

# Jianguo Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

169  
papers

18,610  
citations

44042

48  
h-index

12933

131  
g-index

173  
all docs

173  
docs citations

173  
times ranked

29542  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Draft Sequence of the Rice Genome ( <i>Oryza sativa</i> L. ssp. indica). <i>Science</i> , 2002, 296, 79-92.	6.0	3,146
2	SARS-CoV-2 Infection in Children. <i>New England Journal of Medicine</i> , 2020, 382, 1663-1665.	13.9	1,970
3	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	13.7	1,190
4	A Draft Sequence for the Genome of the Domesticated Silkworm ( <i>Bombyx mori</i> ). <i>Science</i> , 2004, 306, 1937-1940.	6.0	994
5	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008, 456, 60-65.	13.7	834
6	The Genomes of <i>Oryza sativa</i> : A History of Duplications. <i>PLoS Biology</i> , 2005, 3, e38.	2.6	808
7	The draft genome of watermelon ( <i>Citrullus lanatus</i> ) and resequencing of 20 diverse accessions. <i>Nature Genetics</i> , 2013, 45, 51-58.	9.4	731
8	Origin and diversity of novel avian influenza A H7N9 viruses causing human infection: phylogenetic, structural, and coalescent analyses. <i>Lancet</i> , The, 2013, 381, 1926-1932.	6.3	516
9	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.	1.8	480
10	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , 2010, 42, 1027-1030.	9.4	439
11	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004, 432, 717-722.	13.7	391
12	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	13.7	346
13	Fatty Liver Disease Caused by High-Alcohol-Producing <i>Klebsiella pneumoniae</i> . <i>Cell Metabolism</i> , 2019, 30, 675-688.e7.	7.2	294
14	Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases. <i>Nature Biotechnology</i> , 2016, 34, 531-538.	9.4	273
15	Identification of PRRT2 as the causative gene of paroxysmal kinesigenic dyskinesias. <i>Brain</i> , 2011, 134, 3493-3501.	3.7	263
16	Genesis, Evolution and Prevalence of H5N6 Avian Influenza Viruses in China. <i>Cell Host and Microbe</i> , 2016, 20, 810-821.	5.1	257
17	Complete Genome Sequence of <i>Yersinia pestis</i> Strain 91001, an Isolate Avirulent to Humans. <i>DNA Research</i> , 2004, 11, 179-197.	1.5	241
18	High Rate of Chimeric Gene Origination by Retroposition in Plant Genomes. <i>Plant Cell</i> , 2006, 18, 1791-1802.	3.1	207

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19	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.	3.5	199
20	Compositional Gradients in Gramineae Genes. <i>Genome Research</i> , 2002, 12, 851-856.	2.4	166
21	Genetic diversity and evolutionary dynamics of Ebola virus in Sierra Leone. <i>Nature</i> , 2015, 524, 93-96.	13.7	150
22	Mutations of 60 known causative genes in 157 families with retinitis pigmentosa based on exome sequencing. <i>Human Genetics</i> , 2014, 133, 1255-1271.	1.8	148
23	DeNAJCMutations Associated With Early-Onset Parkinson's Disease. <i>Annals of Neurology</i> , 2016, 79, 244-256.	2.8	148
24	Dynamic reassortments and genetic heterogeneity of the human-infecting influenza A (H7N9) virus. <i>Nature Communications</i> , 2014, 5, 3142.	5.8	145
25	Analysis of 142 genes resolves the rapid diversification of the rice genus. <i>Genome Biology</i> , 2008, 9, R49.	13.9	124
26	Poultry carrying H9N2 act as incubators for novel human avian influenza viruses. <i>Lancet</i> , The, 2014, 383, 869.	6.3	113
27	BGI-RIS: an integrated information resource and comparative analysis workbench for rice genomics. <i>Nucleic Acids Research</i> , 2004, 32, 377D-382.	6.5	108
28	Stabilizing mutations of KLHL24 ubiquitin ligase cause loss of keratin 14 and human skin fragility. <i>Nature Genetics</i> , 2016, 48, 1508-1516.	9.4	101
29	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.	1.3	100
30	Comprehensive Mutation Analysis by Whole-Exome Sequencing in 41 Chinese Families With Leber Congenital Amaurosis. , 2013, 54, 4351.		93
31	A Bat-Derived Putative Cross-Family Recombinant Coronavirus with a Reovirus Gene. <i>PLoS Pathogens</i> , 2016, 12, e1005883.	2.1	92
32	Origin and evolution of new exons in rodents. <i>Genome Research</i> , 2005, 15, 1258-1264.	2.4	91
33	RNASEH1 Mutations Impair mtDNA Replication and Cause Adult-Onset Mitochondrial Encephalomyopathy. <i>American Journal of Human Genetics</i> , 2015, 97, 186-193.	2.6	91
34	Identification of CHIP as a Novel Causative Gene for Autosomal Recessive Cerebellar Ataxia. <i>PLoS ONE</i> , 2013, 8, e81884.	1.1	86
35	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, e01280-15.	1.8	86
36	Mouse transcriptome: neutral evolution of 'non-coding' complementary DNAs. <i>Nature</i> , 2004, 431, 1 p following 757; discussion following 757.	13.7	86

