

Xun Xu

List of Publications by Year in descending order

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Version: 2024-02-01

311
papers

83,284
citations

1457

107
h-index

528

266
g-index

385
all docs

385
docs citations

385
times ranked

103483
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	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	2,860
3	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	6.0	2,424
4	Dynamics and Stabilization of the Human Gut Microbiome during the First Year of Life. <i>Cell Host and Microbe</i> , 2015, 17, 690-703.	5.1	2,276
5	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014, 346, 763-767.	6.0	2,096
6	Genome sequence and analysis of the tuber crop potato. <i>Nature</i> , 2011, 475, 189-195.	13.7	1,912
7	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	9.4	1,893
8	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	9.4	1,664
9	Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude. <i>Science</i> , 2010, 329, 75-78.	6.0	1,339
10	The oral and gut microbiomes are perturbed in rheumatoid arthritis and partly normalized after treatment. <i>Nature Medicine</i> , 2015, 21, 895-905.	15.2	1,306
11	Taxonomic structure and functional association of foxtail millet root microbiome. <i>GigaScience</i> , 2017, 6, 1-12.	3.3	1,228
12	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	13.7	1,190
13	Gut microbiome and serum metabolome alterations in obesity and after weight-loss intervention. <i>Nature Medicine</i> , 2017, 23, 859-868.	15.2	1,074
14	Genome sequence of cultivated Upland cotton (<i>Gossypium hirsutum</i> TM-1) provides insights into genome evolution. <i>Nature Biotechnology</i> , 2015, 33, 524-530.	9.4	1,064
15	Gut microbiome development along the colorectal adenoma-carcinoma sequence. <i>Nature Communications</i> , 2015, 6, 6528.	5.8	1,062
16	Draft genome sequence of chickpea (<i>Cicer arietinum</i>) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013, 31, 240-246.	9.4	1,049
17	The gut microbiome in atherosclerotic cardiovascular disease. <i>Nature Communications</i> , 2017, 8, 845.	5.8	1,029
18	Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection. <i>Nature Genetics</i> , 2010, 42, 1053-1059.	9.4	987

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19	The Brassica oleracea genome reveals the asymmetrical evolution of polyploid genomes. Nature Communications, 2014, 5, 3930.	5.8	918
20	Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. Nature, 2014, 512, 194-197.	13.7	904
21	Genome sequence of the cultivated cotton Gossypium arboreum. Nature Genetics, 2014, 46, 567-572.	9.4	883
22	Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer. Gut, 2017, 66, 70-78.	6.1	865
23	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). Genome Research, 2013, 23, 396-408.	2.4	832
24	SOAPdenovo-Trans: <i>de novo</i> transcriptome assembly with short RNA-Seq reads. Bioinformatics, 2014, 30, 1660-1666.	1.8	826
25	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. Nature Biotechnology, 2012, 30, 105-111.	9.4	818
26	Comparative population genomics of maize domestication and improvement. Nature Genetics, 2012, 44, 808-811.	9.4	816
27	Draft genome sequence of pigeonpea (<i>Cajanus cajan</i>), an orphan legume crop of resource-poor farmers. Nature Biotechnology, 2012, 30, 83-89.	9.4	788
28	Correction of a pathogenic gene mutation in human embryos. Nature, 2017, 548, 413-419.	13.7	781
29	Sparse whole-genome sequencing identifies two loci for major depressive disorder. Nature, 2015, 523, 588-591.	13.7	777
30	The genome sequences of <i>Arachis duranensis</i> and <i>Arachis ipaensis</i> , the diploid ancestors of cultivated peanut. Nature Genetics, 2016, 48, 438-446.	9.4	761
31	COLD1 Confers Chilling Tolerance in Rice. Cell, 2015, 160, 1209-1221.	13.5	724
32	The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. Nature Biotechnology, 2011, 29, 735-741.	9.4	699
33	Earth BioGenome Project: Sequencing life for the future of life. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4325-4333.	3.3	652
34	Genome sequence of foxtail millet (<i>Setaria italica</i>) provides insights into grass evolution and biofuel potential. Nature Biotechnology, 2012, 30, 549-554.	9.4	636
35	Single-Cell Exome Sequencing Reveals Single-Nucleotide Mutation Characteristics of a Kidney Tumor. Cell, 2012, 148, 886-895.	13.5	622
36	Maize HapMap2 identifies extant variation from a genome in flux. Nature Genetics, 2012, 44, 803-807.	9.4	577

