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	Predicting the mutational drivers of future SARS-CoV-2 variants of concern. Science Translational Medicine, 2022, 14, eabk3445.	12.4	101
2	Exploring the Natural Origins of SARS-CoV-2 in the Light of Recombination. Genome Biology and Evolution, 2022, 14, .	2.5	93
3	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. Nature, 2022, 603, 679-686.	27.8	1,210
4	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
5	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
6	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
7	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
8	Susceptibility of SARS-CoV-2 Omicron Variants to Therapeutic Monoclonal Antibodies: Systematic Review and Meta-analysis. Microbiology Spectrum, 2022, 10, .	3.0	53
9	Human HspB1, HspB3, HspB5 and HspB8: Shaping these disease factors during vertebrate evolution. Cell Stress and Chaperones, 2022, 27, 309-323.	2.9	3
10	Conserved recombination patterns across coronavirus subgenera. Virus Evolution, 2022, 8, .	4.9	14
11	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
12	Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa. Nature Medicine, 2022, 28, 1785-1790.	30.7	456
13	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
14	Contrast-FELâ€"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
15	Effective Human Immunodeficiency Virus Molecular Surveillance Requires Identification of Incident Cases of Infection. Clinical Infectious Diseases, 2021, 73, 842-849.	5.8	9
16	Extra base hits: Widespread empirical support for instantaneous multiple-nucleotide changes. PLoS ONE, 2021, 16, e0248337.	2.5	13
17	Detection of a SARS-CoV-2 variant of concern in South Africa. Nature, 2021, 592, 438-443.	27.8	1,381
18	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

#	Article	IF	Citations
19	Molecular Evolution of Human Norovirus GII.2 Clusters. Frontiers in Microbiology, 2021, 12, 655567.	3.5	7
20	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
21	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
22	Ancestral transoceanic colonization and recent population reduction in a nonannual killifish from the Seychelles archipelago. Molecular Ecology, 2021, 30, 3610-3623.	3.9	9
23	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
24	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. Cell, 2021, 184, 5189-5200.e7.	28.9	186
25	Characterization of changes in the hemagglutinin that accompanied the emergence of H3N2/1968 pandemic influenza viruses. PLoS Pathogens, 2021, 17, e1009566.	4.7	5
26	Stepwise Evolution and Exceptional Conservation of ORF1a/b Overlap in Coronaviruses. Molecular Biology and Evolution, 2021, 38, 5678-5684.	8.9	6
27	The biological and clinical significance of emerging SARS-CoV-2 variants. Nature Reviews Genetics, 2021, 22, 757-773.	16.3	778
28	Ready-to-use public infrastructure for global SARS-CoV-2 monitoring. Nature Biotechnology, 2021, 39, 1178-1179.	17.5	21
29	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
30	HyPhy 2.5—A Customizable Platform for Evolutionary Hypothesis Testing Using Phylogenies. Molecular Biology and Evolution, 2020, 37, 295-299.	8.9	342
31	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
32	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
33	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
34	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
35	Equiprobable discrete models of site-specific substitution rates underestimate the extent of rate variability. PLoS ONE, 2020, 15, e0229493.	2.5	2
36	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

#	ARTICLE	IF	CITATIONS
37	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. PLoS ONE, 2020, 15, e0225352.	2.5	20
38	A new method for inferring timetrees from temporally sampled molecular sequences. PLoS Computational Biology, 2020, 16, e1007046.	3.2	19
39	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
40	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0
41	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0
42	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0
43	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. , 2020, 15, e0225352.		0
44	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
45	Evolution of Viral Genomes: Interplay Between Selection, Recombination, and Other Forces. Methods in Molecular Biology, 2019, 1910, 427-468.	0.9	48
46	The replication-competent HIV-1 latent reservoir is primarily established near the time of therapy initiation. Science Translational Medicine, 2019, 11, .	12.4	141
47	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
48	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
49	Single-Cell Transcriptomics Reveal a Correlation between Genome Architecture and Gene Family Evolution in Ciliates. MBio, 2019, 10, .	4.1	37
50	Compensatory Evolution within Viral RNA Structure: The Potential Role of Stable Intermediates in RNA Structural Heterogeneity. FASEB Journal, 2019, 33, lb191.	0.5	0
51	Neutral Theory and Rapidly Evolving Viral Pathogens. Molecular Biology and Evolution, 2018, 35, 1348-1354.	8.9	58
52	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
53	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
54	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

