

Jun Wang

List of Publications by Year in descending order

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519
papers

205,647
citations

40

189
h-index

32

428
g-index

543
all docs

543
docs citations

543
times ranked

184059
citing authors

#	ARTICLE	IF	CITATIONS
1	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	27.8	13,998
2	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	27.8	9,342
3	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010, 467, 1061-1073.	27.8	7,209
4	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65.	27.8	7,199
5	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	27.8	5,800
6	A metagenome-wide association study of gut microbiota in type 2 diabetes. <i>Nature</i> , 2012, 490, 55-60.	27.8	5,345
7	SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. <i>GigaScience</i> , 2012, 1, 18.	6.4	4,510
8	Characterization of microRNAs in serum: a novel class of biomarkers for diagnosis of cancer and other diseases. <i>Cell Research</i> , 2008, 18, 997-1006.	12.0	4,084
9	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	27.8	3,641
10	SOAP2: an improved ultrafast tool for short read alignment. <i>Bioinformatics</i> , 2009, 25, 1966-1967.	4.1	3,329
11	A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. <i>indica</i>). <i>Science</i> , 2002, 296, 79-92.	12.6	3,146
12	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	27.8	2,860
13	SOAP: short oligonucleotide alignment program. <i>Bioinformatics</i> , 2008, 24, 713-714.	4.1	2,766
14	WEGO: a web tool for plotting GO annotations. <i>Nucleic Acids Research</i> , 2006, 34, W293-W297.	14.5	2,529
15	De novo assembly of human genomes with massively parallel short read sequencing. <i>Genome Research</i> , 2010, 20, 265-272.	5.5	2,516
16	Dynamics and Stabilization of the Human Gut Microbiome during the First Year of Life. <i>Cell Host and Microbe</i> , 2015, 17, 690-703.	11.0	2,276
17	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014, 346, 763-767.	12.6	2,096
18	The oyster genome reveals stress adaptation and complexity of shell formation. <i>Nature</i> , 2012, 490, 49-54.	27.8	1,966

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19	Genome sequence and analysis of the tuber crop potato. <i>Nature</i> , 2011, 475, 189-195.	27.8	1,912
20	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	21.4	1,893
21	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
22	Independent optical excitation of distinct neural populations. <i>Nature Methods</i> , 2014, 11, 338-346.	19.0	1,879
23	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016, 352, 560-564.	12.6	1,716
24	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	17.5	1,664
25	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	27.8	1,627
26	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016, 535, 376-381.	27.8	1,506
27	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016, 352, 565-569.	12.6	1,398
28	Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude. <i>Science</i> , 2010, 329, 75-78.	12.6	1,339
29	The genome of the cucumber, <i>Cucumis sativus</i> L.. <i>Nature Genetics</i> , 2009, 41, 1275-1281.	21.4	1,317
30	The oral and gut microbiomes are perturbed in rheumatoid arthritis and partly normalized after treatment. <i>Nature Medicine</i> , 2015, 21, 895-905.	30.7	1,306
31	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	27.8	1,190
32	Phylotranscriptomic analysis of the origin and early diversification of land plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4859-68.	7.1	1,123
33	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. <i>Science</i> , 2012, 335, 823-828.	12.6	1,095
34	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.	17.5	1,064
35	Gut microbiome development along the colorectal adenoma-carcinoma sequence. <i>Nature Communications</i> , 2015, 6, 6528.	12.8	1,062
36	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	27.8	1,058

