

Xun Xu

List of PR Articles by Year in descending order

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318

PR articles

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PR citations

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117863

citing authors

#	ARTICLE	IF	PR CITATIONS
1	STOmicsDB: a comprehensive database for spatial transcriptomics data sharing, analysis and visualization. <i>Nucleic Acids Research</i> , 2024, 52, D1053-D1061.	15.7	122
2	A genome-wide association study reveals the relationship between human genetic variation and the nasal microbiome. <i>Communications Biology</i> , 2024, 7, .	4.4	16
3	Region-specific transcriptomic responses to obesity and diabetes in macaque hypothalamus. <i>Cell Metabolism</i> , 2024, 36, 438-453.e6.	26.2	29
4	SAW: an efficient and accurate data analysis workflow for Stereo-seq spatial transcriptomics. <i>GigaByte</i> , 2024, 2024, 1-12.	1.5	33
5	BatchEval Pipeline: batch effect evaluation workflow for multiple datasets joint analysis. <i>GigaByte</i> , 2024, 2024, 1-13.	1.5	1
6	Deciphering spatial domains from spatially resolved transcriptomics with Siamese graph autoencoder. <i>GigaScience</i> , 2024, 13, .	3.2	7
7	Generating single-cell gene expression profiles for high-resolution spatial transcriptomics based on cell boundary images. <i>GigaByte</i> , 2024, 2024, 1-13.	1.5	3
8	EAGS: efficient and adaptive Gaussian smoothing applied to high-resolved spatial transcriptomics. <i>GigaScience</i> , 2024, 13, .	3.2	12
9	Spatially resolved single-cell atlas of ascidian endostyle provides insight into the origin of vertebrate pharyngeal organs. <i>Science Advances</i> , 2024, 10, .	11.0	10
10	A spatiotemporal atlas of mouse liver homeostasis and regeneration. <i>Nature Genetics</i> , 2024, 56, 953-969.	26.1	53
11	Consistent signatures in the human gut microbiome of old- and young-onset colorectal cancer. <i>Nature Communications</i> , 2024, 15, .	13.9	34
12	Multimodal cell atlas of the ageing human skeletal muscle. <i>Nature</i> , 2024, 629, 154-164.	38.7	116
13	A single-cell transcriptome atlas reveals the trajectory of early cell fate transition during callus induction in <i>Arabidopsis</i> . <i>Plant Communications</i> , 2024, 5, 100941.	9.6	25
14	Signatures of Adaptation and Purifying Selection in Highland Populations of <i>Dasiphora fruticosa</i> . <i>Molecular Biology and Evolution</i> , 2024, 41, .	4.7	14
15	A spatial transcriptome map of the developing maize ear. <i>Nature Plants</i> , 2024, 10, 815-827.	11.9	49
16	A single-cell transcriptome atlas of human euploid and aneuploid blastocysts. <i>Nature Genetics</i> , 2024, 56, 1468-1481.	26.1	14
17	Divergent age-associated and metabolism-associated gut microbiome signatures modulate cardiovascular disease risk. <i>Nature Medicine</i> , 2024, 30, 1722-1731.	39.5	44
18	Deciphering spatial domains from spatial multi-omics with SpatialGlue. <i>Nature Methods</i> , 2024, 21, 1658-1667.	25.9	96

