

Xun Xu

List of Publications by Citations

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327
papers

53,540
citations

93
h-index

230
g-index

385
ext. papers

72,004
ext. citations

16
avg, IF

7.23
L-index

#	Paper	IF	Citations
327	A global reference for human genetic variation. <i>Nature</i> , 2015 , 526, 68-74	50.4	8599
326	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012 , 485, 635-41	50.4	2138
325	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011 , 43, 1035-9	36.3	1490
324	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014 , 346, 763-7	33.3	1489
323	Genome sequence and analysis of the tuber crop potato. <i>Nature</i> , 2011 , 475, 189-95	50.4	1438
322	Dynamics and Stabilization of the Human Gut Microbiome during the First Year of Life. <i>Cell Host and Microbe</i> , 2015 , 17, 690-703	23.4	1367
321	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018 , 361,	33.3	1296
320	Taxonomic structure and functional association of foxtail millet root microbiome. <i>GigaScience</i> , 2017 , 6, 1-12	7.6	1155
319	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014 , 32, 834-41	44.5	1088
318	Sequencing of 50 human exomes reveals adaptation to high altitude. <i>Science</i> , 2010 , 329, 75-8	33.3	1020
317	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012 , 491, 393-8	50.4	928
316	The oral and gut microbiomes are perturbed in rheumatoid arthritis and partly normalized after treatment. <i>Nature Medicine</i> , 2015 , 21, 895-905	50.5	849
315	Draft genome sequence of chickpea (<i>Cicer arietinum</i>) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013 , 31, 240-6	44.5	781
314	Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection. <i>Nature Genetics</i> , 2010 , 42, 1053-9	36.3	754
313	Genome sequence of cultivated Upland cotton (<i>Gossypium hirsutum</i> TM-1) provides insights into genome evolution. <i>Nature Biotechnology</i> , 2015 , 33, 524-30	44.5	683
312	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014 , 5, 3930	17.4	676
311	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2011 , 30, 105-11	44.5	635

310	Gut microbiome and serum metabolome alterations in obesity and after weight-loss intervention. <i>Nature Medicine</i> , 2017 , 23, 859-868	50.5	627
309	SOAPdenovo-Trans: de novo transcriptome assembly with short RNA-Seq reads. <i>Bioinformatics</i> , 2014 , 30, 1660-6	7.2	621
308	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013 , 23, 396-408	9.7	615
307	Gut microbiome development along the colorectal adenoma-carcinoma sequence. <i>Nature Communications</i> , 2015 , 6, 6528	17.4	614
306	Genome sequence of the cultivated cotton <i>Gossypium arboreum</i> . <i>Nature Genetics</i> , 2014 , 46, 567-72	36.3	613
305	Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. <i>Nature</i> , 2014 , 512, 194-750.4	50.4	605
304	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012 , 44, 808-11	36.3	600
303	Draft genome sequence of pigeonpea (<i>Cajanus cajan</i>), an orphan legume crop of resource-poor farmers. <i>Nature Biotechnology</i> , 2011 , 30, 83-9	44.5	587
302	Sparse whole-genome sequencing identifies two loci for major depressive disorder. <i>Nature</i> , 2015 , 523, 588-91	50.4	584
301	The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. <i>Nature Biotechnology</i> , 2011 , 29, 735-41	44.5	584
300	The gut microbiome in atherosclerotic cardiovascular disease. <i>Nature Communications</i> , 2017 , 8, 845	17.4	575
299	Correction of a pathogenic gene mutation in human embryos. <i>Nature</i> , 2017 , 548, 413-419	50.4	567
298	Single-cell exome sequencing reveals single-nucleotide mutation characteristics of a kidney tumor. <i>Cell</i> , 2012 , 148, 886-95	56.2	511
297	The genome sequences of <i>Arachis duranensis</i> and <i>Arachis ipaensis</i> , the diploid ancestors of cultivated peanut. <i>Nature Genetics</i> , 2016 , 48, 438-46	36.3	498
296	Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer. <i>Gut</i> , 2017 , 66, 70-78	19.2	488
295	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012 , 44, 803-7	36.3	470
294	Genome sequence of foxtail millet (<i>Setaria italica</i>) provides insights into grass evolution and biofuel potential. <i>Nature Biotechnology</i> , 2012 , 30, 549-54	44.5	447
293	Single-cell exome sequencing and monoclonal evolution of a JAK2-negative myeloproliferative neoplasm. <i>Cell</i> , 2012 , 148, 873-85	56.2	431