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37	The microbiota continuum along the female reproductive tract and its relation to uterine-related diseases. <i>Nature Communications</i> , 2017, 8, 875.	5.8	572
38	An atlas of the protein-coding genes in the human, pig, and mouse brain. <i>Science</i> , 2020, 367, .	6.0	517
39	Single-Cell Exome Sequencing and Monoclonal Evolution of a JAK2-Negative Myeloproliferative Neoplasm. <i>Cell</i> , 2012, 148, 873-885.	13.5	503
40	Rapid, low-input, low-bias construction of shotgun fragment libraries by high-density in vitro transposition. <i>Genome Biology</i> , 2010, 11, R119.	13.9	499
41	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra</i>) Tj ETQq1 1 0.784314 1gBT /Over	9.4	479
42	The genome of <i>Prunus mume</i> . <i>Nature Communications</i> , 2012, 3, 1318.	5.8	441
43	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , 2010, 42, 1027-1030.	9.4	439
44	Spatiotemporal transcriptomic atlas of mouse organogenesis using DNA nanoball-patterned arrays. <i>Cell</i> , 2022, 185, 1777-1792.e21.	13.5	437
45	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	6.0	436
46	The <i>Symbiodinium kawagutii</i> genome illuminates dinoflagellate gene expression and coral symbiosis. <i>Science</i> , 2015, 350, 691-694.	6.0	430
47	A reference gene catalogue of the pig gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16161.	5.9	416
48	The genome sequence of the orchid <i>Phalaenopsis equestris</i> . <i>Nature Genetics</i> , 2015, 47, 65-72.	9.4	413
49	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. <i>Nature Biotechnology</i> , 2019, 37, 179-185.	9.4	402
50	Single-cell landscape of the ecosystem in early-relapse hepatocellular carcinoma. <i>Cell</i> , 2021, 184, 404-421.e16.	13.5	399
51	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
52	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	4.7	391
53	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012, 44, 221-225.	9.4	383
54	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	9.4	356

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55	Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm (<i>Bombyx mori</i>). <i>Genome Biology</i> , 2013, 14, 107. doi:10.1186/gb-2013-14-107	6.0	342
56	Genomic landscapes of Chinese hamster ovary cell lines as revealed by the <i>Cricetulus griseus</i> draft genome. <i>Nature Biotechnology</i> , 2013, 31, 759-765.	9.4	340
57	Structural genomic changes underlie alternative reproductive strategies in the ruff (<i>Philomachus pinnatus</i>). <i>Genome Biology</i> , 2013, 14, 107. doi:10.1186/gb-2013-14-107	9.4	340
58	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , 2018, 361, 1233-1237.	6.0	339
59	Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing. <i>Nature Communications</i> , 2014, 5, 4340.	5.8	332
60	Genome assembly with in vitro proximity ligation data and whole-genome triplication in lettuce. <i>Nature Communications</i> , 2017, 8, 14953.	5.8	330
61	Genomes of Subaerial Zygnematophyceae Provide Insights into Land Plant Evolution. <i>Cell</i> , 2019, 179, 1057-1067.e14.	13.5	320
62	Analyses of gut microbiota and plasma bile acids enable stratification of patients for antidiabetic treatment. <i>Nature Communications</i> , 2017, 8, 1785.	5.8	312
63	The structure and function of the global citrus rhizosphere microbiome. <i>Nature Communications</i> , 2018, 9, 4894.	5.8	304
64	Venom gland transcriptomes of two elapid snakes (<i>Bungarus multicinctus</i> and <i>Naja atra</i>) and evolution of toxin genes. <i>BMC Genomics</i> , 2011, 12, 1.	1.2	300
65	Single-Cell Sequencing of Peripheral Mononuclear Cells Reveals Distinct Immune Response Landscapes of COVID-19 and Influenza Patients. <i>Immunity</i> , 2020, 53, 685-696.e3.	6.6	299
66	The <i>Sinocyclocheilus</i> cavefish genome provides insights into cave adaptation. <i>BMC Biology</i> , 2016, 14, 1.	1.7	292
67	Redefining the structural motifs that determine <i>scp</i> RNA binding and <i>scp</i> RNA editing by pentatricopeptide repeat proteins in land plants. <i>Plant Journal</i> , 2016, 85, 532-547.	2.8	267
68	Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome. <i>Cell Systems</i> , 2016, 3, 572-584.e3.	2.9	261
69	Genesis, Evolution and Prevalence of H5N6 Avian Influenza Viruses in China. <i>Cell Host and Microbe</i> , 2016, 20, 810-821.	5.1	257
70	<i>Ascaris suum</i> draft genome. <i>Nature</i> , 2011, 479, 529-533.	13.7	246
71	Genome sequencing of the high oil crop sesame provides insight into oil biosynthesis. <i>Genome Biology</i> , 2014, 15, R39.	13.9	245
72	CNSA: a data repository for archiving omics data. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	243