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19	spatiAlign: an unsupervised contrastive learning model for data integration of spatially resolved transcriptomics. <i>GigaScience</i> , 2024, 13, .	3.2	6
20	Unlocking plant genetics with telomere-to-telomere genome assemblies. <i>Nature Genetics</i> , 2024, 56, 1788-1799.	26.1	54
21	Mapping the molecular landscape of <i>Lotus japonicus</i> nodule organogenesis through spatiotemporal transcriptomics. <i>Nature Communications</i> , 2024, 15, .	13.9	17
22	Prognostic genome and transcriptome signatures in colorectal cancers. <i>Nature</i> , 2024, 633, 137-146.	38.7	100
23	Spatiotemporal omics for biology and medicine. <i>Cell</i> , 2024, 187, 4488-4519.	34.1	130
24	Global marine microbial diversity and its potential in bioprospecting. <i>Nature</i> , 2024, 633, 371-379.	38.7	111
25	Insights into the assembly of the neovaginal microbiota in Mayer-Rokitansky-K�ster-Hauser (MRKH) syndrome patients. <i>Nature Communications</i> , 2024, 15, .	13.9	3
26	Cross-species single-cell spatial transcriptomic atlases of the cerebellar cortex. <i>Science</i> , 2024, 385, .	36.4	36
27	Single-cell spatiotemporal analysis reveals alveolar dendritic cell�T cell immunity hubs defending against pulmonary infection. <i>Cell Discovery</i> , 2024, 10, .	9.6	19
28	Single-cell spatiotemporal analysis of the lungs reveals Slamf9+ macrophages involved in viral clearance and inflammation resolution. <i>Cell Discovery</i> , 2024, 10, .	9.6	19
29	A spatiotemporal transcriptomic atlas of mouse placentation. <i>Cell Discovery</i> , 2024, 10, .	9.6	30
30	StereoSITE: a framework to spatially and quantitatively profile the cellular neighborhood organized iTME. <i>GigaScience</i> , 2024, 13, .	3.2	7
31	Computational Approaches and Challenges in Spatial Transcriptomics. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 24-47.	6.2	120
32	The genomic landscape of reference genomes of cultivated human gut bacteria. <i>Nature Communications</i> , 2023, 14, .	13.9	53
33	Inbreeding depression explains killer whale population dynamics. <i>Nature Ecology and Evolution</i> , 2023, 7, 675-686.	10.3	89
34	Spatially resolved transcriptomics: a comprehensive review of their technological advances, applications, and challenges. <i>Journal of Genetics and Genomics</i> , 2023, 50, 625-640.	5.0	133
35	An invasive zone in human liver cancer identified by Stereo-seq promotes hepatocyte�tumor cell crosstalk, local immunosuppression and tumor progression. <i>Cell Research</i> , 2023, 33, 585-603.	12.5	153
36	A catalog of bacterial reference genomes from cultivated human oral bacteria. <i>Npj Biofilms and Microbiomes</i> , 2023, 9, .	8.1	27

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37	Single-cell spatial transcriptome reveals cell-type organization in the macaque cortex. <i>Cell</i> , 2023, 186, 3726-3743.e24.	34.1	167
38	The complete and fully-phased diploid genome of a male Han Chinese. <i>Cell Research</i> , 2023, 33, 745-761.	12.5	64
39	The STROMICS genome study: deep whole-genome sequencing and analysis of 10K Chinese patients with ischemic stroke reveal complex genetic and phenotypic interplay. <i>Cell Discovery</i> , 2023, 9, .	9.6	54
40	Chromosome-scale genomes of commercial timber trees (<i>Ochroma pyramidale</i> , <i>Mesua ferrea</i> , and <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50</i>)	5.7	21
41	Spatial transcriptomics drives a new era in plant research. <i>Plant Journal</i> , 2023, 116, 1571-1581.	6.2	59
42	Balanophora genomes display massively convergent evolution with other extreme holoparasites and provide novel insights into parasite-host interactions. <i>Nature Plants</i> , 2023, 9, 1627-1642.	11.9	32
43	A single-cell atlas of West African lungfish respiratory system reveals evolutionary adaptations to terrestrialization. <i>Nature Communications</i> , 2023, 14, .	13.9	6
44	A robust yeast biocontainment system with two-layered regulation switch dependent on unnatural amino acid. <i>Nature Communications</i> , 2023, 14, .	13.9	26
45	A high-resolution haplotype-resolved Reference panel constructed from the China Kadoorie Biobank Study. <i>Nucleic Acids Research</i> , 2023, 51, 11770-11782.	15.7	8
46	Chromosome-level genomes of three key <i>Allium</i> crops and their trait evolution. <i>Nature Genetics</i> , 2023, 55, 1976-1986.	26.1	41
47	Chromosome-scale genomes of commercially important mahoganies, <i>Swietenia macrophylla</i> and <i>Khaya senegalensis</i> . <i>Scientific Data</i> , 2023, 10, .	5.7	7
48	Single cell multi-omics reveal intra-cell-line heterogeneity across human cancer cell lines. <i>Nature Communications</i> , 2023, 14, .	13.9	66
49	Life History Recorded in the Vagino-Cervical Microbiome Along with Multi-Omes. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 304-321.	6.2	33
50	Chromosome-scale assembly and whole-genome sequencing of 266 giant panda roundworms provide insights into their evolution, adaptation and potential drug targets. <i>Molecular Ecology Resources</i> , 2022, 22, 768-785.	4.8	8
51	Over 50,000 Metagenomically Assembled Draft Genomes for the Human Oral Microbiome Reveal New Taxa. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 246-259.	6.2	77
52	Landscapes and dynamic diversifications of B-cell receptor repertoires in COVID-19 patients. <i>Human Immunology</i> , 2022, 83, 119-129.	1.0	28
53	Mendelian randomization analyses support causal relationships between blood metabolites and the gut microbiome. <i>Nature Genetics</i> , 2022, 54, 52-61.	26.1	294
54	Plasma cell-free RNA characteristics in COVID-19 patients. <i>Genome Research</i> , 2022, 32, 228-241.	4.6	44

