

Xinxia Peng

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

1,659
citations

567281

15
h-index

580821

25
g-index

30
all docs

30
docs citations

30
times ranked

3406
citing authors

#	ARTICLE	IF	CITATIONS
1	Unique Signatures of Long Noncoding RNA Expression in Response to Virus Infection and Altered Innate Immune Signaling. MBio, 2010, 1, .	4.1	237
2	Inhalation of lung spheroid cell secretome and exosomes promotes lung repair in pulmonary fibrosis. Nature Communications, 2020, 11, 1064.	12.8	228
3	Infection with MERS-CoV Causes Lethal Pneumonia in the Common Marmoset. PLoS Pathogens, 2014, 10, e1004250.	4.7	186
4	Computational identification of hepatitis C virus associated microRNA-mRNA regulatory modules in human livers. BMC Genomics, 2009, 10, 373.	2.8	178
5	Annotation of long non-coding RNAs expressed in Collaborative Cross founder mice in response to respiratory virus infection reveals a new class of interferon-stimulated transcripts. RNA Biology, 2014, 11, 875-890.	3.1	122
6	The draft genome sequence of the ferret (<i>Mustela putorius furo</i>) facilitates study of human respiratory disease. Nature Biotechnology, 2014, 32, 1250-1255.	17.5	110
7	Fc Characteristics Mediate Selective Placental Transfer of IgG in HIV-Infected Women. Cell, 2019, 178, 190-201.e11.	28.9	93
8	Integrative Deep Sequencing of the Mouse Lung Transcriptome Reveals Differential Expression of Diverse Classes of Small RNAs in Response to Respiratory Virus Infection. MBio, 2011, 2, .	4.1	86
9	Integrated Omics Analysis of Pathogenic Host Responses during Pandemic H1N1 Influenza Virus Infection: The Crucial Role of Lipid Metabolism. Cell Host and Microbe, 2016, 19, 254-266.	11.0	75
10	Virus-host interactions: from systems biology to translational research. Current Opinion in Microbiology, 2009, 12, 432-438.	5.1	61
11	Tissue-specific transcriptome sequencing analysis expands the non-human primate reference transcriptome resource (NHPRT). Nucleic Acids Research, 2015, 43, D737-D742.	14.5	61
12	Deep Sequencing of HIV-Infected Cells: Insights into Nascent Transcription and Host-Directed Therapy. Journal of Virology, 2014, 88, 8768-8782.	3.4	41
13	Evaluation of the innate immune responses to influenza and live-attenuated influenza vaccine infection in primary differentiated human nasal epithelial cells. Vaccine, 2017, 35, 6112-6121.	3.8	27
14	Fc Gamma Receptor Polymorphisms Modulated the Vaccine Effect on HIV-1 Risk in the HVTN 505 HIV Vaccine Trial. Journal of Virology, 2019, 93, .	3.4	26
15	Genomic Profiling of Collaborative Cross Founder Mice Infected with Respiratory Viruses Reveals Novel Transcripts and Infection-Related Strain-Specific Gene and Isoform Expression. G3: Genes, Genomes, Genetics, 2014, 4, 1429-1444.	1.8	25
16	Interleukin-15 response signature predicts RhCMV/SIV vaccine efficacy. PLoS Pathogens, 2021, 17, e1009278.	4.7	18
17	Systematic Profiling of Full-Length Ig and TCR Repertoire Diversity in Rhesus Macaque through Long Read Transcriptome Sequencing. Journal of Immunology, 2020, 204, 3434-3444.	0.8	18
18	Macrophage-associated wound healing contributes to African green monkey SIV pathogenesis control. Nature Communications, 2019, 10, 5101.	12.8	17

#	ARTICLE	IF	CITATIONS
19	Elucidating the Role of Host Long Non-Coding RNA during Viral Infection: Challenges and Paths Forward. <i>Vaccines</i> , 2017, 5, 37.	4.4	12
20	FCGR2C Polymorphisms Associated with HIV-1 Vaccine Protection Are Linked to Altered Gene Expression of Fc- γ Receptors in Human B Cells. <i>PLoS ONE</i> , 2016, 11, e0152425.	2.5	11
21	Deep Transcriptional Sequencing of Mucosal Challenge Compartment from Rhesus Macaques Acutely Infected with Simian Immunodeficiency Virus Implicates Loss of Cell Adhesion Preceding Immune Activation. <i>Journal of Virology</i> , 2014, 88, 7962-7972.	3.4	9
22	Assessment and improvement of Indian origin rhesus macaque and <i>Macaca auricularis</i> origin cynomolgus macaque genome annotations using deep transcriptome sequencing data. <i>Journal of Medical Primatology</i> , 2014, 43, 317-328.	0.6	4
23	Post-GWAS functional analysis identifies CUX1 as a regulator of p16INK4a and cellular senescence. <i>Nature Aging</i> , 2022, 2, 140-154.	11.6	4
24	Single-Cell-Based High-Throughput Ig and TCR Repertoire Sequencing Analysis in Rhesus Macaques. <i>Journal of Immunology</i> , 2022, 208, 762-771.	0.8	2
25	Tumor Necrosis Factor Alpha-Induced Interleukin-1 Alpha Synthesis and Cell Death Is Increased in Mouse Epithelial Cells Infected With <i>Chlamydia muridarum</i> . <i>Journal of Infectious Diseases</i> , 2021, 224, S47-S55.	4.0	0