Shengqiang Shu

List of Publications by Year
in descending order

65 papers	22,472 citations	76326 40 h-index	110387 64 g-index
77 all docs	77 docs citations	77 times ranked	25514 citing authors

#	Article	IF	Citations
1	Phytozome: a comparative platform for green plant genomics. Nucleic Acids Research, 2012, 40, D1178-D1186.	14.5	4,204
2	Genome sequence of the palaeopolyploid soybean. Nature, 2010, 463, 178-183.	27.8	3,854
3	AmiGO: online access to ontology and annotation data. Bioinformatics, 2009, 25, 288-289.	4.1	1,647
4	Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibres. Nature, 2012, 492, 423-427.	27.8	1,204
5	A reference genome for common bean and genome-wide analysis of dual domestications. Nature Genetics, 2014, 46, 707-713.	21.4	1,159
6	The high-quality draft genome of peach (Prunus persica) identifies unique patterns of genetic diversity, domestication and genome evolution. Nature Genetics, 2013, 45, 487-494.	21.4	1,031
7	The Generic Genome Browser: A Building Block for a Model Organism System Database. Genome Research, 2002, 12, 1599-1610.	5.5	1,006
8	Insights into Land Plant Evolution Garnered from the Marchantia polymorpha Genome. Cell, 2017, 171, 287-304.e15.	28.9	973
9	The Amphimedon queenslandica genome and the evolution of animal complexity. Nature, 2010, 466, 720-726.	27.8	917
10	The Genome of the Western Clawed Frog Xenopus tropicalis. Science, 2010, 328, 633-636.	12.6	708
11	The Sorghum bicolor reference genome: improved assembly, gene annotations, a transcriptome atlas, and signatures of genome organization. Plant Journal, 2018, 93, 338-354.	5.7	431
12	The Physcomitrella patens chromosomeâ€scale assembly reveals moss genome structure and evolution. Plant Journal, 2018, 93, 515-533.	5.7	406
13	The Genome of Naegleria gruberi Illuminates Early Eukaryotic Versatility. Cell, 2010, 140, 631-642.	28.9	399
14	The Capsella rubella genome and the genomic consequences of rapid mating system evolution. Nature Genetics, 2013, 45, 831-835.	21.4	374
15	The Peach v2.0 release: high-resolution linkage mapping and deep resequencing improve chromosome-scale assembly and contiguity. BMC Genomics, 2017, 18, 225.	2.8	342
16	Extensive gene content variation in the Brachypodium distachyon pan-genome correlates with population structure. Nature Communications, 2017, 8, 2184.	12.8	269
17	The genome of cowpea (Vigna unguiculata [L.] Walp.). Plant Journal, 2019, 98, 767-782.	5.7	264
18	Genomic diversifications of five Gossypium allopolyploid species and their impact on cotton improvement. Nature Genetics, 2020, 52, 525-533.	21.4	249

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19	Insights into the red algae and eukaryotic evolution from the genome of Porphyra umbilicalis (Bangiophyceae, Rhodophyta). Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6361-E6370.	7.1	233
20	The Reference Genome of the Halophytic Plant Eutrema salsugineum. Frontiers in Plant Science, 2013, 4, 46.	3.6	198
21	Fine-scale variation in meiotic recombination in Mimulus inferred from population shotgun sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19478-19482.	7.1	190
22	The Release 5.1 Annotation of Drosophila melanogaster Heterochromatin. Science, 2007, 316, 1586-1591.	12.6	181
23	The KalanchoÃ« genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. Nature Communications, 2017, 8, 1899.	12.8	159
24	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. Nature, 2021, 590, 438-444.	27.8	144
25	Dynamics of juvenile hormone-mediated gonadotropism in the lepidoptera. Archives of Insect Biochemistry and Physiology, 1997, 35, 539-558.	1.5	138
26	The Aquilegia genome provides insight into adaptive radiation and reveals an extraordinarily polymorphic chromosome with a unique history. ELife, 2018, 7, .	6.0	120
27	Construction and comparison of three referenceâ€quality genome assemblies for soybean. Plant Journal, 2019, 100, 1066-1082.	5.7	113
28	A genome resource for green millet Setaria viridis enables discovery of agronomically valuable loci. Nature Biotechnology, 2020, 38, 1203-1210.	17.5	103
29	The genomic landscape of molecular responses to natural drought stress in Panicum hallii. Nature Communications, 2018, 9, 5213.	12.8	101
30	A willow sex chromosome reveals convergent evolution of complex palindromic repeats. Genome Biology, 2020, 21, 38.	8.8	74
31	A new reference genome for Sorghum bicolor reveals high levels of sequence similarity between sweet and grain genotypes: implications for the genetics of sugar metabolism. BMC Genomics, 2019, 20, 420.	2.8	73
32	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial Populus trichocarpa. Genome Biology, 2020, 21, 259.	8.8	68
33	Gradual polyploid genome evolution revealed by pan-genomic analysis of Brachypodium hybridum and its diploid progenitors. Nature Communications, 2020, 11, 3670.	12.8	67
34	Genome biology of the paleotetraploid perennial biomass crop Miscanthus. Nature Communications, 2020, 11, 5442.	12.8	67
35	A kairomone forTrichogramma nubilale (Hymenoptera: Trichogrammatidae) isolation, identification, and synthesis. Journal of Chemical Ecology, 1990, 16, 521-529.	1.8	61
36	Genome sequence of the model rice variety KitaakeX. BMC Genomics, 2019, 20, 905.	2.8	59

