

# Xiaodong Fang

## 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.

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	Altered metabolome and microbiome features provide clues in understanding irritable bowel syndrome and depression comorbidity. <i>ISME Journal</i> , <b>2021</b> ,	11.9	4
79	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> , <b>2021</b> , 21, 912-923	8.4	6
78	Reply to: Transformation of naked mole-rat cells. <i>Nature</i> , <b>2020</b> , 583, E8-E13	50.4	5
77	A Clostridia-rich microbiota enhances bile acid excretion in diarrhea-predominant irritable bowel syndrome. <i>Journal of Clinical Investigation</i> , <b>2020</b> , 130, 438-450	15.9	43
76	Donkey genomes provide new insights into domestication and selection for coat color. <i>Nature Communications</i> , <b>2020</b> , 11, 6014	17.4	15
75	A comprehensive investigation of metagenome assembly by linked-read sequencing. <i>Microbiome</i> , <b>2020</b> , 8, 156	16.6	4
74	Multi-omics study in monozygotic twins confirm the contribution of de novo mutation to psoriasis. <i>Journal of Autoimmunity</i> , <b>2020</b> , 106, 102349	15.5	8
73	Whole-genome sequencing reveals novel tandem-duplication hotspots and a prognostic mutational signature in gastric cancer. <i>Nature Communications</i> , <b>2019</b> , 10, 2037	17.4	29
72	Clonal architectures predict clinical outcome in clear cell renal cell carcinoma. <i>Nature Communications</i> , <b>2019</b> , 10, 1245	17.4	29
71	<i>Musa balbisiana</i> genome reveals subgenome evolution and functional divergence. <i>Nature Plants</i> , <b>2019</b> , 5, 810-821	11.5	49
70	A draft genome assembly of the solar-powered sea slug <i>Elysia chlorotica</i> . <i>Scientific Data</i> , <b>2019</b> , 6, 190028.2	3.2	30
69	The genetic basis of adaptive evolution in parasitic environment from the <i>Angiostrongylus cantonensis</i> genome. <i>PLoS Neglected Tropical Diseases</i> , <b>2019</b> , 13, e0007846	4.8	7
68	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , <b>2018</b> , 557, 43-49	50.4	582
67	Population genomics of finless porpoises reveal an incipient cetacean species adapted to freshwater. <i>Nature Communications</i> , <b>2018</b> , 9, 1276	17.4	37
66	Genetic Architecture and Selection of Chinese Cattle Revealed by Whole Genome Resequencing. <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 688-699	8.3	47
65	Molecular Footprints of Aquatic Adaptation Including Bone Mass Changes in Cetaceans. <i>Genome Biology and Evolution</i> , <b>2018</b> , 10, 967-975	3.9	17
64	The molecular landscape of synchronous colorectal cancer reveals genetic heterogeneity. <i>Carcinogenesis</i> , <b>2018</b> , 39, 708-718	4.6	23