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37	POPDC1S201F causes muscular dystrophy and arrhythmia by affecting protein trafficking. Journal of Clinical Investigation, 2015, 126, 239-253.	3.9	85
38	Mutations in ABCB6 Cause Dyschromatosis Universalis Hereditaria. Journal of Investigative Dermatology, 2013, 133, 2221-2228.	0.3	80
39	Molecular genetic analysis using targeted NGS analysis of 677 individuals with retinal dystrophy. Scientific Reports, 2019, 9, 1219.	1.6	76
40	Reverse-Transcription Recombinase-Aided Amplification Assay for Rapid Detection of the 2019 Novel Coronavirus (SARS-CoV-2). Analytical Chemistry, 2020, 92, 9699-9705.	3.2	74
41	The genomic underpinnings of apoptosis in the silkworm, Bombyx mori. BMC Genomics, 2010, 11, 611.	1.2	72
42	Intra-host dynamics of Ebola virus during 2014. Nature Microbiology, 2016, 1, 16151.	5.9	70
43	Phylogenetics, Genomic Recombination, and NSP2 Polymorphic Patterns of Porcine Reproductive and Respiratory Syndrome Virus in China and the United States in 2014â€”2018. Journal of Virology, 2020, 94, .	1.5	69
44	H7N9: a low pathogenic avian influenza A virus infecting humans. Current Opinion in Virology, 2014, 5, 91-97.	2.6	65
45	Mutation in mitochondrial ribosomal protein S7 (MRPS7) causes congenital sensorineural deafness, progressive hepatic and renal failure and lactic acidemia. Human Molecular Genetics, 2015, 24, 2297-2307.	1.4	64
46	Next Generation Sequencing Data Analysis in Primary Immunodeficiency Disorders â€” Future Directions. Journal of Clinical Immunology, 2016, 36, 68-75.	2.0	63
47	RePS: A Sequence Assembler That Masks Exact Repeats Identified from the Shotgun Data. Genome Research, 2002, 12, 824-831.	2.4	62
48	Clinical and Immunological Characteristics of Human Infections With H5N6 Avian Influenza Virus. Clinical Infectious Diseases, 2019, 68, 1100-1109.	2.9	56
49	Network pharmacology based investigation into the effect and mechanism of Modified Sijunzi Decoction against the subtypes of chronic atrophic gastritis. Pharmacological Research, 2019, 144, 158-166.	3.1	56
50	<i>CSF1R</i> mosaicism in a family with hereditary diffuse leukoencephalopathy with spheroids. Brain, 2016, 139, 1666-1672.	3.7	53
51	Methyltransferase-like 3 Modulates Severe Acute Respiratory Syndrome Coronavirus-2 RNA N6-Methyladenosine Modification and Replication. MBio, 2021, 12, e0106721.	1.8	53
52	Exome Sequencing of 47 Chinese Families with Cone-Rod Dystrophy: Mutations in 25 Known Causative Genes. PLoS ONE, 2013, 8, e65546.	1.1	52
53	De novo mutation in ATP6V1B2 impairs lysosome acidification and causes dominant deafness-onychodystrophy syndrome. Cell Research, 2014, 24, 1370-1373.	5.7	52
54	Dysfunction of Myosin Lightâ€”Chain 4 (MYL4) Leads to Heritable Atrial Cardiomyopathy With Electrical, Contractile, and Structural Components: Evidence From Geneticallyâ€”Engineered Rats. Journal of the American Heart Association, 2017, 6, .	1.6	52

