

Pei Hao

List of Publications by Year in descending order

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Version: 2024-02-01

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	Molecular dynamic simulation analysis of SARS-CoV-2 spike mutations and evaluation of ACE2 from pets and wild animals for infection risk. <i>Computational Biology and Chemistry</i> , 2022, 96, 107613.	1.1	7
2	DENA: training an authentic neural network model using Nanopore sequencing data of Arabidopsis transcripts for detection and quantification of N6-methyladenosine on RNA. <i>Genome Biology</i> , 2022, 23, 25.	3.8	30
3	Mixed-Weight Neural Bagging for Detecting m^6A Modifications in SARS-CoV-2 RNA Sequencing. <i>IEEE Transactions on Biomedical Engineering</i> , 2022, 69, 2557-2568.	2.5	4
4	Targeted inhibition of Zika virus infection in human cells by CRISPR-Cas13b. <i>Virus Research</i> , 2022, 312, 198707.	1.1	10
5	scSensitiveGeneDefine: sensitive gene detection in single-cell RNA sequencing data by Shannon entropy. <i>BMC Bioinformatics</i> , 2021, 22, 211.	1.2	3
6	Creating RNA Specific C-to-U Editase from APOBEC3A by Separation of Its Activities on DNA and RNA Substrates. <i>ACS Synthetic Biology</i> , 2021, 10, 1106-1115.	1.9	14
7	Comprehensive Comparison of RNA-Seq Data of SARS-CoV-2, SARS-CoV and MERS-CoV Infections: Alternative Entry Routes and Innate Immune Responses. <i>Frontiers in Immunology</i> , 2021, 12, 656433.	2.2	11
8	HIV-1 Infection Alters the Viral Composition of Plasma in Men Who Have Sex with Men. <i>MSphere</i> , 2021, 6, .	1.3	16
9	Rapid screening and identification of viral pathogens in metagenomic data. <i>BMC Medical Genomics</i> , 2021, 14, 289.	0.7	2
10	Is SARS-CoV-2 originated from laboratory? A rebuttal to the claim of formation via laboratory recombination. <i>Emerging Microbes and Infections</i> , 2020, 9, 545-547.	3.0	23
11	Evolution of the novel coronavirus from the ongoing Wuhan outbreak and modeling of its spike protein for risk of human transmission. <i>Science China Life Sciences</i> , 2020, 63, 457-460.	2.3	1,650
12	Interfering with retrotransposition by two types of CRISPR effectors: Cas12a and Cas13a. <i>Cell Discovery</i> , 2020, 6, 30.	3.1	6
13	Two conserved epigenetic regulators prevent healthy ageing. <i>Nature</i> , 2020, 579, 118-122.	13.7	62
14	Molecular simulation of SARS-CoV-2 spike protein binding to pangolin ACE2 or human ACE2 natural variants reveals altered susceptibility to infection. <i>Journal of General Virology</i> , 2020, 101, 921-924.	1.3	42
15	ZIKV infection induces robust Th1-like Tfh cell and long-term protective antibody responses in immunocompetent mice. <i>Nature Communications</i> , 2019, 10, 3859.	5.8	39
16	Foxp1 is critical for the maintenance of regulatory T-cell homeostasis and suppressive function. <i>PLoS Biology</i> , 2019, 17, e3000270.	2.6	44
17	Lupus-associated atypical memory B cells are mTORC1-hyperactivated and functionally dysregulated. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 1090-1100.	0.5	61
18	The nuclear receptor corepressor NCoR1 regulates hematopoiesis and leukemogenesis in vivo. <i>Blood Advances</i> , 2019, 3, 644-657.	2.5	14

