Sergei Pond

List of Publications by Year
in descending order

205 papers	30,119 citations	14655 66 h-index	6300 158 g-index
235 all docs	235 docs citations	235 times ranked	27966 citing authors

#	Article	IF	Citations
1	HyPhy: hypothesis testing using phylogenies. Bioinformatics, 2005, 21, 676-679.	4.1	2,599
2	Not So Different After All: A Comparison of Methods for Detecting Amino Acid Sites Under Selection. Molecular Biology and Evolution, 2005, 22, 1208-1222.	8.9	1,965
3	Detecting Individual Sites Subject to Episodic Diversifying Selection. PLoS Genetics, 2012, 8, e1002764.	3.5	1,455
4	Detection of a SARS-CoV-2 variant of concern in South Africa. Nature, 2021, 592, 438-443.	27.8	1,381
5	Datamonkey: rapid detection of selective pressure on individual sites of codon alignments. Bioinformatics, 2005, 21, 2531-2533.	4.1	1,223
6	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. Nature, 2022, 603, 679-686.	27.8	1,210
7	Datamonkey 2010: a suite of phylogenetic analysis tools for evolutionary biology. Bioinformatics, 2010, 26, 2455-2457.	4.1	1,158
8	FUBAR: A Fast, Unconstrained Bayesian AppRoximation for Inferring Selection. Molecular Biology and Evolution, 2013, 30, 1196-1205.	8.9	1,056
9	Automated Phylogenetic Detection of Recombination Using a Genetic Algorithm. Molecular Biology and Evolution, 2006, 23, 1891-1901.	8.9	866
10	The biological and clinical significance of emerging SARS-CoV-2 variants. Nature Reviews Genetics, 2021, 22, 757-773.	16.3	778
11	GARD: a genetic algorithm for recombination detection. Bioinformatics, 2006, 22, 3096-3098.	4.1	750
12	Datamonkey 2.0: A Modern Web Application for Characterizing Selective and Other Evolutionary Processes. Molecular Biology and Evolution, 2018, 35, 773-777.	8.9	643
13	Less Is More: An Adaptive Branch-Site Random Effects Model for Efficient Detection of Episodic Diversifying Selection. Molecular Biology and Evolution, 2015, 32, 1342-1353.	8.9	631
14	Persistent HIV-1 replication maintains the tissue reservoir during therapy. Nature, 2016, 530, 51-56.	27.8	550
15	RELAX: Detecting Relaxed Selection in a Phylogenetic Framework. Molecular Biology and Evolution, 2015, 32, 820-832.	8.9	535
16	Gene-Wide Identification of Episodic Selection. Molecular Biology and Evolution, 2015, 32, 1365-1371.	8.9	493
17	Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa. Nature Medicine, 2022, 28, 1785-1790.	30.7	456
18	A Random Effects Branch-Site Model for Detecting Episodic Diversifying Selection. Molecular Biology and Evolution, 2011, 28, 3033-3043.	8.9	383

#	Article	IF	Citations
19	Multiple emergences of genetically diverse amphibian-infecting chytrids include a globalized hypervirulent recombinant lineage. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18732-18736.	7.1	375
20	HyPhy 2.5â€"A Customizable Platform for Evolutionary Hypothesis Testing Using Phylogenies. Molecular Biology and Evolution, 2020, 37, 295-299.	8.9	342
21	Neutralizing antibody responses drive the evolution of human immunodeficiency virus type 1 envelope during recent HIV infection. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 18514-18519.	7.1	313
22	Site-to-Site Variation of Synonymous Substitution Rates. Molecular Biology and Evolution, 2005, 22, 2375-2385.	8.9	245
23	Statistics and Truth in Phylogenomics. Molecular Biology and Evolution, 2012, 29, 457-472.	8.9	243
24	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	5.5	237
25	Adaptation to Different Human Populations by HIV-1 Revealed by Codon-Based Analyses. PLoS Computational Biology, 2006, 2, e62.	3.2	209
26	HIV-TRACE (TRAnsmission Cluster Engine): a Tool for Large Scale Molecular Epidemiology of HIV-1 and Other Rapidly Evolving Pathogens. Molecular Biology and Evolution, 2018, 35, 1812-1819.	8.9	206
27	Phylodynamics of Infectious Disease Epidemics. Genetics, 2009, 183, 1421-1430.	2.9	200