63	Genomic analysis of liver cancer unveils novel driver genes and distinct prognostic features. <i>Theranostics</i> , <b>2018</b> , 8, 1740-1751	12.1	51
62	Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , <b>2018</b> , 19, 77	18.3	75
61	Saturated long-chain fatty acid-producing bacteria contribute to enhanced colonic motility in rats. <i>Microbiome</i> , <b>2018</b> , 6, 107	16.6	46
60	CRISPR/Cascade 9-Mediated Genome Editing-Challenges and Opportunities. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 240	4.5	36
59	Bioinformatics applications on Apache Spark. <i>GigaScience</i> , <b>2018</b> , 7,	7.6	35
58	The landscape of somatic mutation in sporadic Chinese colorectal cancer. <i>Oncotarget</i> , <b>2018</b> , 9, 27412-27422	7.6	16
57	Origin and evolution of qingke barley in Tibet. <i>Nature Communications</i> , <b>2018</b> , 9, 5433	17.4	65
56	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , <b>2018</b> , 361,	33.3	167
55	Population genomic data reveal genes related to important traits of quail. <i>GigaScience</i> , <b>2018</b> , 7,	7.6	16
54	Genome of the pitcher plant <i>Cephalotus</i> reveals genetic changes associated with carnivory. <i>Nature Ecology and Evolution</i> , <b>2017</b> , 1, 59	12.3	61
53	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> , <b>2017</b> , 6, 1-13	7.6	54
52	Genome-wide sequencing of longan ( <i>Dimocarpus longan</i> Lour.) provides insights into molecular basis of its polyphenol-rich characteristics. <i>GigaScience</i> , <b>2017</b> , 6, 1-14	7.6	63
51	A reference gene set construction using RNA-seq of multiple tissues of Chinese giant salamander, <i>Andrias davidianus</i> . <i>GigaScience</i> , <b>2017</b> , 6, 1-7	7.6	15
50	ISN Forefronts Symposium 2015: IgA Nephropathy, the Gut Microbiota, and Gut Kidney Crosstalk. <i>Kidney International Reports</i> , <b>2016</b> , 1, 189-196	4.1	6
49	High expression of new genes in trochophore enlightening the ontogeny and evolution of trochozoans. <i>Scientific Reports</i> , <b>2016</b> , 6, 34664	4.9	22
48	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> , <b>2016</b> , 113, 7584-9	11.5	17
47	Distinct Subtypes of Gastric Cancer Defined by Molecular Characterization Include Novel Mutational Signatures with Prognostic Capability. <i>Cancer Research</i> , <b>2016</b> , 76, 1724-32	10.1	86
46	Whole-Genome Sequencing Reveals Diverse Models of Structural Variations in Esophageal Squamous Cell Carcinoma. <i>American Journal of Human Genetics</i> , <b>2016</b> , 98, 256-74	11	87

45	Marine Genomics: Recent Advancement and Wide-Area Applications <b>2016</b> , 97-108		
44	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> , <b>2015</b> , 47, 158-63	36.3	264
43	Genetic blueprint of the zoonotic pathogen <i>Toxocara canis</i> . <i>Nature Communications</i> , <b>2015</b> , 6, 6145	17.4	77
42	A global reference for human genetic variation. <i>Nature</i> , <b>2015</b> , 526, 68-74	50.4	8599
41	BS-SNPper: SNP calling in bisulfite-seq data. <i>Bioinformatics</i> , <b>2015</b> , 31, 4006-8	7.2	28
40	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> , <b>2015</b> , 112, E5907-15	11.5	172
39	A Massively Parallel Computational Method of Reading Index Files for SOAPsnv. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , <b>2015</b> , 7, 397-404	3.5	1
38	Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies. <i>Nature Communications</i> , <b>2015</b> , 6, 8212	17.4	111
37	Adaptation and possible ancient interspecies introgression in pigs identified by whole-genome sequencing. <i>Nature Genetics</i> , <b>2015</b> , 47, 217-25	36.3	188
36	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> , <b>2015</b> , 112, 1095-100	11.5	102
35	Spider genomes provide insight into composition and evolution of venom and silk. <i>Nature Communications</i> , <b>2014</b> , 5, 3765	17.4	169
34	Genome-wide adaptive complexes to underground stresses in blind mole rats <i>Spalax</i> . <i>Nature Communications</i> , <b>2014</b> , 5, 3966	17.4	101
33	Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. <i>Nature Communications</i> , <b>2014</b> , 5, 5594	17.4	89
32	Aragonite shells are more ancient than calcite ones in bivalves: new evidence based on omics. <i>Molecular Biology Reports</i> , <b>2014</b> , 41, 7067-71	2.8	4
31	The locust genome provides insight into swarm formation and long-distance flight. <i>Nature Communications</i> , <b>2014</b> , 5, 2957	17.4	294
30	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> , <b>2014</b> , 111, 5135-40	11.5	466
29	Adaptations to a subterranean environment and longevity revealed by the analysis of mole rat genomes. <i>Cell Reports</i> , <b>2014</b> , 8, 1354-64	10.6	124
28	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> , <b>2014</b> , 15, 1119	4.5	72

