Xun Xu

List of Publications by Year in Descending Order

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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	The Earth BioGenome Project 2020: Starting the clock.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	15
326	Genome-wide annotation of protein-coding genes in pig.. *BMC Biology*, **2022**, 20, 25	7.3	3
325	Genomes shed light on the evolution of Begonia, a mega-diverse genus.. *New Phytologist*, **2022**,	9.8	1
324	Clinical challenges of tissue preparation for spatial transcriptome.. *Clinical and Translational Medicine*, **2022**, 12, e669	5.7	1
323	The genome of Hippophae rhamnoides provides insights into a conserved molecular mechanism in actinorhizal and rhizobial symbiosis.. *New Phytologist*, **2022**,	9.8	2
322	Mendelian randomization analyses support causal relationships between blood metabolites and the gut microbiome.. *Nature Genetics*, **2022**,	36.3	10
321	Distinct biological ages of organs and systems identified from a multi-omics study.. *Cell Reports*, **2022**, 38, 110459	10.6	4
320	Rolling back of human pluripotent stem cells to an 8-cell embryo-like stage.. *Nature*, **2022**,	50.4	3
319	Clinical and translational values of spatial transcriptomics.. *Signal Transduction and Targeted Therapy*, **2022**, 7, 111	21	1
318	The Cycas genome and the early evolution of seed plants.. *Nature Plants*, **2022**,	11.5	5
317	Towards practical and robust DNA-based data archiving using the yin▯yang codec system. *Nature Computational Science*, **2022**, 2, 234-242		2
316	The single-cell stereo-seq reveals region-specific cell subtypes and transcriptome profiling in Arabidopsis leaves.. *Developmental Cell*, **2022**,	10.2	2
315	Spatiotemporal mapping of gene expression landscapes and developmental trajectories during zebrafish embryogenesis.. *Developmental Cell*, **2022**,	10.2	2
314	High-resolution 3D spatiotemporal transcriptomic maps of developing Drosophila embryos and larvae.. *Developmental Cell*, **2022**,	10.2	1
313	Spatiotemporal transcriptomic atlas of mouse organogenesis using DNA nanoball-patterned arrays.. *Cell*, **2022**, 185, 1777-1792.e21	56.2	14
312	Genomic architecture of fetal central nervous system anomalies using whole-genome sequencing.. *Npj Genomic Medicine*, **2022**, 7, 31	6.2	0
311	Single cell atlas for 11 non-model mammals, reptiles and birds. *Nature Communications*, **2021**, 12, 7083	17.4	5

310	Landscapes and dynamic diversifications of B-cell receptor repertoires in COVID-19 patients. *Human Immunology*, **2021**, 83, 119-119	2.3	3
309	Chloranthus genome provides insights into the early diversification of angiosperms. *Nature Communications*, **2021**, 12, 6930	17.4	5
308	A chickpea genetic variation map based on the sequencing of 3,366 genomes. *Nature*, **2021**, 599, 622-627	50.4	15
307	Network of Interactions Between Gut Microbiome, Host Biomarkers, and Urine Metabolome in Carotid Atherosclerosis. *Frontiers in Cellular and Infection Microbiology*, **2021**, 11, 708088	5.9	1
306	SLR-superscaffolder: a de novo scaffolding tool for synthetic long reads using a top-to-bottom scheme. *BMC Bioinformatics*, **2021**, 22, 158	3.6	1
305	Integrated genetic analyses revealed novel human longevity loci and reduced risks of multiple diseases in a cohort study of 15,651 Chinese individuals. *Aging Cell*, **2021**, 20, e13323	9.9	7
304	Characterization of respiratory microbial dysbiosis in hospitalized COVID-19 patients. *Cell Discovery* , **2021**, 7, 23	22.3	10
303	Whole-genome resequencing of 445 Lactuca accessions reveals the domestication history of cultivated lettuce. *Nature Genetics*, **2021**, 53, 752-760	36.3	9
302	Enhancing CRISPR-Cas9 gRNA efficiency prediction by data integration and deep learning. *Nature Communications*, **2021**, 12, 3238	17.4	13
301	A transomic cohort as a reference point for promoting a healthy human gut microbiome. *Medicine in Microecology*, **2021**, 8, 100039	4.3	13
300	Life History Recorded in the Vagino-cervical Microbiome Along with Multi-omics. *Genomics, Proteomics and Bioinformatics*, **2021**,	6.5	8
299	Single-cell atlas of domestic pig cerebral cortex and hypothalamus. *Science Bulletin*, **2021**, 66, 1448-1461	10.6	3
298	Dynamic cell transition and immune response landscapes of axolotl limb regeneration revealed by single-cell analysis. *Protein and Cell*, **2021**, 12, 57-66	7.2	20
297	Single-cell landscape of the ecosystem in early-relapse hepatocellular carcinoma. *Cell*, **2021**, 184, 404-421.e16	56.2	96
296	Sex- and age-related trajectories of the adult human gut microbiota shared across populations of different ethnicities. *Nature Aging*, **2021**, 1, 87-100		22
295	A genome-wide association study for gut metagenome in Chinese adults illuminates complex diseases. *Cell Discovery*, **2021**, 7, 9	22.3	17
294	Characterization of the human skin resistome and identification of two microbiota cutotypes. *Microbiome*, **2021**, 9, 47	16.6	8
293	stLFRsv: A Germline Structural Variant Analysis Pipeline Using Co-barcoded Reads. *Frontiers in Genetics*, **2021**, 12, 636239	4.5	1