#	Article	IF	Citations
55	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
56	Full-Length Envelope Analyzer (FLEA): A tool for longitudinal analysis of viral amplicons. PLoS Computational Biology, 2018, 14, e1006498.	3.2	5
57	Evaluation of global HIV/SIV envelope gp120 RNA structure and evolution within and among infected hosts. Virus Evolution, 2018, 4, vey018.	4.9	2
58	Relative Evolutionary Rates in Proteins Are Largely Insensitive to the Substitution Model. Molecular Biology and Evolution, 2018, 35, 2307-2317.	8.9	19
59	phylotree.js - a JavaScript library for application development and interactive data visualization in phylogenetics. BMC Bioinformatics, 2018, 19, 276.	2.6	40
60	Growth of HIV-1 Molecular Transmission Clusters in New York City. Journal of Infectious Diseases, 2018, 218, 1943-1953.	4.0	75
61	Selection analyses of paired HIV-1 gag and gp41 sequences obtained before and after antiretroviral therapy. Scientific Data, 2018, 5, 180147.	5.3	1
62	Relative evolutionary rate inference in HyPhy with LEISR. PeerJ, 2018, 6, e4339.	2.0	16
63	Genotype-Specific Evolution of Hepatitis E Virus. Journal of Virology, 2017, 91, .	3.4	27
64	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
65	Intrasubtype B HIV-1 Superinfection Correlates with Delayed Neutralizing Antibody Response. Journal of Virology, 2017, 91, .	3.4	10
66	Evolution of gag and gp41 in Patients Receiving Ritonavir-Boosted Protease Inhibitors. Scientific Reports, 2017, 7, 11559.	3.3	12
67	Partner services in adults with acute and early HIV infection. Aids, 2017, 31, 287-293.	2.2	27
68	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
69	Lorenzo-Redondo et al. reply. Nature, 2017, 551, E10-E10.	27.8	5
70	Unbiased RACE-Based Massive Parallel Surveys of Human IgA Antibody Repertoires. Methods in Molecular Biology, 2017, 1643, 45-73.	0.9	5
71	Evolution and spread of Venezuelan equine encephalitis complex alphavirus in the Americas. PLoS Neglected Tropical Diseases, 2017, 11, e0005693.	3.0	56
72	Social and Genetic Networks of HIV-1 Transmission in New York City. PLoS Pathogens, 2017, 13, e1006000.	4.7	157

#	Article	IF	Citations
73	Characterizing the multiplicity of HIV founder variants during sexual transmission among MSM. Virus Evolution, 2016, 2, vew012.	4.9	14
74	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
75	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
76	Viral Evolution and Cytotoxic T Cell Restricted Selection in Acute Infant HIV-1 Infection. Scientific Reports, 2016, 6, 29536.	3.3	13
77	Compartmentalized HIV rebound in the central nervous system after interruption of antiretroviral therapy. Virus Evolution, 2016, 2, vew020.	4.9	49
78	HIV-associated neurocognitive disorder is associated with HIV-1 dual infection. Aids, 2016, 30, 2591-2597.	2.2	8
79	Persistent HIV-1 replication maintains the tissue reservoir during therapy. Nature, 2016, 530, 51-56.	27.8	550
80	Rapid Sequencing of Complete *env* Genes from Primary HIV-1 Samples. Virus Evolution, 2016, 2, vew018.	4.9	30
81	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
82	Assigning and visualizing germline genes in antibody repertoires. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140240.	4.0	20
83	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
84	RELAX: Detecting Relaxed Selection in a Phylogenetic Framework. Molecular Biology and Evolution, 2015, 32, 820-832.	8.9	535
85	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
86	Comprehensive Sieve Analysis of Breakthrough HIV-1 Sequences in the RV144 Vaccine Efficacy Trial. PLoS Computational Biology, 2015, 11, e1003973.	3.2	51
87	Gene-Wide Identification of Episodic Selection. Molecular Biology and Evolution, 2015, 32, 1365-1371.	8.9	493
88	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
89	HIV-1 neutralizing antibody response and viral genetic diversity characterized with next generation sequencing. Virology, 2015, 474, 34-40.	2.4	19
90	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