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55	The Earth BioGenome Project 2020: Starting the clock. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.6	279
56	Genome-wide annotation of protein-coding genes in pig. BMC Biology, 2022, 20, .	4.0	29
57	Genomes shed light on the evolution of <i>Begonia</i> , a mega-diverse genus. New Phytologist, 2022, 234, 295-310.	8.1	37
58	Clinical challenges of tissue preparation for spatial transcriptome. Clinical and Translational Medicine, 2022, 12, .	5.7	35
59	Genome of <i>Hippophae rhamnoides</i> provides insights into a conserved molecular mechanism in actinorhizal and rhizobial symbioses. New Phytologist, 2022, 235, 276-291.	8.1	40
60	Distinct biological ages of organs and systems identified from a multi-omics study. Cell Reports, 2022, 38, 110459.	6.4	195
61	Rolling back human pluripotent stem cells to an eight-cell embryo-like stage. Nature, 2022, 605, 315-324.	38.7	203
62	Clinical and translational values of spatial transcriptomics. Signal Transduction and Targeted Therapy, 2022, 7, .	43.9	158
63	The tRNA discriminator base defines the mutual orthogonality of two distinct pyrrolysyl-tRNA synthetase/tRNAPyl pairs in the same organism. Nucleic Acids Research, 2022, 50, 4601-4615.	15.7	11
64	The Cycas genome and the early evolution of seed plants. Nature Plants, 2022, 8, 389-401.	11.9	175
65	Cell transcriptomic atlas of the non-human primate <i>Macaca fascicularis</i> . Nature, 2022, 604, 723-731.	38.7	175
66	Towards practical and robust DNA-based data archiving using the yin-yang codec system. Nature Computational Science, 2022, 2, 234-242.	11.8	127
67	The single-cell stereo-seq reveals region-specific cell subtypes and transcriptome profiling in Arabidopsis leaves. Developmental Cell, 2022, 57, 1299-1310.e4.	7.8	220
68	Spatiotemporal mapping of gene expression landscapes and developmental trajectories during zebrafish embryogenesis. Developmental Cell, 2022, 57, 1284-1298.e5.	7.8	139
69	High-resolution 3D spatiotemporal transcriptomic maps of developing Drosophila embryos and larvae. Developmental Cell, 2022, 57, 1271-1283.e4.	7.8	135
70	Spatiotemporal transcriptomic atlas of mouse organogenesis using DNA nanoball-patterned arrays. Cell, 2022, 185, 1777-1792.e21.	34.1	1,391
71	Genomic architecture of fetal central nervous system anomalies using whole-genome sequencing. Npj Genomic Medicine, 2022, 7, .	4.3	21
72	A single-cell transcriptomic atlas tracking the neural basis of division of labour in an ant superorganism. Nature Ecology and Evolution, 2022, 6, 1191-1204.	10.3	47