292	The trans-omics landscape of COVID-19. *Nature Communications*, **2021**, 12, 4543	17.4	17
291	Chromosome-level genome of Himalayan yew provides insights into the origin and evolution of the paclitaxel biosynthetic pathway. *Molecular Plant*, **2021**, 14, 1199-1209	14.4	10
290	Identification of HSC/MPP expansion units in fetal liver by single-cell spatiotemporal transcriptomics. *Cell Research*, **2021**,	24.7	9
289	Cervicovaginal microbiome dynamics after taking oral probiotics. *Journal of Genetics and Genomics*, **2021**, 48, 716-726	4	4
288	A Chinese host genetic study discovered IFNs and causality of laboratory traits on COVID-19 severity. *IScience*, **2021**, 24, 103186	6.1	2
287	Over 50,000 Metagenomically Assembled Draft Genomes for the Human Oral Microbiome Reveal New Taxa. *Genomics, Proteomics and Bioinformatics*, **2021**,	6.5	7
286	Analysis of 427 genomes reveals moso bamboo population structure and genetic basis of property traits. *Nature Communications*, **2021**, 12, 5466	17.4	3
285	Dairy consumption and physical fitness tests associated with fecal microbiome in a Chinese cohort. *Medicine in Microecology*, **2021**, 100038	4.3	2
284	Disease trends in a young Chinese cohort according to fecal metagenome and plasma metabolites. *Medicine in Microecology*, **2021**, 100037	4.3	2
283	Metagenome-genome-wide association studies reveal human genetic impact on the oral microbiome. *Cell Discovery*, **2021**, 7, 117	22.3	3
282	The White-Spotted Bamboo Shark Genome Reveals Chromosome Rearrangements and Fast-Evolving Immune Genes of Cartilaginous Fish. *IScience*, **2020**, 23, 101754	6.1	8
281	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. *GigaScience*, **2020**, 9,	7.6	21
280	Dissecting the genome of star fruit (L.). *Horticulture Research*, **2020**, 7, 94	7.7	8
279	The genome of Prasinoderma coloniale unveils the existence of a third phylum within green plants. *Nature Ecology and Evolution*, **2020**, 4, 1220-1231	12.3	31
278	Genetic Association Reveals Protection against Recurrence of Infection with Bezlotoxumab Treatment. *MSphere*, **2020**, 5,	5	6
277	An atlas of the protein-coding genes in the human, pig, and mouse brain. *Science*, **2020**, 367,	33.3	130
276	Metagenome-wide association of gut microbiome features for schizophrenia. *Nature Communications*, **2020**, 11, 1612	17.4	73
275	Multiple approaches for massively parallel sequencing of SARS-CoV-2 genomes directly from clinical samples. *Genome Medicine*, **2020**, 12, 57	14.4	60

