

Art F Y Poon

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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.

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	Datamonkey 2010: a suite of phylogenetic analysis tools for evolutionary biology. <i>Bioinformatics</i> , 2010 , 26, 2455-7	7.2	942
97	Compensating for our load of mutations: freezing the meltdown of small populations. <i>Evolution; International Journal of Organic Evolution</i> , 2000 , 54, 1467-79	3.8	154
96	An evolutionary model-based algorithm for accurate phylogenetic breakpoint mapping and subtype prediction in HIV-1. <i>PLoS Computational Biology</i> , 2009 , 5, e1000581	5	130
95	Near real-time monitoring of HIV transmission hotspots from routine HIV genotyping: an implementation case study. <i>Lancet HIV,the</i> , 2016 , 3, e231-8	7.8	122
94	The rate of compensatory mutation in the DNA bacteriophage phiX174. <i>Genetics</i> , 2005 , 170, 989-99	4	120
93	HyPhy 2.5-A Customizable Platform for Evolutionary Hypothesis Testing Using Phylogenies. <i>Molecular Biology and Evolution</i> , 2020 , 37, 295-299	8.3	111
92	Characterizing HIV transmission networks across the United States. <i>Clinical Infectious Diseases</i> , 2012 , 55, 1135-43	11.6	98
91	A maximum likelihood method for detecting directional evolution in protein sequences and its application to influenza A virus. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1809-24	8.3	88
90	An evolutionary-network model reveals stratified interactions in the V3 loop of the HIV-1 envelope. <i>PLoS Computational Biology</i> , 2007 , 3, e231	5	88
89	Ancestral Reconstruction. <i>PLoS Computational Biology</i> , 2016 , 12, e1004763	5	84
88	Immune-driven recombination and loss of control after HIV superinfection. <i>Journal of Experimental Medicine</i> , 2008 , 205, 1789-96	16.6	83
87	The impact of clinical, demographic and risk factors on rates of HIV transmission: a population-based phylogenetic analysis in British Columbia, Canada. <i>Journal of Infectious Diseases</i> , 2015 , 211, 926-35	7	73
86	The coupon collector and the suppressor mutation: estimating the number of compensatory mutations by maximum likelihood. <i>Genetics</i> , 2005 , 170, 1323-32	4	69
85	Detecting signatures of selection from DNA sequences using Datamonkey. <i>Methods in Molecular Biology</i> , 2009 , 537, 163-83	1.4	59
84	Spidermonkey: rapid detection of co-evolving sites using Bayesian graphical models. <i>Bioinformatics</i> , 2008 , 24, 1949-50	7.2	57
83	Evolutionary fingerprinting of genes. <i>Molecular Biology and Evolution</i> , 2010 , 27, 520-36	8.3	55
82	Phylogenetic analysis of population-based and deep sequencing data to identify coevolving sites in the nef gene of HIV-1. <i>Molecular Biology and Evolution</i> , 2010 , 27, 819-32	8.3	55