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73	CRISPR-mediated MECOM depletion retards tumor growth by reducing cancer stem cell properties in lung squamous cell carcinoma. <i>Molecular Therapy</i> , 2022, 30, 3341-3357.	10.4	18
74	Endothelial cell heterogeneity and microglia regulons revealed by a pig cell landscape at single-cell level. <i>Nature Communications</i> , 2022, 13, .	13.9	77
75	Massively targeted evaluation of therapeutic CRISPR off-targets in cells. <i>Nature Communications</i> , 2022, 13, .	13.9	33
76	Single-cell Stereo-seq reveals induced progenitor cells involved in axolotl brain regeneration. <i>Science</i> , 2022, 377, .	36.4	254
77	GWAS, MWAS and mGWAS provide insights into precision agriculture based on genotype-dependent microbial effects in foxtail millet. <i>Nature Communications</i> , 2022, 13, .	13.9	109
78	Spatiotemporal Omics-Refining the landscape of precision medicine. , 2022, 1, 84-102.		22
79	Spatially resolved gene regulatory and disease-related vulnerability map of the adult Macaque cortex. <i>Nature Communications</i> , 2022, 13, .	13.9	39
80	Spatial-ID: a cell typing method for spatially resolved transcriptomics via transfer learning and spatial embedding. <i>Nature Communications</i> , 2022, 13, .	13.9	69
81	Single-cell landscape of the ecosystem in early-relapse hepatocellular carcinoma. <i>Cell</i> , 2021, 184, 404-421.e16.	34.1	728
82	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.	16.0	203
83	A genome-wide association study for gut metagenome in Chinese adults illuminates complex diseases. <i>Cell Discovery</i> , 2021, 7, .	9.6	68
84	Accurate haplotype-resolved assembly reveals the origin of structural variants for human trios. <i>Bioinformatics</i> , 2021, 37, 2095-2102.	4.8	8
85	Characterization of the human skin resistome and identification of two microbiota cutotypes. <i>Microbiome</i> , 2021, 9, .	11.5	80
86	stLFRsv: A Germline Structural Variant Analysis Pipeline Using Co-barcoded Reads. <i>Frontiers in Genetics</i> , 2021, 12, .	2.4	6
87	Integrated genetic analyses revealed novel human longevity loci and reduced risks of multiple diseases in a cohort study of 15,651 Chinese individuals. <i>Aging Cell</i> , 2021, 20, .	7.0	38
88	Characterization of respiratory microbial dysbiosis in hospitalized COVID-19 patients. <i>Cell Discovery</i> , 2021, 7, .	9.6	57
89	Whole-genome resequencing of 445 <i>Lactuca</i> accessions reveals the domestication history of cultivated lettuce. <i>Nature Genetics</i> , 2021, 53, 752-760.	26.1	129
90	Enhancing CRISPR-Cas9 gRNA efficiency prediction by data integration and deep learning. <i>Nature Communications</i> , 2021, 12, .	13.9	163