#	Article	IF	Citations
91	On the Validity of Evolutionary Models with Site-Specific Parameters. PLoS ONE, 2014, 9, e94534.	2.5	12
92	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
93	Detecting phylogenetic signal in mutualistic interaction networks using a Markov process model. Oikos, 2014, 123, 1250-1260.	2.7	23
94	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
95	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
96	The Global Transmission Network of HIV-1. Journal of Infectious Diseases, 2014, 209, 304-313.	4.0	194
97	Evolutionary Origins of Human Herpes Simplex Viruses 1 and 2. Molecular Biology and Evolution, 2014, 31, 2356-2364.	8.9	139
98	Phylodynamic Analysis of Ebola Virus in the 2014 Sierra Leone Epidemic. PLOS Currents, 2014, 6, .	1.4	39
99	Using HIV Networks to Inform Real Time Prevention Interventions. PLoS ONE, 2014, 9, e98443.	2.5	158
100	Dynamics of Viral Evolution and Neutralizing Antibody Response after HIV-1 Superinfection. Journal of Virology, 2013, 87, 12737-12744.	3.4	22
101	A Case for the Ancient Origin of Coronaviruses. Journal of Virology, 2013, 87, 7039-7045.	3.4	186
102	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
103	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
104	Phylogenetic Relatedness of HIV-1 Donor and Recipient Populations. Journal of Infectious Diseases, 2013, 207, 1181-1182.	4.0	6
105	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
106	FUBAR: A Fast, Unconstrained Bayesian AppRoximation for Inferring Selection. Molecular Biology and Evolution, 2013, 30, 1196-1205.	8.9	1,056
107	HIV-1 Clade B pol Evolution following Primary Infection. PLoS ONE, 2013, 8, e68188.	2.5	43
108	Characterizing HIV Transmission Networks Across the United States. Clinical Infectious Diseases, 2012, 55, 1135-1143.	5.8	120

#	Article	IF	Citations
109	Detecting Individual Sites Subject to Episodic Diversifying Selection. PLoS Genetics, 2012, 8, e1002764.	3.5	1,455
110	Statistics and Truth in Phylogenomics. Molecular Biology and Evolution, 2012, 29, 457-472.	8.9	243
111	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
112	Inconsistencies in Estimating the Age of HIV-1 Subtypes Due to Heterotachy. Molecular Biology and Evolution, 2012, 29, 451-456.	8.9	65
113	In Vivo VL-Targeted Microbial Superantigen Induced Global Shifts in the B Cell Repertoire. Journal of Immunology, 2012, 189, 850-859.	0.8	9
114	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
115	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
116	Higher HIV-1 genetic diversity is associated with AIDS and neuropsychological impairment. Virology, 2012, 433, 498-505.	2.4	11
117	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
118	Workshop: Error correction, noise filtering, and phylogenetic analysis of HIV sequences using the 454 platform. , 2012, , .		0
119	Impact of seminal cytomegalovirus replication on HIV–1 dynamics between blood and semen. Journal of Medical Virology, 2012, 84, 1703-1709.	5.0	19
120	Evolution of Viral Genomes: Interplay Between Selection, Recombination, and Other Forces. Methods in Molecular Biology, 2012, 856, 239-272.	0.9	31
121	Deep Sequencing Reveals Minor Protease Resistance Mutations in Patients Failing a Protease Inhibitor Regimen. Journal of Virology, 2012, 86, 6231-6237.	3.4	63
122	Modeling HIV-1 Drug Resistance as Episodic Directional Selection. PLoS Computational Biology, 2012, 8, e1002507.	3.2	36
123	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
124	Computational analysis of HIV-1 evolution and epidemiology. , 2011, , .		2
125	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
126	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
127	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
128	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
129	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
130	Purifying Selection Can Obscure the Ancient Age of Viral Lineages. Molecular Biology and Evolution, 2011, 28, 3355-3365.	8.9	186
131	Using HIV Transmission Networks to Investigate Community Effects in HIV Prevention Trials. PLoS ONE, 2011, 6, e27775.	2.5	34
132	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
133	Benchmarking Multi-Rate Codon Models. PLoS ONE, 2010, 5, e11587.	2.5	11
134	DIVEIN: a web server to analyze phylogenies, sequence divergence, diversity, and informative sites. BioTechniques, 2010, 48, 405-408.	1.8	184
135	Datamonkey 2010: a suite of phylogenetic analysis tools for evolutionary biology. Bioinformatics, 2010, 26, 2455-2457.	4.1	1,158
136	Evolutionary Fingerprinting of Genes. Molecular Biology and Evolution, 2010, 27, 520-536.	8.9	57
137	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
138	Comparison of Methods to Detect HIV Dual Infection. AIDS Research and Human Retroviruses, 2010, 26, 1291-1298.	1.1	35
139	The Relatedness of HIV Epidemics in the United States–Mexico Border Region. AIDS Research and Human Retroviruses, 2010, 26, 1273-1277.	1.1	11
140	The Origins of Sexually Transmitted HIV Among Men Who Have Sex with Men. Science Translational Medicine, 2010, 2, 18re1.	12.4	66
141	Phylodynamic Reconstruction Reveals Norovirus GII.4 Epidemic Expansions and their Molecular Determinants. PLoS Pathogens, 2010, 6, e1000884.	4.7	124
142	CodonTest: Modeling Amino Acid Substitution Preferences in Coding Sequences. PLoS Computational Biology, 2010, 6, e1000885.	3.2	73
143	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
144	Correcting the Bias of Empirical Frequency Parameter Estimators in Codon Models. PLoS ONE, 2010, 5, e11230.	2.5	49