292	COLD1 confers chilling tolerance in rice. <i>Cell</i> , 2015 , 160, 1209-21	56.2	414
291	Rapid, low-input, low-bias construction of shotgun fragment libraries by high-density in vitro transposition. <i>Genome Biology</i> , 2010 , 11, R119	18.3	377
290	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , 2010 , 42, 1027-30	36.3	365
289	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra hircus</i>). <i>Nature Biotechnology</i> , 2013 , 31, 135-41	44.5	355
288	Earth BioGenome Project: Sequencing life for the future of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 4325-4333	11.5	334
287	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012 , 44, 221-5	36.3	325
286	The microbiota continuum along the female reproductive tract and its relation to uterine-related diseases. <i>Nature Communications</i> , 2017 , 8, 875	17.4	308
285	The genome of <i>Prunus mume</i> . <i>Nature Communications</i> , 2012 , 3, 1318	17.4	295
284	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014 , 344, 1168-1173	33.3	294
283	Genomic landscapes of Chinese hamster ovary cell lines as revealed by the <i>Cricetulus griseus</i> draft genome. <i>Nature Biotechnology</i> , 2013 , 31, 759-65	44.5	289
282	The <i>Symbiodinium kawagutii</i> genome illuminates dinoflagellate gene expression and coral symbiosis. <i>Science</i> , 2015 , 350, 691-4	33.3	283
281	Complete resequencing of 40 genomes reveals domestication events and genes in silkworm (<i>Bombyx</i>). <i>Science</i> , 2009 , 326, 433-6	33.3	277
280	The genome sequence of the orchid <i>Phalaenopsis equestris</i> . <i>Nature Genetics</i> , 2015 , 47, 65-72	36.3	265
279	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
278	A reference gene catalogue of the pig gut microbiome. <i>Nature Microbiology</i> , 2016 , 1, 16161	26.6	233
277	Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing. <i>Nature Communications</i> , 2014 , 5, 4340	17.4	230
276	<i>Ascaris suum</i> draft genome. <i>Nature</i> , 2011 , 479, 529-33	50.4	217
275	Structural genomic changes underlie alternative reproductive strategies in the ruff (<i>Philomachus pugnax</i>). <i>Nature Genetics</i> , 2016 , 48, 84-8	36.3	214

274	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. <i>Nature Biotechnology</i> , 2019 , 37, 179-185	44.5	213
273	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017 , 35, 969-976	44.5	197
272	Genome assembly with in vitro proximity ligation data and whole-genome triplication in lettuce. <i>Nature Communications</i> , 2017 , 8, 14953	17.4	196
271	Analyses of gut microbiota and plasma bile acids enable stratification of patients for antidiabetic treatment. <i>Nature Communications</i> , 2017 , 8, 1785	17.4	192
270	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	4.5	188
269	Genesis, Evolution and Prevalence of H5N6 Avian Influenza Viruses in China. <i>Cell Host and Microbe</i> , 2016 , 20, 810-821	23.4	187
268	Genome sequencing of the high oil crop sesame provides insight into oil biosynthesis. <i>Genome Biology</i> , 2014 , 15, R39	18.3	179
267	Redefining the structural motifs that determine RNA binding and RNA editing by pentatricopeptide repeat proteins in land plants. <i>Plant Journal</i> , 2016 , 85, 532-47	6.9	176
266	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018 , 4, 460-475	17.5	176
265	Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome. <i>Cell Systems</i> , 2016 , 3, 572-584.e3	10.6	172
264	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , 2018 , 361,	33.3	167
263	Molecular signatures of major depression. <i>Current Biology</i> , 2015 , 25, 1146-56	6.3	162
262	Draft genome of the living fossil <i>Ginkgo biloba</i> . <i>GigaScience</i> , 2016 , 5, 49	7.6	161
261	The structure and function of the global citrus rhizosphere microbiome. <i>Nature Communications</i> , 2018 , 9, 4894	17.4	157
260	Genomic and oncogenic preference of HBV integration in hepatocellular carcinoma. <i>Nature Communications</i> , 2016 , 7, 12992	17.4	151
259	Genomes of Subaerial Zygnematophyceae Provide Insights into Land Plant Evolution. <i>Cell</i> , 2019 , 179, 1057-1067.e14	56.2	151
258	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	32.3	148
257	The <i>Sinocyclocheilus</i> cavefish genome provides insights into cave adaptation. <i>BMC Biology</i> , 2016 , 14, 1	7.3	144