81	Evolutionary interactions between N-linked glycosylation sites in the HIV-1 envelope. <i>PLoS Computational Biology</i> , 2007 , 3, e11	5	53
80	Compensatory mutations are repeatable and clustered within proteins. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009 , 276, 1823-7	4.4	50
79	Impacts and shortcomings of genetic clustering methods for infectious disease outbreaks. <i>Virus Evolution</i> , 2016 , 2, vew031	3.7	49
78	Adaptation to human populations is revealed by within-host polymorphisms in HIV-1 and hepatitis C virus. <i>PLoS Pathogens</i> , 2007 , 3, e45	7.6	45
77	Global origin and transmission of hepatitis C virus nonstructural protein 3 Q80K polymorphism. <i>Journal of Infectious Diseases</i> , 2015 , 211, 1288-95	7	42
76	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , 2017 , 34, 185-203	8.3	41
75	COMPENSATING FOR OUR LOAD OF MUTATIONS: FREEZING THE MELTDOWN OF SMALL POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2000 , 54, 1467	3.8	39
74	Drift increases the advantage of sex in RNA bacteriophage Phi6. <i>Genetics</i> , 2004 , 166, 19-24	4	38
73	Reconstructing the dynamics of HIV evolution within hosts from serial deep sequence data. <i>PLoS Computational Biology</i> , 2012 , 8, e1002753	5	37
72	An open-source k-mer based machine learning tool for fast and accurate subtyping of HIV-1 genomes. <i>PLoS ONE</i> , 2018 , 13, e0206409	3.7	36
71	The spread of hepatitis C virus genotype 1a in North America: a retrospective phylogenetic study. <i>Lancet Infectious Diseases</i> , 2016 , 16, 698-702	25.5	35
70	Genotypic and functional impact of HIV-1 adaptation to its host population during the North American epidemic. <i>PLoS Genetics</i> , 2014 , 10, e1004295	6	34
69	Phylogenetic Inference with Kernel ABC and Its Application to HIV Epidemiology. <i>Molecular Biology and Evolution</i> , 2015 , 32, 2483-95	8.3	30
68	Mapping the shapes of phylogenetic trees from human and zoonotic RNA viruses. <i>PLoS ONE</i> , 2013 , 8, e78122	3.7	28
67	Transmitted drug resistance in the CFAR network of integrated clinical systems cohort: prevalence and effects on pre-therapy CD4 and viral load. <i>PLoS ONE</i> , 2011 , 6, e21189	3.7	28
66	Theoretical and experimental assessment of degenerate primer tagging in ultra-deep applications of next-generation sequencing. <i>Nucleic Acids Research</i> , 2014 , 42, e98	20.1	27
65	Use of cellular HIV DNA to predict virologic response to maraviroc: performance of population-based and deep sequencing. <i>Clinical Infectious Diseases</i> , 2013 , 56, 1659-66	11.6	27
64	Genetic Cluster Analysis for HIV Prevention. <i>Current HIV/AIDS Reports</i> , 2018 , 15, 182-189	5.9	26

63	HIV-1 nef protein structures associated with brain infection and dementia pathogenesis. <i>PLoS ONE</i> , 2011 , 6, e16659	3.7	26
62	Dates of HIV infection can be estimated for seroprevalent patients by coalescent analysis of serial next-generation sequencing data. <i>Aids</i> , 2011 , 25, 2019-26	3.5	25
61	Phylogenetic approach to recover integration dates of latent HIV sequences within-host. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E8958-E8967 ^{11.5}	11.5	23
60	Functional origins of fitness effect-sizes of compensatory mutations in the DNA bacteriophage phiX174. <i>Evolution; International Journal of Organic Evolution</i> , 2006 , 60, 2032-43	3.8	21
59	Addressing Ethical Challenges in US-Based HIV Phylogenetic Research. <i>Journal of Infectious Diseases</i> , 2020 , 222, 1997-2006	7	20
58	Promises and pitfalls of Illumina sequencing for HIV resistance genotyping. <i>Virus Research</i> , 2017 , 239, 97-105	6.4	18
57	A molecular phylogenetics-based approach for identifying recent hepatitis C virus transmission events. <i>Infection, Genetics and Evolution</i> , 2015 , 33, 101-9	4.5	18
56	Mapping protease inhibitor resistance to human immunodeficiency virus type 1 sequence polymorphisms within patients. <i>Journal of Virology</i> , 2007 , 81, 13598-607	6.6	18
55	HIV Diversity and Genetic Compartmentalization in Blood and Testes during Suppressive Antiretroviral Therapy. <i>Journal of Virology</i> , 2019 , 93,	6.6	17
54	A model-based clustering method to detect infectious disease transmission outbreaks from sequence variation. <i>PLoS Computational Biology</i> , 2017 , 13, e1005868	5	15
53	Higher sequence diversity in the vaginal tract than in blood at early HIV-1 infection. <i>PLoS Pathogens</i> , 2018 , 14, e1006754	7.6	15
52	Comparison of population and 454 "deep" sequence analysis for HIV type 1 tropism versus the original trofile assay in non-B subtypes. <i>AIDS Research and Human Retroviruses</i> , 2013 , 29, 979-84	1.6	15
51	Selection in coastal <i>Synechococcus</i> (cyanobacteria) populations evaluated from environmental metagenomes. <i>PLoS ONE</i> , 2011 , 6, e24249	3.7	15
50	HIV-1 Transmission Clustering and Phylodynamics Highlight the Important Role of Young Men Who Have Sex with Men. <i>AIDS Research and Human Retroviruses</i> , 2018 , 34, 879-888	1.6	14
49	Parsing social network survey data from hidden populations using stochastic context-free grammars. <i>PLoS ONE</i> , 2009 , 4, e6777	3.7	14
48	Absence of HIV-1 Drug Resistance Mutations Supports the Use of Dolutegravir in Uganda. <i>AIDS Research and Human Retroviruses</i> , 2018 , 34, 404-414	1.6	13
47	Evolution of viral genomes: interplay between selection, recombination, and other forces. <i>Methods in Molecular Biology</i> , 2012 , 856, 239-72	1.4	13
46	In vitro selection of clinically relevant bevirimat resistance mutations revealed by "deep" sequencing of serially passaged, quasispecies-containing recombinant HIV-1. <i>Journal of Clinical Microbiology</i> , 2011 , 49, 201-8	9.7	13

