

Di Liu

List of Publications by Year in descending order

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140
papers

12,282
citations

41344

49
h-index

27406

106
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149
all docs

149
docs citations

149
times ranked

19496
citing authors

#	ARTICLE	IF	CITATIONS
1	Ginseng polysaccharides alter the gut microbiota and kynurenine/tryptophan ratio, potentiating the antitumour effect of antiprogrammed cell death 1/programmed cell death ligand 1 (anti-PD-1/PD-L1) immunotherapy. <i>Gut</i> , 2022, 71, 734-745.	12.1	177
2	Synergistic effect of the responses of different tissues against African swine fever virus. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	3.0	10
3	A global assessment of the impact of school closure in reducing COVID-19 spread. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2022, 380, 20210124.	3.4	13
4	Circulation, genomic characteristics, and evolutionary dynamics of class I Newcastle disease virus in China. <i>Virulence</i> , 2022, 13, 414-427.	4.4	4
5	Association of C-reactive Protein with Cardiovascular Outcomes: A Mendelian Randomization Study in the Japanese Population.. <i>Biomedical and Environmental Sciences</i> , 2022, 35, 126-132.	0.2	3
6	Hemagglutinin Gene Variation Rate of H9N2 Avian Influenza Virus by Vaccine Intervention in China. <i>Viruses</i> , 2022, 14, 1043.	3.3	4
7	Identifying Japanese Encephalitis Virus Using Metatranscriptomic Sequencing, Xinjiang Province, China. <i>Emerging Infectious Diseases</i> , 2022, 28, .	4.3	0
8	Assessment of the Causal Effect of IgG N-Glycosylation Level on Risk of Dementia: A 2-Sample Mendelian Randomization Study. <i>Journal of Alzheimer's Disease</i> , 2022, 88, 1435-1441.	2.6	2
9	Potential m6A and m5C Methylations within the Genome of A Chinese African Swine Fever Virus Strain. <i>Virologica Sinica</i> , 2021, 36, 321-324.	3.0	6
10	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.	4.9	1
11	Cadmium chloride-induced transgenerational neurotoxicity in zebrafish development. <i>Environmental Toxicology and Pharmacology</i> , 2021, 81, 103545.	4.0	36
12	Computational predicting the human infectivity of H7N9 influenza viruses isolated from avian hosts. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 846-856.	3.0	6
13	Light stimulates anoxic and oligotrophic growth of glacial <i>Flavobacterium</i> strains that produce zeaxanthin. <i>ISME Journal</i> , 2021, 15, 1844-1857.	9.8	16
14	Integrated characterization of SARS-CoV-2 genome, microbiome, antibiotic resistance and host response from single throat swabs. <i>Cell Discovery</i> , 2021, 7, 19.	6.7	11
15	SARS-CoV-2 infection induces sustained humoral immune responses in convalescent patients following symptomatic COVID-19. <i>Nature Communications</i> , 2021, 12, 1813.	12.8	198
16	Molecular evolution and genetic diversity analysis of SFTS virus based on next-generation sequencing. <i>Biosafety and Health</i> , 2021, 3, 105-115.	2.7	11
17	Rapid Acquisition of High-Quality SARS-CoV-2 Genome via Amplicon-Oxford Nanopore Sequencing. <i>Virologica Sinica</i> , 2021, 36, 901-912.	3.0	18
18	Avian influenza A (H7N9) virus: from low pathogenic to highly pathogenic. <i>Frontiers of Medicine</i> , 2021, 15, 507-527.	3.4	30