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37	A chromosomeâ€scale reference genome of trifoliate orange (Poncirus trifoliata) provides insights into disease resistance, cold tolerance and genome evolution in Citrus. Plant Journal, 2020, 104, 1215-1232.	5.7	56
38	Genome sequence and evolution ofBetula platyphylla. Horticulture Research, 2021, 8, 37.	6.3	53
39	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. Science Advances, 2021, 7, .	10.3	53
40	Hemolymph juvenile hormone titers in pupal and adult stages of southwestern corn borer [Diatraea grandiosella (pyralidae)] and relationship with egg development. Journal of Insect Physiology, 1997, 43, 719-726.	2.0	50
41	Four chromosome scale genomes and a pan-genome annotation to accelerate pecan tree breeding. Nature Communications, 2021, 12, 4125.	12.8	49
42	Mating inHeliothis virescens: Transfer of juvenile hormone during copulation by male to female and stimulation of biosynthesis of endogenous juvenile hormone. , 1998, 38, 100-107.		45
43	Lipophorin of female Blattella germanica (L.): characterization and relation to hemolymph titers of juvenile hormone and hydrocarbons. Journal of Insect Physiology, 1999, 45, 431-441.	2.0	43
44	Sex pheromone production in Callosobruchus maculatus (Coleoptera: Bruchidae): Electroantennographic and behavioral responses. Journal of Stored Products Research, 1996, 32, 21-30.	2.6	39
45	Chromosome evolution and the genetic basis of agronomically important traits in greater yam. Nature Communications, 2022, 13, 2001.	12.8	35
46	Temporal profiles of juvenile hormone titers and egg production in virgin and mated females of Heliothis virescens (Noctuidae). Journal of Insect Physiology, 1998, 44, 1111-1117.	2.0	33
47	A computational and experimental approach to validating annotations and gene predictions in the Drosophila melanogaster genome. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1566-1571.	7.1	32
48	Genome mapping of quantitative trait loci (QTL) controlling domestication traits of intermediate wheatgrass (Thinopyrum intermedium). Theoretical and Applied Genetics, 2019, 132, 2325-2351.	3.6	30
49	Rhythmicity of mating and oviposition inCallosobruchus subinnotatus (Pic) (Coleoptera: Bruchidae). Journal of Insect Behavior, 1997, 10, 409-423.	0.7	27
50	Evidence for a multicomponent sex pheromone inEriborus terebrans (Gravenhorst) (HYM.:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td 2563-2576.	1.8	26
51	Influence of juvenile hormone and mating on oogenesis and oviposition in the codling moth,Cydia pomonella. , 1999, 41, 186-200.		23
52	Draft Nuclear Genome Sequence of the Liquid Hydrocarbonâ€“Accumulating Green Microalga Botryococcus braunii Race B (Showa). Genome Announcements, 2017, 5, .	0.8	21
53	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. Genome Research, 2021, 31, 799-810.	5.5	21
54	Pests, diseases, and aridity have shaped the genome of Corymbia citriodora. Communications Biology, 2021, 4, 537.	4.4	21

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55	Evidence for Reproductive Diapause in the Fritillary <I>Speyeria idalia</I> (Lepidoptera: Nymphalidae). Annals of the Entomological Society of America, 2001, 94, 427-432.	2.5	20
56	Kinetic effects of a kairomone in moth scales of the European corn borer onTrichogramma nubilale Ertle & Davis (Hymenoptera: Trichogrammatidae). Journal of Insect Behavior, 1989, 2, 123-131.	0.7	19
57	Multiplex knockout of trichome-regulating MYB duplicates in hybrid poplar using a single gRNA. Plant Physiology, 2022, 189, 516-526.	4.8	18
58	Ultrastructure and potential role of integumentary glandular cells in adult male and female Callosobruchus subinnotatus (Pic) and C. maculatus (Fabricius) (Coleoptera : Bruchidae). Arthropod Structure and Development, 1995, 24, 51-61.	0.4	17
59	Role of juvenile hormone-esterase in mating-stimulated egg development in the moth Heliothis virescens. Insect Biochemistry and Molecular Biology, 2000, 30, 785-791.	2.7	16
60	Sex Pheromone of Callosobruchus subinnotatus. Journal of Chemical Ecology, 1999, 25, 2715-2727.	1.8	14
61	Identification, characterization, and gene expression analysis of nucleotide binding site (NB)-type resistance gene homologues in switchgrass. BMC Genomics, 2016, 17, 892.	2.8	14
62	Genomic variation within the maize stiffâ€stalk heterotic germplasm pool. Plant Genome, 2021, 14, e20114.	2.8	14
63	Hybridization History and Repetitive Element Content in the Genome of a Homoploid Hybrid, Yucca gloriosa (Asparagaceae). Frontiers in Plant Science, 2020, 11, 573767.	3.6	9
64	Female Sex Pheromone in Callosobruchus subinnotatus (Coleoptera: Bruchidae): Production and Male Responses. Annals of the Entomological Society of America, 1998, 91, 840-844.	2.5	8
65	Responses of Normal and Active Males of Callosobruchus Subinnotatus to Female Sex Pheromone. Annals of the Entomological Society of America, 1999, 92, 594-600.	2.5	5