

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 | Single-Cellâ€Based High-Throughput Ig and TCR Repertoire Sequencing Analysis in Rhesus Macaques. <i>Journal of Immunology</i> , 2022, 208, 762-771. | 0.8 | 2 |
| 2 | 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 |
| 3 | Interleukin-15 response signature predicts RhCMV/SIV vaccine efficacy. <i>PLoS Pathogens</i> , 2021, 17, e1009278. | 4.7 | 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. | 4.0 | 0 |
| 5 | Inhalation of lung spheroid cell secretome and exosomes promotes lung repair in pulmonary fibrosis. <i>Nature Communications</i> , 2020, 11, 1064. | 12.8 | 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. | 0.8 | 18 |
| 7 | Fc Characteristics Mediate Selective Placental Transfer of IgG in HIV-Infected Women. <i>Cell</i> , 2019, 178, 190-201.e11. | 28.9 | 93 |
| 8 | Macrophage-associated wound healing contributes to African green monkey SIV pathogenesis control. <i>Nature Communications</i> , 2019, 10, 5101. | 12.8 | 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, . | 3.4 | 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. | 3.8 | 27 |
| 11 | 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 |
| 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. | 11.0 | 75 |
| 13 | FCGR2C Polymorphisms Associated with HIV-1 Vaccine Protection Are Linked to Altered Gene Expression of Fc-Î³ Receptors in Human B Cells. <i>PLoS ONE</i> , 2016, 11, e0152425. | 2.5 | 11 |
| 14 | Tissue-specific transcriptome sequencing analysis expands the non-human primate reference transcriptome resource (NHPRTR). <i>Nucleic Acids Research</i> , 2015, 43, D737-D742. | 14.5 | 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. | 3.4 | 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. | 3.1 | 122 |
| 17 | Infection with MERS-CoV Causes Lethal Pneumonia in the Common Marmoset. <i>PLoS Pathogens</i> , 2014, 10, e1004250. | 4.7 | 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. | 17.5 | 110 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Assessment and improvement of Indian origin rhesus macaque and <i>Macaca auritiana</i> origin cynomolgus macaque genome annotations using deep transcriptome sequencing data. Journal of Medical Primatology, 2014, 43, 317-328. | 0.6 | 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. Journal of Virology, 2014, 88, 7962-7972. | 3.4 | 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. G3: Genes, Genomes, Genetics, 2014, 4, 1429-1444. | 1.8 | 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. MBio, 2011, 2, . | 4.1 | 86 |
| 23 | Unique Signatures of Long Noncoding RNA Expression in Response to Virus Infection and Altered Innate Immune Signaling. MBio, 2010, 1, . | 4.1 | 237 |
| 24 | Computational identification of hepatitis C virus associated microRNA-mRNA regulatory modules in human livers. BMC Genomics, 2009, 10, 373. | 2.8 | 178 |
| 25 | Virus-host interactions: from systems biology to translational research. Current Opinion in Microbiology, 2009, 12, 432-438. | 5.1 | 61 |