## Long term trends in the evolution of H(3) HA1 human in

Proceedings of the National Academy of Sciences of the Unite 94, 7712-7718

DOI: 10.1073/pnas.94.15.7712

**Citation Report** 

#	Article	IF	CITATIONS
1	Genetics and the origin of species: An introduction. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 7691-7697.	7.1	40
2	A structural difference between the cell surfaces of humans and the great apes. American Journal of Physical Anthropology, 1998, 107, 187-198.	2.1	155
3	Rapid evolution as an ecological process. Trends in Ecology and Evolution, 1998, 13, 329-332.	8.7	754
4	Antigenic Variation in Influenza Viruses. , 1999, , 377-390.		27
5	Replication of Orthomyxoviruses. Advances in Virus Research, 1999, 54, 319-348.	2.1	28
6	Positive selection on the H3 hemagglutinin gene of human influenza virus A. Molecular Biology and Evolution, 1999, 16, 1457-1465.	8.9	344
7	Genomic evolution during a 10,000-generation experiment with bacteria. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 3807-3812.	7.1	233
8	A complex of influenza hemagglutinin with a neutralizing antibody that binds outside the virus receptor binding site. Nature Structural Biology, 1999, 6, 530-534.	9.7	149
9	Selection of Receptor-Binding Variants of Human Influenza A and B Viruses in Baby Hamster Kidney Cells. Virology, 1999, 262, 31-38.	2.4	47
10	A novel amino acid substitution at the receptor-binding site on the hemagglutinin of H3N2 influenza A viruses isolated from 6 cases with acute encephalopathy during the 1997–1998 season in Tokyo. Archives of Virology, 1999, 144, 147-155.	2.1	33
11	Predicting the Evolution of Human Influenza A. Science, 1999, 286, 1921-1925.	12.6	444
12	EVOLUTIONARY BIOLOGY:Enhanced: Predictive Evolution. Science, 1999, 286, 1866-1867.	12.6	7
13	A method for detecting positive selection at single amino acid sites. Molecular Biology and Evolution, 1999, 16, 1315-1328.	8.9	451
14	Molecular epidemiology of viral infections. How sequence information helps us understand the evolution and dissemination of viruses. Review article. Apmis, 2000, 108, 81-97.	2.0	32
15	Evolution of avian influenza viruses. Veterinary Microbiology, 2000, 74, 15-27.	1.9	166
16	Evidence for evolutionary stasis and genetic drift by genetic analysis of two equine influenza H3 viruses isolated in France. Veterinary Microbiology, 2000, 74, 59-70.	1.9	21
17	Both point mutation and RNA recombination contribute to the sequence diversity of citrus viroid III. Virus Genes, 2000, 20, 243-252.	1.6	34
18	Effective Construction of DNA Vaccines Against Variable Influenza Genes by Homologous Recombination. Virology, 2000, 268, 244-250.	2.4	18

		CITATION REPORT		
#	Article		IF	CITATIONS
19	Are RNA Viruses Adapting or Merely Changing?. Journal of Molecular Evolution, 2000, 5	1, 12-20.	1.8	38
20	Maximum Likelihood Estimation on Large Phylogenies and Analysis of Adaptive Evolutic Influenza Virus A. Journal of Molecular Evolution, 2000, 51, 423-432.	on in Human	1.8	202
21	Evolution of Bovine Respiratory Syncytial Virus. Journal of Virology, 2000, 74, 10714-10	)728.	3.4	82
22	The Wilhelmine E Key 1999 invitational lecture. Predicting the evolution of human influ 91, 183-185.	enza A. , 2000,		32
23	Reevaluation of Amino Acid Variability of the Human Immunodeficiency Virus Type 1 gp Glycoprotein and Prediction of New Discontinuous Epitopes. Journal of Virology, 2000,	120 Envelope 74, 4335-4350.	3.4	98
24	Rapid Antiviral Effect of Inhaled Zanamivir in the Treatment of Naturally Occurring Influ Otherwise Healthy Adults. Journal of Infectious Diseases, 2000, 181, 1471-1474.	enza in	4.0	73
25	Immunology of avian influenza virus: a review. Developmental and Comparative Immun 269-283.	ology, 2000, 24,	2.3	196
26	Statistical methods for detecting molecular adaptation. Trends in Ecology and Evolutio 496-503.	n, 2000, 15,	8.7	1,532
27	Experimental evolution recapitulates natural evolution. Philosophical Transactions of th Society B: Biological Sciences, 2000, 355, 1677-1684.	e Royal	4.0	79
28	Global Epidemiology of Influenza: Past and Present. Annual Review of Medicine, 2000, S	51, 407-421.	12.2	686
29	Applied Evolution. Annual Review of Ecology, Evolution, and Systematics, 2001, 32, 18	3-217.	6.7	59
30	Positively selected amino acid sites in the entire coding region of hepatitis C virus subty 2001, 276, 83-87.	/pe 1b. Gene,	2.2	22
31	Changes in the HA and NA genes prior to the emergence of HPAI H7N1 avian influenza International Congress Series, 2001, 1219, 363-367.	viruses in Italy.	0.2	0
32	Phylogenetic studies of South African influenza A viruses: 1997–1999. International 2001, 1219, 139-145.	Congress Series,	0.2	0
33	Molecular evolution of influenza A/H3N2 viruses in the province of Québec (Canada) 1997–2000 period. Virus Research, 2001, 77, 89-96.	during the	2.2	10
34	Diagnosis of influenza virus: Coming to grips with the molecular era. Molecular Diagnos Therapy, 2001, 6, 291-305.	sis and	1.1	17
36	Strain variation, based on the hemagglutinin gene, in Norwegian ISA virus isolates colle to 2001: indications of recombination. Diseases of Aquatic Organisms, 2001, 47, 119-1	cted from 1987 .28.	1.0	67
37	Molecular Evolution of the ocnus and janus Genes in the Drosophila melanogaster Spec Molecular Biology and Evolution, 2001, 18, 801-811.	ies Subgroup.	8.9	47