28	The Global Transmission Network of HIV-1. Journal of Infectious Diseases, 2014, 209, 304-313.	4.0	194
29	Persistence of Transmitted Drug Resistance among Subjects with Primary Human Immunodeficiency Virus Infection. Journal of Virology, 2008, 82, 5510-5518.	3.4	192
30	Purifying Selection Can Obscure the Ancient Age of Viral Lineages. Molecular Biology and Evolution, 2011, 28, 3355-3365.	8.9	186
31	A Case for the Ancient Origin of Coronaviruses. Journal of Virology, 2013, 87, 7039-7045.	3.4	186
32	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. Cell, 2021, 184, 5189-5200.e7.	28.9	186
33	DIVEIN: a web server to analyze phylogenies, sequence divergence, diversity, and informative sites. BioTechniques, 2010, 48, 405-408.	1.8	184
34	A Genetic Algorithm Approach to Detecting Lineage-Specific Variation in Selection Pressure. Molecular Biology and Evolution, 2005, 22, 478-485.	8.9	178
35	Natural selection in the evolution of SARS-CoV-2 in bats created a generalist virus and highly capable human pathogen. PLoS Biology, 2021, 19, e3001115.	5.6	172
36	Characterization of Human Immunodeficiency Virus Type 1 (HIV-1) Envelope Variation and Neutralizing Antibody Responses during Transmission of HIV-1 Subtype B. Journal of Virology, 2005, 79, 6523-6527.	3.4	171

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37	Using HIV Networks to Inform Real Time Prevention Interventions. PLoS ONE, 2014, 9, e98443.	2.5	158
38	Social and Genetic Networks of HIV-1 Transmission in New York City. PLoS Pathogens, 2017, 13, e1006000.	4.7	157
39	Synonymous Substitution Rates Predict HIV Disease Progression as a Result of Underlying Replication Dynamics. PLoS Computational Biology, 2007, 3, e29.	3.2	152
40	An Evolutionary Model-Based Algorithm for Accurate Phylogenetic Breakpoint Mapping and Subtype Prediction in HIV-1. PLoS Computational Biology, 2009, 5, e1000581.	3.2	151
41	The replication-competent HIV-1 latent reservoir is primarily established near the time of therapy initiation. Science Translational Medicine, 2019, 11, .	12.4	141
42	Evolutionary Origins of Human Herpes Simplex Viruses 1 and 2. Molecular Biology and Evolution, 2014, 31, 2356-2364.	8.9	139
43	Early Antibody Lineage Diversification and Independent Limb Maturation Lead to Broad HIV-1 Neutralization Targeting the Env High-Mannose Patch. Immunity, 2016, 44, 1215-1226.	14.3	138
44	Phylodynamic Reconstruction Reveals Norovirus GII.4 Epidemic Expansions and their Molecular Determinants. PLoS Pathogens, 2010, 6, e1000884.	4.7	124
45	Mode and Rate of Evolution of Haemosporidian Mitochondrial Genomes: Timing the Radiation of Avian Parasites. Molecular Biology and Evolution, 2018, 35, 383-403.	8.9	122
46	Characterizing HIV Transmission Networks Across the United States. Clinical Infectious Diseases, 2012, 55, 1135-1143.	5.8	120
47	HyPhy: Hypothesis Testing Using Phylogenies. , 2005, , 125-181.		117
48	Transmitted HIV Type 1 Drug Resistance Among Individuals with Recent HIV Infection in East and Southern Africa. AIDS Research and Human Retroviruses, 2011, 27, 5-12.	1.1	114
49	A public health model for the molecular surveillance of HIV transmission in San Diego, California. Aids, 2009, 23, 225-232.	2.2	111
50	A Maximum Likelihood Method for Detecting Directional Evolution in Protein Sequences and Its Application to Influenza A Virus. Molecular Biology and Evolution, 2008, 25, 1809-1824.	8.9	106
51	An Evolutionary-Network Model Reveals Stratified Interactions in the V3 Loop of the HIV-1 Envelope. PLoS Computational Biology, 2007, 3, e231.	3.2	103
52	Predicting the mutational drivers of future SARS-CoV-2 variants of concern. Science Translational Medicine, 2022, 14, eabk3445.	12.4	101
53	Semen-Specific Genetic Characteristics of Human Immunodeficiency Virus Type 1 env. Journal of Virology, 2005, 79, 1734-1742.	3.4	98
