

# Tommy Tsan-Yuk Lam

## List of Publications by Year in descending order

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97  
papers

27,625  
citations

46918

47  
h-index

37111

96  
g-index

101  
all docs

101  
docs citations

101  
times ranked

47140  
citing authors

#	ARTICLE	IF	CITATIONS
1	Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia. <i>New England Journal of Medicine</i> , 2020, 382, 1199-1207.	13.9	12,326
2	<code>ggtree</code> : an <code>r</code> 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.	2.2	2,998
3	Exploring the temporal structure of heterochronous sequences using TempEst (formerly Path-O-Gen). <i>Virus Evolution</i> , 2016, 2, vew007.	2.2	1,638
4	Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins. <i>Nature</i> , 2020, 583, 282-285.	13.7	1,453
5	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	13.7	1,058
6	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. <i>Nature Microbiology</i> , 2020, 5, 1408-1417.	5.9	772
7	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, .	3.9	584
8	Two Methods for Mapping and Visualizing Associated Data on Phylogeny Using <code>Ggtree</code> . <i>Molecular Biology and Evolution</i> , 2018, 35, 3041-3043.	3.5	535
9	The genesis and source of the H7N9 influenza viruses causing human infections in China. <i>Nature</i> , 2013, 502, 241-244.	13.7	429
10	Co-circulation of three camel coronavirus species and recombination of MERS-CoVs in Saudi Arabia. <i>Science</i> , 2016, 351, 81-84.	6.0	365
11	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.	3.5	348
12	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, 8700-8711.	1.5	321
13	Molecular epidemiology of PRRSV: A phylogenetic perspective. <i>Virus Research</i> , 2010, 154, 7-17.	1.1	300
14	Molecular Characterization of the Fecal Microbiota in Patients with Nonalcoholic Steatohepatitis – A Longitudinal Study. <i>PLoS ONE</i> , 2013, 8, e62885.	1.1	266
15	The ever-expanding diversity of porcine reproductive and respiratory syndrome virus. <i>Virus Research</i> , 2010, 154, 18-30.	1.1	263
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, 3339-3350.	1.5	211
17	Dissemination, divergence and establishment of H7N9 influenza viruses in China. <i>Nature</i> , 2015, 522, 102-105.	13.7	201
18	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, 1819-1826.	1.5	197

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19	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, 1793-1802.	1.0	171
20	Molecular Epidemiology and Evolution of Influenza Viruses Circulating within European Swine between 2009 and 2013. <i>Journal of Virology</i> , 2015, 89, 9920-9931.	1.5	148
21	Large-Scale Comparative Analyses of Tick Genomes Elucidate Their Genetic Diversity and Vector Capacities. <i>Cell</i> , 2020, 182, 1328-1340.e13.	13.5	145
22	Full-Genome Deep Sequencing and Phylogenetic Analysis of Novel Human Betacoronavirus. <i>Emerging Infectious Diseases</i> , 2013, 19, 736-42B.	2.0	131
23	Spatial Dynamics of Human-Origin H1 Influenza A Virus in North American Swine. <i>PLoS Pathogens</i> , 2011, 7, e1002077.	2.1	116
24	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, 8503-8509.	1.5	100
25	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, 1058-1062.	1.3	96
26	Global epidemiology of non-influenza RNA respiratory viruses: data gaps and a growing need for surveillance. <i>Lancet Infectious Diseases</i> , The, 2017, 17, e320-e326.	4.6	92
27	Emergence of human infection with Jingmen tick virus in China: A retrospective study. <i>EBioMedicine</i> , 2019, 43, 317-324.	2.7	91
28	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.	3.0	86
29	Evolutionary and molecular analysis of the emergent severe fever with thrombocytopenia syndrome virus. <i>Epidemics</i> , 2013, 5, 1-10.	1.5	84
30	Novel Reassortment of Eurasian Avian-Like and Pandemic/2009 Influenza Viruses in Swine: Infectious Potential for Humans. <i>Journal of Virology</i> , 2011, 85, 10432-10439.	1.5	80
31	Effect of probiotic bacteria on the intestinal microbiota in irritable bowel syndrome. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2013, 28, 1624-1631.	1.4	79
32	Expansion of Genotypic Diversity and Establishment of 2009 H1N1 Pandemic-Origin Internal Genes in Pigs in China. <i>Journal of Virology</i> , 2014, 88, 10864-10874.	1.5	79
33	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.	3.3	68
34	Emergence and Evolution of Avian H5N2 Influenza Viruses in Chickens in Taiwan. <i>Journal of Virology</i> , 2014, 88, 5677-5686.	1.5	66
35	Evolutionary and Transmission Dynamics of Reassortant H5N1 Influenza Virus in Indonesia. <i>PLoS Pathogens</i> , 2008, 4, e1000130.	2.1	61
36	Emergence and Evolution of H10 Subtype Influenza Viruses in Poultry in China. <i>Journal of Virology</i> , 2015, 89, 3534-3541.	1.5	61

