

Sergei Pond

List of Publications by Year in descending order

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Version: 2024-02-01

205
papers

30,119
citations

16791

66
h-index

7234

158
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235
all docs

235
docs citations

235
times ranked

30607
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting the mutational drivers of future SARS-CoV-2 variants of concern. <i>Science Translational Medicine</i> , 2022, 14, eabk3445.	5.8	101
2	Exploring the Natural Origins of SARS-CoV-2 in the Light of Recombination. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	93
3	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 2022, 603, 679-686.	13.7	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?. <i>BMJ Global Health</i> , 2022, 7, e008386.	2.0	10
5	Coronavirus Resistance Database (CoV-RDB): SARS-CoV-2 susceptibility to monoclonal antibodies, convalescent plasma, and plasma from vaccinated persons. <i>PLoS ONE</i> , 2022, 17, e0261045.	1.1	70
6	Selection Analysis Identifies Clusters of Unusual Mutational Changes in Omicron Lineage BA.1 That Likely Impact Spike Function. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	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. <i>Viruses</i> , 2022, 14, 853.	1.5	11
8	Susceptibility of SARS-CoV-2 Omicron Variants to Therapeutic Monoclonal Antibodies: Systematic Review and Meta-analysis. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	53
9	Human HspB1, HspB3, HspB5 and HspB8: Shaping these disease factors during vertebrate evolution. <i>Cell Stress and Chaperones</i> , 2022, 27, 309-323.	1.2	3
10	Conserved recombination patterns across coronavirus subgenera. <i>Virus Evolution</i> , 2022, 8, .	2.2	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?. <i>Translational Psychiatry</i> , 2022, 12, .	2.4	4
12	Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa. <i>Nature Medicine</i> , 2022, 28, 1785-1790.	15.2	456
13	Detection of SARS-CoV-2 intra-host recombination during superinfection with Alpha and Epsilon variants in New York City. <i>Nature Communications</i> , 2022, 13, .	5.8	22
14	Contrast-FEL A Test for Differences in Selective Pressures at Individual Sites among Clades and Sets of Branches. <i>Molecular Biology and Evolution</i> , 2021, 38, 1184-1198.	3.5	33
15	Effective Human Immunodeficiency Virus Molecular Surveillance Requires Identification of Incident Cases of Infection. <i>Clinical Infectious Diseases</i> , 2021, 73, 842-849.	2.9	9
16	Extra base hits: Widespread empirical support for instantaneous multiple-nucleotide changes. <i>PLoS ONE</i> , 2021, 16, e0248337.	1.1	13
17	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021, 592, 438-443.	13.7	1,381
18	Natural selection in the evolution of SARS-CoV-2 in bats created a generalist virus and highly capable human pathogen. <i>PLoS Biology</i> , 2021, 19, e3001115.	2.6	172

