

Jianguo Zhang

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

164
papers

14,048
citations

45
h-index

117
g-index

173
ext. papers

16,514
ext. citations

10.5
avg, IF

5.68
L-index

#	Paper	IF	Citations
164	Circulation, genomic characteristics, and evolutionary dynamics of class I Newcastle disease virus in China.. <i>Virulence</i> , 2022 , 13, 414-427	4.7	2
163	Comparison of microbial composition and diversity in the upper respiratory tract between SARS-CoV-2 and influenza virus infections.. <i>Science China Life Sciences</i> , 2022 , 1	8.5	1
162	Hemagglutinin Gene Variation Rate of H9N2 Avian Influenza Virus by Vaccine Intervention in China. <i>Viruses</i> , 2022 , 14, 1043	6.2	1
161	Analysis of the evolution, infectivity and antigenicity of circulating rabies virus strains.. <i>Emerging Microbes and Infections</i> , 2022 , 1-30	18.9	2
160	Suppression and Activation of Intracellular Immune Response in Initial Severe Acute Respiratory Syndrome Coronavirus 2 Infection.. <i>Frontiers in Microbiology</i> , 2021 , 12, 768740	5.7	
159	Risk from Cooling Tower Systems in China. <i>Applied and Environmental Microbiology</i> , 2021 , AEM0192121	4.8	0
158	High alcohol-producing causes fatty liver disease through 2,3-butanediol fermentation pathway. <i>Gut Microbes</i> , 2021 , 13, 1979883	8.8	1
157	Genome-wide association study identifies new loci associated with risk of HBV infection and disease progression. <i>BMC Medical Genomics</i> , 2021 , 14, 84	3.7	3
156	Integrated characterization of SARS-CoV-2 genome, microbiome, antibiotic resistance and host response from single throat swabs. <i>Cell Discovery</i> , 2021 , 7, 19	22.3	3
155	Rapid Acquisition of High-Quality SARS-CoV-2 Genome via Amplicon-Oxford Nanopore Sequencing. <i>Virologica Sinica</i> , 2021 , 36, 901-912	6.4	7
154	Platelet-driven coagulopathy in COVID-19 patients: in comparison to seasonal influenza cases. <i>Experimental Hematology and Oncology</i> , 2021 , 10, 34	7.8	6
153	A bioinformatic study revealed serotonergic neurons are involved in the etiology and therapygenetics of anxiety disorders. <i>Translational Psychiatry</i> , 2021 , 11, 297	8.6	0
152	Transcriptome Analyses Implicate Endogenous Retroviruses Involved in the Host Antiviral Immune System through the Interferon Pathway. <i>Virologica Sinica</i> , 2021 , 1	6.4	7
151	Five-day water-only fasting decreased metabolic-syndrome risk factors and increased anti-aging biomarkers without toxicity in a clinical trial of normal-weight individuals. <i>Clinical and Translational Medicine</i> , 2021 , 11, e502	5.7	0
150	Potential m6A and m5C Methylations within the Genome of A Chinese African Swine Fever Virus Strain. <i>Virologica Sinica</i> , 2021 , 36, 321-324	6.4	3
149	Partial recovery of disturbed V-J pairing profiles of T-cell receptor in people living with HIV receiving long-term antiretroviral therapy. <i>Science China Life Sciences</i> , 2021 , 64, 152-161	8.5	0
148	Biosynthetic Polymalic Acid as a Delivery Nanoplatform for Translational Cancer Medicine. <i>Trends in Biochemical Sciences</i> , 2021 , 46, 213-224	10.3	3