#	Article	IF	CITATIONS
38	Molecular and phylogenetic analysis of haemagglutinin and neuraminidase sequences from recent human influenza type A (H3N2) viral isolates in Southern Greece. Archives of Virology, 2001, 146, 1899-1918.	2.1	8
39	Diverged evolution of recent equine-2 influenza (H3N8) viruses in the Western Hemisphere. Archives of Virology, 2001, 146, 1063-1074.	2.1	128
40	Changes in the haemagglutinin and the neuraminidase genes prior to the emergence of highly pathogenic H7N1 avian influenza viruses in Italy. Archives of Virology, 2001, 146, 963-973.	2.1	270
41	Hemagglutinin Residues of Recent Human A(H3N2) Influenza Viruses That Contribute to the Inability to Agglutinate Chicken Erythrocytes. Virology, 2001, 289, 74-85.	2.4	140
42	Bayesian Inference of Phylogeny and Its Impact on Evolutionary Biology. Science, 2001, 294, 2310-2314.	12.6	2,416
43	Predicting adaptive evolution. Nature Reviews Genetics, 2001, 2, 387-392.	16.3	138
44	Ferrets as a Transmission Model for Influenza: Sequence Changes inHA1of Type A (H3N2) Virus. Journal of Infectious Diseases, 2001, 184, 542-546.	4.0	92
45	Influenza virus antigens and â€~antigenic drift'. Perspectives in Medical Virology, 2002, 7, 49-85.	0.1	18
46	Hemagglutinin sequence clusters and the antigenic evolution of influenza A virus. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6263-6268.	7.1	205
48	Dynamics and selection of many-strain pathogens. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 17209-17214.	7.1	255
49	Emergence of an Influenza B Virus with Antigenic Change. Journal of Clinical Microbiology, 2002, 40, 3068-3070.	3.9	24
50	Mathematical Approaches for Emerging and Reemerging Infectious Diseases: Models, Methods, and Theory. The IMA Volumes in Mathematics and Its Applications, 2002, , .	0.5	75
51	Simulation Study of the Reliability and Robustness of the Statistical Methods for Detecting Positive Selection at Single Amino Acid Sites. Molecular Biology and Evolution, 2002, 19, 1865-1869.	8.9	91
52	Characterization of 2 Influenza A(H3N2) Clinical Isolates with Reduced Susceptibility to Neuraminidase Inhibitors Due to Mutations in the Hemagglutinin Gene. Journal of Infectious Diseases, 2002, 186, 1074-1080.	4.0	57
53	A viral sampling design for testing the molecular clock and for estimating evolutionary rates and divergence times. Bioinformatics, 2002, 18, 115-123.	4.1	49
54	Adaptive Evolution of Variable Region Genes Encoding an Unusual Type of Immunoglobulin in Camelids. Molecular Biology and Evolution, 2002, 19, 205-215.	8.9	48
55	Accuracy and Power of Bayes Prediction of Amino Acid Sites Under Positive Selection. Molecular Biology and Evolution, 2002, 19, 950-958.	8.9	388
56	Complex adaptive systems: Exploring the known, the unknown and the unknowable. Bulletin of the American Mathematical Society, 2002, 40, 3-20.	1.5	264

#	Article	IF	CITATIONS
57	Mapping Mutations on Phylogenies. Systematic Biology, 2002, 51, 729-739.	5.6	373
58	Imbroglios of Viral Taxonomy: Genetic Exchange and Failings of Phenetic Approaches. Journal of Bacteriology, 2002, 184, 4891-4905.	2.2	240
59	Inference of selection from multiple species alignments. Current Opinion in Genetics and Development, 2002, 12, 688-694.	3.3	183
60	Ecology and evolution of the flu. Trends in Ecology and Evolution, 2002, 17, 334-340.	8.7	233
61	DNA vaccination of ferrets with chimeric influenza A virus hemagglutinin (H3) genes. Vaccine, 2002, 20, 2045-2052.	3.8	18
62	Realities and enigmas of human viral influenza: pathogenesis, epidemiology and control. Vaccine, 2002, 20, 3068-3087.	3.8	253
63	Red Queen Dynamics of Protein Translation. Journal of Theoretical Biology, 2002, 218, 97-109.	1.7	30
64	Antigenic drift and variability of influenza viruses. Medical Microbiology and Immunology, 2002, 191, 133-138.	4.8	42
65	Implications of high RNA virus mutation rates: lethal mutagenesis and the antiviral drug ribavirin. Microbes and Infection, 2002, 4, 1301-1307.	1.9	80
66	Applications of selective neutrality tests to molecular ecology. Molecular Ecology, 2002, 11, 1245-1262.	3.9	150
67	The evolutionary significance of parasitism: do parasite-driven genetic dynamics occur ex silico?. Journal of Evolutionary Biology, 2002, 15, 1-9.	1.7	97
68	The effect of cross-immunity and seasonal forcing in a multi-strain epidemic model. Physica D: Nonlinear Phenomena, 2002, 165, 228-241.	2.8	95
69	The application of molecular phylogenetics to the analysis of viral genome diversity and evolution. Reviews in Medical Virology, 2002, 12, 221-238.	8.3	29
70	Dynamics of annual influenza A epidemics with immuno-selection. Journal of Mathematical Biology, 2003, 46, 504-536.	1.9	74
71	Receptor-binding properties of modern human influenza viruses primarily isolated in Vero and MDCK cells and chicken embryonated eggs. Virology, 2003, 313, 473-480.	2.4	102
72	Role of viruses in human evolution. American Journal of Physical Anthropology, 2003, 122, 14-46.	2.1	93
73	Ecological and immunological determinants of influenza evolution. Nature, 2003, 422, 428-433.	27.8	580
74	Unravelling angiosperm genome evolution by phylogenetic analysis of chromosomal duplication events. Nature, 2003, 422, 433-438.	27.8	1,470