54	Comparative Study of Methods for Detecting Sequence Compartmentalization in Human Immunodeficiency Virus Type 1. Journal of Virology, 2007, 81, 6643-6651.	3.4	97

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55	Differences in the Selection Bottleneck between Modes of Sexual Transmission Influence the Genetic Composition of the HIV-1 Founder Virus. PLoS Pathogens, 2016, 12, e1005619.	4.7	97
56	HIV-Specific Probabilistic Models of Protein Evolution. PLoS ONE, 2007, 2, e503.	2.5	96
57	Genetic attributes of cerebrospinal fluid-derived HIV-1 env. Brain, 2006, 129, 1872-1883.	7.6	94
58	Exploring the Natural Origins of SARS-CoV-2 in the Light of Recombination. Genome Biology and Evolution, 2022, 14, .	2.5	93
59	HIV Envelope Glycoform Heterogeneity and Localized Diversity Govern the Initiation and Maturation of a V2 Apex Broadly Neutralizing Antibody Lineage. Immunity, 2017, 47, 990-1003.e9.	14.3	90
60	A Dirichlet process model for detecting positive selection in protein-coding DNA sequences. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6263-6268.	7.1	87
61	Detection of Minority Resistance during Early HIV-1 Infection: Natural Variation and Spurious Detection rather than Transmission and Evolution of Multiple Viral Variants. Journal of Virology, 2011, 85, 8359-8367.	3.4	86
62	Selection Analysis Identifies Clusters of Unusual Mutational Changes in Omicron Lineage BA.1 That Likely Impact Spike Function. Molecular Biology and Evolution, 2022, 39, .	8.9	84
63	Coping with Viral Diversity in HIV Vaccine Design. PLoS Computational Biology, 2007, 3, e75.	3.2	83
64	Population structure of the genes encoding the polymorphic *Plasmodium falciparum* apical membrane antigen 1: Implications for vaccine design. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7857-7862.	7.1	83
65	Detection of Mammalian Virulence Determinants in Highly Pathogenic Avian Influenza H5N1 Viruses: Multivariate Analysis of Published Data. Journal of Virology, 2009, 83, 9901-9910.	3.4	76
66	Spidermonkey: rapid detection of co-evolving sites using Bayesian graphical models. Bioinformatics, 2008, 24, 1949-1950.	4.1	75
67	A counting renaissance: combining stochastic mapping and empirical Bayes to quickly detect amino acid sites under positive selection. Bioinformatics, 2012, 28, 3248-3256.	4.1	75
68	Growth of HIV-1 Molecular Transmission Clusters in New York City. Journal of Infectious Diseases, 2018, 218, 1943-1953.	4.0	75
69	CodonTest: Modeling Amino Acid Substitution Preferences in Coding Sequences. PLoS Computational Biology, 2010, 6, e1000885.	3.2	73
70	HIV-1 and SARS-CoV-2: Patterns in the evolution of two pandemic pathogens. Cell Host and Microbe, 2021, 29, 1093-1110.	11.0	73
71	Detecting Signatures of Selection from DNA Sequences Using Datamonkey. Methods in Molecular Biology, 2009, 537, 163-183.	0.9	71
72	Coronavirus Resistance Database (CoV-RDB): SARS-CoV-2 susceptibility to monoclonal antibodies, convalescent plasma, and plasma from vaccinated persons. PLoS ONE, 2022, 17, e0261045.	2.5	70

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73	A First Look at ARFome: Dual-Coding Genes in Mammalian Genomes. PLoS Computational Biology, 2007, 3, e91.	3.2	68
74	Evolution of the interferon alpha gene family in eutherian mammals. Gene, 2007, 397, 38-50.	2.2	68
75	Windshield splatter analysis with the Galaxy metagenomic pipeline. Genome Research, 2009, 19, 2144-2153.	5.5	68
76	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12522-12523.	7.1	68
77	The Origins of Sexually Transmitted HIV Among Men Who Have Sex with Men. Science Translational Medicine, 2010, 2, 18re1.	12.4	66
78	Inconsistencies in Estimating the Age of HIV-1 Subtypes Due to Heterotachy. Molecular Biology and Evolution, 2012, 29, 451-456.	8.9	65