147	Computational predicting the human infectivity of H7N9 influenza viruses isolated from avian hosts. <i>Transboundary and Emerging Diseases</i> , 2021 , 68, 846-856	4.2	3
146	Differentiation of COVID-19 from seasonal influenza: A multicenter comparative study. <i>Journal of Medical Virology</i> , 2021 , 93, 1512-1519	19.7	16
145	Light stimulates anoxic and oligotrophic growth of glacial Flavobacterium strains that produce zeaxanthin. <i>ISME Journal</i> , 2021 , 15, 1844-1857	11.9	2
144	Rapid Spread of Mutant Alleles in Worldwide SARS-CoV-2 Strains Revealed by Genome-Wide Single Nucleotide Polymorphism and Variation Analysis. <i>Genome Biology and Evolution</i> , 2021 , 13,	3.9	10
143	Extracellular vesicles as delivery systems at nano-/micro-scale. <i>Advanced Drug Delivery Reviews</i> , 2021 , 179, 113910	18.5	9
142	Comparative Study of Acute Lung Injury in COVID-19 and Non-COVID-19 Patients. <i>Frontiers in Medicine</i> , 2021 , 8, 666629	4.9	2
141	Synergistic effect of the responses of different tissues against African swine fever virus. <i>Transboundary and Emerging Diseases</i> , 2021 ,	4.2	4
140	Methyltransferase-like 3 Modulates Severe Acute Respiratory Syndrome Coronavirus-2 RNA N6-Methyladenosine Modification and Replication. <i>MBio</i> , 2021 , 12, e0106721	7.8	12
139	Human Adenovirus Type 7 Infections in Hubei, China During 2018-2019: Epidemic Features and Genetic Characterization of the Detected Viruses. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021 , 11, 684606	5.9	0
138	A Novel Bat Coronavirus Closely Related to SARS-CoV-2 Contains Natural Insertions at the S1/S2 Cleavage Site of the Spike Protein. <i>Current Biology</i> , 2020 , 30, 2196-2203.e3	6.3	319
137	SARS-CoV-2 Infection in Children. <i>New England Journal of Medicine</i> , 2020 , 382, 1663-1665	59.2	1411
136	Genomic epidemiological characteristics of dengue fever in Guangdong province, China from 2013 to 2017. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008049	4.8	4
135	Assessing the role of live poultry trade in community-structured transmission of avian influenza in China. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 5949-5954	11.5	16
134	Transcription profile of human endogenous retroviruses in response to dengue virus serotype 2 infection. <i>Virology</i> , 2020 , 544, 21-30	3.6	9
133	Shifts in the Bacterial Community of Supragingival Plaque Associated With Metabolic-Associated Fatty Liver Disease. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020 , 10, 581888	5.9	0
132	Reverse-Transcription Recombinase-Aided Amplification Assay for Rapid Detection of the 2019 Novel Coronavirus (SARS-CoV-2). <i>Analytical Chemistry</i> , 2020 , 92, 9699-9705	7.8	42
131	Nanopore sequencing of African swine fever virus. <i>Science China Life Sciences</i> , 2020 , 63, 160-164	8.5	8
130	Phylogenetics, Genomic Recombination, and NSP2 Polymorphic Patterns of Porcine Reproductive and Respiratory Syndrome Virus in China and the United States in 2014-2018. <i>Journal of Virology</i> , 2020 , 94,	6.6	27