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19	Molecular Evolution of Human Norovirus GII.2 Clusters. <i>Frontiers in Microbiology</i> , 2021, 12, 655567.	1.5	7
20	Diversity of Functionally Distinct Clonal Sets of Human Conventional Memory B Cells That Bind Staphylococcal Protein A. <i>Frontiers in Immunology</i> , 2021, 12, 662782.	2.2	6
21	Weak selection on synonymous codons substantially inflates dN/dS estimates in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	23
22	Ancestral transoceanic colonization and recent population reduction in a nonannual killifish from the Seychelles archipelago. <i>Molecular Ecology</i> , 2021, 30, 3610-3623.	2.0	9
23	HIV-1 and SARS-CoV-2: Patterns in the evolution of two pandemic pathogens. <i>Cell Host and Microbe</i> , 2021, 29, 1093-1110.	5.1	73
24	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. <i>Cell</i> , 2021, 184, 5189-5200.e7.	13.5	186
25	Characterization of changes in the hemagglutinin that accompanied the emergence of H3N2/1968 pandemic influenza viruses. <i>PLoS Pathogens</i> , 2021, 17, e1009566.	2.1	5
26	Stepwise Evolution and Exceptional Conservation of ORF1a/b Overlap in Coronaviruses. <i>Molecular Biology and Evolution</i> , 2021, 38, 5678-5684.	3.5	6
27	The biological and clinical significance of emerging SARS-CoV-2 variants. <i>Nature Reviews Genetics</i> , 2021, 22, 757-773.	7.7	778
28	Ready-to-use public infrastructure for global SARS-CoV-2 monitoring. <i>Nature Biotechnology</i> , 2021, 39, 1178-1179.	9.4	21
29	Multiple Recombination Events and Strong Purifying Selection at the Origin of SARS-CoV-2 Spike Glycoprotein Increased Correlated Dynamic Movements. <i>International Journal of Molecular Sciences</i> , 2021, 22, 80.	1.8	21
30	HyPhy 2.5 – A Customizable Platform for Evolutionary Hypothesis Testing Using Phylogenies. <i>Molecular Biology and Evolution</i> , 2020, 37, 295-299.	3.5	342
31	Viral CpG Deficiency Provides No Evidence That Dogs Were Intermediate Hosts for SARS-CoV-2. <i>Molecular Biology and Evolution</i> , 2020, 37, 2706-2710.	3.5	18
32	No more business as usual: Agile and effective responses to emerging pathogen threats require open data and open analytics. <i>PLoS Pathogens</i> , 2020, 16, e1008643.	2.1	22
33	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	3.3	68
34	Phyloanatomic characterization of the distinct T cell and monocyte contributions to the peripheral blood HIV population within the host. <i>Virus Evolution</i> , 2020, 6, veaa005.	2.2	6
35	Equiprobable discrete models of site-specific substitution rates underestimate the extent of rate variability. <i>PLoS ONE</i> , 2020, 15, e0229493.	1.1	2
36	Synonymous Site-to-Site Substitution Rate Variation Dramatically Inflates False Positive Rates of Selection Analyses: Ignore at Your Own Peril. <i>Molecular Biology and Evolution</i> , 2020, 37, 2430-2439.	3.5	47

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37	Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences. PLoS ONE, 2020, 15, e0225352.	1.1	20
38	A new method for inferring timetrees from temporally sampled molecular sequences. PLoS Computational Biology, 2020, 16, e1007046.	1.5	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, .	1.5	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.	2.9	46
45	Evolution of Viral Genomes: Interplay Between Selection, Recombination, and Other Forces. Methods in Molecular Biology, 2019, 1910, 427-468.	0.4	48
46	The replication-competent HIV-1 latent reservoir is primarily established near the time of therapy initiation. Science Translational Medicine, 2019, 11, .	5.8	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.	0.4	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.	3.3	53
49	Single-Cell Transcriptomics Reveal a Correlation between Genome Architecture and Gene Family Evolution in Ciliates. MBio, 2019, 10, .	1.8	37
50	Compensatory Evolution within Viral RNA Structure: The Potential Role of Stable Intermediates in RNA Structural Heterogeneity. FASEB Journal, 2019, 33, lb191.	0.2	0
51	Neutral Theory and Rapidly Evolving Viral Pathogens. Molecular Biology and Evolution, 2018, 35, 1348-1354.	3.5	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.	3.5	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.	3.5	122
54	Datamonkey 2.0: A Modern Web Application for Characterizing Selective and Other Evolutionary Processes. Molecular Biology and Evolution, 2018, 35, 773-777.	3.5	643

