Art F Y Poon

List of Publications by Year in Descending Order

98 papers	3,619 citations	30 h-index	58 g-index
109 ext. papers	4,409 ext. citations	5.7 avg, IF	5.49 L-index

#	Paper	IF	Citations
98	Using networks to analyze and visualize the distribution of overlapping genes in virus genomes.. *PLoS Pathogens*, **2022**, 18, e1010331	7.6	2
97	Revisiting the recombinant history of HIV-1 group M with dynamic network community detection.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119, e2108815119	11.5	
96	Quantifying the clonality and dynamics of the within-host HIV-1 latent reservoir. *Virus Evolution*, **2021**, 7, veaa104	3.7	1
95	Tuning intrinsic disorder predictors for virus proteins. *Virus Evolution*, **2021**, 7, veaa106	3.7	1
94	Network science inspires novel tree shape statistics.. *PLoS ONE*, **2021**, 16, e0259877	3.7	0
93	Genetic Diversity, Compartmentalization, and Age of HIV Proviruses Persisting in CD4 T Cell Subsets during Long-Term Combination Antiretroviral Therapy. *Journal of Virology*, **2020**, 94,	6.6	9
92	Public health in genetic spaces: a statistical framework to optimize cluster-based outbreak detection. *Virus Evolution*, **2020**, 6, veaa011	3.7	4
91	Addressing Ethical Challenges in US-Based HIV Phylogenetic Research. *Journal of Infectious Diseases*, **2020**, 222, 1997-2006	7	20
90	A targeted reactivation of latent HIV-1 using an activator vector in patient samples from acute infection. *EBioMedicine*, **2020**, 59, 102853	8.8	5
89	Accumulation of integrase strand transfer inhibitor resistance mutations confers high-level resistance to dolutegravir in non-B subtype HIV-1 strains from patients failing raltegravir in Uganda. *Journal of Antimicrobial Chemotherapy*, **2020**, 75, 3525-3533	5.1	3
88	HyPhy 2.5-A Customizable Platform for Evolutionary Hypothesis Testing Using Phylogenies. *Molecular Biology and Evolution*, **2020**, 37, 295-299	8.3	111
87	Evidence for a recombinant origin of HIV-1 Group M from genomic variation. *Virus Evolution*, **2019**, 5, vey039	3.7	6
86	First-line HIV treatment failures in non-B subtypes and recombinants: a cross-sectional analysis of multiple populations in Uganda. *AIDS Research and Therapy*, **2019**, 16, 3	3	3
85	HIV Diversity and Genetic Compartmentalization in Blood and Testes during Suppressive Antiretroviral Therapy. *Journal of Virology*, **2019**, 93,	6.6	17
84	Role of co-expressed APOBEC3F and APOBEC3G in inducing HIV-1 drug resistance. *Heliyon*, **2019**, 5, e01498	3.3	6
83	Phylogenetic measures of indel rate variation among the HIV-1 group M subtypes. *Virus Evolution*, **2019**, 5, vez022	3.7	2
82	Tree shape-based approaches for the comparative study of cophylogeny. *Ecology and Evolution*, **2019**, 9, 6756-6771	2.8	8

