

Xiaodong Fang

List of Publications by Citations

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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.

80
papers

22,911
citations

46
h-index

85
g-index

85
ext. papers

29,636
ext. citations

17
avg, IF

5.2
L-index

#	Paper	IF	Citations
80	A global reference for human genetic variation. <i>Nature</i> , 2015 , 526, 68-74	50.4	8599
79	De novo assembly of human genomes with massively parallel short read sequencing. <i>Genome Research</i> , 2010 , 20, 265-72	9.7	2084
78	The oyster genome reveals stress adaptation and complexity of shell formation. <i>Nature</i> , 2012 , 490, 49-54	50.4	1464
77	The genome of the cucumber, <i>Cucumis sativus</i> L. <i>Nature Genetics</i> , 2009 , 41, 1275-81	36.3	1031
76	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010 , 463, 311-7	50.4	864
75	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008 , 456, 60-5	50.4	744
74	SNP detection for massively parallel whole-genome resequencing. <i>Genome Research</i> , 2009 , 19, 1124-32	9.7	734
73	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018 , 557, 43-49	50.4	582
72	Whole-genome sequencing of cultivated and wild peppers provides insights into Capsicum domestication and specialization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 5135-40	11.5	466
71	Genome sequencing reveals insights into physiology and longevity of the naked mole rat. <i>Nature</i> , 2011 , 479, 223-7	50.4	410
70	Comparative analysis of bat genomes provides insight into the evolution of flight and immunity. <i>Science</i> , 2013 , 339, 456-60	33.3	377
69	Deep RNA sequencing at single base-pair resolution reveals high complexity of the rice transcriptome. <i>Genome Research</i> , 2010 , 20, 646-54	9.7	375
68	Genomic comparison of the ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Science</i> , 2010 , 329, 1068-71	33.3	353
67	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, 1459-63	36.3	326
66	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012 , 44, 221-5	36.3	325
65	The locust genome provides insight into swarm formation and long-distance flight. <i>Nature Communications</i> , 2014 , 5, 2957	17.4	294
64	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, 158-63	36.3	264

63	Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques. <i>Nature Biotechnology</i> , 2011 , 29, 1019-23	44.5	219
62	<i>Ascaris suum</i> draft genome. <i>Nature</i> , 2011 , 479, 529-33	50.4	217
61	Adaptation and possible ancient interspecies introgression in pigs identified by whole-genome sequencing. <i>Nature Genetics</i> , 2015 , 47, 217-25	36.3	188
60	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	11.5	172
59	Spider genomes provide insight into composition and evolution of venom and silk. <i>Nature Communications</i> , 2014 , 5, 3765	17.4	169
58	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , 2018 , 361,	33.3	167
57	Genome analysis reveals insights into physiology and longevity of the Brandt's bat <i>Myotis brandtii</i> . <i>Nature Communications</i> , 2013 , 4, 2212	17.4	160
56	Adaptations to a subterranean environment and longevity revealed by the analysis of mole rat genomes. <i>Cell Reports</i> , 2014 , 8, 1354-64	10.6	124
55	Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies. <i>Nature Communications</i> , 2015 , 6, 8212	17.4	111
54	The draft genome of Tibetan hullless 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, 1095-100	11.5	102
53	Genome-wide adaptive complexes to underground stresses in blind mole rats <i>Spalax</i> . <i>Nature Communications</i> , 2014 , 5, 3966	17.4	101
52	The sequence and analysis of a Chinese pig genome. <i>GigaScience</i> , 2012 , 1, 16	7.6	91
51	Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. <i>Nature Communications</i> , 2014 , 5, 5594	17.4	89
50	Whole-Genome Sequencing Reveals Diverse Models of Structural Variations in Esophageal Squamous Cell Carcinoma. <i>American Journal of Human Genetics</i> , 2016 , 98, 256-74	11	87
49	Distinct Subtypes of Gastric Cancer Defined by Molecular Characterization Include Novel Mutational Signatures with Prognostic Capability. <i>Cancer Research</i> , 2016 , 76, 1724-32	10.1	86
48	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	3.7	85
47	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, 11291-9	6.6	80
46	Genetic blueprint of the zoonotic pathogen <i>Toxocara canis</i> . <i>Nature Communications</i> , 2015 , 6, 6145	17.4	77

