

Tommy Tsan-Yuk Lam

List of Publications by Year in Descending Order

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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.

95
papers

18,630
citations

42
h-index

101
g-index

101
ext. papers

24,032
ext. citations

10.6
avg, IF

6.94
L-index

#	Paper	IF	Citations
95	Genomic epidemiology of SARS-CoV-2 under an elimination strategy in Hong Kong.. <i>Nature Communications</i> , 2022 , 13, 736	17.4	3
94	Association between inflammatory cytokines and anti-SARS-CoV-2 antibodies in hospitalized patients with COVID-19.. <i>Immunity and Ageing</i> , 2022 , 19, 12	9.7	2
93	Australia as a global sink for the genetic diversity of avian influenza A virus.. <i>PLoS Pathogens</i> , 2022 , 18, e1010150	7.6	1
92	Transmission dynamics of the COVID-19 epidemic in England. <i>International Journal of Infectious Diseases</i> , 2021 , 104, 132-138	10.5	7
91	Nowcasting epidemics of novel pathogens: lessons from COVID-19. <i>Nature Medicine</i> , 2021 , 27, 388-395	50.5	11
90	SARS-CoV-2 under an elimination strategy in Hong Kong 2021 ,		3
89	Genetic Variation of Multiple Serotypes of Enteroviruses Associated with Hand, Foot and Mouth Disease in Southern China. <i>Virologica Sinica</i> , 2021 , 36, 61-74	6.4	4
88	Genomic characterization of a new CRF01_AE/CRF07_BC case from a MSM patient in Guangdong, China. <i>Journal of Medical Virology</i> , 2021 , 93, 6383-6387	19.7	1
87	Highly Pathogenic Avian Influenza A(H5N6) Virus Clade 2.3.4.4h in Wild Birds and Live Poultry Markets, Bangladesh. <i>Emerging Infectious Diseases</i> , 2021 , 27, 2492-2494	10.2	2
86	Early transmissibility assessment of the N501Y mutant strains of SARS-CoV-2 in the United Kingdom, October to November 2020. <i>Eurosurveillance</i> , 2021 , 26,	19.8	395
85	Virome and Blood Meal-Associated Host Responses in Naturally Fed on Patients.. <i>Frontiers in Microbiology</i> , 2021 , 12, 728996	5.7	0
84	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 12522-12523	11.5	46
83	Comparative seasonalities of influenza A, B and common cold coronaviruses - setting the scene for SARS-CoV-2 infections and possible unexpected host immune interactions. <i>Journal of Infection</i> , 2020 , 81, e62-e64	18.9	5
82	Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins. <i>Nature</i> , 2020 , 583, 282-285	50.4	1012
81	Sequencing and Characterisation of Complete Mitogenome DNA for Rasbora hobelmani (Cyprinidae) with Phylogenetic Consideration. <i>Journal of Ichthyology</i> , 2020 , 60, 90-98	0.7	5
80	Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia. <i>New England Journal of Medicine</i> , 2020 , 382, 1199-1207	59.2	8694
79	Sequencing and Characterisation of Complete Mitochondrial DNA Genome for (Cypriniformes: Cyprinidae: Danioninae) with Phylogenetic Consideration. <i>Tropical Life Sciences Research</i> , 2020 , 31, 107-121	1.1	4