			(
#	Article	IF	CITATIONS
75	Molecular evolution meets the genomics revolution. Nature Genetics, 2003, 33, 255-265.	21.4	120
76	Traveling waves in a model of influenza A drift. Journal of Theoretical Biology, 2003, 222, 437-445.	1.7	74
77	SEQUENCEDIVERGENCE, FUNCTIONALCONSTRAINT, ANDSELECTION INPROTEINEVOLUTION. Annual Review of Genomics and Human Genetics, 2003, 4, 213-235.	6.2	241
78	Applications of bioinformatics and computational biology to influenza surveillance and vaccine strain selection. Vaccine, 2003, 21, 1758-1761.	3.8	26
79	Measurably evolving populations. Trends in Ecology and Evolution, 2003, 18, 481-488.	8.7	371
81	Codon bias and frequency-dependent selection on the hemagglutinin epitopes of influenza A virus. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7152-7157.	7.1	154
82	Why are dengue virus serotypes so distantly related? Enhancement and limiting serotype similarity between dengue virus strains. Proceedings of the Royal Society B: Biological Sciences, 2003, 270, 2241-2247.	2.6	51
83	Restriction of Amino Acid Change in Influenza A Virus H3HA: Comparison of Amino Acid Changes Observed in Nature and In Vitro. Journal of Virology, 2003, 77, 10088-10098.	3.4	32
84	Influenza Evolution. , 2004, , 175-197.		1
85	The effects of strain heterology on the epidemiology of equine influenza in a vaccinated population. Proceedings of the Royal Society B: Biological Sciences, 2004, 271, 1547-1555.	2.6	40
86	Three-Dimensional Window Analysis for Detecting Positive Selection at Structural Regions of Proteins. Molecular Biology and Evolution, 2004, 21, 2352-2359.	8.9	36
87	Positive Selection Detection in 40,000 HumanImmunodeficiency Virus (HIV) Type 1 Sequences Automatically IdentifiesDrug Resistance and Positive Fitness Mutations in HIV Proteaseand ReverseTranscriptase. Journal of Virology, 2004, 78, 3722-3732.	3.4	91
88	A Universal Evolutionary Index for Amino Acid Changes. Molecular Biology and Evolution, 2004, 21, 1548-1556.	8.9	51
89	Detecting Selection in Noncoding Regions of Nucleotide Sequences. Genetics, 2004, 167, 949-958.	2.9	112
90	Virus Evolution. , 2004, , .		0
91	Genetic analysis of human H2N2 and early H3N2 influenza viruses, 1957–1972: evidence for genetic divergence and multiple reassortment events. Virology, 2004, 328, 101-119.	2.4	158
92	Phylogenetic analysis of a human group B rotavirus WH-1 detected in China in 2002. Journal of Medical Virology, 2004, 74, 662-667.	5.0	30
93	Cytokine induction in human cord blood lymphocytes after pulsing with UV-inactivated influenza viruses. Immunology Letters, 2004, 94, 201-207.	2.5	4

#	Article	IF	CITATIONS
94	Accuracy and Power of Statistical Methods for Detecting Adaptive Evolution in Protein Coding Sequences and for Identifying Positively Selected Sites. Genetics, 2004, 168, 1041-1051.	2.9	543
95	Influenza drift and epidemic size: the race between generating and escaping immunity. Theoretical Population Biology, 2004, 65, 179-191.	1.1	68
96	Alternate circulation of recent equine-2 influenza viruses (H3N8) from two distinct lineages in the United States. Virus Research, 2004, 100, 159-164.	2.2	39
97	Influenza evolution and immune selection. International Congress Series, 2004, 1263, 12-16.	0.2	3
98	Evolution and persistence of influenza A and other diseases. Mathematical Biosciences, 2004, 188, 17-28.	1.9	47
100	Quasispecies Dynamics and Evolution of Foot-and-Mouth Disease Virus. , 2004, , 262-304.		5
101	Adaptive Molecular Evolution. , 2004, , .		2
102	Mapping mutations on phylogenies. , 2005, , .		Ο
103	Challenges for identifying functionally important genetic variation: the promise of combining complementary research strategies. Molecular Ecology, 2005, 14, 3623-3642.	3.9	263
104	Entropy, disease, and new opportunities for chemical engineering research. AICHE Journal, 2005, 51, 3086-3090.	3.6	4
105	Molecular characterization of the HA gene of influenza type B viruses. Journal of Medical Virology, 2005, 77, 541-549.	5.0	34
106	Modelling antigenic drift in weekly flu incidence. Statistics in Medicine, 2005, 24, 3447-3461.	1.6	36
107	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees. PLoS Biology, 2005, 3, e170.	5.6	870
108	Accumulation of Amino Acid Substitutions Promotes Irreversible Structural Changes in the Hemagglutinin of Human Influenza AH3 Virus during Evolution. Journal of Virology, 2005, 79, 6472-6477.	3.4	42
109	High rate of viral evolution associated with the emergence of carnivore parvovirus. Proceedings of the United States of America, 2005, 102, 379-384.	7.1	471
110	Divergence Time of Porcine Reproductive and Respiratory Syndrome Virus Subtypes. Molecular Biology and Evolution, 2005, 22, 2131-2134.	8.9	110
111	Whole-Genome Analysis of Human Influenza A Virus Reveals Multiple Persistent Lineages and Reassortment among Recent H3N2 Viruses. PLoS Biology, 2005, 3, e300.	5.6	340
112	Dynamics of Two-Strain Influenza with Isolation and Partial Cross-Immunity. SIAM Journal on Applied Mathematics, 2005, 65, 964-982.	1.8	113

#	Apticie	IF	CITATIONS
#	Selectionism and Neutralism in Molecular Evolution. Molecular Biology and Evolution, 2005, 22.	IF	CHATIONS
113	2318-2342.	8.9	293
114	Analytical Methods for Studying the Evolution of Paralogs Using Duplicate Gene Datasets. Methods in Enzymology, 2005, 395, 724-745.	1.0	5
115	Molecular Signatures of Natural Selection. Annual Review of Genetics, 2005, 39, 197-218.	7.6	1,406
116	Divergent genetic evolution of hemagglutinin in influenza A H1N1 and A H1N2 subtypes isolated in the south-France since the winter of 2001–2002. Journal of Clinical Virology, 2005, 33, 230-236.	3.1	13
117	Inferring Evolutionary History through Inter- and Intraspecific DNA Sequence Comparison. , 2005, , 1-12.		2
118	Shaping the phylogenetic tree of influenza by cross-immunity. Theoretical Population Biology, 2006, 70, 164-173.	1.1	40
119	Development of Effective Vaccines against Pandemic Influenza. Immunity, 2006, 24, 5-9.	14.3	151
120	Reassortment between human A(H3N2) viruses is an important evolutionary mechanism. Vaccine, 2006, 24, 6683-6690.	3.8	38
121	Molecular clock and estimation of species divergence times. , 2006, , 223-258.		0
122	Detailed analysis of the genetic evolution of influenza virus during the course of an epidemic. Epidemiology and Infection, 2006, 134, 514-520.	2.1	25
123	Evolutionary implications of Avian Infectious Bronchitis Virus (AIBV) analysis. Cell Research, 2006, 16, 323-327.	12.0	7
124	Epochal Evolution Shapes the Phylodynamics of Interpandemic Influenza A (H3N2) in Humans. Science, 2006, 314, 1898-1903.	12.6	423
125	Molecular diversity of proteins in biological offense and defense systems. Molecular Diversity, 2006, 10, 511-514.	3.9	10
126	Prediction of possible mutations in H5N1 hemagglutitins of influenza A virus by means of logistic regression. Comparative Clinical Pathology, 2006, 15, 255-261.	0.7	20
127	Prediction of Mutations in H5N1 Hemagglutinins from Influenza A Virus. Protein and Peptide Letters, 2006, 13, 971-976.	0.9	21
128	Stochastic Processes Are Key Determinants of Short-Term Evolution in Influenza A Virus. PLoS Pathogens, 2006, 2, e125.	4.7	173
129	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
130	On the Varied Pattern of Evolution of 2 Fungal Genomes: A Critique of Hughes and Friedman. Molecular Biology and Evolution, 2006, 23, 2279-2282.	8.9	8

