

# Xinxia Peng

## List of Publications by Year in descending order

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25  
papers

1,659  
citations

566801

15  
h-index

580395

25  
g-index

30  
all docs

30  
docs citations

30  
times ranked

3406  
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-Cellâ€‘Based High-Throughput Ig and TCR Repertoire Sequencing Analysis in Rhesus Macaques. <i>Journal of Immunology</i> , 2022, 208, 762-771.	0.4	2
2	Post-GWAS functional analysis identifies CUX1 as a regulator of p16INK4a and cellular senescence. <i>Nature Aging</i> , 2022, 2, 140-154.	5.3	4
3	Interleukin-15 response signature predicts RhCMV/SIV vaccine efficacy. <i>PLoS Pathogens</i> , 2021, 17, e1009278.	2.1	18
4	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.	1.9	0
5	Inhalation of lung spheroid cell secretome and exosomes promotes lung repair in pulmonary fibrosis. <i>Nature Communications</i> , 2020, 11, 1064.	5.8	228
6	Systematic Profiling of Full-Length Ig and TCR Repertoire Diversity in Rhesus Macaque through Long Read Transcriptome Sequencing. <i>Journal of Immunology</i> , 2020, 204, 3434-3444.	0.4	18
7	Fc Characteristics Mediate Selective Placental Transfer of IgG in HIV-Infected Women. <i>Cell</i> , 2019, 178, 190-201.e11.	13.5	93
8	Macrophage-associated wound healing contributes to African green monkey SIV pathogenesis control. <i>Nature Communications</i> , 2019, 10, 5101.	5.8	17
9	Fc Gamma Receptor Polymorphisms Modulated the Vaccine Effect on HIV-1 Risk in the HVTN 505 HIV Vaccine Trial. <i>Journal of Virology</i> , 2019, 93, .	1.5	26
10	Evaluation of the innate immune responses to influenza and live-attenuated influenza vaccine infection in primary differentiated human nasal epithelial cells. <i>Vaccine</i> , 2017, 35, 6112-6121.	1.7	27
11	Elucidating the Role of Host Long Non-Coding RNA during Viral Infection: Challenges and Paths Forward. <i>Vaccines</i> , 2017, 5, 37.	2.1	12
12	Integrated Omics Analysis of Pathogenic Host Responses during Pandemic H1N1 Influenza Virus Infection: The Crucial Role of Lipid Metabolism. <i>Cell Host and Microbe</i> , 2016, 19, 254-266.	5.1	75
13	FCGR2C Polymorphisms Associated with HIV-1 Vaccine Protection Are Linked to Altered Gene Expression of Fc-Î³3 Receptors in Human B Cells. <i>PLoS ONE</i> , 2016, 11, e0152425.	1.1	11
14	Tissue-specific transcriptome sequencing analysis expands the non-human primate reference transcriptome resource (NHPRT). <i>Nucleic Acids Research</i> , 2015, 43, D737-D742.	6.5	61
15	Deep Sequencing of HIV-Infected Cells: Insights into Nascent Transcription and Host-Directed Therapy. <i>Journal of Virology</i> , 2014, 88, 8768-8782.	1.5	41
16	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. <i>RNA Biology</i> , 2014, 11, 875-890.	1.5	122
17	Infection with MERS-CoV Causes Lethal Pneumonia in the Common Marmoset. <i>PLoS Pathogens</i> , 2014, 10, e1004250.	2.1	186
18	The draft genome sequence of the ferret ( <i>Mustela putorius furo</i> ) facilitates study of human respiratory disease. <i>Nature Biotechnology</i> , 2014, 32, 1250-1255.	9.4	110

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19	Assessment and improvement of Indian origin rhesus macaque and Mauritian origin cynomolgus macaque genome annotations using deep transcriptome sequencing data. <i>Journal of Medical Primatology</i> , 2014, 43, 317-328.	0.3	4
20	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.	1.5	9
21	Genomic Profiling of Collaborative Cross Founder Mice Infected with Respiratory Viruses Reveals Novel Transcripts and Infection-Related Strain-Specific Gene and Isoform Expression. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1429-1444.	0.8	25
22	Integrative Deep Sequencing of the Mouse Lung Transcriptome Reveals Differential Expression of Diverse Classes of Small RNAs in Response to Respiratory Virus Infection. <i>MBio</i> , 2011, 2, .	1.8	86
23	Unique Signatures of Long Noncoding RNA Expression in Response to Virus Infection and Altered Innate Immune Signaling. <i>MBio</i> , 2010, 1, .	1.8	237
24	Computational identification of hepatitis C virus associated microRNA-mRNA regulatory modules in human livers. <i>BMC Genomics</i> , 2009, 10, 373.	1.2	178
25	Virus-host interactions: from systems biology to translational research. <i>Current Opinion in Microbiology</i> , 2009, 12, 432-438.	2.3	61