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37	Draft genome sequence of chickpea (<i>Cicer arietinum</i>) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013, 31, 240-246.	17.5	1,049
38	The gut microbiome in atherosclerotic cardiovascular disease. <i>Nature Communications</i> , 2017, 8, 845.	12.8	1,029
39	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015, 526, 82-90.	27.8	1,014
40	A Draft Sequence for the Genome of the Domesticated Silkworm (<i>Bombyx mori</i>). <i>Science</i> , 2004, 306, 1937-1940.	12.6	994
41	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011, 470, 59-65.	27.8	991
42	Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection. <i>Nature Genetics</i> , 2010, 42, 1053-1059.	21.4	987
43	KaKs_Calculator: Calculating Ka and Ks Through Model Selection and Model Averaging. <i>Genomics, Proteomics and Bioinformatics</i> , 2006, 4, 259-263.	6.9	940
44	The draft genome of a diploid cotton <i>Gossypium raimondii</i> . <i>Nature Genetics</i> , 2012, 44, 1098-1103.	21.4	935
45	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	12.8	918
46	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	17.5	909
47	Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. <i>Nature</i> , 2014, 512, 194-197.	27.8	904
48	Identification of genomic alterations in oesophageal squamous cell cancer. <i>Nature</i> , 2014, 509, 91-95.	27.8	903
49	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	12.6	895
50	Genome sequence of the cultivated cotton <i>Gossypium arboreum</i> . <i>Nature Genetics</i> , 2014, 46, 567-572.	21.4	883
51	Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer. <i>Gut</i> , 2017, 66, 70-78.	12.1	865
52	SNP detection for massively parallel whole-genome resequencing. <i>Genome Research</i> , 2009, 19, 1124-1132.	5.5	855
53	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008, 456, 60-65.	27.8	834
54	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	5.5	832

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55	SOAPdenovo-Trans: <i>de novo</i> transcriptome assembly with short RNA-Seq reads. <i>Bioinformatics</i> , 2014, 30, 1660-1666.	4.1	826
56	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2012, 30, 105-111.	17.5	818
57	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012, 44, 808-811.	21.4	816
58	The Genomes of <i>Oryza sativa</i> : A History of Duplications. <i>PLoS Biology</i> , 2005, 3, e38.	5.6	808
59	Quantitative microbiome profiling links gut community variation to microbial load. <i>Nature</i> , 2017, 551, 507-511.	27.8	791
60	Draft genome sequence of pigeonpea (<i>Cajanus cajan</i>), an orphan legume crop of resource-poor farmers. <i>Nature Biotechnology</i> , 2012, 30, 83-89.	17.5	788
61	Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. <i>Nature Genetics</i> , 2012, 44, 765-769.	21.4	785
62	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010, 463, 757-762.	27.8	750
63	The draft genome of watermelon (<i>Citrullus lanatus</i>) and resequencing of 20 diverse accessions. <i>Nature Genetics</i> , 2013, 45, 51-58.	21.4	731
64	Recalibrating <i>Equus</i> evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78.	27.8	717
65	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	13.3	717
66	<i>Aegilops tauschii</i> draft genome sequence reveals a gene repertoire for wheat adaptation. <i>Nature</i> , 2013, 496, 91-95.	27.8	714
67	The yak genome and adaptation to life at high altitude. <i>Nature Genetics</i> , 2012, 44, 946-949.	21.4	708
68	Draft genome of the wheat A-genome progenitor <i>Triticum urartu</i> . <i>Nature</i> , 2013, 496, 87-90.	27.8	700
69	The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. <i>Nature Biotechnology</i> , 2011, 29, 735-741.	17.5	699
70	Distinct DNA methylomes of newborns and centenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10522-10527.	7.1	687
71	Whole-genome sequence of a flatfish provides insights into ZW sex chromosome evolution and adaptation to a benthic lifestyle. <i>Nature Genetics</i> , 2014, 46, 253-260.	21.4	685
72	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	21.4	676