#	Article	IF	Citations
145	Estimating selection pressures on alignments of coding sequences. , 2009, , 419-490.		14
146	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
147	Windshield splatter analysis with the Galaxy metagenomic pipeline. Genome Research, 2009, 19, 2144-2153.	5.5	68
148	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
149	Are All Subtypes Created Equal? The Effectiveness of Antiretroviral Therapy against Nonâ€"Subtype B HIVâ€1. Clinical Infectious Diseases, 2009, 48, 1306-1309.	5.8	19
150	Phylodynamics of Infectious Disease Epidemics. Genetics, 2009, 183, 1421-1430.	2.9	200
151	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
152	A public health model for the molecular surveillance of HIV transmission in San Diego, California. Aids, 2009, 23, 225-232.	2.2	111
153	Detecting Signatures of Selection from DNA Sequences Using Datamonkey. Methods in Molecular Biology, 2009, 537, 163-183.	0.9	71
154	Parsing Social Network Survey Data from Hidden Populations Using Stochastic Context-Free Grammars. PLoS ONE, 2009, 4, e6777.	2.5	14
155	Estimating selection pressures on HIVâ€1 using phylogenetic likelihood models. Statistics in Medicine, 2008, 27, 4779-4789.	1.6	19
156	Persistence of Transmitted Drug Resistance among Subjects with Primary Human Immunodeficiency Virus Infection. Journal of Virology, 2008, 82, 5510-5518.	3.4	192
157	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
158	Evolutionary and Transmission Dynamics of Reassortant H5N1 Influenza Virus in Indonesia. PLoS Pathogens, 2008, 4, e1000130.	4.7	61
159	Spidermonkey: rapid detection of co-evolving sites using Bayesian graphical models. Bioinformatics, 2008, 24, 1949-1950.	4.1	75
160	Population structure of the genes encoding the polymorphic <i>Plasmodium falciparum</i> 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
161	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
162	Comparison of Immunogen Designs That Optimize Peptide Coverage: Reply to Fischer et al.. PLoS Computational Biology, 2008, 4, e25.	3.2	13