45	Prolonged and substantial discordance in prevalence of raltegravir-resistant HIV-1 in plasma versus PBMC samples revealed by 454 "deep" sequencing. <i>PLoS ONE</i> , 2012 , 7, e46181	3.7	13
44	Comparative analysis of HIV sequences in real time for public health. <i>Current Opinion in HIV and AIDS</i> , 2019 , 14, 213-220	4.2	13
43	Deep sequencing increases hepatitis C virus phylogenetic cluster detection compared to Sanger sequencing. <i>Infection, Genetics and Evolution</i> , 2016 , 43, 329-37	4.5	12
42	Silent mutations are selected in HIV-1 reverse transcriptase and affect enzymatic efficiency. <i>Aids</i> , 2008 , 22, 2501-8	3.5	12
41	node.dating: dating ancestors in phylogenetic trees in R. <i>Bioinformatics</i> , 2017 , 33, 932-934	7.2	11
40	Factors influencing the sensitivity and specificity of conventional sequencing in human immunodeficiency virus type 1 tropism testing. <i>Journal of Clinical Microbiology</i> , 2013 , 51, 444-51	9.7	11
39	Estimating selection pressures on alignments of coding sequences		11
38	Herpes simplex virus type 2 acquisition during recent HIV infection does not influence plasma HIV levels. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2008 , 47, 592-6	3.1	10
37	Genetic Diversity, Compartmentalization, and Age of HIV Proviruses Persisting in CD4 T Cell Subsets during Long-Term Combination Antiretroviral Therapy. <i>Journal of Virology</i> , 2020 , 94,	6.6	9
36	Population-Level Immune-Mediated Adaptation in HIV-1 Polymerase during the North American Epidemic. <i>Journal of Virology</i> , 2016 , 90, 1244-58	6.6	9
35	Differential evolution of a CXCR4-using HIV-1 strain in CCR5wt/wt and CCR5 Δ 32/ Δ 32 hosts revealed by longitudinal deep sequencing and phylogenetic reconstruction. <i>Scientific Reports</i> , 2015 , 5, 17607	4.9	9
34	"Deep" sequencing accuracy and reproducibility using Roche/454 technology for inferring co-receptor usage in HIV-1. <i>PLoS ONE</i> , 2014 , 9, e99508	3.7	9
33	An evaluation of phylogenetic methods for reconstructing transmitted HIV variants using longitudinal clonal HIV sequence data. <i>Journal of Virology</i> , 2014 , 88, 6181-94	6.6	9
32	Tree shape-based approaches for the comparative study of cophylogeny. <i>Ecology and Evolution</i> , 2019 , 9, 6756-6771	2.8	8
31	Replication fitness of multiple nonnucleoside reverse transcriptase-resistant HIV-1 variants in the presence of etravirine measured by 454 deep sequencing. <i>Journal of Virology</i> , 2013 , 87, 8805-7	6.6	8
30	Reconstructing contact network parameters from viral phylogenies. <i>Virus Evolution</i> , 2016 , 2, vew029	3.7	7
29	Early and ongoing importations of SARS-CoV-2 in Canada		7
28	Evidence for a recombinant origin of HIV-1 Group M from genomic variation. <i>Virus Evolution</i> , 2019 , 5, vey039	3.7	6