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55	Identification and Characterization of Bmi-1-responding Element within the Human p16 Promoter*. <i>Journal of Biological Chemistry</i> , 2010, 285, 33219-33229.	1.6	51
56	<i>L</i> YRM7 mutations cause a multifocal cavitating leukoencephalopathy with distinct MRI appearance. <i>Brain</i> , 2016, 139, 782-794.	3.7	51
57	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>Populus</i> (Salicaceae). <i>Frontiers in Plant Science</i> , 2016, 7, 2022.	1.7	49
58	Highly Pathogenic Avian Influenza A(H5N1) Virus Struck Migratory Birds in China in 2015. <i>Scientific Reports</i> , 2015, 5, 12986.	1.6	47
59	Unique Variants in <i>OPN1LW</i> Cause Both Syndromic and Nonsyndromic X-Linked High Myopia Mapped to MYP1. , 2015, 56, 4150.		46
60	Olmsted syndrome: exploration of the immunological phenotype. <i>Orphanet Journal of Rare Diseases</i> , 2013, 8, 79.	1.2	45
61	Extracellular vesicles as delivery systems at nano-/micro-scale. <i>Advanced Drug Delivery Reviews</i> , 2021, 179, 113910.	6.6	45
62	Exome sequencing reveals mutation in <i>GJA1</i> as a cause of keratoderma-hypotrichosis-leukonychia totalis syndrome. <i>Human Molecular Genetics</i> , 2015, 24, 243-250.	1.4	44
63	TCRklass: A New K-String-Based Algorithm for Human and Mouse TCR Repertoire Characterization. <i>Journal of Immunology</i> , 2015, 194, 446-454.	0.4	43
64	Variants of the <i>ACTG2</i> gene correlate with degree of severity and presence of megacystis in chronic intestinal pseudo-obstruction. <i>European Journal of Human Genetics</i> , 2016, 24, 1211-1215.	1.4	43
65	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.	3.3	43
66	Highly pathogenic avian influenza H5N1 Clade 2.3.2.1c virus in migratory birds, 2014-2015. <i>Virologica Sinica</i> , 2016, 31, 300-305.	1.2	39
67	A novel homozygous mutation in <i>SUCLA2</i> gene identified by exome sequencing. <i>Molecular Genetics and Metabolism</i> , 2012, 107, 403-408.	0.5	38
68	Phylogeography, Transmission, and Viral Proteins of Nipah Virus. <i>Virologica Sinica</i> , 2018, 33, 385-393.	1.2	37
69	Mutations in topoisomerase $\text{II}^2$ result in a B cell immunodeficiency. <i>Nature Communications</i> , 2019, 10, 3644.	5.8	37
70	Loss-of-Function Mutations in <i>CAST</i> Cause Peeling Skin, Leukonychia, Acral Punctate Keratoses, Cheilitis, and Knuckle Pads. <i>American Journal of Human Genetics</i> , 2015, 96, 440-447.	2.6	36
71	A draft sequence of the rice ( <i>Oryza sativa ssp.indica</i> ) genome. <i>Science Bulletin</i> , 2001, 46, 1937-1942.	1.7	35
72	Exome sequencing identifies a <i>COL14A1</i> mutation in a large Chinese pedigree with punctate palmoplantar keratoderma. <i>Journal of Medical Genetics</i> , 2012, 49, 563-568.	1.5	34

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73	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.	1.6	33
74	Interspecies transmission and host restriction of avian H5N1 influenza virus. <i>Science in China Series C: Life Sciences</i> , 2009, 52, 428-438.	1.3	32
75	Temporal antibody responses to SARS-CoV-2 in patients of coronavirus disease 2019. <i>Cell Discovery</i> , 2020, 6, 64.	3.1	32
76	Differentiation of COVID-19 from seasonal influenza: A multicenter comparative study. <i>Journal of Medical Virology</i> , 2021, 93, 1512-1519.	2.5	30
77	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.	1.4	29
78	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, 573-577.	1.8	28
79	Naturally Occurring Single Mutations in Ebola Virus Observably Impact Infectivity. <i>Journal of Virology</i> , 2019, 93, .	1.5	28
80	Revealing Alzheimer's disease genes spectrum in the whole-genome by machine learning. <i>BMC Neurology</i> , 2018, 18, 5.	0.8	27
81	Genomic surveillance of COVID-19 cases in Beijing. <i>Nature Communications</i> , 2020, 11, 5503.	5.8	26
82	Phylogenomic analysis unravels evolution of yellow fever virus within hosts. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006738.	1.3	24
83	Identification of a Novel GJA3 Mutation in Congenital Nuclear Cataract. <i>Optometry and Vision Science</i> , 2015, 92, 337-342.	0.6	23
84	Homozygous <i>GNAL</i> mutation associated with familial childhood-onset generalized dystonia. <i>Neurology: Genetics</i> , 2016, 2, e78.	0.9	22
85	Transcription profile of human endogenous retroviruses in response to dengue virus serotype 2 infection. <i>Virology</i> , 2020, 544, 21-30.	1.1	22
86	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.	1.2	21
87	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.	1.6	21
88	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.	1.1	21
89	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, 151-159.	1.0	20
90	High alcohol-producing <i>Klebsiella pneumoniae</i> causes fatty liver disease through 2,3-butanediol fermentation pathway <i>in vivo</i> . <i>Gut Microbes</i> , 2021, 13, 1979883.	4.3	20