256	The high-quality genome of Brassica napus cultivar 'ZS11' reveals the introgression history in semi-winter morphotype. <i>Plant Journal</i> , 2017 , 92, 452-468	6.9	132
255	High-purity prostate circulating tumor cell isolation by a polymer nanofiber-embedded microchip for whole exome sequencing. <i>Advanced Materials</i> , 2013 , 25, 2897-902	24	131
254	An atlas of the protein-coding genes in the human, pig, and mouse brain. <i>Science</i> , 2020 , 367,	33.3	130
253	Deep sequencing of the MHC region in the Chinese population contributes to studies of complex disease. <i>Nature Genetics</i> , 2016 , 48, 740-6	36.3	129
252	Construction of the third-generation Zea mays haplotype map. <i>GigaScience</i> , 2018 , 7, 1-12	7.6	127
251	Genome-wide characteristics of mutations in autism. <i>Npj Genomic Medicine</i> , 2016 , 1, 160271-1602710	6.2	126
250	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	56.2	123
249	Design and characterization of a 52K SNP chip for goats. <i>PLoS ONE</i> , 2014 , 9, e86227	3.7	121
248	Allelic diversity in an NLR gene 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	11.5	120
247	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. <i>Nature Communications</i> , 2015 , 6, 5969	17.4	119
246	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	36.3	116
245	Rapid detection of structural variation in a human genome using nanochannel-based genome mapping technology. <i>GigaScience</i> , 2014 , 3, 34	7.6	113
244	10KP: A phylo diverse genome sequencing plan. <i>GigaScience</i> , 2018 , 7, 1-9	7.6	108
243	Comparison of variations detection between whole-genome amplification methods used in single-cell resequencing. <i>GigaScience</i> , 2015 , 4, 37	7.6	107
242	Novel loci and pathways significantly associated with longevity. <i>Scientific Reports</i> , 2016 , 6, 21243	4.9	105
241	The genetic basis for ecological adaptation of the Atlantic herring revealed by genome sequencing. <i>ELife</i> , 2016 , 5,	8.9	103
240	Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. <i>Science</i> , 2017 , 355,	33.3	101
239	Discovery of biclonal origin and a novel oncogene SLC12A5 in colon cancer by single-cell sequencing. <i>Cell Research</i> , 2014 , 24, 701-12	24.7	99