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91	A transomic cohort as a reference point for promoting a healthy human gut microbiome. <i>Medicine in Microecology</i> , 2021, 8, 100039.	3.6	38
92	Single-cell atlas of domestic pig cerebral cortex and hypothalamus. <i>Science Bulletin</i> , 2021, 66, 1448-1461.	9.6	28
93	The trans-omics landscape of COVID-19. <i>Nature Communications</i> , 2021, 12, .	13.9	106
94	Identification of HSC/MPP expansion units in fetal liver by single-cell spatiotemporal transcriptomics. <i>Cell Research</i> , 2021, 32, 38-53.	12.5	96
95	Cervicovaginal microbiome dynamics after taking oral probiotics. <i>Journal of Genetics and Genomics</i> , 2021, 48, 716-726.	5.0	21
96	A Chinese host genetic study discovered IFNs and causality of laboratory traits on COVID-19 severity. <i>IScience</i> , 2021, 24, 103186.	3.6	14
97	Analysis of 427 genomes reveals moso bamboo population structure and genetic basis of property traits. <i>Nature Communications</i> , 2021, 12, .	13.9	56
98	Dairy consumption and physical fitness tests associated with fecal microbiome in a Chinese cohort. <i>Medicine in Microecology</i> , 2021, 9, 100038.	3.6	8
99	Disease trends in a young Chinese cohort according to fecal metagenome and plasma metabolites. <i>Medicine in Microecology</i> , 2021, 9, 100037.	3.6	2
100	Network of Interactions Between Gut Microbiome, Host Biomarkers, and Urine Metabolome in Carotid Atherosclerosis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, .	4.3	12
101	<i>Chloranthus</i> genome provides insights into the early diversification of angiosperms. <i>Nature Communications</i> , 2021, 12, .	13.9	85
102	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	38.7	206
103	Single cell atlas for 11 non-model mammals, reptiles and birds. <i>Nature Communications</i> , 2021, 12, .	13.9	63
104	Metagenome-genome-wide association studies reveal human genetic impact on the oral microbiome. <i>Cell Discovery</i> , 2021, 7, .	9.6	95
105	PIRD: Pan Immune Repertoire Database. <i>Bioinformatics</i> , 2020, 36, 897-903.	4.8	143
106	Genome-wide analysis of epigenetic and transcriptional changes associated with heterosis in pigeonpea. <i>Plant Biotechnology Journal</i> , 2020, 18, 1697-1710.	8.8	57
107	Draft Genomes of Two <i>Artocarpus</i> Plants, Jackfruit (<i>A. heterophyllus</i>) and Breadfruit (<i>A. altilis</i>). <i>Genes</i> , 2020, 11, 27.	2.6	41
108	An Indo-Pacific Humpback Dolphin Genome Reveals Insights into Chromosome Evolution and the Demography of a Vulnerable Species. <i>IScience</i> , 2020, 23, 101640.	3.6	23

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109	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.	23.3	384
110	Initial whole-genome sequencing and analysis of the host genetic contribution to COVID-19 severity and susceptibility. <i>Cell Discovery</i> , 2020, 6, .	9.6	186
111	DNB-based on-chip motif finding: A high-throughput method to profile different types of protein-DNA interactions. <i>Science Advances</i> , 2020, 6, .	11.0	14
112	African Arowana Genome Provides Insights on Ancient Teleost Evolution. <i>IScience</i> , 2020, 23, 101662.	3.6	7
113	CNSA: a data repository for archiving omics data. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	2.8	382
114	TGS-GapCloser: A fast and accurate gap closer for large genomes with low coverage of error-prone long reads. <i>GigaScience</i> , 2020, 9, .	3.2	398
115	Initial data release and announcement of the 10,000 Fish Genomes Project (Fish10K). <i>GigaScience</i> , 2020, 9, .	3.2	81
116	The White-Spotted Bamboo Shark Genome Reveals Chromosome Rearrangements and Fast-Evolving Immune Genes of Cartilaginous Fish. <i>IScience</i> , 2020, 23, 101754.	3.6	55
117	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. <i>GigaScience</i> , 2020, 9, .	3.2	58
118	Dissecting the genome of star fruit (<i>Averrhoa carambola</i> L.). <i>Horticulture Research</i> , 2020, 7, .	7.3	24
119	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.	10.3	135
120	Genetic Association Reveals Protection against Recurrence of <i>Clostridium difficile</i> Infection with Bezlotoxumab Treatment. <i>MSphere</i> , 2020, 5, .	3.0	17
121	36.4	962	
122	Metagenome-wide association of gut microbiome features for schizophrenia. <i>Nature Communications</i> , 2020, 11, .	13.9	331
123	Multiple approaches for massively parallel sequencing of SARS-CoV-2 genomes directly from clinical samples. <i>Genome Medicine</i> , 2020, 12, .	9.7	127
124	Single-cell RNA-seq unveils critical regulators of human FOXP3+ regulatory T cell stability. <i>Science Bulletin</i> , 2020, 65, 1114-1124.	9.6	21
125	The draft genome assembly of the critically endangered <i>Nyssa yunnanensis</i> , a plant species with extremely small populations endemic to Yunnan Province, China. <i>GigaByte</i> , 2020, 2020, 1-12.	1.5	3
126	The female urinary microbiota in relation to the reproductive tract microbiota. <i>GigaByte</i> , 2020, 2020, 1-9.	1.5	6