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91	Rapid gene identification in a Chinese osteopetrosis family by whole exome sequencing. <i>Gene</i> , 2013, 516, 311-315.	1.0	19
92	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.	1.4	19
93	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, .	1.1	19
94	Comparative Study of Acute Lung Injury in COVID-19 and Non-COVID-19 Patients. <i>Frontiers in Medicine</i> , 2021, 8, 666629.	1.2	19
95	Utility of next-generation sequencing technologies for the efficient genetic resolution of haematological disorders. <i>Clinical Genetics</i> , 2016, 89, 163-172.	1.0	18
96	The complete mitochondrial genome of the <i>Sorex araneus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3655-3656.	0.7	18
97	Nanopore sequencing of African swine fever virus. <i>Science China Life Sciences</i> , 2020, 63, 160-164.	2.3	18
98	Rapid Acquisition of High-Quality SARS-CoV-2 Genome via Amplicon-Oxford Nanopore Sequencing. <i>Virologica Sinica</i> , 2021, 36, 901-912.	1.2	18
99	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, 2908-2923.	2.5	16
100	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.	1.1	16
101	Light stimulates anoxic and oligotrophic growth of glacial <i>Flavobacterium</i> strains that produce zeaxanthin. <i>ISME Journal</i> , 2021, 15, 1844-1857.	4.4	16
102	Identification of different regions among strains of <i>Yersinia pestis</i> by suppression subtractive hybridization. <i>Research in Microbiology</i> , 2005, 156, 785-789.	1.0	15
103	Rapid and Specific Detection of All Known Nipah virus Strains'™ Sequences With Reverse Transcription-Loop-Mediated Isothermal Amplification. <i>Frontiers in Microbiology</i> , 2019, 10, 418.	1.5	15
104	Platelet-driven coagulopathy in COVID-19 patients: in comparison to seasonal influenza cases. <i>Experimental Hematology and Oncology</i> , 2021, 10, 34.	2.0	15
105	Transcriptome Analyses Implicate Endogenous Retroviruses Involved in the Host Antiviral Immune System through the Interferon Pathway. <i>Virologica Sinica</i> , 2021, 36, 1315-1326.	1.2	15
106	Evolution and Expression of the Membrane Attack Complex and Perforin Gene Family in the Poaceae. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5736.	1.8	14
107	Biosynthetic Polymalic Acid as a Delivery Nanoplatform for Translational Cancer Medicine. <i>Trends in Biochemical Sciences</i> , 2021, 46, 213-224.	3.7	14
108	Mutation analysis of Leber congenital amaurosis-associated genes in patients with retinitis pigmentosa. <i>Molecular Medicine Reports</i> , 2015, 11, 1827-1832.	1.1	13

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109	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.	1.2	13
110	Web Resources for Microbial Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 69-72.	3.0	12
111	An atypical form of AOA2 with myoclonus associated with mutations in SETX and AFG3L2. <i>BMC Medical Genetics</i> , 2015, 16, 16.	2.1	12
112	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, 1-8.	3.0	12
113	Pan-Genomic Analysis of African Swine Fever Virus. <i>Virologica Sinica</i> , 2020, 35, 662-665.	1.2	12
114	Identification and Expression of the Multidrug and Toxic Compound Extrusion (MATE) Gene Family in <i>Capsicum annuum</i> and <i>Solanum tuberosum</i> . <i>Plants</i> , 2020, 9, 1448.	1.6	12
115	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, 1-7.	0.7	11
116	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> , 2016, 32, 117-124.	0.7	11
117	Two genetically diverse H7N7 avian influenza viruses isolated from migratory birds in central China. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-12.	3.0	11
118	Nanopore sequencing: a rapid solution for infectious disease epidemics. <i>Science China Life Sciences</i> , 2019, 62, 1101-1103.	2.3	11
119	Genome-wide association study identifies new loci associated with risk of HBV infection and disease progression. <i>BMC Medical Genetics</i> , 2021, 14, 84.	0.7	11
120	Integrated characterization of SARS-CoV-2 genome, microbiome, antibiotic resistance and host response from single throat swabs. <i>Cell Discovery</i> , 2021, 7, 19.	3.1	11
121	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.	1.7	11
122	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.	1.1	10
123	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.	1.4	10
124	Synergistic effect of the responses of different tissues against African swine fever virus. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	10
125	Website for avian flu information and bioinformatics. <i>Science in China Series C: Life Sciences</i> , 2009, 52, 470-473.	1.3	9
126	Evolutionary Transients in the Rice Transcriptome. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 211-228.	3.0	9