78	Treeio: An R Package for Phylogenetic Tree Input and Output with Richly Annotated and Associated Data. <i>Molecular Biology and Evolution</i> , 2020 , 37, 599-603	8.3	118
77	Sequencing and characterisation of complete mitogenome DNA for <i>Rasbora sarawakensis</i> (Cypriniformes: Cyprinidae: <i>Rasbora</i>) with phylogenetic consideration. <i>Computational Biology and Chemistry</i> , 2020 , 89, 107403	3.6	2
76	Large-Scale Comparative Analyses of Tick Genomes Elucidate Their Genetic Diversity and Vector Capacities. <i>Cell</i> , 2020 , 182, 1328-1340.e13	56.2	57
75	Tracking the Genomic Footprints of SARS-CoV-2 Transmission. <i>Trends in Genetics</i> , 2020 , 36, 544-546	8.5	8
74	Sequencing and characterization of complete mitogenome DNA of <i>Rasbora tornieri</i> (Cypriniformes: Cyprinidae: <i>Rasbora</i>) and its evolutionary significance. <i>Journal of Genetics</i> , 2020 , 99, 1	1.2	3
73	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. <i>Nature Microbiology</i> , 2020 , 5, 1408-1417	26.6	447
72	Sequencing and characterization of complete mitogenome DNA for <i>Rasbora myersi</i> (Cypriniformes: Cyprinidae: <i>Rasbora</i>) and its evolutionary significance. <i>Gene Reports</i> , 2019 , 17, 100499	1.4	4
71	Emergence of human infection with Jingmen tick virus in China: A retrospective study. <i>EBioMedicine</i> , 2019 , 43, 317-324	8.8	41
70	Comparative global epidemiology of influenza, respiratory syncytial and parainfluenza viruses, 2010-2015. <i>Journal of Infection</i> , 2019 , 79, 373-382	18.9	34
69	Neuraminidase inhibitor susceptibility and evolutionary analysis of human influenza B isolates from three Asian countries during 2012-2015. <i>Infection, Genetics and Evolution</i> , 2018 , 62, 27-33	4.5	1
68	Large-Scale Complete-Genome Sequencing and Phylodynamic Analysis of Eastern Equine Encephalitis Virus Reveals Source-Sink Transmission Dynamics in the United States. <i>Journal of Virology</i> , 2018 , 92,	6.6	20
67	Geographically weighted temporally correlated logistic regression model. <i>Scientific Reports</i> , 2018 , 8, 1417	4.9	10
66	Genomic surveillance of avian-origin influenza A viruses causing human disease. <i>Genome Medicine</i> , 2018 , 10, 50	14.4	4
65	A cluster of Zika virus infection among travellers returning to China from Samoa: a case tracing study. <i>Journal of Travel Medicine</i> , 2018 , 25,	12.9	9
64	The impact of host genetic diversity on virus evolution and emergence. <i>Ecology Letters</i> , 2018 , 21, 253-263	10	12
63	Two Methods for Mapping and Visualizing Associated Data on Phylogeny Using Ggtree. <i>Molecular Biology and Evolution</i> , 2018 , 35, 3041-3043	8.3	223
62	Global epidemiology of non-influenza RNA respiratory viruses: data gaps and a growing need for surveillance. <i>Lancet Infectious Diseases</i> , 2017 , 17, e320-e326	25.5	68
61	A7 Evolution of influenza A(H7N9) viruses from waves I to IV. <i>Virus Evolution</i> , 2017 , 3,	3.7	1

60	ggtree: an r package for visualization and annotation of phylogenetic trees with their covariates and other associated data. <i>Methods in Ecology and Evolution</i> , 2017 , 8, 28-36	7.7	1399
59	Exploring the temporal structure of heterochronous sequences using TempEst (formerly Path-O-Gen). <i>Virus Evolution</i> , 2016 , 2, vew007	3.7	961
58	Genomic Analysis of the Emergence, Evolution, and Spread of Human Respiratory RNA Viruses. <i>Annual Review of Genomics and Human Genetics</i> , 2016 , 17, 193-218	9.7	26
57	Infectivity and Transmissibility of Avian H9N2 Influenza Viruses in Pigs. <i>Journal of Virology</i> , 2016 , 90, 3506-14	6.6	21
56	Molecular Evolution and Intraclade Recombination of Enterovirus D68 during the 2014 Outbreak in the United States. <i>Journal of Virology</i> , 2016 , 90, 1997-2007	6.6	45
55	Emergence and development of H7N9 influenza viruses in China. <i>Current Opinion in Virology</i> , 2016 , 16, 106-113	7.5	40
54	Co-circulation of three camel coronavirus species and recombination of MERS-CoVs in Saudi Arabia. <i>Science</i> , 2016 , 351, 81-4	33.3	276
53	Genetic characterization of highly pathogenic H5 influenza viruses from poultry in Taiwan, 2015. <i>Infection, Genetics and Evolution</i> , 2016 , 38, 96-100	4.5	12
52	Emergence and evolution of H10 subtype influenza viruses in poultry in China. <i>Journal of Virology</i> , 2015 , 89, 3534-41	6.6	52
51	Dissemination, divergence and establishment of H7N9 influenza viruses in China. <i>Nature</i> , 2015 , 522, 102-5.4	5.4	165
50	Molecular Epidemiology and Evolution of Influenza Viruses Circulating within European Swine between 2009 and 2013. <i>Journal of Virology</i> , 2015 , 89, 9920-31	6.6	113
49	Puzzling Origins of the Ebola Outbreak in the Democratic Republic of the Congo, 2014. <i>Journal of Virology</i> , 2015 , 89, 10130-2	6.6	12
48	Epidemiological and Evolutionary Dynamics of Influenza B Viruses in Malaysia, 2012-2014. <i>PLoS ONE</i> , 2015 , 10, e0136254	3.7	22
47	Emergence and evolution of avian H5N2 influenza viruses in chickens in Taiwan. <i>Journal of Virology</i> , 2014 , 88, 5677-86	6.6	40
46	Increasing similarity in the dynamics of influenza in two adjacent subtropical Chinese cities following the relaxation of border restrictions. <i>Journal of General Virology</i> , 2014 , 95, 531-538	4.9	11
45	Occurrence and reassortment of avian influenza A (H7N9) viruses derived from coinfecting birds in China. <i>Journal of Virology</i> , 2014 , 88, 13344-51	6.6	13
44	Diffusion of influenza viruses among migratory birds with a focus on the Southwest United States. <i>Infection, Genetics and Evolution</i> , 2014 , 26, 185-93	4.5	11
43	Expansion of genotypic diversity and establishment of 2009 H1N1 pandemic-origin internal genes in pigs in China. <i>Journal of Virology</i> , 2014 , 88, 10864-74	6.6	60