274	Single-cell RNA-seq unveils critical regulators of human FOXP3+ regulatory T cell stability. *Science Bulletin*, **2020**, 65, 1114-1124	10.6	5
273	PIRD: Pan Immune Repertoire Database. *Bioinformatics*, **2020**, 36, 897-903	7.2	12
272	CNGBdb: China National GeneBank DataBase. *Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji*, **2020**, 42, 799-809	1.4	50
271	Genome-wide analysis of epigenetic and transcriptional changes associated with heterosis in pigeonpea. *Plant Biotechnology Journal*, **2020**, 18, 1697-1710	11.6	17
270	Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. *Nature Plants*, **2020**, 6, 95-106	11.5	73
269	An Indo-Pacific Humpback Dolphin Genome Reveals Insights into Chromosome Evolution and the Demography of a Vulnerable Species. *IScience*, **2020**, 23, 101640	6.1	8
268	Single-Cell Sequencing of Peripheral Mononuclear Cells Reveals Distinct Immune Response Landscapes of COVID-19 and Influenza Patients. *Immunity*, **2020**, 53, 685-696.e3	32.3	148
267	Initial whole-genome sequencing and analysis of the host genetic contribution to COVID-19 severity and susceptibility. *Cell Discovery*, **2020**, 6, 83	22.3	75
266	DNB-based on-chip motif finding: A high-throughput method to profile different types of protein-DNA interactions. *Science Advances*, **2020**, 6, eabb3350	14.3	0
265	African Arowana Genome Provides Insights on Ancient Teleost Evolution. *IScience*, **2020**, 23, 101662	6.1	1
264	CNSA: a data repository for archiving omics data. *Database: the Journal of Biological Databases and Curation*, **2020**, 2020,	5	65
263	TGS-GapCloser: A fast and accurate gap closer for large genomes with low coverage of error-prone long reads. *GigaScience*, **2020**, 9,	7.6	30
262	Initial data release and announcement of the 10,000 Fish Genomes Project (Fish10K). *GigaScience*, **2020**, 9,	7.6	12
261	Transplantation of microbiota from drug-free patients with schizophrenia causes schizophrenia-like abnormal behaviors and dysregulated kynurenine metabolism in mice. *Molecular Psychiatry*, **2020**, 25, 2905-2918	15.1	82
260	Distinct gut metagenomics and metaproteomics signatures in prediabetics and treatment-naïve type 2 diabetics. *EBioMedicine*, **2019**, 47, 373-383	8.8	44
259	Resequencing 545 ginkgo genomes across the world reveals the evolutionary history of the living fossil. *Nature Communications*, **2019**, 10, 4201	17.4	41
258	Draft genome sequence of Solanum aethiopicum provides insights into disease resistance, drought tolerance, and the evolution of the genome. *GigaScience*, **2019**, 8,	7.6	24
257	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. *Nature Communications*, **2019**, 10, 470	17.4	84

256	Molecular digitization of a botanical garden: high-depth whole-genome sequencing of 689 vascular plant species from the Ruili Botanical Garden. *GigaScience*, **2019**, 8,	7.6	24
255	Characterization and validation of somatic mutation spectrum to reveal heterogeneity in gastric cancer by single cell sequencing. *Science Bulletin*, **2019**, 64, 236-244	10.6	2
254	New insights from Opisthorchis felineus genome: update on genomics of the epidemiologically important liver flukes. *BMC Genomics*, **2019**, 20, 399	4.5	17
253	Development of coupling controlled polymerizations by adapter-ligation in mate-pair sequencing for detection of various genomic variants in one single assay. *DNA Research*, **2019**, 26, 313-325	4.5	7
252	Single-cell transcriptomic landscape of nucleated cells in umbilical cord blood. *GigaScience*, **2019**, 8,	7.6	12
251	Resequencing of 429 chickpea accessions from 45 countries provides insights into genome diversity, domestication and agronomic traits. *Nature Genetics*, **2019**, 51, 857-864	36.3	116
250	Reliable multiplex sequencing with rare index mis-assignment on DNB-based NGS platform. *BMC Genomics*, **2019**, 20, 215	4.5	20
249	Sequencing of the MHC region defines as the major genetic risk for seropositive rheumatoid arthritis in Han Chinese population. *Annals of the Rheumatic Diseases*, **2019**, 78, 773-780	2.4	16
248	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	9.7	74
247	The first chromosome-level genome for a marine mammal as a resource to study ecology and evolution. *Molecular Ecology Resources*, **2019**, 19, 944-956	8.4	15
246	Mutations in topoisomerase II□result in a B cell immunodeficiency. *Nature Communications*, **2019**, 10, 3644	17.4	24
245	A single bacterium restores the microbiome dysbiosis to protect bones from destruction in a rat model of rheumatoid arthritis. *Microbiome*, **2019**, 7, 107	16.6	55
244	The genomic landscape of Epstein-Barr virus-associated pulmonary lymphoepithelioma-like carcinoma. *Nature Communications*, **2019**, 10, 3108	17.4	36
243	African Orphan Crops Consortium (AOCC): status of developing genomic resources for African orphan crops. *Planta*, **2019**, 250, 989-1003	4.7	42
242	Elimination of a Retrotransposon for Quenching Genome Instability in Modern Rice. *Molecular Plant* , **2019**, 12, 1395-1407	14.4	4
241	Sequencing and comparative analysis of three Chlorella genomes provide insights into strain-specific adaptation to wastewater. *Scientific Reports*, **2019**, 9, 9514	4.9	11
240	3’ Branch ligation: a novel method to ligate non-complementary DNA to recessed or internal 3’OH ends in DNA or RNA. *DNA Research*, **2019**, 26, 45-53	4.5	8
239	Genomes of Subaerial Zygnematophyceae Provide Insights into Land Plant Evolution. *Cell*, **2019**, 179, 1057-1067.e14	56.2	151

