Pei Hao

List of Publications by Year
in descending order

94 papers	8,339 citations	185998 28 h-index	48187 88 g-index
96 all docs	96 docs citations	96 times ranked	13421 citing authors

#	Article	IF	Citations
1	Human Infection with a Novel Avian-Origin Influenza A (H7N9) Virus. New England Journal of Medicine, 2013, 368, 1888-1897.	13.9	2,122
2	Evolution of the novel coronavirus from the ongoing Wuhan outbreak and modeling of its spike protein for risk of human transmission. Science China Life Sciences, 2020, 63, 457-460.	2.3	1,650
3	Cross-host evolution of severe acute respiratory syndrome coronavirus in palm civet and human. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2430-2435.	3.3	602
4	Sequence and analysis of rice chromosome 4. Nature, 2002, 420, 316-320.	13.7	471
5	Optimizing de novo transcriptome assembly from short-read RNA-Seq data: a comparative study. BMC Bioinformatics, 2011, 12, S2.	1.2	462
6	Comparative and functional genomic analyses of the pathogenicity of phytopathogen Xanthomonas campestris pv. campestris. Genome Research, 2005, 15, 757-767.	2.4	371
7	Association between adverse clinical outcome in human disease caused by novel influenza A H7N9 virus and sustained viral shedding and emergence of antiviral resistance. Lancet, The, 2013, 381, 2273-2279.	6.3	308
8	The genome of Mesobuthus martensii reveals a unique adaptation model of arthropods. Nature Communications, 2013, 4, 2602.	5.8	187
9	Identification of Two Critical Amino Acid Residues of the Severe Acute Respiratory Syndrome Coronavirus Spike Protein for Its Variation in Zoonotic Tropism Transition via a Double Substitution Strategy. Journal of Biological Chemistry, 2005, 280, 29588-29595.	1.6	152
10	Metabolic Profiling Reveals Distinct Variations Linked to Nicotine Consumption in Humans â€" First Results from the KORA Study. PLoS ONE, 2008, 3, e3863.	1.1	107
11	Full-length genome sequences of two SARS-like coronaviruses in horseshoe bats and genetic variation analysis. Journal of General Virology, 2006, 87, 3355-3359.	1.3	96
12	Complete Sequencing and Pan-Genomic Analysis of Lactobacillus delbrueckii subsp. bulgaricus Reveal Its Genetic Basis for Industrial Yogurt Production. PLoS ONE, 2011, 6, e15964.	1.1	90
13	Genome-Wide Identification of Schistosoma japonicum MicroRNAs Using a Deep-Sequencing Approach. PLoS ONE, 2009, 4, e8206.	1.1	87
14	The Landscape of A-to-I RNA Editome Is Shaped by Both Positive and Purifying Selection. PLoS Genetics, 2016, 12, e1006191.	1.5	72
15	A High-throughput Approach for Subcellular Proteome. Molecular and Cellular Proteomics, 2004, 3, 441-455.	2.5	71
16	A Fine Physical Map of the Rice Chromosome 4. Genome Research, 2002, 12, 817-823.	2.4	64
17	Two conserved epigenetic regulators prevent healthy ageing. Nature, 2020, 579, 118-122.	13.7	62
18	Lupus-associated atypical memory B cells are mTORC1-hyperactivated and functionally dysregulated. Annals of the Rheumatic Diseases, 2019, 78, 1090-1100.	0.5	61