79	Evolutionary Interactions between N-Linked Glycosylation Sites in the HIV-1 Envelope. PLoS Computational Biology, 2007, 3, e11.	3.2	63
80	Deep Sequencing Reveals Minor Protease Resistance Mutations in Patients Failing a Protease Inhibitor Regimen. Journal of Virology, 2012, 86, 6231-6237.	3.4	63
81	Evolutionary and Transmission Dynamics of Reassortant H5N1 Influenza Virus in Indonesia. PLoS Pathogens, 2008, 4, e1000130.	4.7	61
82	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. Nature, 0, , .	27.8	61
83	Column Sorting: Rapid Calculation of the Phylogenetic Likelihood Function. Systematic Biology, 2004, 53, 685-692.	5.6	59
84	A Simple Hierarchical Approach to Modeling Distributions of Substitution Rates. Molecular Biology and Evolution, 2005, 22, 223-234.	8.9	59
85	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, 819-832.	8.9	59
86	Identification of an HIV-1 Clade A Envelope That Exhibits Broad Antigenicity and Neutralization Sensitivity and Elicits Antibodies Targeting Three Distinct Epitopes. Journal of Virology, 2013, 87, 5372-5383.	3.4	59
87	Neutral Theory and Rapidly Evolving Viral Pathogens. Molecular Biology and Evolution, 2018, 35, 1348-1354.	8.9	58
88	Evolutionary Fingerprinting of Genes. Molecular Biology and Evolution, 2010, 27, 520-536.	8.9	57
89	Evolution and spread of Venezuelan equine encephalitis complex alphavirus in the Americas. PLoS Neglected Tropical Diseases, 2017, 11, e0005693.	3.0	56
90	A structural basis for antibody-mediated neutralization of Nipah virus reveals a site of vulnerability at the fusion glycoprotein apex. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25057-25067.	7.1	53

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91	Susceptibility of SARS-CoV-2 Omicron Variants to Therapeutic Monoclonal Antibodies: Systematic Review and Meta-analysis. Microbiology Spectrum, 2022, 10, .	3.0	53
92	Neuropathy- and myopathy-associated mutations in human small heat shock proteins: Characteristics and evolutionary history of the mutation sites. Mutation Research - Reviews in Mutation Research, 2014, 761, 15-30.	5.5	52
93	Adaptation to Human Populations Is Revealed by Within-Host Polymorphisms in HIV-1 and Hepatitis C Virus. PLoS Pathogens, 2007, 3, e45.	4.7	51
94	A Massively Parallel Sequencing Approach Uncovers Ancient Origins and High Genetic Variability of Endangered Przewalski's Horses. Genome Biology and Evolution, 2011, 3, 1096-1106.	2.5	51
95	Suppressors of RNAi from plant viruses are subject to episodic positive selection. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20130965.	2.6	51
96	Comprehensive Sieve Analysis of Breakthrough HIV-1 Sequences in the RV144 Vaccine Efficacy Trial. PLoS Computational Biology, 2015, 11, e1003973.	3.2	51
97	A Survey of the Molecular Evolutionary Dynamics of Twenty-Five Multigene Families from Four Grass Taxa. Journal of Molecular Evolution, 2001, 52, 144-156.	1.8	49
98	Compartmentalized HIV rebound in the central nervous system after interruption of antiretroviral therapy. Virus Evolution, 2016, 2, vew020.	4.9	49
99	Correcting the Bias of Empirical Frequency Parameter Estimators in Codon Models. PLoS ONE, 2010, 5, e11230.	2.5	49
100	Evolution of Viral Genomes: Interplay Between Selection, Recombination, and Other Forces. Methods in Molecular Biology, 2019, 1910, 427-468.	0.9	48
101	Synonymous Site-to-Site Substitution Rate Variation Dramatically Inflates False Positive Rates of Selection Analyses: Ignore at Your Own Peril. Molecular Biology and Evolution, 2020, 37, 2430-2439.	8.9	47
102	Trends in the Molecular Epidemiology and Genetic Mechanisms of Transmitted Human Immunodeficiency Virus Type 1 Drug Resistance in a Large US Clinic Population. Clinical Infectious Diseases, 2019, 68, 213-221.	5.8	46
103	HIV-1 Clade B pol Evolution following Primary Infection. PLoS ONE, 2013, 8, e68188.	2.5	43