238	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. *Nature Biotechnology*, **2019**, 37, 179-185	44.5	213
237	Draft Genomes of Two Artocarpus Plants, Jackfruit (A. heterophyllus) and Breadfruit (A. altilis). *Genes*, **2019**, 11,	4.2	12
236	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, 903	4.5	2
235	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	5.8	24
234	Genomic sequencing and editing revealed the GRM8 signaling pathway as potential therapeutic targets of squamous cell lung cancer. *Cancer Letters*, **2019**, 442, 53-67	9.9	16
233	Impact of early events and lifestyle on the gut microbiota and metabolic phenotypes in young school-age children. *Microbiome*, **2019**, 7, 2	16.6	82
232	The draft genomes of five agriculturally important African orphan crops. *GigaScience*, **2019**, 8,	7.6	68
231	10KP: A phylodiverse genome sequencing plan. *GigaScience*, **2018**, 7, 1-9	7.6	108
230	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	11.5	334
229	Genome-wide determination of on-target and off-target characteristics for RNA-guided DNA methylation by dCas9 methyltransferases. *GigaScience*, **2018**, 7, 1-19	7.6	43
228	Assessment of the cPAS-based BGISEQ-500 platform for metagenomic sequencing. *GigaScience*, **2018**, 7, 1-8	7.6	82
227	Bph6 encodes an exocyst-localized protein and confers broad resistance to planthoppers in rice. *Nature Genetics*, **2018**, 50, 297-306	36.3	88
226	Construction of the third-generation Zea mays haplotype map. *GigaScience*, **2018**, 7, 1-12	7.6	127
225	The genetic architecture of floral traits in the woody plant Prunus mume. *Nature Communications*, **2018**, 9, 1702	17.4	46
224	Stromal Gene Expression is Predictive for Metastatic Primary Prostate Cancer. *European Urology*, **2018**, 73, 524-532	10.2	35
223	Novel genetic loci associated HLA-B*08:01 positive myasthenia gravis. *Journal of Autoimmunity*, **2018**, 88, 43-49	15.5	14
222	Whole-genome and Transcriptome Sequencing of Prostate Cancer Identify New Genetic Alterations Driving Disease Progression. *European Urology*, **2018**, 73, 322-339	10.2	71
221	A western Sahara centre of domestication inferred from pearl millet genomes. *Nature Ecology and Evolution*, **2018**, 2, 1377-1380	12.3	48

