carbonic Anhydrases Function in Anther Cell Differentiation Downstream of the Receptor-Like Kinase EMS1. Plant Cell, 2017, 29, 1335-1356.	6.6	52
21	The asparagus genome sheds light on the origin and evolution of a young Y chromosome. Nature Communications, 2017, 8, 1279.	12.8	240
22	Plant evolutionary developmental biology. Introduction to a special issue. New Phytologist, 2017, 216, 335-336.	7.3	1
23	How did the flower originate?. Chinese Science Bulletin, 2017, 62, 2323-2334.	0.7	1
24	Prevalent Exon-Intron Structural Changes in the APETALA1/FRUITFULL, SEPALLATA, AGAMOUS-LIKE6, and FLOWERING LOCUS C MADS-Box Gene Subfamilies Provide New Insights into Their Evolution. Frontiers in Plant Science, 2016, 7, 598.	3.6	19
25	Gain of An Auto-regulatory Site Led to Divergence of the Arabidopsis APETALA1 and CAULIFLOWER Duplicate Genes in the Time, Space and Level of Expression and Regulation of One Paralog by the Other. Plant Physiology, 2016, 171, pp.00320.2016.	4.8	42
26	Flexibility in the structure of spiral flowers and its underlying mechanisms. Nature Plants, 2016, 2, 15188.	9.3	88
27	Interactions among proteins of floral MADSâ€box genes in <i>Nuphar pumila</i> (Nymphaeaceae) and the most recent common ancestor of extant angiosperms help understand the underlying mechanisms of the origin of the flower. Journal of Systematics and Evolution, 2015, 53, 285-296.	3.1	17
28	Resolution of deep angiosperm phylogeny using conserved nuclear genes and estimates of early divergence times. Nature Communications, 2014, 5, 4956.	12.8	330
29	MeioBase: a comprehensive database for meiosis. Frontiers in Plant Science, 2014, 5, 728.	3.6	3
30	Evolution of the cyclin gene family in plants. Journal of Systematics and Evolution, 2014, 52, 651-659.	3.1	5
31	Effects of regulatory evolution on morphological diversity. Biodiversity Science, 2014, 22, 72.	0.6	0
32	Developmental repatterning and biodiversity. Biodiversity Science, 2014, 22, 66.	0.6	1
33	Structural, Expression and Interaction Analysis of Rice SKP1-Like Genes. DNA Research, 2013, 20, 67-78.	3.4	24
34	The <i>Amborella</i> Genome and the Evolution of Flowering Plants. Science, 2013, 342, 1241089.	12.6	743
35	Disruption of the petal identity gene <i>APETALA3-3</i> is highly correlated with loss of petals within the buttercup family (Ranunculaceae). Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5074-5079.	7.1	88
36	Divergence of duplicate genes in exonâ€“intron structure. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1187-1192.	7.1	671

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37	Evolutionary divergence of the APETALA1 and CAULIFLOWER proteins. Journal of Systematics and Evolution, 2012, 50, 502-511.	3.1	14
38	Petalâ€specific subfunctionalization of an <i>APETALA3</i> paralog in the Ranunculales and its implications for petal evolution. New Phytologist, 2011, 191, 870-883.	7.3	65
39	Revisiting taxonomy, morphological evolution, and fossil calibration strategies in Chloranthaceae. Journal of Systematics and Evolution, 2011, 49, 315-329.	3.1	25
40	Evolutionary pattern of the regulatory network for flower development: Insights gained from a comparison of two <i>Arabidopsis</i> species. Journal of Systematics and Evolution, 2011, 49, 528-538.	3.1	7
41	The AGL6-like gene OsMADS6 regulates floral organ and meristem identities in rice. Cell Research, 2010, 20, 299-313.	12.0	134
42	The <i>SEPALLATA-</i>Like Gene <i>OsMADS34</i> Is Required for Rice Inflorescence and Spikelet Development Â Â Â. Plant Physiology, 2010, 153, 728-740.	4.8	193
43	Interactions among Proteins of Floral MADS-Box Genes in Basal Eudicots: Implications for Evolution of the Regulatory Network for Flower Development. Molecular Biology and Evolution, 2010, 27, 1598-1611.	8.9	72
44	F-box proteins regulate ethylene signaling and more. Genes and Development, 2009, 23, 391-396.	5.9	26