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73	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. <i>Science</i> , 2011, 334, 94-98.	12.6	675
74	Non-invasive prenatal assessment of trisomy 21 by multiplexed maternal plasma DNA sequencing: large scale validity study. <i>BMJ: British Medical Journal</i> , 2011, 342, c7401-c7401.	2.3	641
75	Frequent mutations of chromatin remodeling genes in transitional cell carcinoma of the bladder. <i>Nature Genetics</i> , 2011, 43, 875-878.	21.4	638
76	Genome sequence of foxtail millet (<i>Setaria italica</i>) provides insights into grass evolution and biofuel potential. <i>Nature Biotechnology</i> , 2012, 30, 549-554.	17.5	636
77	The <i>Schistosoma japonicum</i> genome reveals features of host-parasite interplay. <i>Nature</i> , 2009, 460, 345-351.	27.8	635
78	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. <i>Science</i> , 2012, 337, 100-104.	12.6	626
79	Single-Cell Exome Sequencing Reveals Single-Nucleotide Mutation Characteristics of a Kidney Tumor. <i>Cell</i> , 2012, 148, 886-895.	28.9	622
80	Metagenome-wide analysis of antibiotic resistance genes in a large cohort of human gut microbiota. <i>Nature Communications</i> , 2013, 4, 2151.	12.8	606
81	The genome of a lepidopteran model insect, the silkworm <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 1036-1045.	2.7	592
82	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	6.4	582
83	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , 2014, 3, 17.	6.4	582
84	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	21.4	577
85	Integrated Profiling of MicroRNAs and mRNAs: MicroRNAs Located on Xq27.3 Associate with Clear Cell Renal Cell Carcinoma. <i>PLoS ONE</i> , 2010, 5, e15224.	2.5	573
86	The microbiota continuum along the female reproductive tract and its relation to uterine-related diseases. <i>Nature Communications</i> , 2017, 8, 875.	12.8	572
87	Comparative Analysis of Bat Genomes Provides Insight into the Evolution of Flight and Immunity. <i>Science</i> , 2013, 339, 456-460.	12.6	522
88	Genome sequencing reveals insights into physiology and longevity of the naked mole rat. <i>Nature</i> , 2011, 479, 223-227.	27.8	517
89	Single-Cell Exome Sequencing and Monoclonal Evolution of a JAK2-Negative Myeloproliferative Neoplasm. <i>Cell</i> , 2012, 148, 873-885.	28.9	503
90	Whole-Genome Sequencing in Autism Identifies Hot Spots for De Novo Germline Mutation. <i>Cell</i> , 2012, 151, 1431-1442.	28.9	501

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91	Recovery of gut microbiota of healthy adults following antibiotic exposure. <i>Nature Microbiology</i> , 2018, 3, 1255-1265.	13.3	483
92	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra</i>) Tj ETQq0 0 0rgBT /Overlock 10 T	17.5	479
93	A heterozygous moth genome provides insights into herbivory and detoxification. <i>Nature Genetics</i> , 2013, 45, 220-225.	21.4	472
94	TreeFam: a curated database of phylogenetic trees of animal gene families. <i>Nucleic Acids Research</i> , 2006, 34, D572-D580.	14.5	465
95	Comprehensive analysis of RNA-Seq data reveals extensive RNA editing in a human transcriptome. <i>Nature Biotechnology</i> , 2012, 30, 253-260.	17.5	461
96	Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. <i>Genome Research</i> , 2013, 23, 1422-1433.	5.5	457
97	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	19.0	442
98	The genome of <i>Prunus mume</i> . <i>Nature Communications</i> , 2012, 3, 1318.	12.8	441
99	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , 2010, 42, 1027-1030.	21.4	439
100	The locust genome provides insight into swarm formation and long-distance flight. <i>Nature Communications</i> , 2014, 5, 2957.	12.8	437
101	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	12.6	436
102	Deep RNA sequencing at single base-pair resolution reveals high complexity of the rice transcriptome. <i>Genome Research</i> , 2010, 20, 646-654.	5.5	435
103	The <i>Symbiodinium kawagutii</i> genome illuminates dinoflagellate gene expression and coral symbiosis. <i>Science</i> , 2015, 350, 691-694.	12.6	430
104	Detection of Clinically Relevant Genetic Variants in Autism Spectrum Disorder by Whole-Genome Sequencing. <i>American Journal of Human Genetics</i> , 2013, 93, 249-263.	6.2	429
105	Genome sequencing of 161 <i>Mycobacterium tuberculosis</i> isolates from China identifies genes and intergenic regions associated with drug resistance. <i>Nature Genetics</i> , 2013, 45, 1255-1260.	21.4	426
106	A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2015, 33, 1103-1108.	17.5	422
107	Genomic Comparison of the Ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Science</i> , 2010, 329, 1068-1071.	12.6	420
108	A reference gene catalogue of the pig gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16161.	13.3	416