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73	The high-quality genome of <i>Brassica napus</i> cultivar 'ZS11' reveals the introgression history in semi-winter morphotype. <i>Plant Journal</i> , 2017, 92, 452-468.	2.8	233
74	Draft genome of the living fossil <i>Ginkgo biloba</i> . <i>GigaScience</i> , 2016, 5, 49.	3.3	232
75	Genomic and oncogenic preference of HBV integration in hepatocellular carcinoma. <i>Nature Communications</i> , 2016, 7, 12992.	5.8	228
76	Molecular Signatures of Major Depression. <i>Current Biology</i> , 2015, 25, 1146-1156.	1.8	224
77	Design and Characterization of a 52K SNP Chip for Goats. <i>PLoS ONE</i> , 2014, 9, e86227.	1.1	220
78	Resequencing of 429 chickpea accessions from 45 countries provides insights into genome diversity, domestication and agronomic traits. <i>Nature Genetics</i> , 2019, 51, 857-864.	9.4	219
79	Genomic Analyses from Non-invasive Prenatal Testing Reveal Genetic Associations, Patterns of Viral Infections, and Chinese Population History. <i>Cell</i> , 2018, 175, 347-359.e14.	13.5	213
80	Metagenome-wide association of gut microbiome features for schizophrenia. <i>Nature Communications</i> , 2020, 11, 1612.	5.8	204
81	Transplantation of microbiota from drug-free patients with schizophrenia causes schizophrenia-like abnormal behaviors and dysregulated kynurenine metabolism in mice. <i>Molecular Psychiatry</i> , 2020, 25, 2905-2918.	4.1	202
82	Genome-wide characteristics of de novo mutations in autism. <i>Npj Genomic Medicine</i> , 2016, 1, 160271-1602710.	1.7	200
83	Allelic diversity in an NLR gene <i>BPH9</i> enables rice to combat planthopper variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12850-12855.	3.3	196
84	Construction of the third-generation <i>Zea mays</i> haplotype map. <i>GigaScience</i> , 2018, 7, 1-12.	3.3	191
85	Deep sequencing of the MHC region in the Chinese population contributes to studies of complex disease. <i>Nature Genetics</i> , 2016, 48, 740-746.	9.4	188
86	Efficient and unique cobarcoding of second-generation sequencing reads from long DNA molecules enabling cost-effective and accurate sequencing, haplotyping, and de novo assembly. <i>Genome Research</i> , 2019, 29, 798-808.	2.4	176
87	CNGBdb: China National GeneBank DataBase. <i>Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji</i> , 2020, 42, 799-809.	0.1	170
88	10KP: A phylodiverse genome sequencing plan. <i>GigaScience</i> , 2018, 7, 1-9.	3.3	169
89	Assessment of the cPAS-based BGISEQ-500 platform for metagenomic sequencing. <i>GigaScience</i> , 2018, 7, 1-8.	3.3	168
90	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. <i>Nature Communications</i> , 2015, 6, 5969.	5.8	164