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19	Implementation of the CRISPR-Cas13a system in fission yeast and its repurposing for precise RNA editing. Nucleic Acids Research, 2018, 46, e90-e90.	6.5	52
20	Foxp1 is critical for the maintenance of regulatory T-cell homeostasis and suppressive function. PLoS Biology, 2019, 17, e3000270.	2.6	44
21	Molecular simulation of SARS-CoV-2 spike protein binding to pangolin ACE2 or human ACE2 natural variants reveals altered susceptibility to infection. Journal of General Virology, 2020, 101, 921-924.	1.3	42
22	A comparative analysis of liver transcriptome suggests divergent liver function among human, mouse and rat. Genomics, 2010, 96, 281-289.	1.3	41
23	ZIKV infection induces robust Th1-like Tfh cell and long-term protective antibody responses in immunocompetent mice. Nature Communications, 2019, 10, 3859.	5.8	39
24	In silico discovery of human natural antisense transcripts. BMC Bioinformatics, 2006, 7, 18.	1.2	38
25	Comparison of Next-Generation Sequencing and Clone-Based Sequencing in Analysis of Hepatitis B Virus Reverse Transcriptase Quasispecies Heterogeneity. Journal of Clinical Microbiology, 2013, 51, 4087-4094.	1.8	37
26	Microbiota in the apical root canal system of tooth with apical periodontitis. BMC Genomics, 2019, 20, 189.	1.2	37
27	Pediatric Drug Nitazoxanide: A Potential Choice for Control of Zika. Open Forum Infectious Diseases, 2017, 4, ofx009.	0.4	35
28	Global transcriptome analysis reveals extensive gene remodeling, alternative splicing and differential transcription profiles in non-seed vascular plant Selaginella moellendorffii. BMC Genomics, 2017, 18, 1042.	1.2	34
29	Iguratimod represses B cell terminal differentiation linked with the inhibition of PKC/EGR1 axis. Arthritis Research and Therapy, 2019, 21, 92.	1.6	32
30	A molecular docking model of SARS-CoV S1 protein in complex with its receptor, human ACE2. Computational Biology and Chemistry, 2005, 29, 254-257.	1.1	31
31	The Domain Landscape of Virus-Host Interactomes. BioMed Research International, 2014, 2014, 1-13.	0.9	30
32	DENA: training an authentic neural network model using Nanopore sequencing data of Arabidopsis transcripts for detection and quantification of N6-methyladenosine on RNA. Genome Biology, 2022, 23, 25.	3.8	30
33	A Comparison of Computational Methods for Identifying Virulence Factors. PLoS ONE, 2012, 7, e42517.	1.1	29
34	Differential responses of innate immunity triggered by different subtypes of influenza a viruses in human and avian hosts. BMC Medical Genomics, 2017, 10, 70.	0.7	29
35	KDE Bioscience: Platform for bioinformatics analysis workflows. Journal of Biomedical Informatics, 2006, 39, 440-450.	2.5	28
36	Elaboration of tetravalent antibody responses against dengue viruses using a subunit vaccine comprised of a single consensus dengue envelope sequence. Vaccine, 2017, 35, 6308-6320.	1.7	28

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37	Association of tissue lineage and gene expression: conservatively and differentially expressed genes define common and special functions of tissues. BMC Bioinformatics, 2010, 11, S1.	1.2	27
38	Detection of human novel influenza A (H1N1) viruses using multi-fluorescent real-time RT-PCR. Virus Research, 2010, 147, 85-90.	1.1	25
39	Molecular Dynamics Studies on the Conformational Transitions of Adenylate Kinase: A Computational Evidence for the Conformational Selection Mechanism. BioMed Research International, 2013, 2013, 1-7.	0.9	25
40	Genome-wide analysis of homeobox genes from Mesobuthus martensii reveals Hox gene duplication in scorpions. Insect Biochemistry and Molecular Biology, 2015, 61, 25-33.	1.2	25
41	Optimizing hybrid assembly of next-generation sequence data from Enterococcus faecium: a microbe with highly divergent genome. BMC Systems Biology, 2012, 6, S21.	3.0	24
42	Putative hAPN receptor binding sites in SARS_CoV spike protein. Acta Pharmacologica Sinica, 2003, 24, 481-8.	2.8	24
43	Gene expression module-based chemical function similarity search. Nucleic Acids Research, 2008, 36, e137-e137.	6.5	23
44	Is SARS-CoV-2 originated from laboratory? A rebuttal to the claim of formation via laboratory recombination. Emerging Microbes and Infections, 2020, 9, 545-547.	3.0	23
45	Revealing parasite influence in metabolic pathways in Apicomplexa infected patients. BMC Bioinformatics, 2010, 11, S13.	1.2	22
46	Prediction of quaternary assembly of SARS coronavirus peplomer. Biochemical and Biophysical Research Communications, 2004, 325, 1210-1214.	1.0	20
47	Modelling BioNano optical data and simulation study of genome map assembly. Bioinformatics, 2018, 34, 3966-3974.	1.8	20
48	OrysPSSP: a comparative Platform for Small Secreted Proteins from rice and other plants. Nucleic Acids Research, 2012, 41, D1192-D1198.	6.5	18
49	The evolutionary landscape of intergenic trans-splicing events in insects. Nature Communications, 2015, 6, 8734.	5.8	17
50	Veratramine modulates AP-1-dependent gene transcription by directly binding to programmable DNA. Nucleic Acids Research, 2018, 46, 546-557.	6.5	17
51	Comprehensive mapping of antigen specific T cell responses in hepatitis C virus infected patients with or without spontaneous viral clearance. PLoS ONE, 2017, 12, e0171217.	1.1	16
52	HIV-1 Infection Alters the Viral Composition of Plasma in Men Who Have Sex with Men. MSphere, 2021, 6, .	1.3	16
53	Exploring mitochondrial evolution and metabolism organization principles by comparative analysis of metabolic networks. Genomics, 2010, 95, 339-344.	1.3	15
54	Combining ZHENG Theory and High-Throughput Expression Data to Predict New Effects of Chinese Herbal Formulae. Evidence-based Complementary and Alternative Medicine, 2012, 2012, 1-8.	0.5	15