129	Pan-Genomic Analysis of African Swine Fever Virus. <i>Virologica Sinica</i> , 2020 , 35, 662-665	6.4	6
128	Temporal antibody responses to SARS-CoV-2 in patients of coronavirus disease 2019. <i>Cell Discovery</i> , 2020 , 6, 64	22.3	24
127	Analysis of ACE2 Gene-Encoded Proteins Across Mammalian Species. <i>Frontiers in Veterinary Science</i> , 2020 , 7, 457	3.1	5
126	Evolution and Expression of the Membrane Attack Complex and Perforin Gene Family in the Poaceae. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	4
125	Genomic surveillance of COVID-19 cases in Beijing. <i>Nature Communications</i> , 2020 , 11, 5503	17.4	16
124	Identification and Expression of the Multidrug and Toxic Compound Extrusion (MATE) Gene Family in and. <i>Plants</i> , 2020 , 9,	4.5	4
123	Comprehensive genetic testing of Chinese SNHL patients and variants interpretation using ACMG guidelines and ethnically matched normal controls. <i>European Journal of Human Genetics</i> , 2020 , 28, 231-243	5.3	16
122	New Gene Variants Associated with the Risk of Chronic HBV Infection. <i>Virologica Sinica</i> , 2020 , 35, 378-388	7.4	3
121	Fatty Liver Disease Caused by High-Alcohol-Producing <i>Klebsiella pneumoniae</i> . <i>Cell Metabolism</i> , 2019 , 30, 675-688.e7	24.6	148
120	Gene pathogenicity prediction of Mendelian diseases via the random forest algorithm. <i>Human Genetics</i> , 2019 , 138, 673-679	6.3	4
119	The plasmid-borne quinolone resistance protein QnrB, a novel DnaA-binding protein, increases the bacterial mutation rate by triggering DNA replication stress. <i>Molecular Microbiology</i> , 2019 , 111, 1529-1543	4.1	8
118	Rapid and Specific Detection of All Known Strains Sequences With Reverse Transcription-Loop-Mediated Isothermal Amplification. <i>Frontiers in Microbiology</i> , 2019 , 10, 418	5.7	7
117	Network pharmacology based investigation into the effect and mechanism of Modified Sijunzi Decoction against the subtypes of chronic atrophic gastritis. <i>Pharmacological Research</i> , 2019 , 144, 158-166	10.2	24
116	Intra-host Ebola viral adaption during human infection. <i>Biosafety and Health</i> , 2019 , 1, 14-24	4.7	7
115	Clinical and Immunological Characteristics of Human Infections With H5N6 Avian Influenza Virus. <i>Clinical Infectious Diseases</i> , 2019 , 68, 1100-1109	11.6	35
114	Mutations in topoisomerase III result in a B cell immunodeficiency. <i>Nature Communications</i> , 2019 , 10, 3644	17.4	24
113	Nanopore sequencing: a rapid solution for infectious disease epidemics. <i>Science China Life Sciences</i> , 2019 , 62, 1101-1103	8.5	4
112	Circulation, Evolution and Transmission of H5N8 virus, 2016-2018. <i>Journal of Infection</i> , 2019 , 79, 363-372	18.9	2

111	Plants Engineered To Produce Astaxanthin Show Enhanced Oxidative Stress Tolerance and Bacterial Pathogen Resistance. <i>Journal of Agricultural and Food Chemistry</i> , 2019 , 67, 12590-12598	5.7	3
110	Molecular genetic analysis using targeted NGS analysis of 677 individuals with retinal dystrophy. <i>Scientific Reports</i> , 2019 , 9, 1219	4.9	45
109	Low Pathogenic Avian Influenza A (H5N7) Virus Isolated from a Domestic Duck in Dongting Lake Wetland of China, 2016. <i>Virologica Sinica</i> , 2019 , 34, 97-101	6.4	1
108	Naturally Occurring Single Mutations in Ebola Virus Observably Impact Infectivity. <i>Journal of Virology</i> , 2019 , 93,	6.6	18
107	Homozygous Recessive Versican Missense Variation Is Associated With Early Teeth Loss in a Pakistani Family. <i>Frontiers in Genetics</i> , 2018 , 9, 723	4.5	2
106	Three amino acid substitutions in the NS1 protein change the virus replication of H5N1 influenza virus in human cells. <i>Virology</i> , 2018 , 519, 64-73	3.6	7
105	Identified OAS3 gene variants associated with coexistence of HBsAg and anti-HBs in chronic HBV infection. <i>Journal of Viral Hepatitis</i> , 2018 , 25, 904-910	3.4	7
104	Two genetically diverse H7N7 avian influenza viruses isolated from migratory birds in central China. <i>Emerging Microbes and Infections</i> , 2018 , 7, 62	18.9	11
103	Two reassortant types of highly pathogenic H5N8 avian influenza virus from wild birds in Central China in 2016. <i>Emerging Microbes and Infections</i> , 2018 , 7, 14	18.9	11
102	Biological data processing based on bio-processor unit (BPU), a new concept for next generation computational biology. <i>Science China Life Sciences</i> , 2018 , 61, 597-598	8.5	1
101	A Promising IFN-Deficient System to Manufacture IFN-Sensitive Influenza Vaccine Virus. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018 , 8, 127	5.9	3
100	Revealing Alzheimer's disease genes spectrum in the whole-genome by machine learning. <i>BMC Neurology</i> , 2018 , 18, 5	3.1	18
99	An Assessment of Amplicon-Sequencing Based Method for Viral Intrahost Analysis. <i>Virologica Sinica</i> , 2018 , 33, 557-560	6.4	2
98	Phylogeography, Transmission, and Viral Proteins of Nipah Virus. <i>Virologica Sinica</i> , 2018 , 33, 385-393	6.4	18
97	Phylogenomic analysis unravels evolution of yellow fever virus within hosts. <i>PLoS Neglected Tropical Diseases</i> , 2018 , 12, e0006738	4.8	16
96	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315	50.4	238
95	Genome-wide analysis of structural variants reveals genetic differences in Chinese pigs. <i>PLoS ONE</i> , 2017 , 12, e0186721	3.7	5
94	A47 Origin and possible genetic recombination of the middle east respiratory syndrome coronavirus from the first imported case in china: phylogenetics and coalescence analysis. <i>Virus Evolution</i> , 2017 , 3,	3.7	2

