Jianfei Hu

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Fc-mediated effector function contributes to the in vivo antiviral effect of an HIV neutralizing antibody. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 18754-18763.	7.1	53
2	A high throughput lentivirus sieving assay identifies neutralization resistant Envelope sequences and predicts in vivo sieving. Journal of Immunological Methods, 2019, 464, 64-73.	1.4	2
3	Global Identification of Small Ubiquitin-related Modifier (SUMO) Substrates Reveals Crosstalk between SUMOylation and Phosphorylation Promotes Cell Migration. Molecular and Cellular Proteomics, 2018, 17, 871-888.	3.8	24
4	The long non-coding RNA NEAT1 is responsive to neuronal activity and is associated with hyperexcitability states. Scientific Reports, 2017, 7, 40127.	3.3	92
5	Global Analysis of SUMO-Binding Proteins Identifies SUMOylation as a Key Regulator of the INO80 Chromatin Remodeling Complex. Molecular and Cellular Proteomics, 2017, 16, 812-823.	3.8	15
6	Stochastic principles governing alternative splicing of RNA. PLoS Computational Biology, 2017, 13, e1005761.	3.2	16
7	ScaPD: a database for human scaffold proteins. BMC Bioinformatics, 2017, 18, 386.	2.6	8
8	Multiple Origins of Virus Persistence during Natural Control of HIV Infection. Cell, 2016, 166, 1004-1015.	28.9	156
9	βA3/A1-crystallin is a critical mediator of STAT3 signaling in optic nerve astrocytes. Scientific Reports, 2015, 5, 8755.	3.3	11
10	Systematic Prediction of Scaffold Proteins Reveals New Design Principles in Scaffold-Mediated Signal Transduction. PLoS Computational Biology, 2015, 11, e1004508.	3.2	13
11	A Screen for Extracellular Signal-Regulated Kinase-Primed Glycogen Synthase Kinase 3 Substrates Identifies the p53 Inhibitor iASPP. Journal of Virology, 2015, 89, 9232-9241.	3.4	10
12	Protein Microarray Characterization of the S-Nitrosoproteome. Molecular and Cellular Proteomics, 2014, 13, 63-72.	3.8	56
13	PhosphoNetworks: a database for human phosphorylation networks. Bioinformatics, 2014, 30, 141-142.	4.1	106
14	A Selective Phenelzine Analogue Inhibitor of Histone Demethylase LSD1. ACS Chemical Biology, 2014, 9, 1284-1293.	3.4	88
15	Global analysis of phosphorylation networks in humans. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 224-231.	2.3	20
16	Lhx1 Controls Terminal Differentiation and Circadian Function of the Suprachiasmatic Nucleus. Cell Reports, 2014, 7, 609-622.	6.4	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. Journal of Biological Chemistry, 2014, 289, 12908-12921.	3.4	49

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19	Construction of human activityâ€based phosphorylation networks. Molecular Systems Biology, 2013, 9, 655.	7.2	153
20	Profiling the Dynamics of a Human Phosphorylome Reveals New Components in HGF/c-Met Signaling. PLoS ONE, 2013, 8, e72671.	2.5	19
21	Phosphorylation of the Chromatin Binding Domain of KSHV LANA. PLoS Pathogens, 2012, 8, e1002972.	4.7	32
22	Rapid Identification of Monospecific Monoclonal Antibodies Using a Human Proteome Microarray. Molecular and Cellular Proteomics, 2012, 11, 0111.016253.	3.8	136
23	Expression of brain-derived neurotrophic factor is regulated by the Wnt signaling pathway. NeuroReport, 2012, 23, 189-194.	1.2	76
24	Computational analysis of tissue-specific gene networks: application to murine retinal functional studies. Bioinformatics, 2010, 26, 2289-2297.	4.1	26
25	MOPAT: a graph-based method to predict recurrent cis -regulatory modules from known motifs. Nucleic Acids Research, 2008, 36, 4488-4497.	14.5	29
26	Compositional dynamics of guanine and cytosine content in prokaryotic genomes. Research in Microbiology, 2007, 158, 363-370.	2.1	31
27	Replication-associated purine asymmetry may contribute to strand-biased gene distribution. Genomics, 2007, 90, 186-194.	2.9	27
28	Applications of the double-barreled data in whole-genome shotgun sequence assembly and analysis. Science in China Series C: Life Sciences, 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. Genomics, Proteomics and Bioinformatics, 2003, 1, 101-107.	6.9	17
30	The E Protein Is a Multifunctional Membrane Protein of SARS-CoV. Genomics, Proteomics and Bioinformatics, 2003, 1, 131-144.	6.9	41
31	The Structure Analysis and Antigenicity Study of the N Protein of SARS-CoV. Genomics, Proteomics and Bioinformatics, 2003, 1, 145-154.	6.9	24
32	Complete Genome Sequences of the SARS-CoV: the BJ Group (Isolates BJ01-BJ04). Genomics, Proteomics and Bioinformatics, 2003, 1, 180-192.	6.9	15
33	Evolution and Variation of the SARS-CoV Genome. Genomics, Proteomics and Bioinformatics, 2003, 1, 216-225.	6.9	16
34	Genome Organization of the SARS-CoV. Genomics, Proteomics and Bioinformatics, 2003, 1, 226-235.	6.9	17
35	RePS: A Sequence Assembler That Masks Exact Repeats Identified from the Shotgun Data. Genome Research, 2002, 12, 824-831.	5.5	62
36	A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. <i>indica</i>). Science, 2002, 296, 79-92.	12.6	3,146

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