220	Chromosome-level reference genome of the Siamese fighting fish Betta splendens, a model species for the study of aggression. *GigaScience*, **2018**, 7,	7.6	14
219	Shifting the limits in wheat research and breeding using a fully annotated reference genome. *Science*, **2018**, 361,	33.3	1296
218	The correlation of copy number variations with longevity in a genome-wide association study of Han Chinese. *Aging*, **2018**, 10, 1206-1222	5.6	12
217	Ma et al. reply. *Nature*, **2018**, 560, E10-E23	50.4	27
216	The structure and function of the global citrus rhizosphere microbiome. *Nature Communications*, **2018**, 9, 4894	17.4	157
215	Whole-genome sequencing of 175 Mongolians uncovers population-specific genetic architecture and gene flow throughout North and East Asia. *Nature Genetics*, **2018**, 50, 1696-1704	36.3	27
214	Single-cell RNA-seq reveals dynamic transcriptome profiling in human early neural differentiation. *GigaScience*, **2018**, 7,	7.6	11
213	MetaPGN: a pipeline for construction and graphical visualization of annotated pangenome networks. *GigaScience*, **2018**, 7,	7.6	4
212	Genomic Analyses from Non-invasive Prenatal Testing Reveal Genetic Associations, Patterns of Viral Infections, and Chinese Population History. *Cell*, **2018**, 175, 347-359.e14	56.2	123
211	The metagenome of the female upper reproductive tract. *GigaScience*, **2018**, 7,	7.6	43
210	Sex Differences in Genetic Associations With Longevity. *JAMA Network Open*, **2018**, 1, e181670	10.4	40
209	A gene catalogue of the Sprague-Dawley rat gut metagenome. *GigaScience*, **2018**, 7,	7.6	41
208	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. *Science*, **2018**, 361,	33.3	167
207	Population genomic data reveal genes related to important traits of quail. *GigaScience*, **2018**, 7,	7.6	16
206	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. *Nature Plants*, **2018**, 4, 460-472	11.5	176
205	Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer. *Gut*, **2017**, 66, 70-78	19.2	488
204	Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. *Science*, **2017**, 355,	33.3	101
203	A novel Enterovirus 96 circulating in China causes hand, foot, and mouth disease. *Virus Genes*, **2017**, 53, 352-356	2.3	1

202	Transcriptome profiling of Galaxea fascicularis and its endosymbiont Symbiodinium reveals chronic eutrophication tolerance pathways and metabolic mutualism between partners. *Scientific Reports*, **2017**, 7, 42100	4.9	20
201	Genome assembly with in vitro proximity ligation data and whole-genome triplication in lettuce. *Nature Communications*, **2017**, 8, 14953	17.4	196
200	Isolation and phylogenetic study of Rift Valley fever virus from the first imported case to China. *Virologica Sinica*, **2017**, 32, 253-256	6.4	4
199	Draft genome sequence of the Tibetan medicinal herb Rhodiola crenulata. *GigaScience*, **2017**, 6, 1-5	7.6	20
198	Gut microbiome and serum metabolome alterations in obesity and after weight-loss intervention. *Nature Medicine*, **2017**, 23, 859-868	50.5	627
197	The Different T-cell Receptor Repertoires in Breast Cancer Tumors, Draining Lymph Nodes, and Adjacent Tissues. *Cancer Immunology Research*, **2017**, 5, 148-156	12.5	49
196	The gut microbiome in atherosclerotic cardiovascular disease. *Nature Communications*, **2017**, 8, 845	17.4	575
195	The microbiota continuum along the female reproductive tract and its relation to uterine-related diseases. *Nature Communications*, **2017**, 8, 875	17.4	308
194	Taxonomic structure and functional association of foxtail millet root microbiome. *GigaScience*, **2017** , 6, 1-12	7.6	1155
193	Whole Exome Sequencing Identifies the Genetic Basis of Late-Onset Leigh Syndrome in a Patient with MRI but Little Biochemical Evidence of a Mitochondrial Disorder. *JIMD Reports*, **2017**, 32, 117-124	1.9	7
192	The high-quality genome of Brassica napus cultivar 'ZS11' reveals the introgression history in semi-winter morphotype. *Plant Journal*, **2017**, 92, 452-468	6.9	132
191	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. *Nature Biotechnology*, **2017**, 35, 969-976	44.5	197
190	Genome-wide Target Enrichment-aided Chip Design: a 66 K SNP Chip for Cashmere Goat. *Scientific Reports*, **2017**, 7, 8621	4.9	5
189	RED-ML: a novel, effective RNA editing detection method based on machine learning. *GigaScience*, **2017**, 6, 1-8	7.6	19
188	Correction of a pathogenic gene mutation in human embryos. *Nature*, **2017**, 548, 413-419	50.4	567
187	Deep whole-genome sequencing of 90 Han Chinese genomes. *GigaScience*, **2017**, 6, 1-7	7.6	22
186	Assembly and analysis of 100 full MHC haplotypes from the Danish population. *Genome Research*, **2017**, 27, 1597-1607	9.7	10
185	Analyses of gut microbiota and plasma bile acids enable stratification of patients for antidiabetic treatment. *Nature Communications*, **2017**, 8, 1785	17.4	192

