

Xiaodong Fang

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

33,372
citations

38720

50
h-index

64755

79
g-index

85
all docs

85
docs citations

85
times ranked

59045
citing authors

#	ARTICLE	IF	CITATIONS
1	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
2	De novo assembly of human genomes with massively parallel short read sequencing. <i>Genome Research</i> , 2010, 20, 265-272.	2.4	2,516
3	The oyster genome reveals stress adaptation and complexity of shell formation. <i>Nature</i> , 2012, 490, 49-54.	13.7	1,966
4	The genome of the cucumber, <i>Cucumis sativus</i> L.. <i>Nature Genetics</i> , 2009, 41, 1275-1281.	9.4	1,317
5	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018, 557, 43-49.	13.7	1,091
6	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	13.7	1,058
7	SNP detection for massively parallel whole-genome resequencing. <i>Genome Research</i> , 2009, 19, 1124-1132.	2.4	855
8	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008, 456, 60-65.	13.7	834
9	Whole-genome sequencing of cultivated and wild peppers provides insights into <i>Capsicum</i> domestication and specialization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5135-5140.	3.3	674
10	Comparative Analysis of Bat Genomes Provides Insight into the Evolution of Flight and Immunity. <i>Science</i> , 2013, 339, 456-460.	6.0	522
11	Genome sequencing reveals insights into physiology and longevity of the naked mole rat. <i>Nature</i> , 2011, 479, 223-227.	13.7	517
12	The locust genome provides insight into swarm formation and long-distance flight. <i>Nature Communications</i> , 2014, 5, 2957.	5.8	437
13	Deep RNA sequencing at single base-pair resolution reveals high complexity of the rice transcriptome. <i>Genome Research</i> , 2010, 20, 646-654.	2.4	435
14	Genomic Comparison of the Ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Science</i> , 2010, 329, 1068-1071.	6.0	420
15	Whole-genome and whole-exome sequencing of bladder cancer identifies frequent alterations in genes involved in sister chromatid cohesion and segregation. <i>Nature Genetics</i> , 2013, 45, 1459-1463.	9.4	400
16	Genome-wide profiling of HPV integration in cervical cancer identifies clustered genomic hot spots and a potential microhomology-mediated integration mechanism. <i>Nature Genetics</i> , 2015, 47, 158-163.	9.4	393
17	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012, 44, 221-225.	9.4	383
18	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , 2018, 361, .	6.0	339

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19	Adaptation and possible ancient interspecies introgression in pigs identified by whole-genome sequencing. <i>Nature Genetics</i> , 2015, 47, 217-225.	9.4	288
20	Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques. <i>Nature Biotechnology</i> , 2011, 29, 1019-1023.	9.4	284
21	Genome sequence of the Asian Tiger mosquito, <i>Aedes albopictus</i> , reveals insights into its biology, genetics, and evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5907-15.	3.3	251
22	<i>Ascaris suum</i> draft genome. <i>Nature</i> , 2011, 479, 529-533.	13.7	246
23	Spider genomes provide insight into composition and evolution of venom and silk. <i>Nature Communications</i> , 2014, 5, 3765.	5.8	235
24	Genome analysis reveals insights into physiology and longevity of the Brandt's bat <i>Myotis brandtii</i> . <i>Nature Communications</i> , 2013, 4, 2212.	5.8	213
25	Adaptations to a Subterranean Environment and Longevity Revealed by the Analysis of Mole Rat Genomes. <i>Cell Reports</i> , 2014, 8, 1354-1364.	2.9	162
26	Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , 2018, 19, 77.	3.8	149
27	The draft genome of Tibetan hulless barley reveals adaptive patterns to the high stressful Tibetan Plateau. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1095-1100.	3.3	147
28	Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies. <i>Nature Communications</i> , 2015, 6, 8212.	5.8	146
29	Origin and evolution of qingke barley in Tibet. <i>Nature Communications</i> , 2018, 9, 5433.	5.8	141
30	Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. <i>Nature Communications</i> , 2014, 5, 5594.	5.8	135
31	Genome and Transcriptome Analysis of the Fungal Pathogen <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> Causing Banana Vascular Wilt Disease. <i>PLoS ONE</i> , 2014, 9, e95543.	1.1	135
32	<i>Musa balbisiana</i> genome reveals subgenome evolution and functional divergence. <i>Nature Plants</i> , 2019, 5, 810-821.	4.7	132
33	The sequence and analysis of a Chinese pig genome. <i>GigaScience</i> , 2012, 1, 16.	3.3	125
34	Genome-wide adaptive complexes to underground stresses in blind mole rats <i>Spalax</i> . <i>Nature Communications</i> , 2014, 5, 3966.	5.8	124
35	Distinct Subtypes of Gastric Cancer Defined by Molecular Characterization Include Novel Mutational Signatures with Prognostic Capability. <i>Cancer Research</i> , 2016, 76, 1724-1732.	0.4	120
36	Genome-wide and single-base resolution DNA methylomes of the Pacific oyster <i>Crassostrea gigas</i> provide insight into the evolution of invertebrate CpG methylation. <i>BMC Genomics</i> , 2014, 15, 1119.	1.2	110