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55	Combining Phylogenetic and Network Approaches to Identify HIV-1 Transmission Links in San Mateo County, California. <i>Frontiers in Microbiology</i> , 2018, 9, 2799.	1.5	9
56	Full-Length Envelope Analyzer (FLEA): A tool for longitudinal analysis of viral amplicons. <i>PLoS Computational Biology</i> , 2018, 14, e1006498.	1.5	5
57	Evaluation of global HIV/SIV envelope gp120 RNA structure and evolution within and among infected hosts. <i>Virus Evolution</i> , 2018, 4, vey018.	2.2	2
58	Relative Evolutionary Rates in Proteins Are Largely Insensitive to the Substitution Model. <i>Molecular Biology and Evolution</i> , 2018, 35, 2307-2317.	3.5	19
59	phylotree.js - a JavaScript library for application development and interactive data visualization in phylogenetics. <i>BMC Bioinformatics</i> , 2018, 19, 276.	1.2	40
60	Growth of HIV-1 Molecular Transmission Clusters in New York City. <i>Journal of Infectious Diseases</i> , 2018, 218, 1943-1953.	1.9	75
61	Selection analyses of paired HIV-1 gag and gp41 sequences obtained before and after antiretroviral therapy. <i>Scientific Data</i> , 2018, 5, 180147.	2.4	1
62	Relative evolutionary rate inference in HyPhy with LEISR. <i>PeerJ</i> , 2018, 6, e4339.	0.9	16
63	Genotype-Specific Evolution of Hepatitis E Virus. <i>Journal of Virology</i> , 2017, 91, .	1.5	27
64	Molecular Features of the V1-V4 Coding Region of Sexually Transmitted Human Immunodeficiency Virus Type 1. <i>Journal of Infectious Diseases</i> , 2017, 215, 1506-1513.	1.9	2
65	Intrasubtype B HIV-1 Superinfection Correlates with Delayed Neutralizing Antibody Response. <i>Journal of Virology</i> , 2017, 91, .	1.5	10
66	Evolution of gag and gp41 in Patients Receiving Ritonavir-Boosted Protease Inhibitors. <i>Scientific Reports</i> , 2017, 7, 11559.	1.6	12
67	Partner services in adults with acute and early HIV infection. <i>Aids</i> , 2017, 31, 287-293.	1.0	27
68	HIV Envelope Glycoform Heterogeneity and Localized Diversity Govern the Initiation and Maturation of a V2 Apex Broadly Neutralizing Antibody Lineage. <i>Immunity</i> , 2017, 47, 990-1003.e9.	6.6	90
69	Lorenzo-Redondo et al. reply. <i>Nature</i> , 2017, 551, E10-E10.	13.7	5
70	Unbiased RACE-Based Massive Parallel Surveys of Human IgA Antibody Repertoires. <i>Methods in Molecular Biology</i> , 2017, 1643, 45-73.	0.4	5
71	Evolution and spread of Venezuelan equine encephalitis complex alphavirus in the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005693.	1.3	56
72	Social and Genetic Networks of HIV-1 Transmission in New York City. <i>PLoS Pathogens</i> , 2017, 13, e1006000.	2.1	157