238	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	18.3	97
237	Integrated genome sequence and linkage map of physic nut (<i>Jatropha curcas</i> L.), a biodiesel plant. <i>Plant Journal</i> , 2015 , 81, 810-21	6.9	96
236	Single-cell landscape of the ecosystem in early-relapse hepatocellular carcinoma. <i>Cell</i> , 2021 , 184, 404-421	16.16	96
235	Integrated metabolomics and metagenomics analysis of plasma and urine identified microbial metabolites associated with coronary heart disease. <i>Scientific Reports</i> , 2016 , 6, 22525	4.9	89
234	Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. <i>Nature Communications</i> , 2014 , 5, 5594	17.4	89
233	Bph6 encodes an exocyst-localized protein and confers broad resistance to planthoppers in rice. <i>Nature Genetics</i> , 2018 , 50, 297-306	36.3	88
232	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017 , 548, 87-91	50.4	87
231	A comparison of isolated circulating tumor cells and tissue biopsies using whole-genome sequencing in prostate cancer. <i>Oncotarget</i> , 2015 , 6, 44781-93	3.3	85
230	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. <i>Nature Communications</i> , 2019 , 10, 470	17.4	84
229	Smart enrichment and facile separation of oil from emulsions and mixtures by superhydrophobic/superoleophilic particles. <i>ACS Applied Materials & Interfaces</i> , 2015 , 7, 10475-81	9.5	84
228	A method for noninvasive detection of fetal large deletions/duplications by low coverage massively parallel sequencing. <i>Prenatal Diagnosis</i> , 2013 , 33, 584-90	3.2	84
227	cPAS-based sequencing on the BGISEQ-500 to explore small non-coding RNAs. <i>Clinical Epigenetics</i> , 2016 , 8, 123	7.7	83
226	Assessment of the cPAS-based BGISEQ-500 platform for metagenomic sequencing. <i>GigaScience</i> , 2018 , 7, 1-8	7.6	82
225	Single-cell sequencing analysis characterizes common and cell-lineage-specific mutations in a muscle-invasive bladder cancer. <i>GigaScience</i> , 2012 , 1, 12	7.6	82
224	Impact of early events and lifestyle on the gut microbiota and metabolic phenotypes in young school-age children. <i>Microbiome</i> , 2019 , 7, 2	16.6	82
223	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	15.1	82
222	SCRaMBLE generates designed combinatorial stochastic diversity in synthetic chromosomes. <i>Genome Research</i> , 2016 , 26, 36-49	9.7	78
221	Influenza H7N9 and H9N2 viruses: coexistence in poultry linked to human H7N9 infection and genome characteristics. <i>Journal of Virology</i> , 2014 , 88, 3423-31	6.6	78

220	Clinical outcome of preimplantation genetic diagnosis and screening using next generation sequencing. <i>GigaScience</i> , 2014 , 3, 30	7.6	77
219	Baiji genomes reveal low genetic variability and new insights into secondary aquatic adaptations. <i>Nature Communications</i> , 2013 , 4, 2708	17.4	76
218	Inherited bone marrow failure associated with germline mutation of ACD, the gene encoding telomere protein TPP1. <i>Blood</i> , 2014 , 124, 2767-74	2.2	75
217	Initial whole-genome sequencing and analysis of the host genetic contribution to COVID-19 severity and susceptibility. <i>Cell Discovery</i> , 2020 , 6, 83	22.3	75
216	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	9.7	74
215	IMonitor: A Robust Pipeline for TCR and BCR Repertoire Analysis. <i>Genetics</i> , 2015 , 201, 459-72	4	73
214	Metagenome-wide association of gut microbiome features for schizophrenia. <i>Nature Communications</i> , 2020 , 11, 1612	17.4	73
213	Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. <i>Nature Plants</i> , 2020 , 6, 95-106	11.5	73
212	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	11	72
211	Whole-genome and Transcriptome Sequencing of Prostate Cancer Identify New Genetic Alterations Driving Disease Progression. <i>European Urology</i> , 2018 , 73, 322-339	10.2	71
210	The draft genomes of five agriculturally important African orphan crops. <i>GigaScience</i> , 2019 , 8,	7.6	68
209	Frequent alterations in cytoskeleton remodelling genes in primary and metastatic lung adenocarcinomas. <i>Nature Communications</i> , 2015 , 6, 10131	17.4	67
208	The <i>Tarenaya hassleriana</i> genome provides insight into reproductive trait and genome evolution of crucifers. <i>Plant Cell</i> , 2013 , 25, 2813-30	11.6	67
207	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	4.9	66
206	The Power of Inbreeding: NGS-Based GWAS of Rice Reveals Convergent Evolution during Rice Domestication. <i>Molecular Plant</i> , 2016 , 9, 975-85	14.4	66
205	Pregnancy-induced metabolic phenotype variations in maternal plasma. <i>Journal of Proteome Research</i> , 2014 , 13, 1527-36	5.6	65
204	HIVID: an efficient method to detect HBV integration using low coverage sequencing. <i>Genomics</i> , 2013 , 102, 338-44	4.3	65
203	CNSA: a data repository for archiving omics data. <i>Database: the Journal of Biological Databases and Curation</i> , 2020 , 2020,	5	65