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55	A comprehensive study on cellular RNA editing activity in response to infections with different subtypes of influenza a viruses. BMC Genomics, 2018, 19, 925.	1.2	15
56	Conserved amino acids W423 and N424 in receptor-binding domain of SARS-CoV are potential targets for therapeutic monoclonal antibody. Virology, 2009, 383, 39-46.	1.1	14
57	The nuclear receptor corepressor NCoR1 regulates hematopoiesis and leukemogenesis in vivo. Blood Advances, 2019, 3, 644-657.	2.5	14
58	Creating RNA Specific C-to-U Editase from APOBEC3A by Separation of Its Activities on DNA and RNA Substrates. ACS Synthetic Biology, 2021, 10, 1106-1115.	1.9	14
59	Discovering multiple transcripts of human hepatocytes using massively parallel signature sequencing (MPSS). BMC Genomics, 2007, 8, 207.	1.2	13
60	Negatively Cooperative Binding Properties of Human Cytochrome P450 2E1 with Monocyclic Substrates. Current Drug Metabolism, 2012, 13, 1024-1031.	0.7	13
61	A Model of Proteolysis and Amino Acid Biosynthesis for Lactobacillus delbrueckii subsp. bulgaricus in Whey. Current Microbiology, 2012, 65, 742-751.	1.0	13
62	Exploration of conformational transition in the aryl-binding site of human FXa using molecular dynamics simulations. Journal of Molecular Modeling, 2012, 18, 2717-2725.	0.8	13
63	Comprehensive Comparison of RNA-Seq Data of SARS-CoV-2, SARS-CoV and MERS-CoV Infections: Alternative Entry Routes and Innate Immune Responses. Frontiers in Immunology, 2021, 12, 656433.	2.2	11
64	MPSS: an integrated database system for surveying a set of proteins. Bioinformatics, 2005, 21, 2142-2143.	1.8	10
65	Human gene expression sensitivity according to large scale meta-analysis. BMC Bioinformatics, 2009, 10, S56.	1.2	10
66	Prediction of Protein Modification Sites of Pyrrolidone Carboxylic Acid Using mRMR Feature Selection and Analysis. PLoS ONE, 2011, 6, e28221.	1.1	10
67	In silico analysis of amino acid biosynthesis and proteolysis in Lactobacillus delbrueckii subsp. bulgaricus 2038 and the implications for bovine milk fermentation. Biotechnology Letters, 2012, 34, 1545-1551.	1.1	10
68	Ï€â€"Ï€ Stacking mediated drugâ€"drug interactions in human CYP2E1. Proteins: Structure, Function and Bioinformatics, 2013, 81, 945-954.	1.5	10
69	Targeted inhibition of Zika virus infection in human cells by CRISPR-Cas13b. Virus Research, 2022, 312, 198707.	1.1	10
70	Feature-matching Pattern-based Support Vector Machines for Robust Peptide Mass Fingerprinting. Molecular and Cellular Proteomics, 2011, 10, M110.005785.	2.5	8
71	Designing Peptide-Based HIV Vaccine for Chinese. BioMed Research International, 2014, 2014, 1-8.	0.9	8
72	A cross-species analysis method to analyze animal models' similarity to human's disease state. BMC Systems Biology, 2012, 6, S18.	3.0	7