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19	Transcriptome Analyses Implicate Endogenous Retroviruses Involved in the Host Antiviral Immune System through the Interferon Pathway. <i>Virologica Sinica</i> , 2021, 36, 1315-1326.	3.0	15
20	Visualization and Analysis of Gene Expression in Stanford Type A Aortic Dissection Tissue Section by Spatial Transcriptomics. <i>Frontiers in Genetics</i> , 2021, 12, 698124.	2.3	12
21	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.	3.9	7
22	Discriminating Clonotypes of Influenza A Virus Genes by Nanopore Sequencing. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10069.	4.1	2
23	Cost-effectiveness of strategies for preventing paediatric lower respiratory infections associated with respiratory syncytial virus in eight Chinese cities. <i>Vaccine</i> , 2021, 39, 5490-5498.	3.8	7
24	Ecology of avian influenza viruses in migratory birds wintering within the Yangtze River wetlands. <i>Science Bulletin</i> , 2021, 66, 2014-2024.	9.0	6
25	Development of a highly sensitive digital PCR assay to quantify long non-coding RNA MYU in urine samples which exhibited great potential as an alternative diagnostic biomarker for prostate cancer. <i>Translational Andrology and Urology</i> , 2021, 10, 3815-3825.	1.4	4
26	Nanopore sequencing of African swine fever virus. <i>Science China Life Sciences</i> , 2020, 63, 160-164.	4.9	18
27	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, .	3.4	69
28	Pan-Genomic Analysis of African Swine Fever Virus. <i>Virologica Sinica</i> , 2020, 35, 662-665.	3.0	12
29	Analysis of ACE2 Gene-Encoded Proteins Across Mammalian Species. <i>Frontiers in Veterinary Science</i> , 2020, 7, 457.	2.2	7
30	Genomic surveillance of COVID-19 cases in Beijing. <i>Nature Communications</i> , 2020, 11, 5503.	12.8	26
31	Cancer attributable to human papillomavirus infection in China: Burden and trends. <i>Cancer</i> , 2020, 126, 3719-3732.	4.1	35
32	SARS-CoV-2 Infection in Children. <i>New England Journal of Medicine</i> , 2020, 382, 1663-1665.	27.0	1,970
33	Genomic epidemiological characteristics of dengue fever in Guangdong province, China from 2013 to 2017. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008049.	3.0	9
34	Vaccination with Consensus H7 Elicits Broadly Reactive and Protective Antibodies against Eurasian and North American Lineage H7 Viruses. <i>Vaccines</i> , 2020, 8, 143.	4.4	4
35	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.	7.1	43
36	Transcription profile of human endogenous retroviruses in response to dengue virus serotype 2 infection. <i>Virology</i> , 2020, 544, 21-30.	2.4	22

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37	First-wave COVID-19 transmissibility and severity in China outside Hubei after control measures, and second-wave scenario planning: a modelling impact assessment. <i>Lancet, The</i> , 2020, 395, 1382-1393.	13.7	703
38	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.	6.5	74
39	Clinical and Immunological Characteristics of Human Infections With H5N6 Avian Influenza Virus. <i>Clinical Infectious Diseases</i> , 2019, 68, 1100-1109.	5.8	56
40	Nanopore sequencing: a rapid solution for infectious disease epidemics. <i>Science China Life Sciences</i> , 2019, 62, 1101-1103.	4.9	11
41	Circulation, Evolution and Transmission of H5N8 virus, 2016â€“2018. <i>Journal of Infection</i> , 2019, 79, 363-372.	3.3	6
42	Fatty Liver Disease Caused by High-Alcohol-Producing <i>Klebsiella pneumoniae</i> . <i>Cell Metabolism</i> , 2019, 30, 675-688.e7.	16.2	294
43	Rapid and Specific Detection of All Known Nipah virus Strainsâ€™ Sequences With Reverse Transcription-Loop-Mediated Isothermal Amplification. <i>Frontiers in Microbiology</i> , 2019, 10, 418.	3.5	15
44	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.	7.1	56
45	Intra-host Ebola viral adaption during human infection. <i>Biosafety and Health</i> , 2019, 1, 14-24.	2.7	9
46	Endogenous Retroviruses Function as Gene Expression Regulatory Elements During Mammalian Pre-implantation Embryo Development. <i>International Journal of Molecular Sciences</i> , 2019, 20, 790.	4.1	37
47	Integration of biosafety surveillance through Biosafety Surveillance Conceptual Data Model. <i>Biosafety and Health</i> , 2019, 1, 98-104.	2.7	1
48	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.	3.0	1
49	Naturally Occurring Single Mutations in Ebola Virus Observably Impact Infectivity. <i>Journal of Virology</i> , 2019, 93, .	3.4	28
50	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.	2.4	16
51	Two genetically diverse H7N7 avian influenza viruses isolated from migratory birds in central China. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-12.	6.5	11
52	Sudden emergence of human infections with H7N9 avian influenza A virus in Hubei province, central China. <i>Scientific Reports</i> , 2018, 8, 2486.	3.3	4
53	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.	6.5	12
54	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.	4.9	1