104	Incidence and Prevalence of Intrasubtype HIV-1 Dual Infection in At-Risk Men in the United States. Journal of Infectious Diseases, 2014, 209, 1032-1038.	4.0	42
105	phylotree.js - a JavaScript library for application development and interactive data visualization in phylogenetics. BMC Bioinformatics, 2018, 19, 276.	2.6	40
106	Phylodynamic Analysis of Ebola Virus in the 2014 Sierra Leone Epidemic. PLOS Currents, 2014, 6, .	1.4	39
107	Single-Cell Transcriptomics Reveal a Correlation between Genome Architecture and Gene Family Evolution in Ciliates. MBio, 2019, 10, .	4.1	37
108	Next generation sequencing improves detection of drug resistance mutations in infants after PMTCT failure. Journal of Clinical Virology, 2015, 62, 48-53.	3.1	36

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109	Modeling HIV-1 Drug Resistance as Episodic Directional Selection. PLoS Computational Biology, 2012, 8, e1002507.	3.2	36
110	Comparison of Methods to Detect HIV Dual Infection. AIDS Research and Human Retroviruses, 2010, 26, 1291-1298.	1.1	35
111	Computational analysis and identification of amino acid sites in dengue E proteins relevant to development of diagnostics and vaccines. Virus Genes, 2007, 35, 175-186.	1.6	34
112	Using HIV Transmission Networks to Investigate Community Effects in HIV Prevention Trials. PLoS ONE, 2011, 6, e27775.	2.5	34
113	Contrast-FEL—A Test for Differences in Selective Pressures at Individual Sites among Clades and Sets of Branches. Molecular Biology and Evolution, 2021, 38, 1184-1198.	8.9	33
114	Using phylogeography to characterize the origins of the HIV-1 subtype F epidemic in Romania. Infection, Genetics and Evolution, 2011, 11, 975-979.	2.3	32
115	EVOLUTION OF DUPLICATED ALPH?-TUBULIN GENES IN CILIATES. Evolution; International Journal of Organic Evolution, 2002, 56, 1110-1122.	2.3	31
116	Evolution of Viral Genomes: Interplay Between Selection, Recombination, and Other Forces. Methods in Molecular Biology, 2012, 856, 239-272.	0.9	31
117	Rapid Sequencing of Complete *env* Genes from Primary HIV-1 Samples. Virus Evolution, 2016, 2, vew018.	4.9	30
118	Clinical, virologic, and immunologic correlates of HIV-1 intraclade B dual infection among men who have sex with men. Aids, 2012, 26, 157-165.	2.2	29
119	Antiretroviral Drug Resistance and Risk Behavior Among Recently HIV-Infected Men Who Have Sex With Men. Journal of Acquired Immune Deficiency Syndromes (1999), 2008, 47, 639-643.	2.1	28
120	Genotype-Specific Evolution of Hepatitis E Virus. Journal of Virology, 2017, 91, .	3.4	27
121	Partner services in adults with acute and early HIV infection. Aids, 2017, 31, 287-293.	2.2	27
122	Maintenance of Nef-Mediated Modulation of Major Histocompatibility Complex Class I and CD4 after Sexual Transmission of Human Immunodeficiency Virus Type 1. Journal of Virology, 2007, 81, 4776-4786.	3.4	24
123	IDEPI: Rapid Prediction of HIV-1 Antibody Epitopes and Other Phenotypic Features from Sequence Data Using a Flexible Machine Learning Platform. PLoS Computational Biology, 2014, 10, e1003842.	3.2	24
124	Detecting phylogenetic signal in mutualistic interaction networks using a Markov process model. Oikos, 2014, 123, 1250-1260.	2.7	23
125	Weak selection on synonymous codons substantially inflates *dN/dS* estimates in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	23
126	Rapid asymmetric evolution of a dual-coding tumor suppressor INK4a/ARF locus contradicts its function. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12807-12812.	7.1	22

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127	Dynamics of Viral Evolution and Neutralizing Antibody Response after HIV-1 Superinfection. Journal of Virology, 2013, 87, 12737-12744.	3.4	22