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73	Characterizing the multiplicity of HIV founder variants during sexual transmission among MSM. <i>Virus Evolution</i> , 2016, 2, vew012.	2.2	14
74	Early Antibody Lineage Diversification and Independent Limb Maturation Lead to Broad HIV-1 Neutralization Targeting the Env High-Mannose Patch. <i>Immunity</i> , 2016, 44, 1215-1226.	6.6	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. <i>Clinical Infectious Diseases</i> , 2016, 63, 101-107.	2.9	20
76	Viral Evolution and Cytotoxic T Cell Restricted Selection in Acute Infant HIV-1 Infection. <i>Scientific Reports</i> , 2016, 6, 29536.	1.6	13
77	Compartmentalized HIV rebound in the central nervous system after interruption of antiretroviral therapy. <i>Virus Evolution</i> , 2016, 2, vew020.	2.2	49
78	HIV-associated neurocognitive disorder is associated with HIV-1 dual infection. <i>Aids</i> , 2016, 30, 2591-2597.	1.0	8
79	Persistent HIV-1 replication maintains the tissue reservoir during therapy. <i>Nature</i> , 2016, 530, 51-56.	13.7	550
80	Rapid Sequencing of Complete <i>env</i> Genes from Primary HIV-1 Samples. <i>Virus Evolution</i> , 2016, 2, vew018.	2.2	30
81	Differences in the Selection Bottleneck between Modes of Sexual Transmission Influence the Genetic Composition of the HIV-1 Founder Virus. <i>PLoS Pathogens</i> , 2016, 12, e1005619.	2.1	97
82	Assigning and visualizing germline genes in antibody repertoires. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140240.	1.8	20
83	Comparative Analysis of Cell-Associated HIV DNA Levels in Cerebrospinal Fluid and Peripheral Blood by Droplet Digital PCR. <i>PLoS ONE</i> , 2015, 10, e0139510.	1.1	22
84	RELAX: Detecting Relaxed Selection in a Phylogenetic Framework. <i>Molecular Biology and Evolution</i> , 2015, 32, 820-832.	3.5	535
85	Less Is More: An Adaptive Branch-Site Random Effects Model for Efficient Detection of Episodic Diversifying Selection. <i>Molecular Biology and Evolution</i> , 2015, 32, 1342-1353.	3.5	631
86	Comprehensive Sieve Analysis of Breakthrough HIV-1 Sequences in the RV144 Vaccine Efficacy Trial. <i>PLoS Computational Biology</i> , 2015, 11, e1003973.	1.5	51
87	Gene-Wide Identification of Episodic Selection. <i>Molecular Biology and Evolution</i> , 2015, 32, 1365-1371.	3.5	493
88	Next generation sequencing improves detection of drug resistance mutations in infants after PMTCT failure. <i>Journal of Clinical Virology</i> , 2015, 62, 48-53.	1.6	36
89	HIV-1 neutralizing antibody response and viral genetic diversity characterized with next generation sequencing. <i>Virology</i> , 2015, 474, 34-40.	1.1	19
90	Structure-function analysis of hepatitis C virus envelope glycoproteins E1 and E2. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 1682-1694.	2.0	13

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91	On the Validity of Evolutionary Models with Site-Specific Parameters. PLoS ONE, 2014, 9, e94534.	1.1	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.	1.5	24
93	Detecting phylogenetic signal in mutualistic interaction networks using a Markov process model. Oikos, 2014, 123, 1250-1260.	1.2	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.	2.4	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.	1.9	42
96	The Global Transmission Network of HIV-1. Journal of Infectious Diseases, 2014, 209, 304-313.	1.9	194
97	Evolutionary Origins of Human Herpes Simplex Viruses 1 and 2. Molecular Biology and Evolution, 2014, 31, 2356-2364.	3.5	139
98	Phylogenetic 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.	1.1	158
100	Dynamics of Viral Evolution and Neutralizing Antibody Response after HIV-1 Superinfection. Journal of Virology, 2013, 87, 12737-12744.	1.5	22
101	A Case for the Ancient Origin of Coronaviruses. Journal of Virology, 2013, 87, 7039-7045.	1.5	186
102	Using Ultradeep Pyrosequencing to Study HIV-1 Coreceptor Usage in Primary and Dual Infection. Journal of Infectious Diseases, 2013, 208, 271-274.	1.9	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.	1.2	51
104	Phylogenetic Relatedness of HIV-1 Donor and Recipient Populations. Journal of Infectious Diseases, 2013, 207, 1181-1182.	1.9	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.	1.5	59
106	FUBAR: A Fast, Unconstrained Bayesian Approximation for Inferring Selection. Molecular Biology and Evolution, 2013, 30, 1196-1205.	3.5	1,056
107	HIV-1 Clade B pol Evolution following Primary Infection. PLoS ONE, 2013, 8, e68188.	1.1	43
108	Characterizing HIV Transmission Networks Across the United States. Clinical Infectious Diseases, 2012, 55, 1135-1143.	2.9	120