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73	Ionophore A23187 shows anti-tuberculosis activity and synergy with tebipenem. Tuberculosis, 2017, 107, 111-118.	0.8	7
74	Molecular dynamic simulation analysis of SARS-CoV-2 spike mutations and evaluation of ACE2 from pets and wild animals for infection risk. Computational Biology and Chemistry, 2022, 96, 107613.	1.1	7
75	Acquisition of amino acids by Lactobacillus delbrueckii subsp. bulgaricus 2038 when grown in the presence of casein. International Dairy Journal, 2014, 35, 145-152.	1.5	6
76	Interfering with retrotransposition by two types of CRISPR effectors: Cas12a and Cas13a. Cell Discovery, 2020, 6, 30.	3.1	6
77	Computational Studies on the Substrate Interactions of Influenza A Virus PB2 Subunit. PLoS ONE, 2012, 7, e44079.	1.1	6
78	Causal co-expression method with module analysis to screen drugs with specific target. Gene, 2013, 518, 145-151.	1.0	5
79	<i>De novo</i> assembly of transcriptome from next‑generation sequencing data. Quantitative Biology, 2016, 4, 94-105.	0.3	5
80	Med23 serves as a gatekeeper of the myeloid potential of hematopoietic stem cells. Nature Communications, 2018, 9, 3746.	5.8	5
81	Cloning and characterization of the chromosomal replication origin region of Amycolatopsis mediterranei U32. Biochemical and Biophysical Research Communications, 2005, 333, 14-20.	1.0	4
82	Bioinformatics Research on the SARS Coronavirus (SARS_CoV) in China. Current Pharmaceutical Design, 2006, 12, 4565-4572.	0.9	4
83	MPSQ: a web tool for protein-state searching. Bioinformatics, 2008, 24, 2412-2413.	1.8	4
84	GEOGLE: context mining tool for the correlation between gene expression and the phenotypic distinction. BMC Bioinformatics, 2009, 10, 264.	1.2	4
85	ASSOCIATION OF FEATURE GENE EXPRESSION WITH STRUCTURAL FINGERPRINTS OF CHEMICAL COMPOUNDS. Journal of Bioinformatics and Computational Biology, 2011, 09, 503-519.	0.3	4
86	A comparative analysis of tissue gene expression data from high-throughput studies. Science Bulletin, 2012, 57, 2920-2927.	1.7	4
87	A survey on cellular RNA editing activity in response to Candida albicans infections. BMC Genomics, 2018, 19, 43.	1.2	4
88	Mixed-Weight Neural Bagging for Detecting m^6A Modifications in SARS-CoV-2 RNA Sequencing. IEEE Transactions on Biomedical Engineering, 2022, 69, 2557-2568.	2.5	4
89	Comparative analysis of whole-genome sequences of Streptococcus suis. Science Bulletin, 2006, 51, 1199-1209.	1.7	3
90	scSensitiveGeneDefine: sensitive gene detection in single-cell RNA sequencing data by Shannon entropy. BMC Bioinformatics, 2021, 22, 211.	1.2	3

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91	The contribution of cis-regulatory elements to head-to-head gene pairs' co-expression pattern. Science in China Series C: Life Sciences, 2009, 52, 74-79.	1.3	2
92	Rapid screening and identification of viral pathogens in metagenomic data. BMC Medical Genomics, 2021, 14, 289.	0.7	2
93	Research/Review: Structure and Linkage Disequilibrium Analysis of Adamantane Resistant Mutations in Influenza Virus M2 Proton Channel. Current Drug Metabolism, 2014, 15, 526-534.	0.7	1
94	Expression Sensitivity Analysis of Human Disease Related Genes. BioMed Research International, 2013, 2013, 1-8.	0.9	0