81	sierra-local: A lightweight standalone application for drug resistance prediction. *Journal of Open Source Software*, **2019**, 4, 1186	5.2	2
80	Comparative analysis of HIV sequences in real time for public health. *Current Opinion in HIV and AIDS*, **2019**, 14, 213-220	4.2	13
79	A systematic, deep sequencing-based methodology for identification of mixed-genotype hepatitis C virus infections. *Infection, Genetics and Evolution*, **2019**, 69, 76-84	4.5	5
78	Detecting Amino Acid Coevolution with Bayesian Graphical Models. *Methods in Molecular Biology*, **2019**, 1851, 105-122	1.4	3
77	Genetic Cluster Analysis for HIV Prevention. *Current HIV/AIDS Reports*, **2018**, 15, 182-189	5.9	26
76	What Proportion of HIV-Infected Foreign-Born Individuals in the United States Have Been Infected After Immigrating to the United States?. *Journal of Acquired Immune Deficiency Syndromes (1999)*, **2018**, 77, e35-e36	3.1	2
75	Absence of HIV-1 Drug Resistance Mutations Supports the Use of Dolutegravir in Uganda. *AIDS Research and Human Retroviruses*, **2018**, 34, 404-414	1.6	13
74	Quantitation of the latent HIV-1 reservoir from the sequence diversity in viral outgrowth assays. *Retrovirology*, **2018**, 15, 47	3.6	2
73	HIV-1 Transmission Clustering and Phylodynamics Highlight the Important Role of Young Men Who Have Sex with Men. *AIDS Research and Human Retroviruses*, **2018**, 34, 879-888	1.6	14
72	Higher sequence diversity in the vaginal tract than in blood at early HIV-1 infection. *PLoS Pathogens*, **2018**, 14, e1006754	7.6	15
71	An open-source k-mer based machine learning tool for fast and accurate subtyping of HIV-1 genomes. *PLoS ONE*, **2018**, 13, e0206409	3.7	36
70	Phylogenetic approach to recover integration dates of latent HIV sequences within-host. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E8958-E8967	11.5	23
69	node.dating: dating ancestors in phylogenetic trees in R. *Bioinformatics*, **2017**, 33, 932-934	7.2	11
68	Genotypic susceptibility score (GSS) and CD4+ T cell recovery in HIV-1 patients with suppressed viral load. *Journal of Antimicrobial Chemotherapy*, **2017**, 72, 496-503	5.1	2
67	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. *Molecular Biology and Evolution*, **2017**, 34, 185-203	8.3	41
66	Promises and pitfalls of Illumina sequencing for HIV resistance genotyping. *Virus Research*, **2017**, 239, 97-105	6.4	18
65	A model-based clustering method to detect infectious disease transmission outbreaks from sequence variation. *PLoS Computational Biology*, **2017**, 13, e1005868	5	15
64	Sensitive detection of HIV-1 resistance to Zidovudine and impact on treatment outcomes in low- to middle-income countries. *Infectious Diseases of Poverty*, **2017**, 6, 163	10.4	6

63	Potential for immune-driven viral polymorphisms to compromise antiretroviral-based preexposure prophylaxis for prevention of HIV-1 infection. *Aids*, **2017**, 31, 1935-1943	3.5	6
62	Reconstructing contact network parameters from viral phylogenies. *Virus Evolution*, **2016**, 2, vew029	3.7	7
61	Deep sequencing increases hepatitis C virus phylogenetic cluster detection compared to Sanger sequencing. *Infection, Genetics and Evolution*, **2016**, 43, 329-37	4.5	12
60	Population-Level Immune-Mediated Adaptation in HIV-1 Polymerase during the North American Epidemic. *Journal of Virology*, **2016**, 90, 1244-58	6.6	9
59	Ancestral Reconstruction. *PLoS Computational Biology*, **2016**, 12, e1004763	5	84
58	Impacts and shortcomings of genetic clustering methods for infectious disease outbreaks. *Virus Evolution*, **2016**, 2, vew031	3.7	49
57	The spread of hepatitis C virus genotype 1a in North America: a retrospective phylogenetic study. *Lancet Infectious Diseases, The*, **2016**, 16, 698-702	25.5	35
56	Near real-time monitoring of HIV transmission hotspots from routine HIV genotyping: an implementation case study. *Lancet HIV,the*, **2016**, 3, e231-8	7.8	122
55	The impact of clinical, demographic and risk factors on rates of HIV transmission: a population-based phylogenetic analysis in British Columbia, Canada. *Journal of Infectious Diseases*, **2015**, 211, 926-35	7	73
54	A molecular phylogenetics-based approach for identifying recent hepatitis C virus transmission events. *Infection, Genetics and Evolution*, **2015**, 33, 101-9	4.5	18
53	Phylodynamic Inference with Kernel ABC and Its Application to HIV Epidemiology. *Molecular Biology and Evolution*, **2015**, 32, 2483-95	8.3	30
52	Global Database-Driven Assessment of HIV-1 Adaptation to the Immune Repertoires of Human Populations. *Journal of Virology*, **2015**, 89, 10693-5	6.6	5
51	Global origin and transmission of hepatitis C virus nonstructural protein 3 Q80K polymorphism. *Journal of Infectious Diseases*, **2015**, 211, 1288-95	7	42
50	Differential evolution of a CXCR4-using HIV-1 strain in CCR5wt/wt and CCR5Δ2/Δ2 hosts revealed by longitudinal deep sequencing and phylogenetic reconstruction. *Scientific Reports*, **2015**, 5, 17607	4.9	9
49	Origin and Evolution of Human Immunodeficiency Viruses **2015**, 587-611		3
48	"Deep" sequencing accuracy and reproducibility using Roche/454 technology for inferring co-receptor usage in HIV-1. *PLoS ONE*, **2014**, 9, e99508	3.7	9
47	Genotypic and functional impact of HIV-1 adaptation to its host population during the North American epidemic. *PLoS Genetics*, **2014**, 10, e1004295	6	34
46	Theoretical and experimental assessment of degenerate primer tagging in ultra-deep applications of next-generation sequencing. *Nucleic Acids Research*, **2014**, 42, e98	20.1	27

