Hufeng Zhou

List of Publications by Year
in descending order

30 papers	1,487 citations	331670 21 h-index	454955 30 g-index
32 all docs	32 docs citations	32 times ranked	2490 citing authors

#	ARTICLE	IF	CITATIONS
1	The NF-κB Genomic Landscape in Lymphoblastoid B Cells. Cell Reports, 2014, 8, 1595-1606.	6.4	147
2	Epstein-Barr Virus Oncoprotein Super-enhancers Control B Cell Growth. Cell Host and Microbe, 2015, 17, 205-216.	11.0	146
3	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146
4	The Epstein-Barr Virus Regulome in Lymphoblastoid Cells. Cell Host and Microbe, 2017, 22, 561-573.e4.	11.0	89
5	Epstein–Barr Virus Nuclear Antigen 3C binds to BATF/IRF4 or SPI1/IRF4 composite sites and recruits Sin3A to repress CDKN2A. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 421-426.	7.1	81
6	Epstein–Barr virus super-enhancer eRNAs are essential for MYC oncogene expression and lymphoblast proliferation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14121-14126.	7.1	77
7	Stringent homology-based prediction of H. sapiens-M. tuberculosis H37Rv protein-protein interactions. Biology Direct, 2014, 9, 5.	4.6	74
8	Epstein-Barr Virus (EBV) Infection in Chinese Children: A Retrospective Study of Age-Specific Prevalence. PLoS ONE, 2014, 9, e99857.	2.5	69
9	TRAF1 Coordinates Polyubiquitin Signaling to Enhance Epstein-Barr Virus LMP1-Mediated Growth and Survival Pathway Activation. PLoS Pathogens, 2015, 11, e1004890.	4.7	67
10	Epstein–Barr virus nuclear antigen leader protein localizes to promoters and enhancers with cell transcription factors and EBNA2. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18537-18542.	7.1	61
11	PROGRESS IN COMPUTATIONAL STUDIES OF HOST–PATHOGEN INTERACTIONS. Journal of Bioinformatics and Computational Biology, 2013, 11, 1230001.	0.8	54
12	Epstein–Barr virus nuclear antigen 3A partially coincides with EBNA3C genome-wide and is tethered to DNA through BATF complexes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 554-559.	7.1	45
13	Mouse model of Epstein–Barr virus LMP1- and LMP2A-driven germinal center B-cell lymphoproliferative disease. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4751-4756.	7.1	44
14	Evasion of affinity-based selection in germinal centers by Epstein–Barr virus LMP2A. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11612-11617.	7.1	43
15	Nasopharyngeal carcinoma super-enhancer–driven ETV6 correlates with prognosis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9683-9688.	7.1	43
16	Dynamic Scan Procedure for Detecting Rare-Variant Association Regions in Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 802-814.	6.2	43
17	IntPath--an integrated pathway gene relationship database for model organisms and important pathogens. BMC Systems Biology, 2012, 6, S2.	3.0	41
18	Stringent DDI-based Prediction of H. sapiens-M. tuberculosis H37Rv Protein-Protein Interactions. BMC Systems Biology, 2013, 7, S6.	3.0	34

#	Article	IF	Citations
19	Comparative analysis and assessment of M. tuberculosis H37Rv protein-protein interaction datasets. BMC Genomics, 2011, 12, S20.	2.8	29
20	Haemophilus parasuis Infection Disrupts Adherens Junctions and Initializes EMT Dependent on Canonical Wnt/Î²-Catenin Signaling Pathway. Frontiers in Cellular and Infection Microbiology, 2018, 8, 324.	3.9	27
21	Epstein-Barr Virus Episome Physically Interacts with Active Regions of the Host Genome in Lymphoblastoid Cells. Journal of Virology, 2020, 94, .	3.4	26
22	The Association Between Indwelling Arterial Catheters and Mortality in Hemodynamically Stable Patients With Respiratory Failure. Chest, 2015, 148, 1470-1476.	0.8	24
23	A multi-dimensional integrative scoring framework for predicting functional variants in the human genome. American Journal of Human Genetics, 2022, 109, 446-456.	6.2	18
24	Epstein-Barr Virus Nuclear Antigen Leader Protein Coactivates EP300. Journal of Virology, 2018, 92, .	3.4	15
25	Haemophilus parasuis infection activates NOD1/2-RIP2 signaling pathway in PK-15Âcells. Developmental and Comparative Immunology, 2018, 79, 158-165.	2.3	12
26	Genome-wide association study of neck circumference identifies sex-specific loci independent of generalized adiposity. International Journal of Obesity, 2021, 45, 1532-1541.	3.4	8
27	Transcriptional responses of Haemophilus parasuis to iron-restriction stress in vitro. BioMetals, 2009, 22, 907-916.	4.1	7
28	Integration of multiomic annotation data to prioritize and characterize inflammation and immuneâ€related risk variants in squamous cell lung cancer. Genetic Epidemiology, 2021, 45, 99-114.	1.3	7
29	Identification of a nucleoside analog active against adenosine kinaseâ€"expressing plasma cell malignancies. Journal of Clinical Investigation, 2017, 127, 2066-2080.	8.2	7
30	LipidGO: database for lipid-related GO terms and applications. Bioinformatics, 2014, 30, 1043-1044.	4.1	2