184	Isolation and whole genome sequencing of fetal cells from maternal blood towards the ultimate non-invasive prenatal testing. *Prenatal Diagnosis*, **2017**, 37, 1311-1321	3.2	25
183	Improvement of peptide identification with considering the abundance of mRNA and peptide. *BMC Bioinformatics*, **2017**, 18, 109	3.6	6
182	Two distinct metacommunities characterize the gut microbiota in Crohn's disease patients. *GigaScience*, **2017**, 6, 1-11	7.6	40
181	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. *Nature*, **2017**, 548, 87-91	50.4	87
180	Copy number variations of HLA-I and activation of NKp30 pathway determine the sensitivity of gastric cancer cells to the cytotoxicity of natural killer cells. *Oncogene*, **2016**, 35, 2584-91	9.2	4
179	Exome sequencing identified FGF12 as a novel candidate gene for Kashin-Beck disease. *Functional and Integrative Genomics*, **2016**, 16, 13-7	3.8	7
178	cPAS-based sequencing on the BGISEQ-500 to explore small non-coding RNAs. *Clinical Epigenetics*, **2016**, 8, 123	7.7	83
177	Draft genome of the living fossil Ginkgo biloba. *GigaScience*, **2016**, 5, 49	7.6	161
176	First report of human salivirus/klassevirus in respiratory specimens of a child with fatal adenovirus infection. *Virus Genes*, **2016**, 52, 620-4	2.3	2
175	A reference gene catalogue of the pig gut microbiome. *Nature Microbiology*, **2016**, 1, 16161	26.6	233
174	Integrated metabolomics and metagenomics analysis of plasma and urine identified microbial metabolites associated with coronary heart disease. *Scientific Reports*, **2016**, 6, 22525	4.9	89
173	Allelic diversity in an NLR gene enables rice to combat planthopper variation. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 12850-12855	11.5	120
172	Genome-wide characteristics of mutations in autism. *Npj Genomic Medicine*, **2016**, 1, 160271-1602710	6.2	126
171	The stepwise evolution of the exome during acquisition of docetaxel resistance in breast cancer cells. *BMC Genomics*, **2016**, 17, 442	4.5	21
170	Genomic and oncogenic preference of HBV integration in hepatocellular carcinoma. *Nature Communications*, **2016**, 7, 12992	17.4	151
169	Case report of a Li-Fraumeni syndrome-like phenotype with a de novo mutation in CHEK2. *Medicine (United States)*, **2016**, 95, e4251	1.8	4
168	PGA: an R/Bioconductor package for identification of novel peptides using a customized database derived from RNA-Seq. *BMC Bioinformatics*, **2016**, 17, 244	3.6	39
167	Multiple IgH Isotypes Including IgD, Subclasses of IgM, and IgY Are Expressed in the Common Ancestors of Modern Birds. *Journal of Immunology*, **2016**, 196, 5138-47	5.3	21

166	Utility of next-generation sequencing technologies for the efficient genetic resolution of haematological disorders. *Clinical Genetics*, **2016**, 89, 163-72	4	13
165	Search for the potential "second-hit" mechanism underlying the onset of familial hemophagocytic lymphohistiocytosis type 2 by whole-exome sequencing analysis. *Translational Research*, **2016**, 170, 26-39	11	7
164	SCRaMbLE generates designed combinatorial stochastic diversity in synthetic chromosomes. *Genome Research*, **2016**, 26, 36-49	9.7	78
163	Analytical and Decision Support Tools for Genomics-Assisted Breeding. *Trends in Plant Science*, **2016**, 21, 354-363	13.1	46
162	The genome sequences of Arachis duranensis and Arachis ipaensis, the diploid ancestors of cultivated peanut. *Nature Genetics*, **2016**, 48, 438-46	36.3	498
161	Reply to Artifacts in the data of Hu et al. *Nature Genetics*, **2016**, 48, 3-4	36.3	1
160	The Sinocyclocheilus cavefish genome provides insights into cave adaptation. *BMC Biology*, **2016**, 14, 1	7.3	144
159	Structural genomic changes underlie alternative reproductive strategies in the ruff (Philomachus pugnax). *Nature Genetics*, **2016**, 48, 84-8	36.3	214
158	POPDC1(S201F) causes muscular dystrophy and arrhythmia by affecting protein trafficking. *Journal of Clinical Investigation*, **2016**, 126, 239-53	15.9	55
157	Single-cell analyses of transcriptional heterogeneity in squamous cell carcinoma of urinary bladder. *Oncotarget*, **2016**, 7, 66069-66076	3.3	23
156	The genetic basis for ecological adaptation of the Atlantic herring revealed by genome sequencing. *ELife*, **2016**, 5,	8.9	103
155	Minimal Residual Disease Detection and Evolved Clones Analysis in Acute B Lymphoblastic Leukemia Using Deep Sequencing. *Frontiers in Immunology*, **2016**, 7, 403	8.4	24
154	Systematic Comparative Evaluation of Methods for Investigating the TCR□Repertoire. *PLoS ONE*, **2016**, 11, e0152464	3.7	29
153	Signatures of Crested Ibis MHC Revealed by Recombination Screening and Short-Reads Assembly Strategy. *PLoS ONE*, **2016**, 11, e0168744	3.7	2
152	Redefining the structural motifs that determine RNA binding and RNA editing by pentatricopeptide repeat proteins in land plants. *Plant Journal*, **2016**, 85, 532-47	6.9	176
151	Recent breeding programs enhanced genetic diversity in both desi and kabuli varieties of chickpea (Cicer arietinum L.). *Scientific Reports*, **2016**, 6, 38636	4.9	53
150	Genesis, Evolution and Prevalence of H5N6 Avian Influenza Viruses in China. *Cell Host and Microbe*, **2016**, 20, 810-821	23.4	187
149	Novel loci and pathways significantly associated with longevity. *Scientific Reports*, **2016**, 6, 21243	4.9	105