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109	The genome of flax (<i>Linum usitatissimum</i>) assembled <i>de novo</i> from short shotgun sequence reads. <i>Plant Journal</i> , 2012, 72, 461-473.	5.7	415
110	The genome sequence of the orchid <i>Phalaenopsis equestris</i> . <i>Nature Genetics</i> , 2015, 47, 65-72.	21.4	413
111	The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. <i>Nature Genetics</i> , 2013, 45, 701-706.	21.4	409
112	Whole-genome sequencing reveals untapped genetic potential in Africa's indigenous cereal crop sorghum. <i>Nature Communications</i> , 2013, 4, 2320.	12.8	405
113	Genomes of the rice pest brown planthopper and its endosymbionts reveal complex complementary contributions for host adaptation. <i>Genome Biology</i> , 2014, 15, 521.	8.8	404
114	Whole-genome and whole-exome sequencing of bladder cancer identifies frequent alterations in genes involved in sister chromatid cohesion and segregation. <i>Nature Genetics</i> , 2013, 45, 1459-1463.	21.4	400
115	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.	21.4	393
116	Open-Source Genomic Analysis of Shiga-Toxin-Producing <i>E. coli</i> O104:H4. <i>New England Journal of Medicine</i> , 2011, 365, 718-724.	27.0	392
117	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004, 432, 717-722.	27.8	391
118	A genome triplication associated with early diversification of the core eudicots. <i>Genome Biology</i> , 2012, 13, R3.	9.6	389
119	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012, 44, 221-225.	21.4	383
120	Historical variations in mutation rate in an epidemic pathogen, <i>Yersinia pestis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 577-582.	7.1	373
121	Molecular traces of alternative social organization in a termite genome. <i>Nature Communications</i> , 2014, 5, 3636.	12.8	371
122	Prebiotic inulin-type fructans induce specific changes in the human gut microbiota. <i>Gut</i> , 2017, 66, 1968-1974.	12.1	370
123	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. <i>Cell</i> , 2014, 157, 785-794.	28.9	363
124	Genome-wide and Caste-Specific DNA Methylomes of the Ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Current Biology</i> , 2012, 22, 1755-1764.	3.9	361
125	Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 2015, 348, 1139-1143.	12.6	357
126	Epigenetic modification and inheritance in sexual reversal of fish. <i>Genome Research</i> , 2014, 24, 604-615.	5.5	356

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127	Metagenome-wide association studies: fine-mining the microbiome. <i>Nature Reviews Microbiology</i> , 2016, 14, 508-522.	28.6	356
128	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	17.5	356
129	RNA-seq analysis of prostate cancer in the Chinese population identifies recurrent gene fusions, cancer-associated long noncoding RNAs and aberrant alternative splicings. <i>Cell Research</i> , 2012, 22, 806-821.	12.0	352
130	Lanosterol reverses protein aggregation in cataracts. <i>Nature</i> , 2015, 523, 607-611.	27.8	351
131	Single base-resolution methylome of the silkworm reveals a sparse epigenomic map. <i>Nature Biotechnology</i> , 2010, 28, 516-520.	17.5	349
132	The Dynamic Distribution of Porcine Microbiota across Different Ages and Gastrointestinal Tract Segments. <i>PLoS ONE</i> , 2015, 10, e0117441.	2.5	349
133	Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm (<i>Bombyx mori</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 11	12.6	342
134	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.	17.5	340
135	A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. <i>Nature</i> , 2014, 512, 190-193.	27.8	338
136	The 3,000 rice genomes project: new opportunities and challenges for future rice research. <i>GigaScience</i> , 2014, 3, 8.	6.4	337
137	SNP Calling, Genotype Calling, and Sample Allele Frequency Estimation from New-Generation Sequencing Data. <i>PLoS ONE</i> , 2012, 7, e37558.	2.5	336
138	The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. <i>Nature Genetics</i> , 2013, 45, 776-783.	21.4	327
139	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015, 16, 133.	8.8	325
140	Whole-genome sequencing of giant pandas provides insights into demographic history and local adaptation. <i>Nature Genetics</i> , 2013, 45, 67-71.	21.4	303
141	Camelid genomes reveal evolution and adaptation to desert environments. <i>Nature Communications</i> , 2014, 5, 5188.	12.8	299
142	Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. <i>Nature Genetics</i> , 2010, 42, 969-972.	21.4	297
143	Frequent mutations of genes encoding ubiquitin-mediated proteolysis pathway components in clear cell renal cell carcinoma. <i>Nature Genetics</i> , 2012, 44, 17-19.	21.4	295
144	TreeFam: 2008 Update. <i>Nucleic Acids Research</i> , 2007, 36, D735-D740.	14.5	294