93	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. <i>JIMD Reports</i> , 2017 , 32, 117-124	1.9	7
92	Epidemiology, Evolution, and Pathogenesis of H7N9 Influenza Viruses in Five Epidemic Waves since 2013 in China. <i>Trends in Microbiology</i> , 2017 , 25, 713-728	12.4	151
91	Dysfunction of Myosin Light-Chain 4 (MYL4) Leads to Heritable Atrial Cardiomyopathy With Electrical, Contractile, and Structural Components: Evidence From Genetically-Engineered Rats. <i>Journal of the American Heart Association</i> , 2017 , 6,	6	26
90	Mapping the clinical outcomes and genetic evolution of Ebola virus in Sierra Leone. <i>JCI Insight</i> , 2017 , 2,	9.9	3
89	Next-generation sequencing reveals a novel NDP gene mutation in a Chinese family with Norrie disease. <i>Indian Journal of Ophthalmology</i> , 2017 , 65, 1161-1165	1.6	0
88	The complete mitochondrial genome of the <i>Sorex araneus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3655-6	1.3	14
87	Identification of MFRP Mutations in Chinese Families with High Hyperopia. <i>Optometry and Vision Science</i> , 2016 , 93, 19-26	2.1	9
86	Highly pathogenic avian influenza H5N1 Clade 2.3.2.1c virus in migratory birds, 2014-2015. <i>Virologica Sinica</i> , 2016 , 31, 300-5	6.4	28
85	Intra-host dynamics of Ebola virus during 2014. <i>Nature Microbiology</i> , 2016 , 1, 16151	26.6	54
84	Stabilizing mutations of KLHL24 ubiquitin ligase cause loss of keratin 14 and human skin fragility. <i>Nature Genetics</i> , 2016 , 48, 1508-1516	36.3	73
83	DNAJC6 Mutations Associated With Early-Onset Parkinson's Disease. <i>Annals of Neurology</i> , 2016 , 79, 244-54	9.4	104
82	aKMT Catalyzes Extensive Protein Lysine Methylation in the Hyperthermophilic Archaeon <i>Sulfolobus islandicus</i> but is Dispensable for the Growth of the Organism. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2908-23	7.6	10
81	Utility of next-generation sequencing technologies for the efficient genetic resolution of haematological disorders. <i>Clinical Genetics</i> , 2016 , 89, 163-72	4	13
80	Variants of the ACTG2 gene correlate with degree of severity and presence of megacystis in chronic intestinal pseudo-obstruction. <i>European Journal of Human Genetics</i> , 2016 , 24, 1211-5	5.3	27
79	LYRM7 mutations cause a multifocal cavitating leukoencephalopathy with distinct MRI appearance. <i>Brain</i> , 2016 , 139, 782-94	11.2	44
78	Next Generation Sequencing Data Analysis in Primary Immunodeficiency Disorders - Future Directions. <i>Journal of Clinical Immunology</i> , 2016 , 36 Suppl 1, 68-75	5.7	46
77	The complete mitochondrial genome of the <i>Poecilia formosa</i> (Amazon molly). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3523-4	1.3	1
76	Phylogenetic and Taxonomic Status Analyses of the Abaso Section from Multiple Nuclear Genes and Plastid Fragments Reveal New Insights into the North America Origin of (<i>Salicaceae</i>). <i>Frontiers in Plant Science</i> , 2016 , 7, 2022	6.2	21