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109	Detecting Individual Sites Subject to Episodic Diversifying Selection. <i>PLoS Genetics</i> , 2012, 8, e1002764.	1.5	1,455
110	Statistics and Truth in Phylogenomics. <i>Molecular Biology and Evolution</i> , 2012, 29, 457-472.	3.5	243
111	A counting renaissance: combining stochastic mapping and empirical Bayes to quickly detect amino acid sites under positive selection. <i>Bioinformatics</i> , 2012, 28, 3248-3256.	1.8	75
112	Inconsistencies in Estimating the Age of HIV-1 Subtypes Due to Heterotachy. <i>Molecular Biology and Evolution</i> , 2012, 29, 451-456.	3.5	65
113	In Vivo VL-Targeted Microbial Superantigen Induced Global Shifts in the B Cell Repertoire. <i>Journal of Immunology</i> , 2012, 189, 850-859.	0.4	9
114	Associations Between Phylogenetic Clustering and HLA Profile Among HIV-Infected Individuals in San Diego, California. <i>Journal of Infectious Diseases</i> , 2012, 205, 1529-1533.	1.9	10
115	Clinical, virologic, and immunologic correlates of HIV-1 intraclade B dual infection among men who have sex with men. <i>Aids</i> , 2012, 26, 157-165.	1.0	29
116	Higher HIV-1 genetic diversity is associated with AIDS and neuropsychological impairment. <i>Virology</i> , 2012, 433, 498-505.	1.1	11
117	Sexual transmission of predicted CXCR4-tropic HIV-1 likely originating from the source partner's seminal cells. <i>Virology</i> , 2012, 434, 2-4.	1.1	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. <i>Journal of Medical Virology</i> , 2012, 84, 1703-1709.	2.5	19
120	Evolution of Viral Genomes: Interplay Between Selection, Recombination, and Other Forces. <i>Methods in Molecular Biology</i> , 2012, 856, 239-272.	0.4	31
121	Deep Sequencing Reveals Minor Protease Resistance Mutations in Patients Failing a Protease Inhibitor Regimen. <i>Journal of Virology</i> , 2012, 86, 6231-6237.	1.5	63
122	Modeling HIV-1 Drug Resistance as Episodic Directional Selection. <i>PLoS Computational Biology</i> , 2012, 8, e1002507.	1.5	36
123	Transmitted HIV Type 1 Drug Resistance Among Individuals with Recent HIV Infection in East and Southern Africa. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 5-12.	0.5	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18732-18736.	3.3	375
126	A Random Effects Branch-Site Model for Detecting Episodic Diversifying Selection. <i>Molecular Biology and Evolution</i> , 2011, 28, 3033-3043.	3.5	383

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127	A Massively Parallel Sequencing Approach Uncovers Ancient Origins and High Genetic Variability of Endangered Przewalski's Horses. <i>Genome Biology and Evolution</i> , 2011, 3, 1096-1106.	1.1	51
128	Using phylogeography to characterize the origins of the HIV-1 subtype F epidemic in Romania. <i>Infection, Genetics and Evolution</i> , 2011, 11, 975-979.	1.0	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. <i>Journal of Virology</i> , 2011, 85, 8359-8367.	1.5	86
130	Purifying Selection Can Obscure the Ancient Age of Viral Lineages. <i>Molecular Biology and Evolution</i> , 2011, 28, 3355-3365.	3.5	186
131	Using HIV Transmission Networks to Investigate Community Effects in HIV Prevention Trials. <i>PLoS ONE</i> , 2011, 6, e27775.	1.1	34
132	Protease polymorphisms in HIV-1 subtype CRF01_AE represent selection by antiretroviral therapy and host immune pressure. <i>Aids</i> , 2010, 24, 411-416.	1.0	17
133	Benchmarking Multi-Rate Codon Models. <i>PLoS ONE</i> , 2010, 5, e11587.	1.1	11
134	DIVEIN: a web server to analyze phylogenies, sequence divergence, diversity, and informative sites. <i>BioTechniques</i> , 2010, 48, 405-408.	0.8	184
135	Datamonkey 2010: a suite of phylogenetic analysis tools for evolutionary biology. <i>Bioinformatics</i> , 2010, 26, 2455-2457.	1.8	1,158
136	Evolutionary Fingerprinting of Genes. <i>Molecular Biology and Evolution</i> , 2010, 27, 520-536.	3.5	57
137	Response to Comment on "The Origins of Sexually Transmitted HIV Among Men Who Have Sex with Men". <i>Science Translational Medicine</i> , 2010, 2, 501r1.	5.8	8
138	Comparison of Methods to Detect HIV Dual Infection. <i>AIDS Research and Human Retroviruses</i> , 2010, 26, 1291-1298.	0.5	35
139	The Relatedness of HIV Epidemics in the United States-Mexico Border Region. <i>AIDS Research and Human Retroviruses</i> , 2010, 26, 1273-1277.	0.5	11
140	The Origins of Sexually Transmitted HIV Among Men Who Have Sex with Men. <i>Science Translational Medicine</i> , 2010, 2, 18re1.	5.8	66
141	Phylodynamic Reconstruction Reveals Norovirus GII.4 Epidemic Expansions and their Molecular Determinants. <i>PLoS Pathogens</i> , 2010, 6, e1000884.	2.1	124
142	CodonTest: Modeling Amino Acid Substitution Preferences in Coding Sequences. <i>PLoS Computational Biology</i> , 2010, 6, e1000885.	1.5	73
143	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, 819-832.	3.5	59
144	Correcting the Bias of Empirical Frequency Parameter Estimators in Codon Models. <i>PLoS ONE</i> , 2010, 5, e11230.	1.1	49