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19	Microbiota in the apical root canal system of tooth with apical periodontitis. BMC Genomics, 2019, 20, 189.	1.2	37
20	Iguratimod represses B cell terminal differentiation linked with the inhibition of PKC/EGR1 axis. Arthritis Research and Therapy, 2019, 21, 92.	1.6	32
21	Veratramine modulates AP-1-dependent gene transcription by directly binding to programmable DNA. Nucleic Acids Research, 2018, 46, 546-557.	6.5	17
22	Med23 serves as a gatekeeper of the myeloid potential of hematopoietic stem cells. Nature Communications, 2018, 9, 3746.	5.8	5
23	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
24	A survey on cellular RNA editing activity in response to Candida albicans infections. BMC Genomics, 2018, 19, 43.	1.2	4
25	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
26	Modelling BioNano optical data and simulation study of genome map assembly. Bioinformatics, 2018, 34, 3966-3974.	1.8	20
27	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
28	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
29	lonophore A23187 shows anti-tuberculosis activity and synergy with tebipenem. Tuberculosis, 2017, 107, 111-118.	0.8	7
30	Pediatric Drug Nitazoxanide: A Potential Choice for Control of Zika. Open Forum Infectious Diseases, 2017, 4, ofx009.	0.4	35
31	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
32	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
33	De novo assembly of transcriptome from next-generation sequencing data. Quantitative Biology, 2016, 4, 94-105.	0.3	5
34	The Landscape of A-to-I RNA Editome Is Shaped by Both Positive and Purifying Selection. PLoS Genetics, 2016, 12, e1006191.	1.5	72
35	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
36	The evolutionary landscape of intergenic trans-splicing events in insects. Nature Communications, 2015, 6, 8734.	5.8	17

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37	The Domain Landscape of Virus-Host Interactomes. <i>BioMed Research International</i> , 2014, 2014, 1-13.	0.9	30
38	Designing Peptide-Based HIV Vaccine for Chinese. <i>BioMed Research International</i> , 2014, 2014, 1-8.	0.9	8
39	Acquisition of amino acids by <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> 2038 when grown in the presence of casein. <i>International Dairy Journal</i> , 2014, 35, 145-152.	1.5	6
40	Research/Review: Structure and Linkage Disequilibrium Analysis of Adamantane Resistant Mutations in Influenza Virus M2 Proton Channel. <i>Current Drug Metabolism</i> , 2014, 15, 526-534.	0.7	1
41	Comparison of Next-Generation Sequencing and Clone-Based Sequencing in Analysis of Hepatitis B Virus Reverse Transcriptase Quasispecies Heterogeneity. <i>Journal of Clinical Microbiology</i> , 2013, 51, 4087-4094.	1.8	37
42	Stacking mediated drug-drug interactions in human CYP2E1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 945-954.	1.5	10
43	Causal co-expression method with module analysis to screen drugs with specific target. <i>Gene</i> , 2013, 518, 145-151.	1.0	5
44	Human Infection with a Novel Avian-Origin Influenza A (H7N9) Virus. <i>New England Journal of Medicine</i> , 2013, 368, 1888-1897.	13.9	2,122
45	Association between adverse clinical outcome in human disease caused by novel influenza A H7N9 virus and sustained viral shedding and emergence of antiviral resistance. <i>Lancet, The</i> , 2013, 381, 2273-2279.	6.3	308
46	The genome of <i>Mesobuthus martensii</i> reveals a unique adaptation model of arthropods. <i>Nature Communications</i> , 2013, 4, 2602.	5.8	187
47	Expression Sensitivity Analysis of Human Disease Related Genes. <i>BioMed Research International</i> , 2013, 2013, 1-8.	0.9	0
48	Molecular Dynamics Studies on the Conformational Transitions of Adenylate Kinase: A Computational Evidence for the Conformational Selection Mechanism. <i>BioMed Research International</i> , 2013, 2013, 1-7.	0.9	25
49	Combining ZHENG Theory and High-Throughput Expression Data to Predict New Effects of Chinese Herbal Formulae. <i>Evidence-based Complementary and Alternative Medicine</i> , 2012, 2012, 1-8.	0.5	15
50	OrySPSSP: a comparative Platform for Small Secreted Proteins from rice and other plants. <i>Nucleic Acids Research</i> , 2012, 41, D1192-D1198.	6.5	18
51	Negatively Cooperative Binding Properties of Human Cytochrome P450 2E1 with Monocyclic Substrates. <i>Current Drug Metabolism</i> , 2012, 13, 1024-1031.	0.7	13
52	In silico analysis of amino acid biosynthesis and proteolysis in <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> 2038 and the implications for bovine milk fermentation. <i>Biotechnology Letters</i> , 2012, 34, 1545-1551.	1.1	10
53	A Model of Proteolysis and Amino Acid Biosynthesis for <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> in Whey. <i>Current Microbiology</i> , 2012, 65, 742-751.	1.0	13
54	A comparative analysis of tissue gene expression data from high-throughput studies. <i>Science Bulletin</i> , 2012, 57, 2920-2927.	1.7	4