27	Role of co-expressed APOBEC3F and APOBEC3G in inducing HIV-1 drug resistance. <i>Heliyon</i> , 2019 , 5, e01498	4.8	6
26	Sensitive detection of HIV-1 resistance to Zidovudine and impact on treatment outcomes in low- to middle-income countries. <i>Infectious Diseases of Poverty</i> , 2017 , 6, 163	10.4	6
25	Potential for immune-driven viral polymorphisms to compromise antiretroviral-based preexposure prophylaxis for prevention of HIV-1 infection. <i>Aids</i> , 2017 , 31, 1935-1943	3.5	6
24	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. <i>Journal of Antimicrobial Chemotherapy</i> , 2013 , 68, 2007-14	5.1	6
23	Global Database-Driven Assessment of HIV-1 Adaptation to the Immune Repertoires of Human Populations. <i>Journal of Virology</i> , 2015 , 89, 10693-5	6.6	5
22	A targeted reactivation of latent HIV-1 using an activator vector in patient samples from acute infection. <i>EBioMedicine</i> , 2020 , 59, 102853	8.8	5
21	A systematic, deep sequencing-based methodology for identification of mixed-genotype hepatitis C virus infections. <i>Infection, Genetics and Evolution</i> , 2019 , 69, 76-84	4.5	5
20	Public health in genetic spaces: a statistical framework to optimize cluster-based outbreak detection. <i>Virus Evolution</i> , 2020 , 6, veaa011	3.7	4
19	A novel codon insert in protease of clade B HIV type 1. <i>AIDS Research and Human Retroviruses</i> , 2009 , 25, 547-50	1.6	4
18	First-line HIV treatment failures in non-B subtypes and recombinants: a cross-sectional analysis of multiple populations in Uganda. <i>AIDS Research and Therapy</i> , 2019 , 16, 3	3	3
17	Origin and Evolution of Human Immunodeficiency Viruses 2015 , 587-611		3
16	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. <i>Journal of Antimicrobial Chemotherapy</i> , 2020 , 75, 3525-3533	5.1	3
15	Detecting Amino Acid Coevolution with Bayesian Graphical Models. <i>Methods in Molecular Biology</i> , 2019 , 1851, 105-122	1.4	3
14	Genotypic susceptibility score (GSS) and CD4+ T cell recovery in HIV-1 patients with suppressed viral load. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 496-503	5.1	2
13	What Proportion of HIV-Infected Foreign-Born Individuals in the United States Have Been Infected After Immigrating to the United States?. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2018 , 77, e35-e36	3.1	2
12	Quantitation of the latent HIV-1 reservoir from the sequence diversity in viral outgrowth assays. <i>Retrovirology</i> , 2018 , 15, 47	3.6	2
11	Phylogenetic measures of indel rate variation among the HIV-1 group M subtypes. <i>Virus Evolution</i> , 2019 , 5, vez022	3.7	2
10	FUNCTIONAL ORIGINS OF FITNESS EFFECT-SIZES OF COMPENSATORY MUTATIONS IN THE DNA BACTERIOPHAGE ϕ 174. <i>Evolution; International Journal of Organic Evolution</i> , 2006 , 60, 2032-2043	3.8	2

9	sierra-local: A lightweight standalone application for drug resistance prediction. <i>Journal of Open Source Software</i> , 2019 , 4, 1186	5.2	2
8	Tree Shape-based approaches for the Comparative study of Cophylogeny		2
7	Using networks to analyze and visualize the distribution of overlapping genes in virus genomes.. <i>PLoS Pathogens</i> , 2022 , 18, e1010331	7.6	2
6	sierra-local: A lightweight standalone application for secure HIV-1 drug resistance prediction		1
5	Quantifying the clonality and dynamics of the within-host HIV-1 latent reservoir. <i>Virus Evolution</i> , 2021 , 7, veaa104	3.7	1
4	Tuning intrinsic disorder predictors for virus proteins. <i>Virus Evolution</i> , 2021 , 7, veaa106	3.7	1
3	Network science inspires novel tree shape statistics.. <i>PLoS ONE</i> , 2021 , 16, e0259877	3.7	0
2	An Evolutionary-Network Model Reveals Stratified Interactions in the V3 Loop of the HIV-1 Envelope. <i>PLoS Computational Biology</i> , 2005 , preprint, e231	5	
1	Revisiting the recombinant history of HIV-1 group M with dynamic network community detection.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2108815119 ^{11.5}		