#	Article	IF	CITATIONS
131	Longitudinal Analysis of Genotype Distribution of Influenza A Virus from 2003 to 2005. Journal of Clinical Microbiology, 2006, 44, 3583-3588.	3.9	7
132	Epidemic dynamics and antigenic evolution in a single season of influenza A. Proceedings of the Royal Society B: Biological Sciences, 2006, 273, 1307-1316.	2.6	85
133	Avian Influenza Virus Exhibits Rapid Evolutionary Dynamics. Molecular Biology and Evolution, 2006, 23, 2336-2341.	8.9	203
134	Relaxed Phylogenetics and Dating with Confidence. PLoS Biology, 2006, 4, e88.	5.6	5,566
135	Influenza Escapes Immunity Along Neutral Networks. Science, 2006, 314, 1884-1886.	12.6	54
136	Simultaneous amino acid substitutions at antigenic sites drive influenza A hemagglutinin evolution. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6283-6288.	7.1	210
137	The generation of influenza outbreaks by a network of host immune responses against a limited set of antigenic types. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7711-7716.	7.1	96
138	Phylogenetic Analysis Reveals the Global Migration of Seasonal Influenza A Viruses. PLoS Pathogens, 2007, 3, e131.	4.7	136
139	On State-Space Reduction in Multi-Strain Pathogen Models, with an Application to Antigenic Drift in Influenza A. PLoS Computational Biology, 2007, 3, e159.	3.2	50
140	Evolution and Variation of the H3 Gene of Influenza A Virus and Interaction among Hosts. Intervirology, 2007, 50, 287-295.	2.8	12
141	Up to new tricks – A review of cross-species transmission of influenza A viruses. Animal Health Research Reviews, 2007, 8, 1-21.	3.1	51
142	Inferring natural selection operating on conservative and radical substitution at single amino acid sites. Genes and Genetic Systems, 2007, 82, 341-360.	0.7	12
143	Influenza vaccine: The challenge of antigenic drift. Vaccine, 2007, 25, 6852-6862.	3.8	568
144	The perpetuation and epidemic recurrence of communicable diseases in human populations. Comptes Rendus - Biologies, 2007, 330, 356-363.	0.2	4
145	Expression and diversity of Echinococcus multilocularis AgB genes in secondarily infected mice: evaluating the influence of T-cell immune selection on antigenic variation. Gene, 2007, 392, 98-105.	2.2	11
146	Ancestral Inference and the Study of Codon Bias Evolution: Implications for Molecular Evolutionary Analyses of the Drosophila melanogaster Subgroup. PLoS ONE, 2007, 2, e1065.	2.5	31
147	New methods for inferring population dynamics from microbial sequences. Infection, Genetics and Evolution, 2007, 7, 24-43.	2.3	18
148	The evolution of epidemic influenza. Nature Reviews Genetics, 2007, 8, 196-205.	16.3	462

	CHAIL	JN REPORT	
#	Article	IF	CITATIONS
149	The quest for natural selection in the age of comparative genomics. Heredity, 2007, 99, 567-579.	2.6	78
150	Exploring Variation in the d N /d S Ratio Among Sites and Lineages Using Mutational Mappings: Applications to the Influenza Virus. Journal of Molecular Evolution, 2007, 65, 340-348.	1.8	15
151	Counting labeled transitions in continuous-time Markov models of evolution. Journal of Mathematical Biology, 2007, 56, 391-412.	1.9	235
152	The variable codons of H3 influenza A virus haemagglutinin genes. Archives of Virology, 2007, 152, 11-24.	2.1	13
153	Prediction of Mutations Initiated by Internal Power in H3N2 Hemagglutinins of Influenza A Virus from North America. International Journal of Peptide Research and Therapeutics, 2008, 14, 41-51.	1.9	15
154	Rapid Evolution by Positive Darwinian Selection in T-Cell Antigen CD4 in Primates. Journal of Molecular Evolution, 2008, 66, 446-456.	1.8	33
155	The Evolutionary Dynamics of Human Influenza B Virus. Journal of Molecular Evolution, 2008, 66, 655-663.	1.8	194
156	Heterogeneous Selective Pressure Acting on Influenza B Victoria- and Yamagata-Like Hemagglutinins. Journal of Molecular Evolution, 2008, 67, 427-435.	1.8	7
157	Molecular evolution of influenza A (H3N2) viruses circulated in Fujian Province, China during the 1996–2004 period. Science in China Series C: Life Sciences, 2008, 51, 373-380.	1.3	2
158	Prediction of mutations engineered by randomness in H5N1 neuraminidases from influenza A virus. Amino Acids, 2008, 34, 81-90.	2.7	24
159	Prediction of mutations engineered by randomness in H5N1 hemagglutinins of influenza A virus. Amino Acids, 2008, 35, 365-373.	2.7	20
160	Fully Bayesian tests of neutrality using genealogical summary statistics. BMC Genetics, 2008, 9, 68.	2.7	27
161	Adaptive Molecular Evolution. , 2008, , 375-406.		13
162	Effects of single-point amino acid substitutions on the structure and function neuraminidase proteins in influenza A virus. Microbiology and Immunology, 2008, 52, 216-223.	1.4	13
163	Correlating novel variable and conserved motifs in the Hemagglutinin protein with significant biological functions. Virology Journal, 2008, 5, 91.	3.4	4
165	Methods for Analyzing Viral Evolution. , 2008, , 165-204.		5
166	Capturing escape in infectious disease dynamics. Trends in Ecology and Evolution, 2008, 23, 572-577.	8.7	26
167	Natural Selection for Nucleotide Usage at Synonymous and Nonsynonymous Sites in Influenza A Virus Genes. Journal of Virology, 2008, 82, 4938-4945.	3.4	25

