

# Duleepa Jayasundara

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/927018/publications.pdf>

Version: 2024-02-01

10  
papers

99  
citations

1684188  
5  
h-index

1474206  
9  
g-index

10  
all docs

10  
docs citations

10  
times ranked

151  
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole of population-based cohort study of recovery time from COVID-19 in New South Wales Australia. <i>The Lancet Regional Health - Western Pacific</i> , 2021, 12, 100193.	2.9	29
2	Emergence of pertactin-deficient pertussis strains in Australia can be explained by models of vaccine escape. <i>Epidemics</i> , 2020, 31, 100388.	3.0	9
3	ENViT: inference of ecological characteristics of viruses from metagenomic data. <i>BMC Bioinformatics</i> , 2019, 19, 377.	2.6	2
4	Modelling the in-host dynamics of <i>Neisseria gonorrhoeae</i> infection. <i>Pathogens and Disease</i> , 2019, 77, .	2.0	4
5	Modelling the decline and future of hepatitis A transmission in Australia. <i>Journal of Viral Hepatitis</i> , 2019, 26, 199-207.	2.0	5
6	Human Body to Water Reservoirs: Estimating Viral Population Characteristics Using High-Throughput Sequencing. , 2018, , 139-155.		0
7	Assessing Species Diversity Using Metavirome Data: Methods and Challenges. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 447-455.	4.1	10
8	Quantifying the population effects of vaccination and migration on hepatitis A seroepidemiology in Australia. <i>Vaccine</i> , 2017, 35, 5228-5234.	3.8	4
9	Accurate reconstruction of viral quasispecies spectra through improved estimation of strain richness. <i>BMC Bioinformatics</i> , 2015, 16, S3.	2.6	3
10	ViQuaS: an improved reconstruction pipeline for viral quasispecies spectra generated by next-generation sequencing. <i>Bioinformatics</i> , 2015, 31, 886-896.	4.1	33