

Jianfei Hu

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

4,759
citations

331538

21
h-index

360920

35
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37
all docs

37
docs citations

37
times ranked

7737
citing authors

#	ARTICLE	IF	CITATIONS
1	Fc-mediated effector function contributes to the in vivo antiviral effect of an HIV neutralizing antibody. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18754-18763.	3.3	53
2	A high throughput lentivirus sieving assay identifies neutralization resistant Envelope sequences and predicts in vivo sieving. <i>Journal of Immunological Methods</i> , 2019, 464, 64-73.	0.6	2
3	Global Identification of Small Ubiquitin-related Modifier (SUMO) Substrates Reveals Crosstalk between SUMOylation and Phosphorylation Promotes Cell Migration. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 871-888.	2.5	24
4	The long non-coding RNA NEAT1 is responsive to neuronal activity and is associated with hyperexcitability states. <i>Scientific Reports</i> , 2017, 7, 40127.	1.6	92
5	Global Analysis of SUMO-Binding Proteins Identifies SUMOylation as a Key Regulator of the INO80 Chromatin Remodeling Complex. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 812-823.	2.5	15
6	Stochastic principles governing alternative splicing of RNA. <i>PLoS Computational Biology</i> , 2017, 13, e1005761.	1.5	16
7	ScaPD: a database for human scaffold proteins. <i>BMC Bioinformatics</i> , 2017, 18, 386.	1.2	8
8	Multiple Origins of Virus Persistence during Natural Control of HIV Infection. <i>Cell</i> , 2016, 166, 1004-1015.	13.5	156
9	β A3/A1-crystallin is a critical mediator of STAT3 signaling in optic nerve astrocytes. <i>Scientific Reports</i> , 2015, 5, 8755.	1.6	11
10	Systematic Prediction of Scaffold Proteins Reveals New Design Principles in Scaffold-Mediated Signal Transduction. <i>PLoS Computational Biology</i> , 2015, 11, e1004508.	1.5	13
11	A Screen for Extracellular Signal-Regulated Kinase-Primed Glycogen Synthase Kinase 3 Substrates Identifies the p53 Inhibitor iASPP. <i>Journal of Virology</i> , 2015, 89, 9232-9241.	1.5	10
12	Protein Microarray Characterization of the S-Nitrosoproteome. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 63-72.	2.5	56
13	PhosphoNetworks: a database for human phosphorylation networks. <i>Bioinformatics</i> , 2014, 30, 141-142.	1.8	106
14	A Selective Phenelzine Analogue Inhibitor of Histone Demethylase LSD1. <i>ACS Chemical Biology</i> , 2014, 9, 1284-1293.	1.6	88
15	Global analysis of phosphorylation networks in humans. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 224-231.	1.1	20
16	Lhx1 Controls Terminal Differentiation and Circadian Function of the Suprachiasmatic Nucleus. <i>Cell Reports</i> , 2014, 7, 609-622.	2.9	88
17	Endothelial Cell MicroRNA Expression in Human Late-Onset Fuchs' Dystrophy. , 2014, 55, 216.		50
18	Transcription Factor SOX9 Plays a Key Role in the Regulation of Visual Cycle Gene Expression in the Retinal Pigment Epithelium. <i>Journal of Biological Chemistry</i> , 2014, 289, 12908-12921.	1.6	49

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19	Construction of human activityâ€based phosphorylation networks. <i>Molecular Systems Biology</i> , 2013, 9, 655.	3.2	153
20	Profiling the Dynamics of a Human Phosphorylome Reveals New Components in HGF/c-Met Signaling. <i>PLoS ONE</i> , 2013, 8, e72671.	1.1	19
21	Phosphorylation of the Chromatin Binding Domain of KSHV LANA. <i>PLoS Pathogens</i> , 2012, 8, e1002972.	2.1	32
22	Rapid Identification of Monospecific Monoclonal Antibodies Using a Human Proteome Microarray. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.016253.	2.5	136
23	Expression of brain-derived neurotrophic factor is regulated by the Wnt signaling pathway. <i>NeuroReport</i> , 2012, 23, 189-194.	0.6	76
24	Computational analysis of tissue-specific gene networks: application to murine retinal functional studies. <i>Bioinformatics</i> , 2010, 26, 2289-2297.	1.8	26
25	MOPAT: a graph-based method to predict recurrent cis -regulatory modules from known motifs. <i>Nucleic Acids Research</i> , 2008, 36, 4488-4497.	6.5	29
26	Compositional dynamics of guanine and cytosine content in prokaryotic genomes. <i>Research in Microbiology</i> , 2007, 158, 363-370.	1.0	31
27	Replication-associated purine asymmetry may contribute to strand-biased gene distribution. <i>Genomics</i> , 2007, 90, 186-194.	1.3	27
28	Applications of the double-barreled data in whole-genome shotgun sequence assembly and analysis. <i>Science in China Series C: Life Sciences</i> , 2005, 48, 300-306.	1.3	0
29	A Genome Sequence of Novel SARS-CoV Isolates: the Genotype, GD-Ins29, Leads to a Hypothesis of Viral Transmission in South China. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 101-107.	3.0	17
30	The E Protein Is a Multifunctional Membrane Protein of SARS-CoV. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 131-144.	3.0	41
31	The Structure Analysis and Antigenicity Study of the N Protein of SARS-CoV. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 145-154.	3.0	24
32	Complete Genome Sequences of the SARS-CoV: the BJ Group (Isolates BJ01-BJ04). <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 180-192.	3.0	15
33	Evolution and Variation of the SARS-CoV Genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 216-225.	3.0	16
34	Genome Organization of the SARS-CoV. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 226-235.	3.0	17
35	RePS: A Sequence Assembler That Masks Exact Repeats Identified from the Shotgun Data. <i>Genome Research</i> , 2002, 12, 824-831.	2.4	62
36	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

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37	A draft sequence of the rice (<i>Oryza sativa</i> ssp.indica) genome. Science Bulletin, 2001, 46, 1937-1942.	1.7	35