ARTICLE IF CITATIONS Physiochemical Constraints in Influenza A Hemagglutinin., 2008,,. 0 168 Homologous Recombination Is Very Rare or Absent in Human Influenza A Virus. Journal of Virology, 3.4 2008, 82, 4807-4811. Smooth Skyride through a Rough Skyline: Bayesian Coalescent-Based Inference of Population 170 8.9 626 Dynamics. Molecular Biology and Evolution, 2008, 25, 1459-1471. Evolutionary Dynamics and Emergence of Panzootic H5N1 Influenza Viruses. PLoS Pathogens, 2008, 4, 171 143 e1000161. Molecular Epidemiology of A/H3N2 and A/H1N1 Influenza Virus during a Single Epidemic Season in the 172 4.7 97 United States. PLoS Pathogens, 2008, 4, e1000133. Genetic and Epidemiological Analysis of Influenza Virus Epidemics in Taiwan during 2003 to 2006. Journal of Clinical Microbiology, 2008, 46, 1426-1434. Genetic Analysis of Influenza A/H3N2 and A/H1N1 Viruses Circulating in Vietnam from 2001 to 2006. 174 3.9 17 Journal of Clinical Microbiology, 2008, 46, 399-405. Directionality in the evolution of influenza A haemagglutinin. Proceedings of the Royal Society B: 2.6 21 Biological Sciences, 2008, 275, 2455-2464. Bayesian analysis of amino acid substitution models. Philosophical Transactions of the Royal Society 176 4.0 42 B: Biological Sciences, 2008, 363, 3941-3953. Prediction of sites under adaptive evolution in cytochrome P450 sequences and their relationship to 1.5 substrate recognition sites. Pharmacogenetics and Genomics, 2008, 18, 467-476. Three Sampling Strategies to Predict Mutations in H5N1 Hemagglutitins from Influenza A Virus. 178 9 0.9 Protein and Peptide Letters, 2008, 15, 731-738. Learning to Count: Robust Estimates for Labeled Distances between Molecular Sequences. Molecular 179 8.9 Biology and Evolution, 2009, 26, 801-814. The Role of Genomics in Tracking the Evolution of Influenza A Virus. PLoS Pathogens, 2009, 5, e1000566. 180 4.7 81 Using a mutual information-based site transition network to map the genetic evolution of influenza 4.1 A/H3N2 virus. Bioinformatics, 2009, 25, 2309-2317. Molecular evolution of human influenza A viruses in a local area during eight influenza epidemics 182 2.1 24 from 2000 to 2007. Archives of Virology, 2009, 154, 285-295. Molecular characterization and phylogenetic analysis of H3N2 human influenza A viruses in Cheongiu, South Korea. Journal of Microbiology, 2009, 47, 91-100. Evolutionary analysis of the dynamics of viral infectious disease. Nature Reviews Genetics, 2009, 10, 184 16.3526 540-550. Influenza outbreaks. Cellular Microbiology, 2009, 11, 1016-1024. 2.1

#	Article	IF	CITATIONS
186	Genomic events underlying the changes in adamantane resistance among influenza A(H3N2) viruses during 2006–2008. Influenza and Other Respiratory Viruses, 2009, 3, 297-314.	3.4	21
187	Evolutionary epidemiology 20 years on: Challenges and prospects. Infection, Genetics and Evolution, 2009, 9, 108-123.	2.3	42
188	Evidence of a major role of GP64 in group I alphabaculovirus evolution. Virus Research, 2009, 142, 85-91.	2.2	17
189	Panorama phylogenetic diversity and distribution of type A influenza viruses based on their six internal gene sequences. Virology Journal, 2009, 6, 137.	3.4	27
191	Measuring Natural Selection on Genotypes and Phenotypes in the Wild. Cold Spring Harbor Symposia on Quantitative Biology, 2009, 74, 155-168.	1.1	55
192	Influenza epidemiology and characterization of influenza viruses in patients seeking treatment for acute fever in Cambodia. Epidemiology and Infection, 2010, 138, 199-209.	2.1	38
193	Statistical methods for detecting natural selection from genomic data. Genes and Genetic Systems, 2010, 85, 359-376.	0.7	31
194	Comparison of selection pressures on the HA gene of pandemic (2009) and seasonal human and swine influenza A H1 subtype viruses. Virology, 2010, 405, 314-321.	2.4	38
195	Models of RNA virus evolution and their roles in vaccine design. Immunome Research, 2010, 6, S5.	0.1	19
196	Guidelines for Identifying Homologous Recombination Events in Influenza A Virus. PLoS ONE, 2010, 5, e10434.	2.5	72
197	Genomic Signature-Based Identification of Influenza A Viruses Using RT-PCR/Electro-Spray Ionization Mass Spectrometry (ESI-MS) Technology. PLoS ONE, 2010, 5, e13293.	2.5	38
198	Low-dimensional clustering detects incipient dominant influenza strain clusters. Protein Engineering, Design and Selection, 2010, 23, 935-946.	2.1	28
199	Evolutionary Genetics of Human Enterovirus 71: Origin, Population Dynamics, Natural Selection, and Seasonal Periodicity of the VP1 Gene. Journal of Virology, 2010, 84, 3339-3350.	3.4	211
200	Microevolution of Canine Influenza Virus in Shelters and Its Molecular Epidemiology in the United States. Journal of Virology, 2010, 84, 12636-12645.	3.4	46
201	A two-tiered model for simulating the ecological and evolutionary dynamics of rapidly evolving viruses, with an application to influenza. Journal of the Royal Society Interface, 2010, 7, 1257-1274.	3.4	54
202	Occurrence of Mixed Populations of Influenza A Viruses That Can Be Maintained through Transmission in a Single Host and Potential for Reassortment. Journal of Clinical Microbiology, 2010, 48, 369-374.	3.9	18
203	Sustained oscillations in an evolutionary epidemiological model of influenza A drift. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2010, 466, 965-992.	2.1	21
204	Global Migration Dynamics Underlie Evolution and Persistence of Human Influenza A (H3N2). PLoS Pathogens, 2010, 6, e1000918.	4.7	151