75	POPDC1(S201F) causes muscular dystrophy and arrhythmia by affecting protein trafficking. <i>Journal of Clinical Investigation</i> , 2016 , 126, 239-53	15.9	55
74	Exome Sequencing of a Pedigree Reveals S339L Mutation in the TLN2 Gene as a Cause of Fifth Finger Camptodactyly. <i>PLoS ONE</i> , 2016 , 11, e0155180	3.7	6
73	A Bat-Derived Putative Cross-Family Recombinant Coronavirus with a Reovirus Gene. <i>PLoS Pathogens</i> , 2016 , 12, e1005883	7.6	70
72	High-Throughput Analysis of the T Cell Receptor Beta Chain Repertoire in PBMCs from Chronic Hepatitis B Patients with HBeAg Seroconversion. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2016 , 2016, 8594107	2.6	8
71	Genesis, Evolution and Prevalence of H5N6 Avian Influenza Viruses in China. <i>Cell Host and Microbe</i> , 2016 , 20, 810-821	23.4	187
70	A new reassortment of influenza A (H7N9) virus causing human infection in Beijing, 2014. <i>Scientific Reports</i> , 2016 , 6, 26624	4.9	7
69	Homozygous GNAL mutation associated with familial childhood-onset generalized dystonia. <i>Neurology: Genetics</i> , 2016 , 2, e78	3.8	17
68	Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases. <i>Nature Biotechnology</i> , 2016 , 34, 531-8	44.5	196
67	CSF1R mosaicism in a family with hereditary diffuse leukoencephalopathy with spheroids. <i>Brain</i> , 2016 , 139, 1666-72	11.2	38
66	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
65	Web resources for microbial data. <i>Genomics, Proteomics and Bioinformatics</i> , 2015 , 13, 69-72	6.5	11
64	RNASEH1 Mutations Impair mtDNA Replication and Cause Adult-Onset Mitochondrial Encephalomyopathy. <i>American Journal of Human Genetics</i> , 2015 , 97, 186-93	11	76
63	An atypical form of AOA2 with myoclonus associated with mutations in SETX and AFG3L2. <i>BMC Medical Genetics</i> , 2015 , 16, 16	2.1	8
62	Genetic diversity and evolutionary dynamics of Ebola virus in Sierra Leone. <i>Nature</i> , 2015 , 524, 93-6	50.4	121
61	Identification of a novel GJA3 mutation in congenital nuclear cataract. <i>Optometry and Vision Science</i> , 2015 , 92, 337-42	2.1	19
60	Origin and Possible Genetic Recombination of the Middle East Respiratory Syndrome Coronavirus from the First Imported Case in China: Phylogenetics and Coalescence Analysis. <i>MBio</i> , 2015 , 6, e01280-13	7.8	70
59	Phylogeny of section Leuce (<i>Populus</i> , Salicaceae) inferred from 34 chloroplast DNA fragments. <i>Biochemical Systematics and Ecology</i> , 2015 , 63, 212-217	1.4	6
58	TCRklass: a new K-string-based algorithm for human and mouse TCR repertoire characterization. <i>Journal of Immunology</i> , 2015 , 194, 446-54	5.3	29