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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. <i>Journal of Virology</i> , 2009, 83, 9901-9910.	1.5	76
147	Windshield splatter analysis with the Galaxy metagenomic pipeline. <i>Genome Research</i> , 2009, 19, 2144-2153.	2.4	68
148	An Evolutionary Model-Based Algorithm for Accurate Phylogenetic Breakpoint Mapping and Subtype Prediction in HIV-1. <i>PLoS Computational Biology</i> , 2009, 5, e1000581.	1.5	151
149	Are All Subtypes Created Equal? The Effectiveness of Antiretroviral Therapy against Non-Subtype B HIV-1. <i>Clinical Infectious Diseases</i> , 2009, 48, 1306-1309.	2.9	19
150	Phylogenetics of Infectious Disease Epidemics. <i>Genetics</i> , 2009, 183, 1421-1430.	1.2	200
151	Detection in 2009 of the Swine Origin Influenza A (H1N1) Virus by a Subtyping Microarray. <i>Journal of Clinical Microbiology</i> , 2009, 47, 3060-3061.	1.8	15
152	A public health model for the molecular surveillance of HIV transmission in San Diego, California. <i>Aids</i> , 2009, 23, 225-232.	1.0	111
153	Detecting Signatures of Selection from DNA Sequences Using Datamonkey. <i>Methods in Molecular Biology</i> , 2009, 537, 163-183.	0.4	71
154	Parsing Social Network Survey Data from Hidden Populations Using Stochastic Context-Free Grammars. <i>PLoS ONE</i> , 2009, 4, e6777.	1.1	14
155	Estimating selection pressures on HIV-1 using phylogenetic likelihood models. <i>Statistics in Medicine</i> , 2008, 27, 4779-4789.	0.8	19
156	Persistence of Transmitted Drug Resistance among Subjects with Primary Human Immunodeficiency Virus Infection. <i>Journal of Virology</i> , 2008, 82, 5510-5518.	1.5	192
157	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, 1809-1824.	3.5	106
158	Evolutionary and Transmission Dynamics of Reassortant H5N1 Influenza Virus in Indonesia. <i>PLoS Pathogens</i> , 2008, 4, e1000130.	2.1	61
159	Spidermonkey: rapid detection of co-evolving sites using Bayesian graphical models. <i>Bioinformatics</i> , 2008, 24, 1949-1950.	1.8	75
160	Population structure of the genes encoding the polymorphic <i>Plasmodium falciparum</i> apical membrane antigen 1: Implications for vaccine design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7857-7862.	3.3	83
161	Antiretroviral Drug Resistance and Risk Behavior Among Recently HIV-Infected Men Who Have Sex With Men. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2008, 47, 639-643.	0.9	28
162	Comparison of Immunogen Designs That Optimize Peptide Coverage: Reply to Fischer et al.. <i>PLoS Computational Biology</i> , 2008, 4, e25.	1.5	13

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