#	Article	IF	CITATIONS
205	Antigenic variations of human influenza virus in Shiraz, Iran. Indian Journal of Medical Microbiology, 2010, 28, 114-119.	0.8	5
206	A 27-Amino-Acid Deletion in the Neuraminidase Stalk Supports Replication of an Avian H2N2 Influenza A Virus in the Respiratory Tract of Chickens. Journal of Virology, 2010, 84, 11831-11840.	3.4	69
207	Macrophage Receptors for Influenza A Virus: Role of the Macrophage Galactose-Type Lectin and Mannose Receptor in Viral Entry. Journal of Virology, 2010, 84, 3730-3737.	3.4	116
208	A new antigenic variant of human influenza A (H3N2) virus isolated from airport and community surveillance in Taiwan in early 2009. Virus Research, 2010, 151, 33-38.	2.2	14
209	Phylodynamic Analyses of Rotavirus Genotypes G9 and G12 Underscore Their Potential for Swift Global Spread. Molecular Biology and Evolution, 2010, 27, 2431-2436.	8.9	253
210	Development of real-time RT-PCR for human metapneumovirus. Acta Virologica, 2011, 55, 285-286.	0.8	2
212	Molecular characterization and pathogenicity of swine influenza H9N2 subtype virus A/swine/HeBei/012/2008/(H9N2). Acta Virologica, 2011, 55, 219-226.	0.8	7
213	Variation in the Analysis of Positively Selected Sites Using Nonsynonymous/Synonymous Rate Ratios: An Example Using Influenza Virus. PLoS ONE, 2011, 6, e19996.	2.5	21
214	Gnarled-Trunk Evolutionary Model of Influenza A Virus Hemagglutinin. PLoS ONE, 2011, 6, e25953.	2.5	30
215	Rohlin Distance and the Evolution of Influenza A Virus: Weak Attractors and Precursors. PLoS ONE, 2011, 6, e27924.	2.5	1
216	Equine influenza: A review of an unpredictable virus. Veterinary Journal, 2011, 189, 7-14.	1.7	76
217	Isolation and characterisation of equine influenza viruses (H3N8) from Europe and North America from 2008 to 2009. Veterinary Microbiology, 2011, 147, 19-27.	1.9	57
218	The Genomic Rate of Molecular Adaptation of the Human Influenza A Virus. Molecular Biology and Evolution, 2011, 28, 2443-2451.	8.9	150
219	Is There a Twelfth Protein-Coding Gene in the Genome of Influenza A? A Selection-Based Approach to the Detection of Overlapping Genes in Closely Related Sequences. Journal of Molecular Evolution, 2011, 73, 305-315.	1.8	18
220	Strength and tempo of selection revealed in viral gene genealogies. BMC Evolutionary Biology, 2011, 11, 220.	3.2	69
221	Characterization of Dihydrofolate Reductases from Multiple Strains of <i>Plasmodium falciparum</i> Using Mathematical Descriptors of Their Inhibitors. Chemistry and Biodiversity, 2011, 8, 440-453.	2.1	4
222	A dimensionless number for understanding the evolutionary dynamics of antigenically variable RNA viruses. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 3723-3730.	2.6	12
223	Quantifying selection and diversity in viruses by entropy methods, with application to the haemagglutinin of H3N2 influenza. Journal of the Royal Society Interface, 2011, 8, 1644-1653.	3.4	40

#	Article	IF	CITATIONS
224	Genetic analysis of HA gene of pandemic H1N1 2009 influenza viruses circulating in India. Indian Journal of Medical Microbiology, 2012, 30, 346-349.	0.8	2
225	Impact of cross-protective vaccines on epidemiological and evolutionary dynamics of influenza. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3173-3177.	7.1	60
226	Influenza emergence in the face of evolutionary constraints. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 645-652.	2.6	22
227	Detecting Patches of Protein Sites of Influenza A Viruses under Positive Selection. Molecular Biology and Evolution, 2012, 29, 2063-2071.	8.9	27
228	Clonal Interference in the Evolution of Influenza. Genetics, 2012, 192, 671-682.	2.9	158
229	Computational analysis of adaptive antigenic mutations of the human influenza hemagglutinin for vaccine strain selection. International Journal of Bioinformatics Research and Applications, 2012, 8, 81.	0.2	2
230	Canalization of the evolutionary trajectory of the human influenza virus. BMC Biology, 2012, 10, 38.	3.8	84
231	The evolutionary dynamics of a spatial multi-strain host–pathogen system with cross-immunity. Nonlinear Analysis: Hybrid Systems, 2012, 6, 741-753.	3.5	2
232	Phylogenetic Properties of RNA Viruses. PLoS ONE, 2012, 7, e44849.	2.5	30
233	Genetic evolution of the neuraminidase of influenza A (H3N2) viruses from 1968 to 2009 and its correspondence to haemagglutinin evolution. Journal of General Virology, 2012, 93, 1996-2007.	2.9	57
234	Mapping of H3N2 influenza antigenic evolution in China reveals a strategy for vaccine strain recommendation. Nature Communications, 2012, 3, 709.	12.8	88
235	Two-dimensional antigenic dendrogram and phylogenetic tree of avian influenza virus H5N1. FEMS Immunology and Medical Microbiology, 2012, 64, 205-211.	2.7	4
236	Substitutions Near the Receptor Binding Site Determine Major Antigenic Change During Influenza Virus Evolution. Science, 2013, 342, 976-979.	12.6	500
237	Genome-wide mutagenesis of influenza virus reveals unique plasticity of the hemagglutinin and NS1 proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20248-20253.	7.1	159
238	The evolutionary dynamics of receptor binding avidity in influenza A: a mathematical model for a new antigenic drift hypothesis. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120204.	4.0	12
239	Yeast Reveal a "Druggable―Rsp5/Nedd4 Network that Ameliorates α-Synuclein Toxicity in Neurons. Science, 2013, 342, 979-983.	12.6	234
240	Genome-scale evolution and phylodynamics of H5N1 influenza virus in China during 1996–2012. Veterinary Microbiology, 2013, 167, 383-393.	1.9	16
241	Timing of the emergence of new successful viral strains in seasonal influenza. Journal of Theoretical Biology, 2013, 329, 32-38.	1.7	6