27	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> , <b>2014</b> , 9, e95543	3.7	85
26	Identification of conserved and novel microRNAs in the Pacific oyster <i>Crassostrea gigas</i> by deep sequencing. <i>PLoS ONE</i> , <b>2014</b> , 9, e104371	3.7	25
25	Genome analysis reveals insights into physiology and longevity of the Brandt's bat <i>Myotis brandtii</i> . <i>Nature Communications</i> , <b>2013</b> , 4, 2212	17.4	160
24	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> , <b>2013</b> , 45, 1459-63	36.3	326
23	Comparative analysis of bat genomes provides insight into the evolution of flight and immunity. <i>Science</i> , <b>2013</b> , 339, 456-60	33.3	377
22	Baiji genomes reveal low genetic variability and new insights into secondary aquatic adaptations. <i>Nature Communications</i> , <b>2013</b> , 4, 2708	17.4	76
21	Evolution and functional analysis of the Pif97 gene of the Pacific oyster <i>Crassostrea gigas</i> . <i>Environmental Epigenetics</i> , <b>2013</b> , 59, 109-115	2.4	8
20	Oyster Shell Proteins Originate from Multiple Organs and Their Probable Transport Pathway to the Shell Formation Front. <i>PLoS ONE</i> , <b>2013</b> , 8, e66522	3.7	30
19	The sequence and analysis of a Chinese pig genome. <i>GigaScience</i> , <b>2012</b> , 1, 16	7.6	91
18	The oyster genome reveals stress adaptation and complexity of shell formation. <i>Nature</i> , <b>2012</b> , 490, 49-54	50.4	1464
17	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , <b>2012</b> , 44, 221-5	36.3	325
16	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> , <b>2012</b> , 29, 1545-56	8.3	50
15	An effort to use human-based exome capture methods to analyze chimpanzee and macaque exomes. <i>PLoS ONE</i> , <b>2012</b> , 7, e40637	3.7	24
14	Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques. <i>Nature Biotechnology</i> , <b>2011</b> , 29, 1019-23	44.5	219
13	Genome sequence and global sequence variation map with 5.5 million SNPs in Chinese rhesus macaque. <i>Genome Biology</i> , <b>2011</b> , 12, R63	18.3	29
12	Genome sequencing reveals insights into physiology and longevity of the naked mole rat. <i>Nature</i> , <b>2011</b> , 479, 223-7	50.4	410
11	<i>Ascaris suum</i> draft genome. <i>Nature</i> , <b>2011</b> , 479, 529-33	50.4	217
10	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> , <b>2011</b> , 85, 11291-9	6.6	80

9	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , <b>2010</b> , 463, 311-7	50.4	864
8	Genomic comparison of the ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Science</i> , <b>2010</b> , 329, 1068-71	33.3	353
7	Deep RNA sequencing at single base-pair resolution reveals high complexity of the rice transcriptome. <i>Genome Research</i> , <b>2010</b> , 20, 646-54	9.7	375
6	De novo assembly of human genomes with massively parallel short read sequencing. <i>Genome Research</i> , <b>2010</b> , 20, 265-72	9.7	2084
5	SNP detection for massively parallel whole-genome resequencing. <i>Genome Research</i> , <b>2009</b> , 19, 1124-32	9.7	734
4	The genome of the cucumber, <i>Cucumis sativus</i> L. <i>Nature Genetics</i> , <b>2009</b> , 41, 1275-81	36.3	1031
3	The diploid genome sequence of an Asian individual. <i>Nature</i> , <b>2008</b> , 456, 60-5	50.4	744
2	FGF: a web tool for Fishing Gene Family in a whole genome database. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, W121-5	20.1	4
1	Dampened PI3K/AKT signaling contributes to cancer resistance of the naked mole rat		2