42	The genesis and source of the H7N9 influenza viruses causing human infections in China. <i>Nature</i> , 2013 , 502, 241-4	50.4	337
41	Viral evolution explains the associations among hepatitis C virus genotype, clinical outcomes, and human genetic variation. <i>Infection, Genetics and Evolution</i> , 2013 , 20, 418-21	4.5	11
40	Differing epidemiological dynamics of influenza B virus lineages in Guangzhou, southern China, 2009-2010. <i>Journal of Virology</i> , 2013 , 87, 12447-56	6.6	51
39	Effect of probiotic bacteria on the intestinal microbiota in irritable bowel syndrome. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2013 , 28, 1624-31	4	60
38	The evolutionary dynamics of influenza A virus adaptation to mammalian hosts. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013 , 368, 20120382	5.8	35
37	Systematic phylogenetic analysis of influenza A virus reveals many novel mosaic genome segments. <i>Infection, Genetics and Evolution</i> , 2013 , 18, 367-78	4.5	18
36	Evolutionary and molecular analysis of the emergent severe fever with thrombocytopenia syndrome virus. <i>Epidemics</i> , 2013 , 5, 1-10	5.1	65
35	Successful establishment and global dispersal of genotype VI avian paramyxovirus serotype 1 after cross species transmission. <i>Infection, Genetics and Evolution</i> , 2013 , 17, 260-8	4.5	20
34	Full-genome deep sequencing and phylogenetic analysis of novel human betacoronavirus. <i>Emerging Infectious Diseases</i> , 2013 , 19, 736-42B	10.2	117
33	Migration and persistence of human influenza A viruses, Vietnam, 2001-2008. <i>Emerging Infectious Diseases</i> , 2013 , 19, 1756-65	10.2	14
32	Epidemiological dynamics and phylogeography of influenza virus in southern China. <i>Journal of Infectious Diseases</i> , 2013 , 207, 106-14	7	39
31	The rapidly expanding CRF01_AE epidemic in China is driven by multiple lineages of HIV-1 viruses introduced in the 1990s. <i>Aids</i> , 2013 , 27, 1793-802	3.5	142
30	Molecular characterization of the fecal microbiota in patients with nonalcoholic steatohepatitis--a longitudinal study. <i>PLoS ONE</i> , 2013 , 8, e62885	3.7	205
29	History of Swine influenza viruses in Asia. <i>Current Topics in Microbiology and Immunology</i> , 2013 , 370, 57-68	3.3	42
28	Comparison of mutation patterns in full-genome A/H3N2 influenza sequences obtained directly from clinical samples and the same samples after a single MDCK passage. <i>PLoS ONE</i> , 2013 , 8, e79252	3.7	42
27	Phylogenetics of H5N1 avian influenza virus in Indonesia. <i>Molecular Ecology</i> , 2012 , 21, 3062-77	5.7	28
26	Migratory flyway and geographical distance are barriers to the gene flow of influenza virus among North American birds. <i>Ecology Letters</i> , 2012 , 15, 24-33	10	76
25	The recombinant origin of emerging human norovirus GII.4/2008: intra-genotypic exchange of the capsid P2 domain. <i>Journal of General Virology</i> , 2012 , 93, 817-822	4.9	22