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145	The Sinocyclocheilus cavefish genome provides insights into cave adaptation. BMC Biology, 2016, 14, 1.	3.8	292
146	The DNA Methylome of Human Peripheral Blood Mononuclear Cells. PLoS Biology, 2010, 8, e1000533.	5.6	290
147	Genomic Analyses Reveal Mutational Signatures and Frequently Altered Genes in Esophageal Squamous Cell Carcinoma. American Journal of Human Genetics, 2015, 96, 597-611.	6.2	290
148	Genomic insights into salt adaptation in a desert poplar. Nature Communications, 2013, 4, 2797.	12.8	286
149	Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques. Nature Biotechnology, 2011, 29, 1019-1023.	17.5	284
150	Pulling out the 1%: Whole-Genome Capture for the Targeted Enrichment of Ancient DNA Sequencing Libraries. American Journal of Human Genetics, 2013, 93, 852-864.	6.2	284
151	Genome of the Chinese tree shrew. Nature Communications, 2013, 4, 1426.	12.8	284
152	Pigs in sequence space: A 0.66X coverage pig genome survey based on shotgun sequencing. BMC Genomics, 2005, 6, 70.	2.8	283
153	Draft genome sequence of the mulberry tree <i>Morus notabilis</i> . Nature Communications, 2013, 4, 2445.	12.8	277
154	Mutation in the <i>SYNJ1</i> Gene Associated with Autosomal Recessive, Early-Onset Parkinsonism. Human Mutation, 2013, 34, 1208-1215.	2.5	276
155	Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases. Nature Biotechnology, 2016, 34, 531-538.	17.5	273
156	Insights into salt tolerance from the genome of <i>Thellungiella salsuginea</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12219-12224.	7.1	272
157	Single-base resolution maps of cultivated and wild rice methylomes and regulatory roles of DNA methylation in plant gene expression. BMC Genomics, 2012, 13, 300.	2.8	266
158	Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome. Cell Systems, 2016, 3, 572-584.e3.	6.2	261
159	Roux-en-Y gastric bypass surgery of morbidly obese patients induces swift and persistent changes of the individual gut microbiota. Genome Medicine, 2016, 8, 67.	8.2	260
160	Donor Species Richness Determines Faecal Microbiota Transplantation Success in Inflammatory Bowel Disease. Journal of Crohn's and Colitis, 2016, 10, 387-394.	1.3	256
161	IQuant: An automated pipeline for quantitative proteomics based upon isobaric tags. Proteomics, 2014, 14, 2280-2285.	2.2	253
162	RNA sequencing reveals the complex regulatory network in the maize kernel. Nature Communications, 2013, 4, 2832.	12.8	252

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163	Identification of ten serum microRNAs from a genome-wide serum microRNA expression profile as novel noninvasive biomarkers for nonsmall cell lung cancer diagnosis. <i>International Journal of Cancer</i> , 2012, 130, 1620-1628.	5.1	251
164	<i>Ascaris suum</i> draft genome. <i>Nature</i> , 2011, 479, 529-533.	27.8	246
165	The Genome of the Netherlands: design, and project goals. <i>European Journal of Human Genetics</i> , 2014, 22, 221-227.	2.8	246
166	Genome sequencing of the high oil crop sesame provides insight into oil biosynthesis. <i>Genome Biology</i> , 2014, 15, R39.	9.6	245
167	A Glimpse of Streptococcal Toxic Shock Syndrome from Comparative Genomics of <i>S. suis</i> 2 Chinese Isolates. <i>PLoS ONE</i> , 2007, 2, e315.	2.5	244
168	TGM6 identified as a novel causative gene of spinocerebellar ataxias using exome sequencing. <i>Brain</i> , 2010, 133, 3510-3518.	7.6	243
169	Noninvasive Prenatal Diagnosis of Fetal Trisomy 18 and Trisomy 13 by Maternal Plasma DNA Sequencing. <i>PLoS ONE</i> , 2011, 6, e21791.	2.5	243
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