57	Mutation analysis of Leber congenital amaurosis-associated genes in patients with retinitis pigmentosa. <i>Molecular Medicine Reports</i> , 2015 , 11, 1827-32	2.9	11
56	Identification of climate factors related to human infection with avian influenza A H7N9 and H5N1 viruses in China. <i>Scientific Reports</i> , 2015 , 5, 18094	4.9	26
55	Highly Pathogenic Avian Influenza A(H5N1) Virus Struck Migratory Birds in China in 2015. <i>Scientific Reports</i> , 2015 , 5, 12986	4.9	38
54	Deep sequencing of hepatitis B virus basal core promoter and precore mutants in HBeAg-positive chronic hepatitis B patients. <i>Scientific Reports</i> , 2015 , 5, 17950	4.9	14
53	Unique Variants in OPN1LW Cause Both Syndromic and Nonsyndromic X-Linked High Myopia Mapped to MYP1 2015 , 56, 4150-5		30
52	Molecular genetic testing in clinical diagnostic assessments that demonstrate correlations in patients with autosomal recessive inherited retinal dystrophy. <i>JAMA Ophthalmology</i> , 2015 , 133, 427-36	3.9	16
51	Distribution of sialic acid receptors and experimental infections with different subtypes of influenza A viruses in Qinghai-Tibet plateau wild pika. <i>Virology Journal</i> , 2015 , 12, 63	6.1	8
50	Exome sequencing reveals mutation in GJA1 as a cause of keratoderma-hypotrichosis-leukonychia totalis syndrome. <i>Human Molecular Genetics</i> , 2015 , 24, 243-50	5.6	34
49	Copy number variation in CEP57L1 predisposes to congenital absence of bilateral ACL and PCL ligaments. <i>Human Genomics</i> , 2015 , 9, 31	6.8	5
48	Loss-of-function mutations in CAST cause peeling skin, leukonychia, acral punctate keratoses, cheilitis, and knuckle pads. <i>American Journal of Human Genetics</i> , 2015 , 96, 440-7	11	22
47	Mutation analysis in 129 genes associated with other forms of retinal dystrophy in 157 families with retinitis pigmentosa based on exome sequencing. <i>Molecular Vision</i> , 2015 , 21, 477-86	2.3	19
46	H7N9: a low pathogenic avian influenza A virus infecting humans. <i>Current Opinion in Virology</i> , 2014 , 5, 91-7	7.5	56
45	Dynamic reassortments and genetic heterogeneity of the human-infecting influenza A (H7N9) virus. <i>Nature Communications</i> , 2014 , 5, 3142	17.4	120
44	Mutations of 60 known causative genes in 157 families with retinitis pigmentosa based on exome sequencing. <i>Human Genetics</i> , 2014 , 133, 1255-71	6.3	121
43	The new emerging H7N9 influenza virus indicates poultry as new mixing vessels. <i>Science China Life Sciences</i> , 2014 , 57, 731-2	8.5	7
42	Poultry carrying H9N2 act as incubators for novel human avian influenza viruses. <i>Lancet, The</i> , 2014 , 383, 869	40	80
41	De novo mutation in ATP6V1B2 impairs lysosome acidification and causes dominant deafness-onychodystrophy syndrome. <i>Cell Research</i> , 2014 , 24, 1370-3	24.7	36
40	Exome sequencing reveals CHM mutations in six families with atypical choroideremia initially diagnosed as retinitis pigmentosa. <i>International Journal of Molecular Medicine</i> , 2014 , 34, 573-7	4.4	26

39	Bioinformatics analysis raises candidate genes in blood for early screening of Parkinson's disease. <i>Biomedical and Environmental Sciences</i> , 2014 , 27, 462-5	1.1	6
38	Olmsted syndrome: exploration of the immunological phenotype. <i>Orphanet Journal of Rare Diseases</i> , 2013 , 8, 79	4.2	35
37	Adult-onset Alexander disease, associated with a mutation in an alternative GFAP transcript, may be phenotypically modulated by a non-neutral HDAC6 variant. <i>Orphanet Journal of Rare Diseases</i> , 2013 , 8, 66	4.2	17
36	The draft genome of watermelon (<i>Citrullus lanatus</i>) and resequencing of 20 diverse accessions. <i>Nature Genetics</i> , 2013 , 45, 51-8	36.3	503
35	Origin and diversity of novel avian influenza A H7N9 viruses causing human infection: phylogenetic, structural, and coalescent analyses. <i>Lancet, The</i> , 2013 , 381, 1926-32	4.0	436
34	Rapid gene identification in a Chinese osteopetrosis family by whole exome sequencing. <i>Gene</i> , 2013 , 516, 311-5	3.8	17
33	Mutations in ABCB6 cause dyschromatosis universalis hereditaria. <i>Journal of Investigative Dermatology</i> , 2013 , 133, 2221-8	4.3	61
32	Comprehensive mutation analysis by whole-exome sequencing in 41 Chinese families with Leber congenital amaurosis 2013 , 54, 4351-7		74
31	Exome sequencing of 47 Chinese families with cone-rod dystrophy: mutations in 25 known causative genes. <i>PLoS ONE</i> , 2013 , 8, e65546	3.7	42
30	Identification of CHIP as a novel causative gene for autosomal recessive cerebellar ataxia. <i>PLoS ONE</i> , 2013 , 8, e81884	3.7	72
29	A replicating modified vaccinia tiantan strain expressing an avian-derived influenza H5N1 hemagglutinin induce broadly neutralizing antibodies and cross-clade protective immunity in mice. <i>PLoS ONE</i> , 2013 , 8, e83274	3.7	8
28	Exome sequencing identifies a COL14A1 mutation in a large Chinese pedigree with punctate palmoplantar keratoderma. <i>Journal of Medical Genetics</i> , 2012 , 49, 563-8	5.8	25
27	A novel homozygous mutation in SUCLA2 gene identified by exome sequencing. <i>Molecular Genetics and Metabolism</i> , 2012 , 107, 403-8	3.7	33
26	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012 , 491, 393-8	50.4	928
25	Identification of PRRT2 as the causative gene of paroxysmal kinesigenic dyskinesias. <i>Brain</i> , 2011 , 134, 3493-3501	11.2	226
24	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , 2010 , 42, 1027-30	36.3	365
23	Identification and characterization of Bmi-1-responding element within the human p16 promoter. <i>Journal of Biological Chemistry</i> , 2010 , 285, 33219-33229	5.4	48
22	Evolutionary transients in the rice transcriptome. <i>Genomics, Proteomics and Bioinformatics</i> , 2010 , 8, 211-285		8

