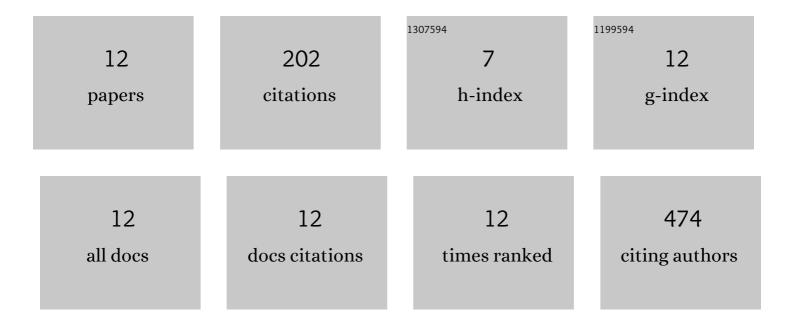
Yee Ling Chong

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7996891/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	The Effect of Vaccination on the Evolution and Population Dynamics of Avian Paramyxovirus-1. PLoS Pathogens, 2010, 6, e1000872.	4.7	65
2	A survey of recently emerged genome-wide computational enhancer predictor tools. Computational Biology and Chemistry, 2018, 74, 132-141.	2.3	29
3	Successful establishment and global dispersal of genotype VI avian paramyxovirus serotype 1 after cross species transmission. Infection, Genetics and Evolution, 2013, 17, 260-268.	2.3	23
4	Systematic phylogenetic analysis of influenza A virus reveals many novel mosaic genome segments. Infection, Genetics and Evolution, 2013, 18, 367-378.	2.3	21
5	Puzzling Origins of the Ebola Outbreak in the Democratic Republic of the Congo, 2014. Journal of Virology, 2015, 89, 10130-10132.	3.4	14
6	Antimicrobial Susceptibilities of Escherichia coli Isolates from Food Animals and Wildlife Animals in Sarawak, East Malaysia. Asian Journal of Animal and Veterinary Advances, 2008, 3, 409-416.	0.0	14
7	Detection of Escherichia coli O157:H7 in Wildlife from Disturbed Habitats in Sarawak, Malaysia. Research Journal of Microbiology, 2011, 6, 132-139.	0.2	11
8	Rodent Species Distribution and Hantavirus Seroprevalence in Residential and Forested areas of Sarawak, Malaysia. Tropical Life Sciences Research, 2017, 28, 151-159.	0.9	8
9	Sequencing and characterization of complete mitogenome DNA of Rasbora tornieri (Cypriniformes:) Tj ETQq1 1 C	0.784314 r 0.7	g&T /Overloo
10	Lineage diversification of pigeon paramyxovirus effect re-emergence potential in chickens. Virology, 2014, 462-463, 309-317.	2.4	4
11	Sequencing and characterisation of complete mitogenome DNA for Rasbora sarawakensis (Cypriniformes: Cyprinidae: Rasbora) with phylogenetic consideration. Computational Biology and Chemistry, 2020, 89, 107403.	2.3	4
12	Genomic recombination in primate bocavirus: inconsistency and alternative interpretations. Virus Genes, 2017, 53, 774-777.	1.6	3