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37	Whole-Genome Sequencing Reveals Diverse Models of Structural Variations in Esophageal Squamous Cell Carcinoma. <i>American Journal of Human Genetics</i> , 2016, 98, 256-274.	2.6	109
38	Genetic blueprint of the zoonotic pathogen <i>Toxocara canis</i> . <i>Nature Communications</i> , 2015, 6, 6145.	5.8	103
39	Genome-wide sequencing of longan (<i>Dimocarpus longan</i> Lour.) provides insights into molecular basis of its polyphenol-rich characteristics. <i>GigaScience</i> , 2017, 6, 1-14.	3.3	103
40	A Clostridia-rich microbiota enhances bile acid excretion in diarrhea-predominant irritable bowel syndrome. <i>Journal of Clinical Investigation</i> , 2019, 130, 438-450.	3.9	101
41	Genome of the pitcher plant <i>Cephalotus</i> reveals genetic changes associated with carnivory. <i>Nature Ecology and Evolution</i> , 2017, 1, 59.	3.4	99
42	Genetic Architecture and Selection of Chinese Cattle Revealed by Whole Genome Resequencing. <i>Molecular Biology and Evolution</i> , 2018, 35, 688-699.	3.5	97
43	The draft genome of blunt snout bream (<i>Megalobrama amblycephala</i>) reveals the development of intermuscular bone and adaptation to herbivorous diet. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	95
44	Direct Sequencing and Characterization of a Clinical Isolate of Epstein-Barr Virus from Nasopharyngeal Carcinoma Tissue by Using Next-Generation Sequencing Technology. <i>Journal of Virology</i> , 2011, 85, 11291-11299.	1.5	93
45	Bajji genomes reveal low genetic variability and new insights into secondary aquatic adaptations. <i>Nature Communications</i> , 2013, 4, 2708.	5.8	93
46	Saturated long-chain fatty acid-producing bacteria contribute to enhanced colonic motility in rats. <i>Microbiome</i> , 2018, 6, 107.	4.9	92
47	Population genomics of finless porpoises reveal an incipient cetacean species adapted to freshwater. <i>Nature Communications</i> , 2018, 9, 1276.	5.8	80
48	Genomic analysis of liver cancer unveils novel driver genes and distinct prognostic features. <i>Theranostics</i> , 2018, 8, 1740-1751.	4.6	80
49	Donkey genomes provide new insights into domestication and selection for coat color. <i>Nature Communications</i> , 2020, 11, 6014.	5.8	63
50	BS-SNPer: SNP calling in bisulfite-seq data. <i>Bioinformatics</i> , 2015, 31, 4006-4008.	1.8	61
51	Bioinformatics applications on Apache Spark. <i>GigaScience</i> , 2018, 7, .	3.3	55
52	Whole-genome sequencing reveals novel tandem-duplication hotspots and a prognostic mutational signature in gastric cancer. <i>Nature Communications</i> , 2019, 10, 2037.	5.8	55
53	Transcriptomic Evidence for the Expression of Horizontally Transferred Algal Nuclear Genes in the Photosynthetic Sea Slug, <i>Elysia chlorotica</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 1545-1556.	3.5	54
54	A draft genome assembly of the solar-powered sea slug <i>Elysia chlorotica</i> . <i>Scientific Data</i> , 2019, 6, 190022.	2.4	48