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91	Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. <i>Science</i> , 2017, 355, .	6.0	163
92	Initial whole-genome sequencing and analysis of the host genetic contribution to COVID-19 severity and susceptibility. <i>Cell Discovery</i> , 2020, 6, 83.	3.1	159
93	Bph6 encodes an exocyst-localized protein and confers broad resistance to planthoppers in rice. <i>Nature Genetics</i> , 2018, 50, 297-306.	9.4	158
94	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. <i>Nature Communications</i> , 2019, 10, 470.	5.8	156
95	TGS-GapCloser: A fast and accurate gap closer for large genomes with low coverage of error-prone long reads. <i>GigaScience</i> , 2020, 9, .	3.3	156
96	Rapid detection of structural variation in a human genome using nanochannel-based genome mapping technology. <i>GigaScience</i> , 2014, 3, 34.	3.3	153
97	Integrated genome sequence and linkage map of physic nut (<i>Jatropha curcas</i> L.), a biodiesel plant. <i>Plant Journal</i> , 2015, 81, 810-821.	2.8	149
98	Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. <i>Nature Plants</i> , 2020, 6, 95-106.	4.7	146
99	Novel loci and pathways significantly associated with longevity. <i>Scientific Reports</i> , 2016, 6, 21243.	1.6	145
100	The genetic basis for ecological adaptation of the Atlantic herring revealed by genome sequencing. <i>ELife</i> , 2016, 5, .	2.8	143
101	Integrated metabolomics and metagenomics analysis of plasma and urine identified microbial metabolites associated with coronary heart disease. <i>Scientific Reports</i> , 2016, 6, 22525.	1.6	143
102	High-purity Prostate Circulating Tumor Cell Isolation by a Polymer Nanofiber-Embedded Microchip for Whole Exome Sequencing. <i>Advanced Materials</i> , 2013, 25, 2897-2902.	11.1	142
103	Comparison of variations detection between whole-genome amplification methods used in single-cell resequencing. <i>GigaScience</i> , 2015, 4, 37.	3.3	141
104	Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. <i>Nature Communications</i> , 2014, 5, 5594.	5.8	135
105	Impact of early events and lifestyle on the gut microbiota and metabolic phenotypes in young school-age children. <i>Microbiome</i> , 2019, 7, 2.	4.9	135
106	Comparative population genomics reveals the domestication history of the peach, <i>Prunus persica</i> , and human influences on perennial fruit crops. <i>Genome Biology</i> , 2014, 15, 415.	3.8	134
107	Mendelian randomization analyses support causal relationships between blood metabolites and the gut microbiome. <i>Nature Genetics</i> , 2022, 54, 52-61.	9.4	134
108	Whole-genome and Transcriptome Sequencing of Prostate Cancer Identify New Genetic Alterations Driving Disease Progression. <i>European Urology</i> , 2018, 73, 322-339.	0.9	130

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109	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017, 548, 87-91.	13.7	130
110	SCRaMble generates designed combinatorial stochastic diversity in synthetic chromosomes. <i>Genome Research</i> , 2016, 26, 36-49.	2.4	124
111	The Earth BioGenome Project 2020: Starting the clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	124
112	Discovery of biclonal origin and a novel oncogene SLC12A5 in colon cancer by single-cell sequencing. <i>Cell Research</i> , 2014, 24, 701-712.	5.7	123
113	cPAS-based sequencing on the BGISEQ-500 to explore small non-coding RNAs. <i>Clinical Epigenetics</i> , 2016, 8, 123.	1.8	122
114	IMonitor: A Robust Pipeline for TCR and BCR Repertoire Analysis. <i>Genetics</i> , 2015, 201, 459-472.	1.2	119
115	The draft genomes of five agriculturally important African orphan crops. <i>GigaScience</i> , 2019, 8, .	3.3	108
116	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	13.7	106
117	Multiple approaches for massively parallel sequencing of SARS-CoV-2 genomes directly from clinical samples. <i>Genome Medicine</i> , 2020, 12, 57.	3.6	104
118	A method for noninvasive detection of fetal large deletions/duplications by low coverage massively parallel sequencing. <i>Prenatal Diagnosis</i> , 2013, 33, 584-590.	1.1	103
119	Reference genome of wild goat (<i>capra aegagrus</i>) and sequencing of goat breeds provide insight into genic basis of goat domestication. <i>BMC Genomics</i> , 2015, 16, 431.	1.2	103
120	The Power of Inbreeding: NGS-Based GWAS of Rice Reveals Convergent Evolution during Rice Domestication. <i>Molecular Plant</i> , 2016, 9, 975-985.	3.9	102
121	A single bacterium restores the microbiome dysbiosis to protect bones from destruction in a rat model of rheumatoid arthritis. <i>Microbiome</i> , 2019, 7, 107.	4.9	101
122	Distinct gut metagenomics and metaproteomics signatures in prediabetics and treatment-naïve type 2 diabetics. <i>EBioMedicine</i> , 2019, 47, 373-383.	2.7	101
123	Single-cell sequencing analysis characterizes common and cell-lineage-specific mutations in a muscle-invasive bladder cancer. <i>GigaScience</i> , 2012, 1, 12.	3.3	99
124	Smart Enrichment and Facile Separation of Oil from Emulsions and Mixtures by Superhydrophobic/Superoleophilic Particles. <i>ACS Applied Materials & Interfaces</i> , 2015, 7, 10475-10481.	4.0	99
125	Resequencing 545 ginkgo genomes across the world reveals the evolutionary history of the living fossil. <i>Nature Communications</i> , 2019, 10, 4201.	5.8	99
126	Clinical outcome of preimplantation genetic diagnosis and screening using next generation sequencing. <i>GigaScience</i> , 2014, 3, 30.	3.3	97