#	Article	IF	CITATIONS
242	Detection of positive selection eliminating effects of structural constraints in hemagglutinin of H3N2 human influenza A virus. Infection, Genetics and Evolution, 2013, 16, 93-98.	2.3	4
243	Tracking recent adaptive evolution in microbial species using TimeZone. Nature Protocols, 2013, 8, 652-665.	12.0	23
244	The Roles of Competition and Mutation in Shaping Antigenic and Genetic Diversity in Influenza. PLoS Pathogens, 2013, 9, e1003104.	4.7	63
245	Viral Phylodynamics. PLoS Computational Biology, 2013, 9, e1002947.	3.2	340
246	Dynamical correlations in the escape strategy of Influenza A virus. Europhysics Letters, 2013, 101, 68003.	2.0	3
247	Identification of Differentially Evolved Genes: An Alternative Approach to Detection of Accelerated Molecular Evolution from Genome-Wide Comparative Data. Evolutionary Bioinformatics, 2013, 9, EBO.S12166.	1.2	2
248	Dynamically correlated mutations drive human Influenza A evolution. Scientific Reports, 2013, 3, 2705.	3.3	14
249	Integrating influenza antigenic dynamics with molecular evolution. ELife, 2014, 3, e01914.	6.0	299
250	Seasonality in the migration and establishment of H3N2 Influenza lineages with epidemic growth and decline. BMC Evolutionary Biology, 2014, 14, 272.	3.2	11
251	Influenza Pathogenesis and Control - Volume I. Current Topics in Microbiology and Immunology, 2014, , ,	1.1	11
252	Models of nucleotide substitution. , 2014, , 1-34.		1
253	Genetic and Antigenic Typing of Seasonal Influenza Virus Breakthrough Cases from a 2008-2009 Vaccine Efficacy Trial. Vaccine Journal, 2014, 21, 271-279.	3.1	9
254	Pathogen evolution and the immunological niche. Annals of the New York Academy of Sciences, 2014, 1320, 1-15.	3.8	59
255	Toward a method for tracking virus evolutionary trajectory applied to the pandemic H1N1 2009 influenza virus. Infection, Genetics and Evolution, 2014, 28, 351-357.	2.3	3
256	The hemagglutinin mutation E391K of pandemic 2009 influenza revisited. Molecular Phylogenetics and Evolution, 2014, 70, 29-36.	2.7	4
257	A synchronized global sweep of the internal genes of modern avian influenza virus. Nature, 2014, 508, 254-257.	27.8	206
258	Genomewide Analysis of Reassortment and Evolution of Human Influenza A(H3N2) Viruses Circulating between 1968 and 2011. Journal of Virology, 2014, 88, 2844-2857.	3.4	137
259	Surveillance of human influenza A(H3N2) virus from 1999 to 2009 in southern Italy. Epidemiology and Infection, 2014, 142, 933-939.	2.1	3

#	Article	IF	CITATIONS
260	Antigenic Analyses of Highly Pathogenic Avian Influenza A Viruses. Current Topics in Microbiology and Immunology, 2014, 385, 403-440.	1.1	5
261	Inter-Seasonal Influenza is Characterized by Extended Virus Transmission and Persistence. PLoS Pathogens, 2015, 11, e1004991.	4.7	25
262	Detection of influenza antigenic variants directly from clinical samples using polyclonal antibody based proximity ligation assays. Virology, 2015, 476, 151-158.	2.4	5
263	Applications in the search for genomic selection signatures in fish. Frontiers in Genetics, 2014, 5, 458.	2.3	53
264	Impact of vaccination on the molecular epidemiology and evolution of group A rotaviruses in Latin America and factors affecting vaccine efficacy. Infection, Genetics and Evolution, 2015, 34, 106-113.	2.3	13
265	Evolution of the hemagglutinin expressed by human influenza A(H1N1)pdm09 and A(H3N2) viruses circulating between 2008–2009 and 2013–2014 in Germany. International Journal of Medical Microbiology, 2015, 305, 762-775.	3.6	19
266	Population genetic processes affecting the mode of selective sweeps and effective population size in influenza virus H3N2. BMC Evolutionary Biology, 2016, 16, 156.	3.2	10
267	Rules of co-occurring mutations characterize the antigenic evolution of human influenza A/H3N2, A/H1N1 and B viruses. BMC Medical Genomics, 2016, 9, 69.	1.5	11
268	Determination of antigenicity-altering patches on the major surface protein of human influenza A/H3N2 viruses. Virus Evolution, 2016, 2, vev025.	4.9	21
269	Profile comparison revealed deviation from structural constraint at the positively selected sites. BioSystems, 2016, 147, 67-77.	2.0	0
270	Dynamic Convergent Evolution Drives the Passage Adaptation across 48 Years' History of H3N2 Influenza Evolution. Molecular Biology and Evolution, 2016, 33, 3133-3143.	8.9	16
271	Smoothed Bootstrap Aggregation for Assessing Selection Pressure at Amino Acid Sites. Molecular Biology and Evolution, 2016, 33, 2976-2989.	8.9	6
272	Phylodynamics of influenza A(H3N2) in South America, 1999–2012. Infection, Genetics and Evolution, 2016, 43, 312-320.	2.3	3
273	Influenza Virus: Dealing with a Drifting and Shifting Pathogen. Viral Immunology, 2018, 31, 174-183.	1.3	232
274	Stability of the Influenza Virus Hemagglutinin Protein Correlates with Evolutionary Dynamics. MSphere, 2018, 3, .	2.9	31
275	Molecular and epidemiological analysis of pandemic and postâ€pandemic influenza A(H1N1)pdm09 virus from central India. Journal of Medical Virology, 2018, 90, 447-455.	5.0	9
276	Causes and Consequences of Spatial Within-Host Viral Spread. Viruses, 2018, 10, 627.	3.3	57
277	Molecular evolution of hemagglutinin gene of Influenza A virus. Frontiers in Bioscience - Scholar, 2018, 10, 101-118.	2.1	12