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37	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.	1.5	59
38	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.	1.3	57
39	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, 10279-10285.	1.5	57
40	Differing Epidemiological Dynamics of Influenza B Virus Lineages in Guangzhou, Southern China, 2009-2010. <i>Journal of Virology</i> , 2013, 87, 12447-12456.	1.5	57
41	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.	1.1	57
42	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.	2.7	56
43	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, 828-834.	1.5	54
44	Comparative global epidemiology of influenza, respiratory syncytial and parainfluenza viruses, 2010-2015. <i>Journal of Infection</i> , 2019, 79, 373-382.	1.7	53
45	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, 2375-2378.	1.5	52
46	Emergence and development of H7N9 influenza viruses in China. <i>Current Opinion in Virology</i> , 2016, 16, 106-113.	2.6	50
47	Phylogenetic evidence for homologous recombination within the family Birnaviridae. <i>Journal of General Virology</i> , 2008, 89, 3156-3164.	1.3	48
48	History of Swine Influenza Viruses in Asia. <i>Current Topics in Microbiology and Immunology</i> , 2011, 370, 57-68.	0.7	47
49	Epidemiological Dynamics and Phylogeography of Influenza Virus in Southern China. <i>Journal of Infectious Diseases</i> , 2013, 207, 106-114.	1.9	41
50	Phylogenetic perspectives on the epidemiology and origins of SARS and SARS-like coronaviruses. <i>Infection, Genetics and Evolution</i> , 2009, 9, 1185-1196.	1.0	40
51	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.	1.8	40
52	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.	2.5	38
53	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	9.0	35
54	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, 235-241.	1.2	33

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55	Phylodynamics of H5N1 avian influenza virus in Indonesia. <i>Molecular Ecology</i> , 2012, 21, 3062-3077.	2.0	33
56	The impact of host genetic diversity on virus evolution and emergence. <i>Ecology Letters</i> , 2018, 21, 253-263.	3.0	33
57	Emerging, Novel, and Known Influenza Virus Infections in Humans. <i>Infectious Disease Clinics of North America</i> , 2010, 24, 603-617.	1.9	32
58	Nowcasting epidemics of novel pathogens: lessons from COVID-19. <i>Nature Medicine</i> , 2021, 27, 388-395.	15.2	32
59	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, .	1.5	31
60	Infectivity and Transmissibility of Avian H9N2 Influenza Viruses in Pigs. <i>Journal of Virology</i> , 2016, 90, 3506-3514.	1.5	29
61	Genetic characterization and evolutionary analysis of 4 Newcastle disease virus isolate full genomes from waterbirds in South China during 2003â€“2007. <i>Veterinary Microbiology</i> , 2011, 152, 46-54.	0.8	27
62	Genomic epidemiology of SARS-CoV-2 under an elimination strategy in Hong Kong. <i>Nature Communications</i> , 2022, 13, 736.	5.8	26
63	Evolutionary analyses of European H1N2 swine influenza A virus by placing timestamps on the multiple reassortment events. <i>Virus Research</i> , 2008, 131, 271-278.	1.1	24
64	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.	1.3	24
65	Epidemiological and Evolutionary Dynamics of Influenza B Viruses in Malaysia, 2012-2014. <i>PLoS ONE</i> , 2015, 10, e0136254.	1.1	24
66	Successful establishment and global dispersal of genotype VI avian paramyxovirus serotype 1 after cross species transmission. <i>Infection, Genetics and Evolution</i> , 2013, 17, 260-268.	1.0	23
67	Association between inflammatory cytokines and anti-SARS-CoV-2 antibodies in hospitalized patients with COVID-19. <i>Immunity and Ageing</i> , 2022, 19, 12.	1.8	23
68	Systematic phylogenetic analysis of influenza A virus reveals many novel mosaic genome segments. <i>Infection, Genetics and Evolution</i> , 2013, 18, 367-378.	1.0	21
69	Geographically weighted temporally correlated logistic regression model. <i>Scientific Reports</i> , 2018, 8, 1417.	1.6	21
70	Occurrence and Reassortment of Avian Influenza A (H7N9) Viruses Derived from Coinfected Birds in China. <i>Journal of Virology</i> , 2014, 88, 13344-13351.	1.5	20
71	Migration and Persistence of Human Influenza A Viruses, Vietnam, 2001â€“2008. <i>Emerging Infectious Diseases</i> , 2013, 19, 1756-1765.	2.0	16
72	Genetic characterization of highly pathogenic H5 influenza viruses from poultry in Taiwan, 2015. <i>Infection, Genetics and Evolution</i> , 2016, 38, 96-100.	1.0	15