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55	Optimizing hybrid assembly of next-generation sequence data from <i>Enterococcus faecium</i> : a microbe with highly divergent genome. <i>BMC Systems Biology</i> , 2012, 6, S21.	3.0	24
56	A cross-species analysis method to analyze animal models' similarity to human's disease state. <i>BMC Systems Biology</i> , 2012, 6, S18.	3.0	7
57	A Comparison of Computational Methods for Identifying Virulence Factors. <i>PLoS ONE</i> , 2012, 7, e42517.	1.1	29
58	Exploration of conformational transition in the aryl-binding site of human FXa using molecular dynamics simulations. <i>Journal of Molecular Modeling</i> , 2012, 18, 2717-2725.	0.8	13
59	Computational Studies on the Substrate Interactions of Influenza A Virus PB2 Subunit. <i>PLoS ONE</i> , 2012, 7, e44079.	1.1	6
60	Complete Sequencing and Pan-Genomic Analysis of <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> Reveal Its Genetic Basis for Industrial Yogurt Production. <i>PLoS ONE</i> , 2011, 6, e15964.	1.1	90
61	Prediction of Protein Modification Sites of Pyrrolidone Carboxylic Acid Using mRMR Feature Selection and Analysis. <i>PLoS ONE</i> , 2011, 6, e28221.	1.1	10
62	Optimizing de novo transcriptome assembly from short-read RNA-Seq data: a comparative study. <i>BMC Bioinformatics</i> , 2011, 12, S2.	1.2	462
63	Feature-matching Pattern-based Support Vector Machines for Robust Peptide Mass Fingerprinting. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.005785.	2.5	8
64	ASSOCIATION OF FEATURE GENE EXPRESSION WITH STRUCTURAL FINGERPRINTS OF CHEMICAL COMPOUNDS. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 503-519.	0.3	4
65	Association of tissue lineage and gene expression: conservatively and differentially expressed genes define common and special functions of tissues. <i>BMC Bioinformatics</i> , 2010, 11, S1.	1.2	27
66	Revealing parasite influence in metabolic pathways in Apicomplexa infected patients. <i>BMC Bioinformatics</i> , 2010, 11, S13.	1.2	22
67	Detection of human novel influenza A (H1N1) viruses using multi-fluorescent real-time RT-PCR. <i>Virus Research</i> , 2010, 147, 85-90.	1.1	25
68	Exploring mitochondrial evolution and metabolism organization principles by comparative analysis of metabolic networks. <i>Genomics</i> , 2010, 95, 339-344.	1.3	15
69	A comparative analysis of liver transcriptome suggests divergent liver function among human, mouse and rat. <i>Genomics</i> , 2010, 96, 281-289.	1.3	41
70	GEOGLE: context mining tool for the correlation between gene expression and the phenotypic distinction. <i>BMC Bioinformatics</i> , 2009, 10, 264.	1.2	4
71	Human gene expression sensitivity according to large scale meta-analysis. <i>BMC Bioinformatics</i> , 2009, 10, S56.	1.2	10
72	Conserved amino acids W423 and N424 in receptor-binding domain of SARS-CoV are potential targets for therapeutic monoclonal antibody. <i>Virology</i> , 2009, 383, 39-46.	1.1	14