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127	Inherited bone marrow failure associated with germline mutation of ACD, the gene encoding telomere protein TPP1. <i>Blood</i> , 2014, 124, 2767-2774.	0.6	97
128	The <i>Tarenaya hassleriana</i> Genome Provides Insight into Reproductive Trait and Genome Evolution of Crucifers. <i>Plant Cell</i> , 2013, 25, 2813-2830.	3.1	95
129	Keppen-Lubinsky Syndrome Is Caused by Mutations in the Inwardly Rectifying K ⁺ Channel Encoded by KCNJ6. <i>American Journal of Human Genetics</i> , 2015, 96, 295-300.	2.6	95
130	HIVID: An efficient method to detect HBV integration using low coverage sequencing. <i>Genomics</i> , 2013, 102, 338-344.	1.3	94
131	Using SOAPaligner for Short Reads Alignment. <i>Current Protocols in Bioinformatics</i> , 2013, 44, 11.11.1-17.	25.8	94
132	A comparison of isolated circulating tumor cells and tissue biopsies using whole-genome sequencing in prostate cancer. <i>Oncotarget</i> , 2015, 6, 44781-44793.	0.8	94
133	Bajji genomes reveal low genetic variability and new insights into secondary aquatic adaptations. <i>Nature Communications</i> , 2013, 4, 2708.	5.8	93
134	Influenza H7N9 and H9N2 Viruses: Coexistence in Poultry Linked to Human H7N9 Infection and Genome Characteristics. <i>Journal of Virology</i> , 2014, 88, 3423-3431.	1.5	93
135	Frequent alterations in cytoskeleton remodelling genes in primary and metastatic lung adenocarcinomas. <i>Nature Communications</i> , 2015, 6, 10131.	5.8	93
136	The Asian arowana (<i>Scleropages formosus</i>) genome provides new insights into the evolution of an early lineage of teleosts. <i>Scientific Reports</i> , 2016, 6, 24501.	1.6	89
137	The single-cell stereo-seq reveals region-specific cell subtypes and transcriptome profiling in <i>Arabidopsis</i> leaves. <i>Developmental Cell</i> , 2022, 57, 1299-1310.e4.	3.1	89
138	Introgression from Domestic Goat Generated Variation at the Major Histocompatibility Complex of Alpine Ibex. <i>PLoS Genetics</i> , 2014, 10, e1004438.	1.5	87
139	The Different T-cell Receptor Repertoires in Breast Cancer Tumors, Draining Lymph Nodes, and Adjacent Tissues. <i>Cancer Immunology Research</i> , 2017, 5, 148-156.	1.6	87
140	Rolling back human pluripotent stem cells to an eight-cell embryo-like stage. <i>Nature</i> , 2022, 605, 315-324.	13.7	87
141	Sex- and age-related trajectories of the adult human gut microbiota shared across populations of different ethnicities. <i>Nature Aging</i> , 2021, 1, 87-100.	5.3	86
142	POPDC1S201F causes muscular dystrophy and arrhythmia by affecting protein trafficking. <i>Journal of Clinical Investigation</i> , 2015, 126, 239-253.	3.9	85
143	Pregnancy-Induced Metabolic Phenotype Variations in Maternal Plasma. <i>Journal of Proteome Research</i> , 2014, 13, 1527-1536.	1.8	84
144	The genome of <i>Prasinoderma coloniale</i> unveils the existence of a third phylum within green plants. <i>Nature Ecology and Evolution</i> , 2020, 4, 1220-1231.	3.4	84