21	The genomic underpinnings of apoptosis in the silkworm, <i>Bombyx mori</i> . <i>BMC Genomics</i> , 2010 , 11, 611	4.5	65
20	Interspecies transmission and host restriction of avian H5N1 influenza virus. <i>Science in China Series C: Life Sciences</i> , 2009 , 52, 428-38		27
19	Website for avian flu information and bioinformatics. <i>Science in China Series C: Life Sciences</i> , 2009 , 52, 470-3		6
18	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008 , 456, 60-5	50.4	744
17	Analysis of 142 genes resolves the rapid diversification of the rice genus. <i>Genome Biology</i> , 2008 , 9, R49	18.3	113
16	H5N1 avian influenza re-emergence of Lake Qinghai: phylogenetic and antigenic analyses of the newly isolated viruses and roles of migratory birds in virus circulation. <i>Journal of General Virology</i> , 2008 , 89, 697-702	4.9	87
15	Genomic comparison of <i>Yersinia pestis</i> and <i>Yersinia pseudotuberculosis</i> by combination of suppression subtractive hybridization and DNA microarray. <i>Archives of Microbiology</i> , 2006 , 186, 151-9	3	17
14	High rate of chimeric gene origination by retroposition in plant genomes. <i>Plant Cell</i> , 2006 , 18, 1791-802	11.6	183
13	Identification of different regions among strains of <i>Yersinia pestis</i> by suppression subtractive hybridization. <i>Research in Microbiology</i> , 2005 , 156, 785-9	4	14
12	OsHT, a Rice Gene Encoding for a Plasma-Membrane Localized Histidine Transporter. <i>Journal of Integrative Plant Biology</i> , 2005 , 47, 92-99	8.3	7
11	The Genomes of <i>Oryza sativa</i> : a history of duplications. <i>PLoS Biology</i> , 2005 , 3, e38	9.7	695
10	Origin and evolution of new exons in rodents. <i>Genome Research</i> , 2005 , 15, 1258-64	9.7	79
9	Complete genome sequence of <i>Yersinia pestis</i> strain 91001, an isolate avirulent to humans. <i>DNA Research</i> , 2004 , 11, 179-97	4.5	201
8	BGI-RIS: an integrated information resource and comparative analysis workbench for rice genomics. <i>Nucleic Acids Research</i> , 2004 , 32, D377-82	20.1	97
7	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004 , 432, 717-22	50.4	341
6	A draft sequence for the genome of the domesticated silkworm (<i>Bombyx mori</i>). <i>Science</i> , 2004 , 306, 1937-40	50.4	859
5	Mouse transcriptome: neutral evolution of non-coding complementary DNAs. <i>Nature</i> , 2004 , 431, 1 p following 757; discussion following 757	50.4	82
4	RePS: a sequence assembler that masks exact repeats identified from the shotgun data. <i>Genome Research</i> , 2002 , 12, 824-31	9.7	48

- 3 Compositional gradients in Gramineae genes. *Genome Research*, **2002**, 12, 851-6 9.7 139
- 2 A draft sequence of the rice genome (*Oryza sativa* L. ssp. indica). *Science*, **2002**, 296, 79-92 33.3 2356
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