202	Introgression from domestic goat generated variation at the major histocompatibility complex of Alpine ibex. <i>PLoS Genetics</i> , 2014 , 10, e1004438	6	62
201	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	4.5	60
200	Multiple approaches for massively parallel sequencing of SARS-CoV-2 genomes directly from clinical samples. <i>Genome Medicine</i> , 2020 , 12, 57	14.4	60
199	De novo assembly of a haplotype-resolved human genome. <i>Nature Biotechnology</i> , 2015 , 33, 617-22	44.5	57
198	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	16.6	55
197	The sacred lotus genome provides insights into the evolution of flowering plants. <i>Plant Journal</i> , 2013 , 76, 557-67	6.9	55
196	POPDC1(S201F) causes muscular dystrophy and arrhythmia by affecting protein trafficking. <i>Journal of Clinical Investigation</i> , 2016 , 126, 239-53	15.9	55
195	A single cell level based method for copy number variation analysis by low coverage massively parallel sequencing. <i>PLoS ONE</i> , 2013 , 8, e54236	3.7	55
194	Generation of hircine-induced pluripotent stem cells by somatic cell reprogramming. <i>Cell Research</i> , 2011 , 21, 849-53	24.7	54
193	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	4.9	53
192	A robust approach for blind detection of balanced chromosomal rearrangements with whole-genome low-coverage sequencing. <i>Human Mutation</i> , 2014 , 35, 625-36	4.7	50
191	CNGBdb: China National GeneBank DataBase. <i>Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji</i> , 2020 , 42, 799-809	1.4	50
190	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	12.5	49
189	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, 2297-307	5.6	48
188	A western Sahara centre of domestication inferred from pearl millet genomes. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1377-1380	12.3	48
187	The genetic architecture of floral traits in the woody plant <i>Prunus mume</i> . <i>Nature Communications</i> , 2018 , 9, 1702	17.4	46
186	Analytical and Decision Support Tools for Genomics-Assisted Breeding. <i>Trends in Plant Science</i> , 2016 , 21, 354-363	13.1	46
185	The <i>Streptococcus suis</i> transcriptional landscape reveals adaptation mechanisms in pig blood and cerebrospinal fluid. <i>Rna</i> , 2014 , 20, 882-98	5.8	46

184	Distinct gut metagenomics and metaproteomics signatures in prediabetics and treatment-naïve type 2 diabetics. <i>EBioMedicine</i> , 2019 , 47, 373-383	8.8	44
183	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	7.6	43
182	The metagenome of the female upper reproductive tract. <i>GigaScience</i> , 2018 , 7,	7.6	43
181	African Orphan Crops Consortium (AOCC): status of developing genomic resources for African orphan crops. <i>Planta</i> , 2019 , 250, 989-1003	4.7	42
180	Full-length single-cell RNA-seq applied to a viral human cancer: applications to HPV expression and splicing analysis in HeLa S3 cells. <i>GigaScience</i> , 2015 , 4, 51	7.6	42
179	Genome-wide characterization of nonreference transposons reveals evolutionary propensities of transposons in soybean. <i>Plant Cell</i> , 2012 , 24, 4422-36	11.6	42
178	Resequencing 545 ginkgo genomes across the world reveals the evolutionary history of the living fossil. <i>Nature Communications</i> , 2019 , 10, 4201	17.4	41
177	A gene catalogue of the Sprague-Dawley rat gut metagenome. <i>GigaScience</i> , 2018 , 7,	7.6	41
176	Two distinct metacommunities characterize the gut microbiota in Crohn's disease patients. <i>GigaScience</i> , 2017 , 6, 1-11	7.6	40
175	Sex Differences in Genetic Associations With Longevity. <i>JAMA Network Open</i> , 2018 , 1, e181670	10.4	40
174	PGA: an R/Bioconductor package for identification of novel peptides using a customized database derived from RNA-Seq. <i>BMC Bioinformatics</i> , 2016 , 17, 244	3.6	39
173	Multiscale bio-inspired honeycomb structure material with high mechanical strength and low density. <i>Journal of Materials Chemistry</i> , 2012 , 22, 10883		39
172	Using SOAPaligner for Short Reads Alignment. <i>Current Protocols in Bioinformatics</i> , 2013 , 44, 11.11.1-17	24.2	39
171	The genomic landscape of Epstein-Barr virus-associated pulmonary lymphoepithelioma-like carcinoma. <i>Nature Communications</i> , 2019 , 10, 3108	17.4	36
170	Noninvasive prenatal testing for autosomal recessive conditions by maternal plasma sequencing in a case of congenital deafness. <i>Genetics in Medicine</i> , 2014 , 16, 972-6	8.1	36
169	Haplotype-based approach for noninvasive prenatal diagnosis of congenital adrenal hyperplasia by maternal plasma DNA sequencing. <i>Gene</i> , 2014 , 544, 252-8	3.8	36
168	Stromal Gene Expression is Predictive for Metastatic Primary Prostate Cancer. <i>European Urology</i> , 2018 , 73, 524-532	10.2	35
167	Comparative methylomics between domesticated and wild silkworms implies possible epigenetic influences on silkworm domestication. <i>BMC Genomics</i> , 2013 , 14, 646	4.5	35