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145	Enhancing CRISPR-Cas9 gRNA efficiency prediction by data integration and deep learning. <i>Nature Communications</i> , 2021, 12, 3238.	5.8	81
146	Cell transcriptomic atlas of the non-human primate <i>Macaca fascicularis</i> . <i>Nature</i> , 2022, 604, 723-731.	13.7	81
147	The <i>Cycas</i> genome and the early evolution of seed plants. <i>Nature Plants</i> , 2022, 8, 389-401.	4.7	80
148	PIRD: Pan Immune Repertoire Database. <i>Bioinformatics</i> , 2020, 36, 897-903.	1.8	79
149	A western Sahara centre of domestication inferred from pearl millet genomes. <i>Nature Ecology and Evolution</i> , 2018, 2, 1377-1380.	3.4	78
150	Recent breeding programs enhanced genetic diversity in both desi and kabuli varieties of chickpea (<i>Cicer arietinum</i> L.). <i>Scientific Reports</i> , 2016, 6, 38636.	1.6	77
151	The sacred lotus genome provides insights into the evolution of flowering plants. <i>Plant Journal</i> , 2013, 76, 557-567.	2.8	75
152	Two distinct metacommunities characterize the gut microbiota in Crohn's disease patients. <i>GigaScience</i> , 2017, 6, 1-11.	3.3	75
153	The trans-omics landscape of COVID-19. <i>Nature Communications</i> , 2021, 12, 4543.	5.8	75
154	Distinct biological ages of organs and systems identified from a multi-omics study. <i>Cell Reports</i> , 2022, 38, 110459.	2.9	74
155	De novo assembly of a haplotype-resolved human genome. <i>Nature Biotechnology</i> , 2015, 33, 617-622.	9.4	73
156	The genetic architecture of floral traits in the woody plant <i>Prunus mume</i> . <i>Nature Communications</i> , 2018, 9, 1702.	5.8	73
157	African Orphan Crops Consortium (AOCC): status of developing genomic resources for African orphan crops. <i>Planta</i> , 2019, 250, 989-1003.	1.6	73
158	Analytical and Decision Support Tools for Genomics-Assisted Breeding. <i>Trends in Plant Science</i> , 2016, 21, 354-363.	4.3	70
159	The genomic landscape of Epstein-Barr virus-associated pulmonary lymphoepithelioma-like carcinoma. <i>Nature Communications</i> , 2019, 10, 3108.	5.8	69
160	The metagenome of the female upper reproductive tract. <i>GigaScience</i> , 2018, 7, .	3.3	68
161	A Single Cell Level Based Method for Copy Number Variation Analysis by Low Coverage Massively Parallel Sequencing. <i>PLoS ONE</i> , 2013, 8, e54236.	1.1	66
162	A Robust Approach for Blind Detection of Balanced Chromosomal Rearrangements with Whole-Genome Low-Coverage Sequencing. <i>Human Mutation</i> , 2014, 35, 625-636.	1.1	65

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163	Mutation in mitochondrial ribosomal protein S7 (MRPS7) causes congenital sensorineural deafness, progressive hepatic and renal failure and lactic acidemia. <i>Human Molecular Genetics</i> , 2015, 24, 2297-2307.	1.4	64
164	Genome-wide determination of on-target and off-target characteristics for RNA-guided DNA methylation by dCas9 methyltransferases. <i>GigaScience</i> , 2018, 7, 1-19.	3.3	64
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