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73	The contribution of cis-regulatory elements to head-to-head gene pairs'™ co-expression pattern. <i>Science in China Series C: Life Sciences</i> , 2009, 52, 74-79.	1.3	2
74	Genome-Wide Identification of <i>Schistosoma japonicum</i> MicroRNAs Using a Deep-Sequencing Approach. <i>PLoS ONE</i> , 2009, 4, e8206.	1.1	87
75	MPSQ: a web tool for protein-state searching. <i>Bioinformatics</i> , 2008, 24, 2412-2413.	1.8	4
76	Gene expression module-based chemical function similarity search. <i>Nucleic Acids Research</i> , 2008, 36, e137-e137.	6.5	23
77	Metabolic Profiling Reveals Distinct Variations Linked to Nicotine Consumption in Humans " First Results from the KORA Study. <i>PLoS ONE</i> , 2008, 3, e3863.	1.1	107
78	Discovering multiple transcripts of human hepatocytes using massively parallel signature sequencing (MPSS). <i>BMC Genomics</i> , 2007, 8, 207.	1.2	13
79	Comparative analysis of whole-genome sequences of <i>Streptococcus suis</i> . <i>Science Bulletin</i> , 2006, 51, 1199-1209.	1.7	3
80	KDE Bioscience: Platform for bioinformatics analysis workflows. <i>Journal of Biomedical Informatics</i> , 2006, 39, 440-450.	2.5	28
81	In silico discovery of human natural antisense transcripts. <i>BMC Bioinformatics</i> , 2006, 7, 18.	1.2	38
82	Bioinformatics Research on the SARS Coronavirus (SARS_CoV) in China. <i>Current Pharmaceutical Design</i> , 2006, 12, 4565-4572.	0.9	4
83	Full-length genome sequences of two SARS-like coronaviruses in horseshoe bats and genetic variation analysis. <i>Journal of General Virology</i> , 2006, 87, 3355-3359.	1.3	96
84	A molecular docking model of SARS-CoV S1 protein in complex with its receptor, human ACE2. <i>Computational Biology and Chemistry</i> , 2005, 29, 254-257.	1.1	31
85	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. <i>Journal of Biological Chemistry</i> , 2005, 280, 29588-29595.	1.6	152
86	MPSS: an integrated database system for surveying a set of proteins. <i>Bioinformatics</i> , 2005, 21, 2142-2143.	1.8	10
87	Cross-host evolution of severe acute respiratory syndrome coronavirus in palm civet and human. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2430-2435.	3.3	602
88	Comparative and functional genomic analyses of the pathogenicity of phytopathogen <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>Genome Research</i> , 2005, 15, 757-767.	2.4	371
89	Cloning and characterization of the chromosomal replication origin region of <i>Amycolatopsis mediterranei</i> U32. <i>Biochemical and Biophysical Research Communications</i> , 2005, 333, 14-20.	1.0	4
90	A High-throughput Approach for Subcellular Proteome. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 441-455.	2.5	71

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91	Prediction of quaternary assembly of SARS coronavirus peplomer. <i>Biochemical and Biophysical Research Communications</i> , 2004, 325, 1210-1214.	1.0	20
92	Putative hAPN receptor binding sites in SARS_CoV spike protein. <i>Acta Pharmacologica Sinica</i> , 2003, 24, 481-8.	2.8	24
93	A Fine Physical Map of the Rice Chromosome 4. <i>Genome Research</i> , 2002, 12, 817-823.	2.4	64
94	Sequence and analysis of rice chromosome 4. <i>Nature</i> , 2002, 420, 316-320.	13.7	471