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55	Emergence and Adaptation of a Novel Highly Pathogenic H7N9 Influenza Virus in Birds and Humans from a 2013 Human-Infecting Low-Pathogenic Ancestor. <i>Journal of Virology</i> , 2018, 92, .	3.4	99
56	An Assessment of Amplicon-Sequencing Based Method for Viral Intrahost Analysis. <i>Virologica Sinica</i> , 2018, 33, 557-560.	3.0	3
57	Phylogeography, Transmission, and Viral Proteins of Nipah Virus. <i>Virologica Sinica</i> , 2018, 33, 385-393.	3.0	37
58	Phylogenomic analysis unravels evolution of yellow fever virus within hosts. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006738.	3.0	24
59	A Promising IFN-Deficient System to Manufacture IFN-Sensitive Influenza Vaccine Virus. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 127.	3.9	8
60	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	27.8	346
61	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.	7.7	199
62	The triphibious warfare against viruses. <i>Science China Life Sciences</i> , 2017, 60, 1295-1298.	4.9	8
63	Highly Pathogenic Avian Influenza A(H5N8) Virus in Wild Migratory Birds, Qinghai Lake, China. <i>Emerging Infectious Diseases</i> , 2017, 23, 637-641.	4.3	82
64	Mapping the clinical outcomes and genetic evolution of Ebola virus in Sierra Leone. <i>JCI Insight</i> , 2017, 2, .	5.0	5
65	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.	1.9	11
66	Genesis, Evolution and Prevalence of H5N6 Avian Influenza Viruses in China. <i>Cell Host and Microbe</i> , 2016, 20, 810-821.	11.0	257
67	A new reassortment of influenza A (H7N9) virus causing human infection in Beijing, 2014. <i>Scientific Reports</i> , 2016, 6, 26624.	3.3	9
68	Novel avian influenza A (H5N6) viruses isolated in migratory waterfowl before the first human case reported in China, 2014. <i>Scientific Reports</i> , 2016, 6, 29888.	3.3	57
69	Highly pathogenic avian influenza H5N1 Clade 2.3.2.1c virus in migratory birds, 2014-2015. <i>Virologica Sinica</i> , 2016, 31, 300-305.	3.0	39
70	Intra-host dynamics of Ebola virus during 2014. <i>Nature Microbiology</i> , 2016, 1, 16151.	13.3	70
71	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.	3.8	16
72	A Bat-Derived Putative Cross-Family Recombinant Coronavirus with a Reovirus Gene. <i>PLoS Pathogens</i> , 2016, 12, e1005883.	4.7	92

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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.	3.3	33
74	Highly Pathogenic Avian Influenza A(H5N1) Virus Struck Migratory Birds in China in 2015. <i>Scientific Reports</i> , 2015, 5, 12986.	3.3	47
75	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.	3.3	21
76	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.	3.4	10
77	Two novel reassortants of avian influenza A (H5N6) virus in China. <i>Journal of General Virology</i> , 2015, 96, 975-981.	2.9	89
78	Web Resources for Microbial Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 69-72.	6.9	12
79	The efficient hemostatic effect of Antarctic krill chitosan is related to its hydration property. <i>Carbohydrate Polymers</i> , 2015, 132, 295-303.	10.2	41
80	BMP2 gene delivery to bone mesenchymal stem cell by chitosan-g-PEI nonviral vector. <i>Nanoscale Research Letters</i> , 2015, 10, 203.	5.7	28
81	Genetic diversity and evolutionary dynamics of Ebola virus in Sierra Leone. <i>Nature</i> , 2015, 524, 93-96.	27.8	150
82	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.	4.1	86
83	Metatranscriptomic Analyses of Plant Cell Wall Polysaccharide Degradation by Microorganisms in the Cow Rumen. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1375-1386.	3.1	206
84	TCRklass: A New K-String-Based Algorithm for Human and Mouse TCR Repertoire Characterization. <i>Journal of Immunology</i> , 2015, 194, 446-454.	0.8	43
85	Human Infection with Influenza Virus A(H10N8) from Live Poultry Markets, China, 2014. <i>Emerging Infectious Diseases</i> , 2014, 20, 2076-9.	4.3	94
86	H7N9: a low pathogenic avian influenza A virus infecting humans. <i>Current Opinion in Virology</i> , 2014, 5, 91-97.	5.4	65
87	Molecular characterization and phylogenetics of a reassortant H13N8 influenza virus isolated from gulls in Mongolia. <i>Virus Genes</i> , 2014, 49, 237-249.	1.6	8
88	Dynamic reassortments and genetic heterogeneity of the human-infecting influenza A (H7N9) virus. <i>Nature Communications</i> , 2014, 5, 3142.	12.8	145
89	Continuous reassortments with local chicken H9N2 virus underlie the human-infecting influenza A (H7N9) virus in the new influenza season, Guangdong, China. <i>Protein and Cell</i> , 2014, 5, 878-882.	11.0	17
90	The new emerging H7N9 influenza virus indicates poultry as new mixing vessels. <i>Science China Life Sciences</i> , 2014, 57, 731-732.	4.9	8