148	First documented case of avian influenza (H5N1) virus infection in a lion. *Emerging Microbes and Infections*, **2016**, 5, e125	18.9	11
147	Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome. *Cell Systems*, **2016**, 3, 572-584.e3	10.6	172
146	Evolution of multiple cell clones over a 29-year period of a CLL patient. *Nature Communications*, **2016**, 7, 13765	17.4	21
145	The Asian arowana (Scleropages formosus) genome provides new insights into the evolution of an early lineage of teleosts. *Scientific Reports*, **2016**, 6, 24501	4.9	66
144	Deep sequencing of the MHC region in the Chinese population contributes to studies of complex disease. *Nature Genetics*, **2016**, 48, 740-6	36.3	129
143	The Power of Inbreeding: NGS-Based GWAS of Rice Reveals Convergent Evolution during Rice Domestication. *Molecular Plant*, **2016**, 9, 975-85	14.4	66
142	An LC-MS based untargeted metabolomics study identified novel biomarkers for coronary heart disease. *Molecular BioSystems*, **2016**, 12, 3425-3434		9
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21	Three genomes of Osteoglossidae shed light on ancient teleost evolution	3
20	Genomic analyses reveal the origin of domestic ducks and identify different genetic underpinnings of wild ducks	1
19	CoolMPS：Advanced massively parallel sequencing using antibodies specific to each natural nucleobase	2
18	Multiple approaches for massively parallel sequencing of HCoV-19 (SARS-CoV-2) genomes directly from clinical samples	9
17	Single-cell atlas of a non-human primate reveals new pathogenic mechanisms of COVID-19	19
16	Initial Whole Genome Sequencing and Analysis of the Host Genetic Contribution to COVID-19 Severity and Susceptibility	3
15	Inter-determination of blood metabolite levels and gut microbiome supported by Mendelian randomization	5
14	The Trans-omics Landscape of COVID-19	1
13	Landscapes and dynamic diversifications of B-cell receptor repertoires in COVID-19 patients	1
12	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment	1
11	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity	5
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9	Recent origin of an XX/XY sex-determination system in the ancient plant lineage Ginkgo biloba	5
8	Draft genome sequence of the Solanum aethiopicum provides insights into disease resistance, drought tolerance and the evolution of the genome	4
7	The vagino-cervical microbiome as a woman's life history	4
6	A multi-omic cohort as a reference point for promoting a healthy human gut microbiome	7
5	Age-dependent sexual dimorphism in the adult human gut microbiota	2

4	SLR-superscaffolder: a de novo scaffolding tool for synthetic long reads using a top-to-bottom scheme	1
3	Over 50000 metagenomically assembled draft genomes for the human oral microbiome reveal new taxa	3
2	TGS-GapCloser: fast and accurately passing through the Bermuda in large genome using error-prone third-generation long reads	3
1	Metagenome-genome-wide association studies reveal human genetic impact on the oral microbiome	2