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55	Oyster Shell Proteins Originate from Multiple Organs and Their Probable Transport Pathway to the Shell Formation Front. PLoS ONE, 2013, 8, e66522.	1.1	46
56	CRISPR/Cascade 9-Mediated Genome Editing-Challenges and Opportunities. Frontiers in Genetics, 2018, 9, 240.	1.1	45
57	Clonal architectures predict clinical outcome in clear cell renal cell carcinoma. Nature Communications, 2019, 10, 1245.	5.8	44
58	Population genomic data reveal genes related to important traits of quail. GigaScience, 2018, 7, .	3.3	38
59	Altered metabolome and microbiome features provide clues in understanding irritable bowel syndrome and depression comorbidity. ISME Journal, 2022, 16, 983-996.	4.4	36
60	Genome sequence and global sequence variation map with 5.5 million SNPs in Chinese rhesus macaque. Genome Biology, 2011, 12, R63.	3.8	35
61	Identification of Conserved and Novel MicroRNAs in the Pacific Oyster <i>Crassostrea gigas</i> by Deep Sequencing. PLoS ONE, 2014, 9, e104371.	1.1	33
62	High expression of new genes in trochophore enlightening the ontogeny and evolution of trochozoans. Scientific Reports, 2016, 6, 34664.	1.6	32
63	The molecular landscape of synchronous colorectal cancer reveals genetic heterogeneity. Carcinogenesis, 2018, 39, 708-718.	1.3	28
64	An Effort to Use Human-Based Exome Capture Methods to Analyze Chimpanzee and Macaque Exomes. PLoS ONE, 2012, 7, e40637.	1.1	28
65	The landscape of somatic mutation in sporadic Chinese colorectal cancer. Oncotarget, 2018, 9, 27412-27422.	0.8	26
66	Transcriptome, genetic editing, and microRNA divergence substantiate sympatric speciation of blind mole rat, <i>Spalax</i> . Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7584-7589.	3.3	25
67	Molecular Footprints of Aquatic Adaptation Including Bone Mass Changes in Cetaceans. Genome Biology and Evolution, 2018, 10, 967-975.	1.1	23
68	A reference gene set construction using RNA-seq of multiple tissues of Chinese giant salamander, <i>Andrias davidianus</i> . GigaScience, 2017, 6, 1-7.	3.3	21
69	Evolution and functional analysis of the Pif97 gene of the Pacific oyster <i>Crassostrea gigas</i> . Environmental Epigenetics, 2013, 59, 109-115.	0.9	17
70	Whole genome sequencing of silver carp (<i>Hypophthalmichthys molitrix</i>) and bighead carp (<i>Hypophthalmichthys nobilis</i>) provide novel insights into their evolution and speciation. Molecular Ecology Resources, 2021, 21, 912-923.	2.2	17
71	Multi-omics study in monozygotic twins confirm the contribution of de novo mutation to psoriasis. Journal of Autoimmunity, 2020, 106, 102349.	3.0	13
72	A comprehensive investigation of metagenome assembly by linked-read sequencing. Microbiome, 2020, 8, 156.	4.9	12

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73	Reply to: Transformation of naked mole-rat cells. <i>Nature</i> , 2020, 583, E8-E13.	13.7	11
74	The genetic basis of adaptive evolution in parasitic environment from the <i>Angiostrongylus cantonensis</i> genome. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007846.	1.3	9
75	Aragonite shells are more ancient than calcite ones in bivalves: new evidence based on omics. <i>Molecular Biology Reports</i> , 2014, 41, 7067-7071.	1.0	7
76	ISN Forefronts Symposium 2015: IgA Nephropathy, the Gut Microbiota, and Gut-Kidney Crosstalk. <i>Kidney International Reports</i> , 2016, 1, 189-196.	0.4	7
77	FGF: A web tool for Fishing Gene Family in a whole genome database. <i>Nucleic Acids Research</i> , 2007, 35, W121-W125.	6.5	6
78	A Massively Parallel Computational Method of Reading Index Files for SOAPsnv. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2015, 7, 397-404.	2.2	1
79	Eliminating heterozygosity from reads through coverage normalization. , 2016, , .		0
80	Marine Genomics: Recent Advancement and Wide-Area Applications. , 2016, , 97-108.		0