45	Evolution of F-box genes in plants: Different modes of sequence divergence and their relationships with functional diversification. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 835-840.	7.1	268
46	Evolution of Plant MADS Box Transcription Factors: Evidence for Shifts in Selection Associated with Early Angiosperm Diversification and Concerted Gene Duplications. Molecular Biology and Evolution, 2009, 26, 2229-2244.	8.9	88
47	Functional divergence of the duplicated <i>AtKIN14a</i> and <i>AtKIN14b</i> genes: critical roles in Arabidopsis meiosis and gametophyte development. Plant Journal, 2008, 53, 1013-1026.	5.7	34
48	The MIK region rather than the Câ€terminal domain of AP3â€like class B floral homeotic proteins determines functional specificity in the development and evolution of petals. New Phytologist, 2008, 178, 544-558.	7.3	32
49	Patterns of gene duplication and functional diversification during the evolution of the AP1/SQUA subfamily of plant MADS-box genes. Molecular Phylogenetics and Evolution, 2007, 44, 26-41.	2.7	104
50	Patterns of gene duplication in the plant SKP1 gene family in angiosperms: evidence for multiple mechanisms of rapid gene birth. Plant Journal, 2007, 50, 873-885.	5.7	361
51	Duplication and Divergence of Floral MADS-Box Genes in Grasses: Evidence for the Generation and Modification of Novel Regulators. Journal of Integrative Plant Biology, 2007, 49, 927-939.	8.5	23
52	Mitochondrial matR sequences help to resolve deep phylogenetic relationships in rosids. BMC Evolutionary Biology, 2007, 7, 217.	3.2	66
53	Conservation and divergence of candidate class B genes in Akebia trifoliata (Lardizabalaceae). Development Genes and Evolution, 2006, 216, 785-795.	0.9	31
54	Origins and evolution of the recA/RAD51 gene family: Evidence for ancient gene duplication and endosymbiotic gene transfer. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 10328-10333.	7.1	268

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55	Expression of floral MADS-box genes in basal angiosperms: implications for the evolution of floral regulators. Plant Journal, 2005, 43, 724-744.	5.7	247
56	Characterization of candidate class A, B and E floral homeotic genes from the perianthless basal angiosperm Chloranthus spicatus (Chloranthaceae). Development Genes and Evolution, 2005, 215, 437-449.	0.9	37
57	The Evolution of the SEPALLATA Subfamily of MADS-Box GenesSequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY850178, AY850179, AY850180, AY850181, AY850182, AY850183, AY850184, AY850185, AY850186.. Genetics, 2005, 169, 2209-2223.	2.9	343
58	Genome-Wide Analysis of the Cyclin Family in Arabidopsis and Comparative Phylogenetic Analysis of Plant Cyclin-Like Proteins. Plant Physiology, 2004, 135, 1084-1099.	4.8	252
59	Highly Heterogeneous Rates of Evolution in the SKP1 Gene Family in Plants and Animals: Functional and Evolutionary Implications. Molecular Biology and Evolution, 2004, 21, 117-128.	8.9	69
60	Allozyme variation and population differentiation of the Aconitum delavayi complex (Ranunculaceae) in the Hengduan Mountains of China. Biochemical Genetics, 2003, 41, 47-55.	1.7	9
61	ABC model and floral evolution. Science Bulletin, 2003, 48, 2651-2657.	1.7	6
62	Phylogeny of <i>Chloranthus</i> (Chloranthaceae) based on nuclear ribosomal ITS and plastid TRNLâ€F sequence data. American Journal of Botany, 2002, 89, 940-946.	1.7	25
63	Floral organogenesis of Chloranthus sessilifolius , with special emphasis on the morphological nature of the androecium of Chloranthus (Chloranthaceae). Plant Systematics and Evolution, 2002, 232, 181-188.	0.9	24
64	Comparative morphology of leaf epidermis in the Chloranthaceae. Botanical Journal of the Linnean Society, 2001, 136, 279-294.	1.6	39
65	Comparative morphology of leaf epidermis in the Chloranthaceae. Botanical Journal of the Linnean Society, 2001, 136, 279-294.	1.6	2
66	Karyotypes of Sarcandra Gardn. and Chloranthus Swartz (Chloranthaceae) from China. Botanical Journal of the Linnean Society, 2000, 133, 327-342.	1.6	12