24	Emergence and dissemination of a swine H3N2 reassortant influenza virus with 2009 pandemic H1N1 genes in pigs in China. <i>Journal of Virology</i> , 2012 , 86, 2375-8	6.6	49
23	Genetic characterization and evolutionary analysis of 4 Newcastle disease virus isolate full genomes from waterbirds in South China during 2003-2007. <i>Veterinary Microbiology</i> , 2011 , 152, 46-54	3.3	26
22	Phylogeography of the spring and fall waves of the H1N1/09 pandemic influenza virus in the United States. <i>Journal of Virology</i> , 2011 , 85, 828-34	6.6	46
21	Reassortment events among swine influenza A viruses in China: implications for the origin of the 2009 influenza pandemic. <i>Journal of Virology</i> , 2011 , 85, 10279-85	6.6	50
20	Novel reassortment of Eurasian avian-like and pandemic/2009 influenza viruses in swine: infectious potential for humans. <i>Journal of Virology</i> , 2011 , 85, 10432-9	6.6	69
19	Spatial dynamics of human-origin H1 influenza A virus in North American swine. <i>PLoS Pathogens</i> , 2011 , 7, e1002077	7.6	101
18	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010 , 463, 311-7	50.4	864
17	Intraspecies diversity of SARS-like coronaviruses in <i>Rhinolophus sinicus</i> and its implications for the origin of SARS coronaviruses in humans. <i>Journal of General Virology</i> , 2010 , 91, 1058-62	4.9	84
16	Evolutionary genetics of human enterovirus 71: origin, population dynamics, natural selection, and seasonal periodicity of the VP1 gene. <i>Journal of Virology</i> , 2010 , 84, 3339-50	6.6	182
15	Phylogeny-based evolutionary, demographical, and geographical dissection of North American type 2 porcine reproductive and respiratory syndrome viruses. <i>Journal of Virology</i> , 2010 , 84, 8700-11	6.6	238
14	Emerging, novel, and known influenza virus infections in humans. <i>Infectious Disease Clinics of North America</i> , 2010 , 24, 603-17	6.5	25
13	Use of phylogenetics in the molecular epidemiology and evolutionary studies of viral infections. <i>Critical Reviews in Clinical Laboratory Sciences</i> , 2010 , 47, 5-49	9.4	48
12	Molecular epidemiology of PRRSV: a phylogenetic perspective. <i>Virus Research</i> , 2010 , 154, 7-17	6.4	227
11	The ever-expanding diversity of porcine reproductive and respiratory syndrome virus. <i>Virus Research</i> , 2010 , 154, 18-30	6.4	220
10	Features of the new pandemic influenza A/H1N1/2009 virus: virology, epidemiology, clinical and public health aspects. <i>Current Opinion in Pulmonary Medicine</i> , 2010 , 16, 235-41	3	29
9	Phylogenetic perspectives on the epidemiology and origins of SARS and SARS-like coronaviruses. <i>Infection, Genetics and Evolution</i> , 2009 , 9, 1185-96	4.5	31
8	Comments to the predecessor of human SARS coronavirus in 2003-2004 epidemic. <i>Veterinary Microbiology</i> , 2008 , 126, 390-3	3.3	5
7	Evolutionary analyses of European H1N2 swine influenza A virus by placing timestamps on the multiple reassortment events. <i>Virus Research</i> , 2008 , 131, 271-8	6.4	21

6	Evolutionary and transmission dynamics of reassortant H5N1 influenza virus in Indonesia. <i>PLoS Pathogens</i> , 2008 , 4, e1000130	7.6	52
5	Evidence of the recombinant origin of a bat severe acute respiratory syndrome (SARS)-like coronavirus and its implications on the direct ancestor of SARS coronavirus. <i>Journal of Virology</i> , 2008 , 82, 1819-26	6.6	152
4	Phylogenetic evidence for homologous recombination within the family Birnaviridae. <i>Journal of General Virology</i> , 2008 , 89, 3156-3164	4.9	39
3	Evidence for recombination in natural populations of porcine circovirus type 2 in Hong Kong and mainland China. <i>Journal of General Virology</i> , 2007 , 88, 1733-1737	4.9	55
2	Phylogenetic analysis reveals a correlation between the expansion of very virulent infectious bursal disease virus and reassortment of its genome segment B. <i>Journal of Virology</i> , 2006 , 80, 8503-9	6.6	91
1	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic		54