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127	Copy number variation in CEP57L1 predisposes to congenital absence of bilateral ACL and PCL ligaments. <i>Human Genomics</i> , 2015, 9, 31.	1.4	9
128	Identification of MFRP Mutations in Chinese Families with High Hyperopia. <i>Optometry and Vision Science</i> , 2016, 93, 19-26.	0.6	9
129	A new reassortment of influenza A (H7N9) virus causing human infection in Beijing, 2014. <i>Scientific Reports</i> , 2016, 6, 26624.	1.6	9
130	Identified <i>OAS3</i> gene variants associated with coexistence of <i>HBsAg</i> and anti- <i>HBs</i> in chronic <i>HBV</i> infection. <i>Journal of Viral Hepatitis</i> , 2018, 25, 904-910.	1.0	9
131	Intra-host Ebola viral adaption during human infection. <i>Biosafety and Health</i> , 2019, 1, 14-24.	1.2	9
132	Genomic epidemiological characteristics of dengue fever in Guangdong province, China from 2013 to 2017. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008049.	1.3	9
133	Exome Sequencing of a Pedigree Reveals S339L Mutation in the <i>TLN2</i> Gene as a Cause of Fifth Finger Camptodactyly. <i>PLoS ONE</i> , 2016, 11, e0155180.	1.1	9
134	OsHT, a Rice Gene Encoding for a Plasma-Membrane Localized Histidine Transporter. <i>Journal of Integrative Plant Biology</i> , 2005, 47, 92-99.	4.1	8
135	The new emerging H7N9 influenza virus indicates poultry as new mixing vessels. <i>Science China Life Sciences</i> , 2014, 57, 731-732.	2.3	8
136	The triphibious warfare against viruses. <i>Science China Life Sciences</i> , 2017, 60, 1295-1298.	2.3	8
137	A Promising IFN-Deficient System to Manufacture IFN-Sensitive Influenza Vaccine Virus. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 127.	1.8	8
138	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.	1.8	8
139	Genome-wide analysis of structural variants reveals genetic differences in Chinese pigs. <i>PLoS ONE</i> , 2017, 12, e0186721.	1.1	7
140	Analysis of ACE2 Gene-Encoded Proteins Across Mammalian Species. <i>Frontiers in Veterinary Science</i> , 2020, 7, 457.	0.9	7
141	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.	1.8	7
142	TRIM14 inhibits OPTN-mediated autophagic degradation of KDM4D to epigenetically regulate inflammation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	7
143	Phylogeny of section <i>Leuce</i> ( <i>Populus</i> , <i>Salicaceae</i> ) inferred from 34 chloroplast DNA fragments. <i>Biochemical Systematics and Ecology</i> , 2015, 63, 212-217.	0.6	6
144	Circulation, Evolution and Transmission of H5N8 virus, 2016–2018. <i>Journal of Infection</i> , 2019, 79, 363-372.	1.7	6

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145	Potential m6A and m5C Methylations within the Genome of A Chinese African Swine Fever Virus Strain. <i>Virologica Sinica</i> , 2021, 36, 321-324.	1.2	6
146	Computational predicting the human infectivity of H7N9 influenza viruses isolated from avian hosts. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 846-856.	1.3	6
147	Bioinformatics analysis raises candidate genes in blood for early screening of Parkinson's disease. <i>Biomedical and Environmental Sciences</i> , 2014, 27, 462-5.	0.2	6
148	Evaluation of Clinical and Immune Responses in Recovered Children with Mild COVID-19. <i>Viruses</i> , 2022, 14, 85.	1.5	6
149	Analysis of the evolution, infectivity and antigenicity of circulating rabies virus strains. <i>Emerging Microbes and Infections</i> , 2022, 11, 1474-1487.	3.0	6
150	Arabidopsis thaliana 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.	2.4	5
151	Mapping the clinical outcomes and genetic evolution of Ebola virus in Sierra Leone. <i>JCI Insight</i> , 2017, 2, .	2.3	5
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