45	An evaluation of phylogenetic methods for reconstructing transmitted HIV variants using longitudinal clonal HIV sequence data. *Journal of Virology*, **2014**, 88, 6181-94	6.6	9
44	Comparison of population and 454 "deep" sequence analysis for HIV type 1 tropism versus the original trofile assay in non-B subtypes. *AIDS Research and Human Retroviruses*, **2013**, 29, 979-84	1.6	15
43	Use of cellular HIV DNA to predict virologic response to maraviroc: performance of population-based and deep sequencing. *Clinical Infectious Diseases*, **2013**, 56, 1659-66	11.6	27
42	Maraviroc treatment in non-R5-HIV-1-infected patients results in the selection of extreme CXCR4-using variants with limited effect on the total viral setpoint. *Journal of Antimicrobial Chemotherapy*, **2013**, 68, 2007-14	5.1	6
41	Factors influencing the sensitivity and specificity of conventional sequencing in human immunodeficiency virus type 1 tropism testing. *Journal of Clinical Microbiology*, **2013**, 51, 444-51	9.7	11
40	Replication fitness of multiple nonnucleoside reverse transcriptase-resistant HIV-1 variants in the presence of etravirine measured by 454 deep sequencing. *Journal of Virology*, **2013**, 87, 8805-7	6.6	8
39	Mapping the shapes of phylogenetic trees from human and zoonotic RNA viruses. *PLoS ONE*, **2013**, 8, e78122	3.7	28
38	Evolution of viral genomes: interplay between selection, recombination, and other forces. *Methods in Molecular Biology*, **2012**, 856, 239-72	1.4	13
37	Characterizing HIV transmission networks across the United States. *Clinical Infectious Diseases*, **2012**, 55, 1135-43	11.6	98
36	Reconstructing the dynamics of HIV evolution within hosts from serial deep sequence data. *PLoS Computational Biology*, **2012**, 8, e1002753	5	37
35	Prolonged and substantial discordance in prevalence of raltegravir-resistant HIV-1 in plasma versus PBMC samples revealed by 454 "deep" sequencing. *PLoS ONE*, **2012**, 7, e46181	3.7	13
34	HIV-1 nef protein structures associated with brain infection and dementia pathogenesis. *PLoS ONE*, **2011**, 6, e16659	3.7	26
33	Transmitted drug resistance in the CFAR network of integrated clinical systems cohort: prevalence and effects on pre-therapy CD4 and viral load. *PLoS ONE*, **2011**, 6, e21189	3.7	28
32	Dates of HIV infection can be estimated for seroprevalent patients by coalescent analysis of serial next-generation sequencing data. *Aids*, **2011**, 25, 2019-26	3.5	25
31	In vitro selection of clinically relevant bevirimat resistance mutations revealed by "deep" sequencing of serially passaged, quasispecies-containing recombinant HIV-1. *Journal of Clinical Microbiology*, **2011**, 49, 201-8	9.7	13
30	Selection in coastal Synechococcus (cyanobacteria) populations evaluated from environmental metagenomes. *PLoS ONE*, **2011**, 6, e24249	3.7	15
29	Datamonkey 2010: a suite of phylogenetic analysis tools for evolutionary biology. *Bioinformatics*, **2010**, 26, 2455-7	7.2	942
28	Evolutionary fingerprinting of genes. *Molecular Biology and Evolution*, **2010**, 27, 520-36	8.3	55