128	Comparative Analysis of Cell-Associated HIV DNA Levels in Cerebrospinal Fluid and Peripheral Blood by Droplet Digital PCR. PLoS ONE, 2015, 10, e0139510.	2.5	22
129	No more business as usual: Agile and effective responses to emerging pathogen threats require open data and open analytics. PLoS Pathogens, 2020, 16, e1008643.	4.7	22
130	Detection of SARS-CoV-2 intra-host recombination during superinfection with Alpha and Epsilon variants in New York City. Nature Communications, 2022, 13, .	12.8	22
131	Ready-to-use public infrastructure for global SARS-CoV-2 monitoring. Nature Biotechnology, 2021, 39, 1178-1179.	17.5	21
132	Multiple Recombination Events and Strong Purifying Selection at the Origin of SARS-CoV-2 Spike Glycoprotein Increased Correlated Dynamic Movements. International Journal of Molecular Sciences, 2021, 22, 80.	4.1	21
133	Mapping Protease Inhibitor Resistance to Human Immunodeficiency Virus Type 1 Sequence Polymorphisms within Patients. Journal of Virology, 2007, 81, 13598-13607.	3.4	20
134	Assigning and visualizing germline genes in antibody repertoires. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140240.	4.0	20
135	Using HIV Sequence and Epidemiologic Data to Assess the Effect of Self-referral Testing for Acute HIV Infection on Incident Diagnoses in San Diego, California. Clinical Infectious Diseases, 2016, 63, 101-107.	5.8	20
136	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. PLoS ONE, 2020, 15, e0225352.	2.5	20
137	Evidence for Positive Selection on a Sexual Reproduction Gene in the Diatom Genus Thalassiosira (Bacillariophyta). Journal of Molecular Evolution, 2006, 63, 231-239.	1.8	19
138	Estimating selection pressures on HIV‑1 using phylogenetic likelihood models. Statistics in Medicine, 2008, 27, 4779-4789.	1.6	19
139	Are All Subtypes Created Equal? The Effectiveness of Antiretroviral Therapy against Non–Subtype B HIV‑1. Clinical Infectious Diseases, 2009, 48, 1306-1309.	5.8	19
140	Impact of seminal cytomegalovirus replication on HIV‑1 dynamics between blood and semen. Journal of Medical Virology, 2012, 84, 1703-1709.	5.0	19
141	HIV-1 neutralizing antibody response and viral genetic diversity characterized with next generation sequencing. Virology, 2015, 474, 34-40.	2.4	19
142	Relative Evolutionary Rates in Proteins Are Largely Insensitive to the Substitution Model. Molecular Biology and Evolution, 2018, 35, 2307-2317.	8.9	19
143	A new method for inferring timetrees from temporally sampled molecular sequences. PLoS Computational Biology, 2020, 16, e1007046.	3.2	19
144	Viral CpG Deficiency Provides No Evidence That Dogs Were Intermediate Hosts for SARS-CoV-2. Molecular Biology and Evolution, 2020, 37, 2706-2710.	8.9	18

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145	Evolutionary Model Selection with a Genetic Algorithm: A Case Study Using Stem RNA. Molecular Biology and Evolution, 2006, 24, 159-170.	8.9	17
146	Protease polymorphisms in HIV-1 subtype CRF01_AE represent selection by antiretroviral therapy and host immune pressure. Aids, 2010, 24, 411-416.	2.2	17
147	Relative evolutionary rate inference in HyPhy with LEISR. PeerJ, 2018, 6, e4339.	2.0	16
148	Detection in 2009 of the Swine Origin Influenza A (H1N1) Virus by a Subtyping Microarray. Journal of Clinical Microbiology, 2009, 47, 3060-3061.	3.9	15
149	Codon volatility does not reflect selective pressure on the HIV-1 genome. Virology, 2005, 336, 137-143.	2.4	14
150	Estimating selection pressures on alignments of coding sequences. , 2009, , 419-490.		14
151	Characterizing the multiplicity of HIV founder variants during sexual transmission among MSM. Virus Evolution, 2016, 2, vew012.	4.9	14
152	Parsing Social Network Survey Data from Hidden Populations Using Stochastic Context-Free Grammars. PLoS ONE, 2009, 4, e6777.	2.5	14