166	An integrated tool to study MHC region: accurate SNV detection and HLA genes typing in human MHC region using targeted high-throughput sequencing. <i>PLoS ONE</i> , 2013 , 8, e69388	3.7	34
165	Genome-wide transcriptome and antioxidant analyses on gamma-irradiated phases of deinococcus radiodurans R1. <i>PLoS ONE</i> , 2014 , 9, e85649	3.7	32
164	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	12.3	31
163	TGS-GapCloser: A fast and accurate gap closer for large genomes with low coverage of error-prone long reads. <i>GigaScience</i> , 2020 , 9,	7.6	30
162	Systematic Comparative Evaluation of Methods for Investigating the TCR Repertoire. <i>PLoS ONE</i> , 2016 , 11, e0152464	3.7	29
161	Analysis of elite variety tag SNPs reveals an important allele in upland rice. <i>Nature Communications</i> , 2013 , 4, 2138	17.4	27
160	Ma et al. reply. <i>Nature</i> , 2018 , 560, E10-E23	50.4	27
159	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	36.3	27
158	IPeak: An open source tool to combine results from multiple MS/MS search engines. <i>Proteomics</i> , 2015 , 15, 2916-20	4.8	26
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48	Three genomes of Osteoglossidae shed light on ancient teleost evolution		3
47	Initial Whole Genome Sequencing and Analysis of the Host Genetic Contribution to COVID-19 Severity and Susceptibility		3
46	Over 50000 metagenomically assembled draft genomes for the human oral microbiome reveal new taxa		3
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36	Advanced Whole Genome Sequencing Using an Entirely PCR-free Massively Parallel Sequencing Workflow		2
35	CoolMPS—Advanced massively parallel sequencing using antibodies specific to each natural nucleobase		2
34	Age-dependent sexual dimorphism in the adult human gut microbiota		2
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16	Low Pass Genomes of 141,431 Chinese Reveal Patterns of Viral Infection, Novel Phenotypic Associations, and the Genetic History of China. <i>SSRN Electronic Journal</i> ,	1	1
15	M-GWAS for the gut microbiome in Chinese adults illuminates on complex diseases		1
14	Identification of gut microbiome markers for schizophrenia delineates a potential role of <i>Streptococcus</i>		1
13	Genomic analyses reveal the origin of domestic ducks and identify different genetic underpinnings of wild ducks		1
12	The Trans-omics Landscape of COVID-19		1
11	Landscapes and dynamic diversifications of B-cell receptor repertoires in COVID-19 patients		1
10	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment		1
9	PIRD: Pan immune repertoire database		1
8	SLR-superscaffolder: a de novo scaffolding tool for synthetic long reads using a top-to-bottom scheme		1
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