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127	Mutations in topoisomerase II β result in a B cell immunodeficiency. <i>Nature Communications</i> , 2019, 10, .	13.9	55
128	A single bacterium restores the microbiome dysbiosis to protect bones from destruction in a rat model of rheumatoid arthritis. <i>Microbiome</i> , 2019, 7, .	11.5	141
129	The genomic landscape of Epstein-Barr virus-associated pulmonary lymphoepithelioma-like carcinoma. <i>Nature Communications</i> , 2019, 10, .	13.9	102
130	African Orphan Crops Consortium (AOCC): status of developing genomic resources for African orphan crops. <i>Planta</i> , 2019, 250, 989-1003.	3.3	100
131	Elimination of a Retrotransposon for Quenching Genome Instability in Modern Rice. <i>Molecular Plant</i> , 2019, 12, 1395-1407.	19.0	19
132	Sequencing and comparative analysis of three <i>Chlorella</i> genomes provide insights into strain-specific adaptation to wastewater. <i>Scientific Reports</i> , 2019, 9, .	3.5	33
133	3 α €² Branch ligation: a novel method to ligate non-complementary DNA to recessed or internal 3 α €²OH ends in DNA or RNA. <i>DNA Research</i> , 2019, 26, 45-53.	2.8	12
134	Genomes of Subaerial Zygnematophyceae Provide Insights into Land Plant Evolution. <i>Cell</i> , 2019, 179, 1057-1067.e14.	34.1	469
135	Distinct gut metagenomics and metaproteomics signatures in prediabetics and treatment-naïve type 2 diabetics. <i>EBioMedicine</i> , 2019, 47, 373-383.	9.9	181
136	Resequencing 545 ginkgo genomes across the world reveals the evolutionary history of the living fossil. <i>Nature Communications</i> , 2019, 10, .	13.9	156
137	Draft genome sequence of <i>Solanum aethiopicum</i> provides insights into disease resistance, drought tolerance, and the evolution of the genome. <i>GigaScience</i> , 2019, 8, .	3.2	49
138	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. <i>Nature Communications</i> , 2019, 10, .	13.9	223
139	Molecular digitization of a botanical garden: high-depth whole-genome sequencing of 689 vascular plant species from the Ruili Botanical Garden. <i>GigaScience</i> , 2019, 8, .	3.2	50
140	Characterization and validation of somatic mutation spectrum to reveal heterogeneity in gastric cancer by single cell sequencing. <i>Science Bulletin</i> , 2019, 64, 236-244.	9.6	10
141	New insights from <i>Opisthorchis felinus</i> genome: update on genomics of the epidemiologically important liver flukes. <i>BMC Genomics</i> , 2019, 20, .	3.3	39
142	Development of coupling controlled polymerizations by adapter-ligation in mate-pair sequencing for detection of various genomic variants in one single assay. <i>DNA Research</i> , 2019, 26, 313-325.	2.8	25
143	Single-cell transcriptomic landscape of nucleated cells in umbilical cord blood. <i>GigaScience</i> , 2019, 8, .	3.2	31
144	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.	26.1	285