45	Baiji genomes reveal low genetic variability and new insights into secondary aquatic adaptations. <i>Nature Communications</i> , 2013 , 4, 2708	17.4	76
44	Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , 2018 , 19, 77	18.3	75
43	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	4.5	72
42	Origin and evolution of qingke barley in Tibet. <i>Nature Communications</i> , 2018 , 9, 5433	17.4	65
41	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	7.6	63
40	Genome of the pitcher plant <i>Cephalotus</i> reveals genetic changes associated with carnivory. <i>Nature Ecology and Evolution</i> , 2017 , 1, 59	12.3	61
39	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	7.6	54
38	Genomic analysis of liver cancer unveils novel driver genes and distinct prognostic features. <i>Theranostics</i> , 2018 , 8, 1740-1751	12.1	51
37	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, 1545-56	8.3	50
36	<i>Musa balbisiana</i> genome reveals subgenome evolution and functional divergence. <i>Nature Plants</i> , 2019 , 5, 810-821	11.5	49
35	Genetic Architecture and Selection of Chinese Cattle Revealed by Whole Genome Resequencing. <i>Molecular Biology and Evolution</i> , 2018 , 35, 688-699	8.3	47
34	Saturated long-chain fatty acid-producing bacteria contribute to enhanced colonic motility in rats. <i>Microbiome</i> , 2018 , 6, 107	16.6	46
33	A Clostridia-rich microbiota enhances bile acid excretion in diarrhea-predominant irritable bowel syndrome. <i>Journal of Clinical Investigation</i> , 2020 , 130, 438-450	15.9	43
32	Population genomics of finless porpoises reveal an incipient cetacean species adapted to freshwater. <i>Nature Communications</i> , 2018 , 9, 1276	17.4	37
31	CRISPR/Cascade 9-Mediated Genome Editing-Challenges and Opportunities. <i>Frontiers in Genetics</i> , 2018 , 9, 240	4.5	36
30	Bioinformatics applications on Apache Spark. <i>GigaScience</i> , 2018 , 7,	7.6	35
29	A draft genome assembly of the solar-powered sea slug <i>Elysia chlorotica</i> . <i>Scientific Data</i> , 2019 , 6, 190023.2	28.2	30
28	Oyster Shell Proteins Originate from Multiple Organs and Their Probable Transport Pathway to the Shell Formation Front. <i>PLoS ONE</i> , 2013 , 8, e66522	3.7	30

27	Whole-genome sequencing reveals novel tandem-duplication hotspots and a prognostic mutational signature in gastric cancer. <i>Nature Communications</i> , 2019 , 10, 2037	17.4	29
26	Clonal architectures predict clinical outcome in clear cell renal cell carcinoma. <i>Nature Communications</i> , 2019 , 10, 1245	17.4	29
25	Genome sequence and global sequence variation map with 5.5 million SNPs in Chinese rhesus macaque. <i>Genome Biology</i> , 2011 , 12, R63	18.3	29
24	BS-SNPer: SNP calling in bisulfite-seq data. <i>Bioinformatics</i> , 2015 , 31, 4006-8	7.2	28
23	Identification of conserved and novel microRNAs in the Pacific oyster <i>Crassostrea gigas</i> by deep sequencing. <i>PLoS ONE</i> , 2014 , 9, e104371	3.7	25
22	An effort to use human-based exome capture methods to analyze chimpanzee and macaque exomes. <i>PLoS ONE</i> , 2012 , 7, e40637	3.7	24
21	The molecular landscape of synchronous colorectal cancer reveals genetic heterogeneity. <i>Carcinogenesis</i> , 2018 , 39, 708-718	4.6	23
20	High expression of new genes in trochophore enlightening the ontogeny and evolution of trochozoans. <i>Scientific Reports</i> , 2016 , 6, 34664	4.9	22
19	Molecular Footprints of Aquatic Adaptation Including Bone Mass Changes in Cetaceans. <i>Genome Biology and Evolution</i> , 2018 , 10, 967-975	3.9	17
18	Transcriptome, genetic editing, and microRNA divergence substantiate sympatric speciation of blind mole rat, <i>Spalax</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 7584-9	11.5	17
17	The landscape of somatic mutation in sporadic Chinese colorectal cancer. <i>Oncotarget</i> , 2018 , 9, 27412-27422	3.2	16
16	Population genomic data reveal genes related to important traits of quail. <i>GigaScience</i> , 2018 , 7,	7.6	16
15	A reference gene set construction using RNA-seq of multiple tissues of Chinese giant salamander, <i>Andrias davidianus</i> . <i>GigaScience</i> , 2017 , 6, 1-7	7.6	15
14	Donkey genomes provide new insights into domestication and selection for coat color. <i>Nature Communications</i> , 2020 , 11, 6014	17.4	15
13	Evolution and functional analysis of the Pif97 gene of the Pacific oyster <i>Crassostrea gigas</i> . <i>Environmental Epigenetics</i> , 2013 , 59, 109-115	2.4	8
12	Multi-omics study in monozygotic twins confirm the contribution of de novo mutation to psoriasis. <i>Journal of Autoimmunity</i> , 2020 , 106, 102349	15.5	8
11	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	4.8	7
10	ISN Forefronts Symposium 2015: IgA Nephropathy, the Gut Microbiota, and Gut-Kidney Crosstalk. <i>Kidney International Reports</i> , 2016 , 1, 189-196	4.1	6

9	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. <i>Molecular Ecology Resources</i> , 2021 , 21, 912-923	8.4	6
8	Reply to: Transformation of naked mole-rat cells. <i>Nature</i> , 2020 , 583, E8-E13	50.4	5
7	Aragonite shells are more ancient than calcite ones in bivalves: new evidence based on omics. <i>Molecular Biology Reports</i> , 2014 , 41, 7067-71	2.8	4
6	FGF: a web tool for Fishing Gene Family in a whole genome database. <i>Nucleic Acids Research</i> , 2007 , 35, W121-5	20.1	4
5	Altered metabolome and microbiome features provide clues in understanding irritable bowel syndrome and depression comorbidity. <i>ISME Journal</i> , 2021 ,	11.9	4
4	A comprehensive investigation of metagenome assembly by linked-read sequencing. <i>Microbiome</i> , 2020 , 8, 156	16.6	4
3	Dampened PI3K/AKT signaling contributes to cancer resistance of the naked mole rat		2
2	A Massively Parallel Computational Method of Reading Index Files for SOAPsnv. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2015 , 7, 397-404	3.5	1
1	Marine Genomics: Recent Advancement and Wide-Area Applications 2016 , 97-108		