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91	Analyses of the Similarity and Difference of Global Gene Expression Profiles in Cortex Regions of Three Neurodegenerative Diseases: Sporadic Creutzfeldt-Jakob Disease (sCJD), Fatal Familial Insomnia (FFI), and Alzheimer's Disease (AD). <i>Molecular Neurobiology</i> , 2014, 50, 473-481.	4.0	23
92	Phylogenetics of varied subtypes of avian influenza viruses in China: potential threat to humans. <i>Protein and Cell</i> , 2014, 5, 253-257.	11.0	31
93	Poultry carrying H9N2 act as incubators for novel human avian influenza viruses. <i>Lancet, The</i> , 2014, 383, 869.	13.7	113
94	Characterization of human $\alpha\beta$ TCR repertoire and discovery of D-D fusion in TCR β chains. <i>Protein and Cell</i> , 2014, 5, 603-615.	11.0	27
95	Genesis of the novel human-infecting influenza A(H10N8) virus and potential genetic diversity of the virus in poultry, China. <i>Eurosurveillance</i> , 2014, 19, .	7.0	83
96	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
97	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
98	HTQC: a fast quality control toolkit for Illumina sequencing data. <i>BMC Bioinformatics</i> , 2013, 14, 33.	2.6	142
99	Comparative Analysis of Gene Expression Profiles Between Cortex and Thalamus in Chinese Fatal Familial Insomnia Patients. <i>Molecular Neurobiology</i> , 2013, 48, 36-48.	4.0	26
100	Interaction between DAHP synthase and chorismate mutase endows new regulation on DAHP synthase activity in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 10373-10380.	3.6	12
101	Origin and molecular characterization of the human-infecting H6N1 influenza virus in Taiwan. <i>Protein and Cell</i> , 2013, 4, 846-853.	11.0	86
102	Origin and diversity of novel avian influenza A H7N9 viruses causing human infection: phylogenetic, structural, and coalescent analyses. <i>Lancet, The</i> , 2013, 381, 1926-1932.	13.7	516
103	Environmental connections of novel avian-origin H7N9 influenza virus infection and virus adaptation to the human. <i>Science China Life Sciences</i> , 2013, 56, 485-492.	4.9	81
104	Global transcriptional profiling of the postmortem brain of a patient with G114V genetic Creutzfeldt-Jakob disease. <i>International Journal of Molecular Medicine</i> , 2013, 31, 676-688.	4.0	14
105	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.	2.5	10
106	T4SP: a novel tool and database for type IV secretion systems in bacterial genomes. <i>Biomedical and Environmental Sciences</i> , 2013, 26, 614-7.	0.2	2
107	SARS-like virus in the Middle East: A truly bat-related coronavirus causing human diseases. <i>Protein and Cell</i> , 2012, 3, 803-805.	11.0	64
108	The Genome Characteristics and Predicted Function of Methyl-Group Oxidation Pathway in the Obligate Aceticlastic Methanogens, <i>Methanosaeta</i> spp. <i>PLoS ONE</i> , 2012, 7, e36756.	2.5	38