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145	Reliable multiplex sequencing with rare index mis-assignment on DNB-based NGS platform. BMC Genomics, 2019, 20, .	3.3	55
146	Sequencing of the MHC region defines <i>HLA-DQA1</i> as the major genetic risk for seropositive rheumatoid arthritis in Han Chinese population. Annals of the Rheumatic Diseases, 2019, 78, 773-780.	12.4	37
147	Efficient and unique cobarcoding of second-generation sequencing reads from long DNA molecules enabling cost-effective and accurate sequencing, haplotyping, and de novo assembly. Genome Research, 2019, 29, 798-808.	4.6	229
148	The first chromosome-level genome for a marine mammal as a resource to study ecology and evolution. Molecular Ecology Resources, 2019, 19, 944-956.	4.8	37
149	Enhancement of de novo sequencing, assembly and annotation of the Mongolian gerbil genome with transcriptome sequencing and assembly from several different tissues. BMC Genomics, 2019, 20, .	3.3	8
150	Comprehensive genomic variation profiling of cervical intraepithelial neoplasia and cervical cancer identifies potential targets for cervical cancer early warning. Journal of Medical Genetics, 2019, 56, 186-194.	3.9	56
151	Genomic sequencing and editing revealed the GRM8 signaling pathway as potential therapeutic targets of squamous cell lung cancer. Cancer Letters, 2019, 442, 53-67.	8.8	43
152	Impact of early events and lifestyle on the gut microbiota and metabolic phenotypes in young school-age children. Microbiome, 2019, 7, .	11.5	182
153	The draft genomes of five agriculturally important African orphan crops. GigaScience, 2019, 8, .	3.2	141
154	Transplantation of microbiota from drug-free patients with schizophrenia causes schizophrenia-like abnormal behaviors and dysregulated kynurenine metabolism in mice. Molecular Psychiatry, 2019, 25, 2905-2918.	8.4	293
155	Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. Nature Plants, 2019, 6, 95-106.	11.9	202
156	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. Nature Biotechnology, 2019, 37, 179-185.	32.2	512
157	10KP: A phylodiverse genome sequencing plan. GigaScience, 2018, 7, .	3.2	199
158	Genome-wide determination of on-target and off-target characteristics for RNA-guided DNA methylation by dCas9 methyltransferases. GigaScience, 2018, 7, .	3.2	84
159	Assessment of the cPAS-based BGISEQ-500 platform for metagenomic sequencing. GigaScience, 2018, 7, .	3.2	201
160	Bph6 encodes an exocyst-localized protein and confers broad resistance to planthoppers in rice. Nature Genetics, 2018, 50, 297-306.	26.1	223
161	Construction of the third-generation Zea mays haplotype map. GigaScience, 2018, 7, .	3.2	250
162	The genetic architecture of floral traits in the woody plant Prunus mume. Nature Communications, 2018, 9, .	13.9	102

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163	Stromal Gene Expression is Predictive for Metastatic Primary Prostate Cancer. <i>European Urology</i> , 2018, 73, 524-532.	2.2	74
164	Novel genetic loci associated HLA-B*08:01 positive myasthenia gravis. <i>Journal of Autoimmunity</i> , 2018, 88, 43-49.	6.7	29
165	Whole-genome and Transcriptome Sequencing of Prostate Cancer Identify New Genetic Alterations Driving Disease Progression. <i>European Urology</i> , 2018, 73, 322-339.	2.2	170
166	The structure and function of the global citrus rhizosphere microbiome. <i>Nature Communications</i> , 2018, 9, .	13.9	438
167	Whole-genome sequencing of 175 Mongolians uncovers population-specific genetic architecture and gene flow throughout North and East Asia. <i>Nature Genetics</i> , 2018, 50, 1696-1704.	26.1	49
168	Single-cell RNA-seq reveals dynamic transcriptome profiling in human early neural differentiation. <i>GigaScience</i> , 2018, 7, .	3.2	27
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