

Rebekah Penrice-Randal

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

16 papers	395 citations	8 h-index	19 g-index
20 ext. papers	689 ext. citations	9 avg, IF	3.98 L-index

#	Paper	IF	Citations
16	Tissue-Specific Immunopathology in Fatal COVID-19. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2021 , 203, 192-201	10.2	116
15	Inflammatory profiles across the spectrum of disease reveal a distinct role for GM-CSF in severe COVID-19. <i>Science Immunology</i> , 2021 , 6,	28	82
14	SARS-CoV-2 one year on: evidence for ongoing viral adaptation. <i>Journal of General Virology</i> , 2021 , 102,	4.9	63
13	SARS-CoV-2 Omicron-B.1.1.529 Variant leads to less severe disease than Pango B and Delta variants strains in a mouse model of severe COVID-19		31
12	Amplicon based MinION sequencing of SARS-CoV-2 and metagenomic characterisation of nasopharyngeal swabs from patients with COVID-19		24
11	Amplicon-Based Detection and Sequencing of SARS-CoV-2 in Nasopharyngeal Swabs from Patients With COVID-19 and Identification of Deletions in the Viral Genome That Encode Proteins Involved in Interferon Antagonism. <i>Viruses</i> , 2020 , 12,	6.2	23
10	Tissue-specific tolerance in fatal Covid-19		22
9	Mutations that adapt SARS-CoV-2 to mink or ferret do not increase fitness in the human airway.. <i>Cell Reports</i> , 2022 , 110344	10.6	10
8	Sequential infection with influenza A virus followed by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) leads to more severe disease and encephalitis in a mouse model of COVID-19		7
7	Tissue Proteomic Analysis Identifies Mechanisms and Stages of Immunopathology in Fatal COVID-19. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2021 ,	5.7	5
6	Amplicon and Metagenomic Analysis of Middle East Respiratory Syndrome (MERS) Coronavirus and the Microbiome in Patients with Severe MERS. <i>MSphere</i> , 2021 , 6, e0021921	5	4
5	Sequence analysis of SARS-CoV-2 in nasopharyngeal samples from patients with COVID-19 illustrates population variation and diverse phenotypes, placing the in vitro growth properties of B.1.1.7 and B.1.351 lineage viruses in context		2
4	Mutations that adapt SARS-CoV-2 to mustelid hosts do not increase fitness in the human airway		2
3	Rapid selection of P323L in the SARS-CoV-2 polymerase (NSP12) in humans and non-human primate models and confers a large plaque phenotype		2
2	Identification and quantification of SARS-CoV-2 leader subgenomic mRNA gene junctions in nasopharyngeal samples shows phasic transcription in animal models of COVID-19 and dysregulation at later time points that can also be identified in humans		1
1	Analysis of SARS-CoV-2 in Nasopharyngeal Samples from Patients with COVID-19 Illustrates Population Variation and Diverse Phenotypes, Placing the Growth Properties of Variants of Concern in Context with Other Lineages.. <i>MSphere</i> , 2022 , e0091321	5	0