#	Article	IF	Citations
163	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
164	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
165	Evolutionary Interactions between N-Linked Glycosylation Sites in the HIV-1 Envelope. PLoS Computational Biology, 2007, 3, e11.	3.2	63
166	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	5.5	237
167	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
168	Coping with Viral Diversity in HIV Vaccine Design. PLoS Computational Biology, 2007, 3, e75.	3.2	83
169	Synonymous Substitution Rates Predict HIV Disease Progression as a Result of Underlying Replication Dynamics. PLoS Computational Biology, 2007, 3, e29.	3.2	152
170	A First Look at ARFome: Dual-Coding Genes in Mammalian Genomes. PLoS Computational Biology, 2007, 3, e91.	3.2	68
171	Comparative Study of Methods for Detecting Sequence Compartmentalization in Human Immunodeficiency Virus Type 1. Journal of Virology, 2007, 81, 6643-6651.	3.4	97
172	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
173	Mapping Protease Inhibitor Resistance to Human Immunodeficiency Virus Type 1 Sequence Polymorphisms within Patients. Journal of Virology, 2007, 81, 13598-13607.	3.4	20
174	Evolution of the interferon alpha gene family in eutherian mammals. Gene, 2007, 397, 38-50.	2.2	68
175	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
176	HIV-Specific Probabilistic Models of Protein Evolution. PLoS ONE, 2007, 2, e503.	2.5	96
177	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
178	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
179	Genetic attributes of cerebrospinal fluid-derived HIV-1 env. Brain, 2006, 129, 1872-1883.	7.6	94
180	Evolutionary Model Selection with a Genetic Algorithm: A Case Study Using Stem RNA. Molecular Biology and Evolution, 2006, 24, 159-170.	8.9	17

#	Article	IF	Citations
181	Adaptation to Different Human Populations by HIV-1 Revealed by Codon-Based Analyses. PLoS Computational Biology, 2006, 2, e62.	3.2	209
182	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
183	GARD: a genetic algorithm for recombination detection. Bioinformatics, 2006, 22, 3096-3098.	4.1	750
184	Automated Phylogenetic Detection of Recombination Using a Genetic Algorithm. Molecular Biology and Evolution, 2006, 23, 1891-1901.	8.9	866
185	Codon volatility does not reflect selective pressure on the HIV-1 genome. Virology, 2005, 336, 137-143.	2.4	14
186	A Simple Hierarchical Approach to Modeling Distributions of Substitution Rates. Molecular Biology and Evolution, 2005, 22, 223-234.	8.9	59
187	Datamonkey: rapid detection of selective pressure on individual sites of codon alignments. Bioinformatics, 2005, 21, 2531-2533.	4.1	1,223
188	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
189	A Genetic Algorithm Approach to Detecting Lineage-Specific Variation in Selection Pressure. Molecular Biology and Evolution, 2005, 22, 478-485.	8.9	178
190	Semen-Specific Genetic Characteristics of Human Immunodeficiency Virus Type 1 env. Journal of Virology, 2005, 79, 1734-1742.	3.4	98
191	Site-to-Site Variation of Synonymous Substitution Rates. Molecular Biology and Evolution, 2005, 22, 2375-2385.	8.9	245
192	HyPhy: hypothesis testing using phylogenies. Bioinformatics, 2005, 21, 676-679.	4.1	2,599
193	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
194	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
195	HyPhy: Hypothesis Testing Using Phylogenies. , 2005, , 125-181.		117
196	Adaptation to different human populations by HIV-1 revealed by codon-based analysis. PLoS Computational Biology, 2005, preprint, e62.	3.2	0
197	Synonymous Substitution Rates Predict HIV Disease Progression as a Result of Underlying Replication Dynamics. PLoS Computational Biology, 2005, preprint, e29.	3.2	1
198	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

#	Article	IF	Citations
199	Column Sorting: Rapid Calculation of the Phylogenetic Likelihood Function. Systematic Biology, 2004, 53, 685-692.	5.6	59
200	EVOLUTION OF DUPLICATED ALPHA-TUBULIN GENES IN CILIATES. Evolution; International Journal of Organic Evolution, 2002, 56, 1110.	2.3	7
201	EVOLUTION OF DUPLICATED ALPH?-TUBULIN GENES IN CILIATES. Evolution; International Journal of Organic Evolution, 2002, 56, 1110-1122.	2.3	31
202	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
203	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
204	The Role of Viral Genetic Variability in HIV-Associated Neurocognitive Disorder. , 0, , 201-218.		0
205	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. Nature, 0, , .	27.8	61