27	Phylogenetic analysis of population-based and deep sequencing data to identify coevolving sites in the nef gene of HIV-1. *Molecular Biology and Evolution*, **2010**, 27, 819-32	8.3	55
26	An evolutionary model-based algorithm for accurate phylogenetic breakpoint mapping and subtype prediction in HIV-1. *PLoS Computational Biology*, **2009**, 5, e1000581	5	130
25	A novel codon insert in protease of clade B HIV type 1. *AIDS Research and Human Retroviruses*, **2009**, 25, 547-50	1.6	4
24	Compensatory mutations are repeatable and clustered within proteins. *Proceedings of the Royal Society B: Biological Sciences*, **2009**, 276, 1823-7	4.4	50
23	Parsing social network survey data from hidden populations using stochastic context-free grammars. *PLoS ONE*, **2009**, 4, e6777	3.7	14
22	Detecting signatures of selection from DNA sequences using Datamonkey. *Methods in Molecular Biology*, **2009**, 537, 163-83	1.4	59
21	Immune-driven recombination and loss of control after HIV superinfection. *Journal of Experimental Medicine*, **2008**, 205, 1789-96	16.6	83
20	A maximum likelihood method for detecting directional evolution in protein sequences and its application to influenza A virus. *Molecular Biology and Evolution*, **2008**, 25, 1809-24	8.3	88
19	Spidermonkey: rapid detection of co-evolving sites using Bayesian graphical models. *Bioinformatics*, **2008**, 24, 1949-50	7.2	57
18	Silent mutations are selected in HIV-1 reverse transcriptase and affect enzymatic efficiency. *Aids*, **2008**, 22, 2501-8	3.5	12
17	Herpes simplex virus type 2 acquisition during recent HIV infection does not influence plasma HIV levels. *Journal of Acquired Immune Deficiency Syndromes (1999)*, **2008**, 47, 592-6	3.1	10
16	Adaptation to human populations is revealed by within-host polymorphisms in HIV-1 and hepatitis C virus. *PLoS Pathogens*, **2007**, 3, e45	7.6	45
15	Evolutionary interactions between N-linked glycosylation sites in the HIV-1 envelope. *PLoS Computational Biology*, **2007**, 3, e11	5	53
14	An evolutionary-network model reveals stratified interactions in the V3 loop of the HIV-1 envelope. *PLoS Computational Biology*, **2007**, 3, e231	5	88
13	Mapping protease inhibitor resistance to human immunodeficiency virus type 1 sequence polymorphisms within patients. *Journal of Virology*, **2007**, 81, 13598-607	6.6	18
12	FUNCTIONAL ORIGINS OF FITNESS EFFECT-SIZES OF COMPENSATORY MUTATIONS IN THE DNA BACTERIOPHAGE ⵣX174. *Evolution; International Journal of Organic Evolution*, **2006**, 60, 2032-2043	3.8	2
11	Functional origins of fitness effect-sizes of compensatory mutations in the DNA bacteriophage phiX174. *Evolution; International Journal of Organic Evolution*, **2006**, 60, 2032-43	3.8	21
10	The coupon collector and the suppressor mutation: estimating the number of compensatory mutations by maximum likelihood. *Genetics*, **2005**, 170, 1323-32	4	69

List of Publications

9	The rate of compensatory mutation in the DNA bacteriophage phiX174. *Genetics*, **2005**, 170, 989-99	4	120
8	An Evolutionary-Network Model Reveals Stratified Interactions in the V3 Loop of the HIV-1 Envelope. *PLoS Computational Biology*, **2005**, preprint, e231	5	
7	Drift increases the advantage of sex in RNA bacteriophage Phi6. *Genetics*, **2004**, 166, 19-24	4	38
6	Compensating for our load of mutations: freezing the meltdown of small populations. *Evolution; International Journal of Organic Evolution*, **2000**, 54, 1467-79	3.8	154
5	COMPENSATING FOR OUR LOAD OF MUTATIONS: FREEZING THE MELTDOWN OF SMALL POPULATIONS. *Evolution; International Journal of Organic Evolution*, **2000**, 54, 1467	3.8	39
4	Estimating selection pressures on alignments of coding sequences419-490		11
3	sierra-local: A lightweight standalone application for secure HIV-1 drug resistance prediction		1
2	Tree Shape-based approaches for the Comparative study of Cophylogeny		2
1	Early and ongoing importations of SARS-CoV-2 in Canada		7