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109	Metagenomic Insights into the Fibrolytic Microbiome in Yak Rumen. PLoS ONE, 2012, 7, e40430.	2.5	98
110	Clade T4SS-mediated horizontal transfer of the 89K pathogenicity island in epidemic <i>Streptococcus suis</i> serotype 2. Molecular Microbiology, 2011, 79, 1670-1683.	2.5	86
111	A large scale comparative genomic analysis reveals insertion sites for newly acquired genomic islands in bacterial genomes. BMC Microbiology, 2011, 11, 135.	3.3	10
112	An unexpected similarity between antibiotic-resistant NDM-1 and beta-lactamase II from <i>Erythrobacter litoralis</i> . Protein and Cell, 2011, 2, 250-258.	11.0	34
113	Whole-Genome Sequences of Four <i>Mycobacterium bovis</i> BCG Vaccine Strains. Journal of Bacteriology, 2011, 193, 3152-3153.	2.2	28
114	Clade 2.3.2 Avian Influenza Virus (H5N1), Qinghai Lake Region, China, 2009-2010. Emerging Infectious Diseases, 2011, 17, 560-562.	4.3	38
115	Duck Egg-Drop Syndrome Caused by BYD Virus, a New Tembusu-Related Flavivirus. PLoS ONE, 2011, 6, e18106.	2.5	296
116	Functional Genomic Analysis of Taxonomic and Typing Loci for Pathogenic Bacteria Based on Orthologous Genes. Scientia Sinica Vitae, 2011, 41, 640-648.	0.3	0
117	Crystal structure of the swine-origin A (H1N1)-2009 influenza A virus hemagglutinin (HA) reveals similar antigenicity to that of the 1918 pandemic virus. Protein and Cell, 2010, 1, 459-467.	11.0	94
118	Interaction of Hsp40 with influenza virus M2 protein: implications for PKR signaling pathway. Protein and Cell, 2010, 1, 944-955.	11.0	41
119	In silico characterization of the functional and structural modules of the hemagglutinin protein from the swine-origin influenza virus A (H1N1)-2009. Science China Life Sciences, 2010, 53, 633-642.	4.9	29
120	The 2009 pandemic H1N1 neuraminidase N1 lacks the 150-cavity in its active site. Nature Structural and Molecular Biology, 2010, 17, 1266-1268.	8.2	160
121	Identification and Characterization of Bmi-1-responding Element within the Human p16 Promoter*. Journal of Biological Chemistry, 2010, 285, 33219-33229.	3.4	51
122	Serological Surveillance of Influenza A Virus Infection in Swine Populations in Fujian Province, China: No Evidence of Naturally Occurring H5N1 Infection in Pigs. Zoonoses and Public Health, 2010, 57, 291-298.	2.2	28
123	Autophagy is involved in influenza A virus replication. Autophagy, 2009, 5, 321-328.	9.1	229
124	Avian influenza virus, <i>Streptococcus suis</i> serotype 2, severe acute respiratory syndrome-coronavirus and beyond: molecular epidemiology, ecology and the situation in China. Philosophical Transactions of the Royal Society B: Biological Sciences, 2009, 364, 2725-2737.	4.0	31
125	Interspecies transmission and host restriction of avian H5N1 influenza virus. Science in China Series C: Life Sciences, 2009, 52, 428-438.	1.3	32
126	Website for avian flu information and bioinformatics. Science in China Series C: Life Sciences, 2009, 52, 470-473.	1.3	9

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127	Stable non-synonymous substitutions on NS gene (NS1 and NS2 proteins) of Qinghai Lake H5N1 influenza virus (Clade 2.2) after successive passages in Muscovy ducks. <i>Science in China Series C: Life Sciences</i> , 2009, 52, 847-853.	1.3	0
128	The involvement of sortase A in high virulence of STSS-causing <i>Streptococcus suis</i> serotype 2. <i>Archives of Microbiology</i> , 2009, 191, 23-33.	2.2	65
129	Autophagy protects LNCaP cells under androgen deprivation conditions. <i>Autophagy</i> , 2008, 4, 54-60.	9.1	90
130	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.	2.9	100
131	Porcine Respiratory and Reproductive Syndrome Virus Variants, Vietnam and China, 2007. <i>Emerging Infectious Diseases</i> , 2008, 14, 1774-1776.	4.3	112
132	SalK/SalR, a Two-Component Signal Transduction System, Is Essential for Full Virulence of Highly Invasive <i>Streptococcus suis</i> Serotype 2. <i>PLoS ONE</i> , 2008, 3, e2080.	2.5	132
133	Emergence of Fatal PRRSV Variants: Unparalleled Outbreaks of Atypical PRRS in China and Molecular Dissection of the Unique Hallmark. <i>PLoS ONE</i> , 2007, 2, e526.	2.5	841
134	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
135	Existence and characterization of allelic variants of Sao, a newly identified surface protein from <i>Streptococcus suis</i> . <i>FEMS Microbiology Letters</i> , 2007, 275, 80-88.	1.8	34
136	OsHT, a Rice Gene Encoding for a Plasma-Membrane Localized Histidine Transporter. <i>Journal of Integrative Plant Biology</i> , 2005, 47, 92-99.	8.5	8
137	An Annotation Update via cDNA Sequence Analysis and Comprehensive Profiling of Developmental, Hormonal or Environmental Responsiveness of the Arabidopsis AP2/EREBP Transcription Factor Gene Family. <i>Plant Molecular Biology</i> , 2005, 59, 853-868.	3.9	170
138	DATE: a database of Arabidopsis transcription factors. <i>Bioinformatics</i> , 2005, 21, 2568-2569.	4.1	296
139	Isolation and analyses of genes preferentially expressed during early cotton fiber development by subtractive PCR and cDNA array. <i>Nucleic Acids Research</i> , 2003, 31, 2534-2543.	14.5	226
140	Simplified amino acid alphabets based on deviation of conditional probability from random background. <i>Physical Review E</i> , 2002, 66, 021906.	2.1	23