153	Active Methamphetamine Use is Associated with Transmitted Drug Resistance to Non-Nucleoside Reverse Transcriptase Inhibitors in Individuals with HIV Infection of Unknown Duration. Open AIDS Journal, 2007, 1, 5-10.	0.5	14
154	Conserved recombination patterns across coronavirus subgenera. Virus Evolution, 2022, 8, .	4.9	14
155	Comparison of Immunogen Designs That Optimize Peptide Coverage: Reply to Fischer et al.. PLoS Computational Biology, 2008, 4, e25.	3.2	13
156	Structure–function analysis of hepatitis C virus envelope glycoproteins E1 and E2. Journal of Biomolecular Structure and Dynamics, 2015, 33, 1682-1694.	3.5	13
157	Viral Evolution and Cytotoxic T Cell Restricted Selection in Acute Infant HIV-1 Infection. Scientific Reports, 2016, 6, 29536.	3.3	13
158	Extra base hits: Widespread empirical support for instantaneous multiple-nucleotide changes. PLoS ONE, 2021, 16, e0248337.	2.5	13
159	On the Validity of Evolutionary Models with Site-Specific Parameters. PLoS ONE, 2014, 9, e94534.	2.5	12
160	Evolution of gag and gp41 in Patients Receiving Ritonavir-Boosted Protease Inhibitors. Scientific Reports, 2017, 7, 11559.	3.3	12
161	Benchmarking Multi-Rate Codon Models. PLoS ONE, 2010, 5, e11587.	2.5	11
162	The Relatedness of HIV Epidemics in the United States–Mexico Border Region. AIDS Research and Human Retroviruses, 2010, 26, 1273-1277.	1.1	11

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163	Higher HIV-1 genetic diversity is associated with AIDS and neuropsychological impairment. Virology, 2012, 433, 498-505.	2.4	11
164	Recent Zoonotic Spillover and Tropism Shift of a Canine Coronavirus Is Associated with Relaxed Selection and Putative Loss of Function in NTD Subdomain of Spike Protein. Viruses, 2022, 14, 853.	3.3	11
165	Associations Between Phylogenetic Clustering and HLA Profile Among HIV-Infected Individuals in San Diego, California. Journal of Infectious Diseases, 2012, 205, 1529-1533.	4.0	10
166	Intrasubtype B HIV-1 Superinfection Correlates with Delayed Neutralizing Antibody Response. Journal of Virology, 2017, 91, .	3.4	10
167	Waiting for the truth: is reluctance in accepting an early origin hypothesis for SARS-CoV-2 delaying our understanding of viral emergence?. BMJ Global Health, 2022, 7, e008386.	4.7	10
168	In Vivo VL-Targeted Microbial Superantigen Induced Global Shifts in the B Cell Repertoire. Journal of Immunology, 2012, 189, 850-859.	0.8	9
169	Combining Phylogenetic and Network Approaches to Identify HIV-1 Transmission Links in San Mateo County, California. Frontiers in Microbiology, 2018, 9, 2799.	3.5	9
170	Effective Human Immunodeficiency Virus Molecular Surveillance Requires Identification of Incident Cases of Infection. Clinical Infectious Diseases, 2021, 73, 842-849.	5.8	9
171	Ancestral transoceanic colonization and recent population reduction in a nonannual killifish from the Seychelles archipelago. Molecular Ecology, 2021, 30, 3610-3623.	3.9	9
172	Response to Comment on "The Origins of Sexually Transmitted HIV Among Men Who Have Sex with Men". Science Translational Medicine, 2010, 2, 501r1.	12.4	8
173	Sexual transmission of predicted CXCR4-tropic HIV-1 likely originating from the source partner's seminal cells. Virology, 2012, 434, 2-4.	2.4	8
174	Using Ultradeep Pyrosequencing to Study HIV-1 Coreceptor Usage in Primary and Dual Infection. Journal of Infectious Diseases, 2013, 208, 271-274.	4.0	8
175	HIV-associated neurocognitive disorder is associated with HIV-1 dual infection. Aids, 2016, 30, 2591-2597.	2.2	8
176	Molecular Evidence for SARS-CoV-2 in Samples Collected From Patients With Morbilliform Eruptions Since Late Summer 2019 in Lombardy, Northern Italy. SSRN Electronic Journal, 0, , .	0.4	8
177	EVOLUTION OF DUPLICATED ALPHA-TUBULIN GENES IN CILIATES. Evolution; International Journal of Organic Evolution, 2002, 56, 1110.	2.3	7
178	Molecular Evolution of Human Norovirus GII.2 Clusters. Frontiers in Microbiology, 2021, 12, 655567.	3.5	7