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73	Viral evolution explains the associations among hepatitis C virus genotype, clinical outcomes, and human genetic variation. <i>Infection, Genetics and Evolution</i> , 2013, 20, 418-421.	1.0	14
74	Puzzling Origins of the Ebola Outbreak in the Democratic Republic of the Congo, 2014. <i>Journal of Virology</i> , 2015, 89, 10130-10132.	1.5	14
75	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.	1.3	13
76	Diffusion of influenza viruses among migratory birds with a focus on the Southwest United States. <i>Infection, Genetics and Evolution</i> , 2014, 26, 185-193.	1.0	13
77	Tracking the Genomic Footprints of SARS-CoV-2 Transmission. <i>Trends in Genetics</i> , 2020, 36, 544-546.	2.9	12
78	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.	1.2	11
79	Transmission dynamics of the COVID-19 epidemic in England. <i>International Journal of Infectious Diseases</i> , 2021, 104, 132-138.	1.5	11
80	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, .	1.4	10
81	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.	1.7	9
82	Australia as a global sink for the genetic diversity of avian influenza A virus. <i>PLoS Pathogens</i> , 2022, 18, e1010150.	2.1	9
83	Sequencing and Characterisation of Complete Mitogenome DNA for <i>Rasbora hobelmani</i> (Cyprinidae) with Phylogenetic Consideration. <i>Journal of Ichthyology</i> , 2020, 60, 90-98.	0.2	8
84	Genomic surveillance of avian-origin influenza A viruses causing human disease. <i>Genome Medicine</i> , 2018, 10, 50.	3.6	7
85	Sequencing and characterization of complete mitogenome DNA of <i>Rasbora tornieri</i> (Cypriniformes: Cyprinidae) with Phylogenetic Consideration. <i>Tropical Life Sciences Research</i> , 2020, 31, 107-121.	0.4	6
86	Comments to the predecessor of human SARS coronavirus in 2003"2004 epidemic. <i>Veterinary Microbiology</i> , 2008, 126, 390-393.	0.8	5
87	Sequencing and characterization of complete mitogenome DNA for <i>Rasbora myersi</i> (Cypriniformes: Cyprinidae) with Phylogenetic Consideration. <i>Tropical Life Sciences Research</i> , 2020, 31, 107-121.	0.4	5
88	Sequencing and Characterisation of Complete Mitochondrial DNA Genome for <i>Trigonopoma pauciperforatum</i> (Cypriniformes: Cyprinidae: Danioninae) with Phylogenetic Consideration. <i>Tropical Life Sciences Research</i> , 2020, 31, 107-121.	0.5	5
89	Sequencing and characterisation of complete mitogenome DNA for <i>Rasbora sarawakensis</i> (Cypriniformes: Cyprinidae: Rasbora) with phylogenetic consideration. <i>Computational Biology and Chemistry</i> , 2020, 89, 107403.	1.1	4
90	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.	2.5	4

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91	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.	2.0	4
92	Virome and Blood Meal-Associated Host Responses in <i>Ixodes persulcatus</i> Naturally Fed on Patients. <i>Frontiers in Microbiology</i> , 2021, 12, 728996.	1.5	4
93	Editorial: Biomedical Data Visualization: Methods and Applications. <i>Frontiers in Genetics</i> , 2022, 13, 890775.	1.1	2
94	A7â€fEvolution of influenza A(H7N9) viruses from waves I to IV. <i>Virus Evolution</i> , 2017, 3, .	2.2	1
95	Neuraminidase inhibitor susceptibility and evolutionary analysis of human influenza B isolates from three Asian countries during 2012â€“2015. <i>Infection, Genetics and Evolution</i> , 2018, 62, 27-33.	1.0	1
96	Molecular Epidemiology of H5N1 Avian Influenza Virus: Correlations between Antigenic Drift, Geographical Migration and Expansion of Viral Diversity. <i>International Journal of Infectious Diseases</i> , 2008, 12, e58-e59.	1.5	0
97	A24â€fApplication of large-scale sequencing and data analysis to research on emerging infectious diseases. <i>Virus Evolution</i> , 2017, 3, .	2.2	0