179	Phylogenetic Relatedness of HIV-1 Donor and Recipient Populations. Journal of Infectious Diseases, 2013, 207, 1181-1182.	4.0	6
180	National and International Dimensions of Human Immunodeficiency Virus-1 Sequence Clusters in a Northern California Clinical Cohort. Open Forum Infectious Diseases, 2019, 6, ofz135.	0.9	6

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181	Phyloanatomic characterization of the distinct T cell and monocyte contributions to the peripheral blood HIV population within the host. Virus Evolution, 2020, 6, veaa005.	4.9	6
182	Deep Sequencing Reveals Compartmentalized HIV-1 in the Semen of Men with and without Sexually Transmitted Infection-Associated Urethritis. Journal of Virology, 2020, 94, .	3.4	6
183	Diversity of Functionally Distinct Clonal Sets of Human Conventional Memory B Cells That Bind Staphylococcal Protein A. Frontiers in Immunology, 2021, 12, 662782.	4.8	6
184	Stepwise Evolution and Exceptional Conservation of ORF1a/b Overlap in Coronaviruses. Molecular Biology and Evolution, 2021, 38, 5678-5684.	8.9	6
185	Lorenzo-Redondo et al. reply. Nature, 2017, 551, E10-E10.	27.8	5
186	Unbiased RACE-Based Massive Parallel Surveys of Human IgA Antibody Repertoires. Methods in Molecular Biology, 2017, 1643, 45-73.	0.9	5
187	Full-Length Envelope Analyzer (FLEA): A tool for longitudinal analysis of viral amplicons. PLoS Computational Biology, 2018, 14, e1006498.	3.2	5
188	Characterization of changes in the hemagglutinin that accompanied the emergence of H3N2/1968 pandemic influenza viruses. PLoS Pathogens, 2021, 17, e1009566.	4.7	5
189	The evolution of BDNF is defined by strict purifying selection and prodomain spatial coevolution, but what does it mean for human brain disease?. Translational Psychiatry, 2022, 12, .	4.8	4
190	Human HspB1, HspB3, HspB5 and HspB8: Shaping these disease factors during vertebrate evolution. Cell Stress and Chaperones, 2022, 27, 309-323.	2.9	3
191	Computational analysis of HIV-1 evolution and epidemiology. , 2011, , .		2
192	Molecular Features of the V1–V4 Coding Region of Sexually Transmitted Human Immunodeficiency Virus Type 1. Journal of Infectious Diseases, 2017, 215, 1506-1513.	4.0	2
193	Evaluation of global HIV/SIV envelope gp120 RNA structure and evolution within and among infected hosts. Virus Evolution, 2018, 4, vey018.	4.9	2
194	Equiprobable discrete models of site-specific substitution rates underestimate the extent of rate variability. PLoS ONE, 2020, 15, e0229493.	2.5	2
195	Selection analyses of paired HIV-1 gag and gp41 sequences obtained before and after antiretroviral therapy. Scientific Data, 2018, 5, 180147.	5.3	1
196	Synonymous Substitution Rates Predict HIV Disease Progression as a Result of Underlying Replication Dynamics. PLoS Computational Biology, 2005, preprint, e29.	3.2	1
197	Workshop: Error correction, noise filtering, and phylogenetic analysis of HIV sequences using the 454 platform. , 2012, , .		0
198	Adaptation to different human populations by HIV-1 revealed by codon-based analysis. PLoS Computational Biology, 2005, preprint, e62.	3.2	0

#	Article	IF	Citations
199	An Evolutionary-Network Model Reveals Stratified Interactions in the V3 Loop of the HIV-1 Envelope. PLoS Computational Biology, 2005, preprint, e231.	3.2	0
200	The Role of Viral Genetic Variability in HIV-Associated Neurocognitive Disorder. , 0, , 201-218.		0
201	Compensatory Evolution within Viral RNA Structure: The Potential Role of Stable Intermediates in RNA Structural Heterogeneity. FASEB Journal, 2019, 33, lb191.	0.5	0
202	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0
203	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0
204	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0
205	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0