#	Article	IF	CITATIONS
278	Immunodominance of Antigenic Site B in the Hemagglutinin of the Current H3N2 Influenza Virus in Humans and Mice. Journal of Virology, 2018, 92, .	3.4	24
279	Measuring Immunological Age: From T Cell Repertoires to Populations. , 2018, , 1-62.		4
280	Deep mutational scanning of hemagglutinin helps predict evolutionary fates of human H3N2 influenza variants. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8276-E8285.	7.1	156
281	Changes in the Receptor-Binding Properties of H3N2 Viruses during Long-Term Circulation in Humans. Biochemistry (Moscow), 2019, 84, 1177-1185.	1.5	3
282	Allele-specific nonstationarity in evolution of influenza A virus surface proteins. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 21104-21112.	7.1	10
283	Abundance of HPV L1 Intra-Genotype Variants With Capsid Epitopic Modifications Found Within Low- and High-Grade Pap Smears With Potential Implications for Vaccinology. Frontiers in Genetics, 2019, 10, 489.	2.3	6
284	Structures and functions linked to genome-wide adaptation of human influenza A viruses. Scientific Reports, 2019, 9, 6267.	3.3	4
285	The Value of the Tree of Life. , 2019, , 75-116.		0
286	Anticipating time-dependent antigenic variants of influenza A (H3N2) viruses. Infection, Genetics and Evolution, 2019, 67, 67-72.	2.3	3
287	Individual immune selection pressure has limited impact on seasonal influenza virus evolution. Nature Ecology and Evolution, 2019, 3, 302-311.	7.8	25
288	The Ecology and Evolution of Influenza Viruses. Cold Spring Harbor Perspectives in Medicine, 2020, 10, a038489.	6.2	97
289	An epidemic model for an evolving pathogen with strain-dependent immunity. Mathematical Biosciences, 2020, 330, 108480.	1.9	2
290	Adsorptive mutation and N-linked glycosylation modulate influenza virus antigenicity and fitness. Emerging Microbes and Infections, 2020, 9, 2622-2631.	6.5	7
291	An open source tool to infer epidemiological and immunological dynamics from serological data: serosolver. PLoS Computational Biology, 2020, 16, e1007840.	3.2	13
292	Linking influenza virus evolution within and between human hosts. Virus Evolution, 2020, 6, veaa010.	4.9	47
293	Biased Mutation and Selection in RNA Viruses. Molecular Biology and Evolution, 2021, 38, 575-588.	8.9	43
294	Computational investigations of the immune response to repeated influenza infections and vaccinations. Royal Society Open Science, 2021, 8, 201433.	2.4	1
295	Machine Learning Prediction and Experimental Validation of Antigenic Drift in H3 Influenza A Viruses in Swine. MSphere, 2021, 6, .	2.9	13

#	ARTICLE	IF	CITATIONS
296	A human coronavirus evolves antigenically to escape antibody immunity. PLoS Pathogens, 2021, 17, e1009453.	4.7	183
297	Raman spectroscopy in cell biology and microbiology. Journal of Raman Spectroscopy, 2021, 52, 2348-2443.	2.5	81
298	Inference of population genetic parameters from an irregular time series of seasonal influenza virus sequences. Genetics, 2021, 217, .	2.9	1
300	New Directions in the Mathematics of Infectious Disease. The IMA Volumes in Mathematics and Its Applications, 2002, , 1-5.	0.5	4
301	New Directions in the Mathematics of Infectious Disease. The IMA Volumes in Mathematics and Its Applications, 2002, , 1-5.	0.5	2
302	Generation and Characterization of Candidate Vaccine Viruses for Prepandemic Influenza Vaccines. Current Topics in Microbiology and Immunology, 2009, 333, 83-108.	1.1	21
304	Phylogeny reconstruction: overview. , 2006, , 73-99.		1
305	Maximum likelihood methods. , 2006, , 100-144.		3
306	Bayesian methods. , 2006, , 145-184.		1
307	Neutral and adaptive protein evolution. , 2006, , 259-292.		6
307 309	Neutral and adaptive protein evolution. , 2006, , 259-292. Codon-Substitution Models for Heterogeneous Selection Pressure at Amino Acid Sites. Genetics, 2000, 155, 431-449.	2.9	6 2,064
307 309 310	Neutral and adaptive protein evolution., 2006, , 259-292.         Codon-Substitution Models for Heterogeneous Selection Pressure at Amino Acid Sites. Genetics, 2000, 155, 431-449.         Mutations as Missing Data: Inferences on the Ages and Distributions of Nonsynonymous and Synonymous Mutations. Genetics, 2001, 159, 401-411.	2.9 2.9	6 2,064 23
307 309 310 311	Neutral and adaptive protein evolution. , 2006, , 259-292.         Codon-Substitution Models for Heterogeneous Selection Pressure at Amino Acid Sites. Genetics, 2000, 155, 431-449.         Mutations as Missing Data: Inferences on the Ages and Distributions of Nonsynonymous and Synonymous Mutations. Genetics, 2001, 159, 401-411.         Effect of Recombination on the Accuracy of the Likelihood Method for Detecting Positive Selection at Amino Acid Sites. Genetics, 2003, 164, 1229-1236.	2.9 2.9 2.9	6 2,064 23 507
307 309 310 311 315	Neutral and adaptive protein evolution. , 2006, , 259-292.         Codon-Substitution Models for Heterogeneous Selection Pressure at Amino Acid Sites. Genetics, 2000, 155, 431-449.         Mutations as Missing Data: Inferences on the Ages and Distributions of Nonsynonymous and Synonymous Mutations. Genetics, 2001, 159, 401-411.         Effect of Recombination on the Accuracy of the Likelihood Method for Detecting Positive Selection at Amino Acid Sites. Genetics, 2003, 164, 1229-1236.         Genomic Evolution, Patterns of Global Dissemination, and Interspecies Transmission of Human and Simian T-cell Leukemia/Lymphotropic Viruses. Genome Research, 1999, 9, 525-540.	2.9 2.9 2.9 5.5	6 2,064 23 507 180
307 309 310 311 315 316	Neutral and adaptive protein evolution. , 2006, , 259-292.Codon-Substitution Models for Heterogeneous Selection Pressure at Amino Acid Sites. Genetics, 2000, 155, 431-449.Mutations as Missing Data: Inferences on the Ages and Distributions of Nonsynonymous and Synonymous Mutations. Genetics, 2001, 159, 401-411.Effect of Recombination on the Accuracy of the Likelihood Method for Detecting Positive Selection at Amino Acid Sites. Genetics, 2003, 164, 1229-1236.Genomic Evolution, Patterns of Global Dissemination, and Interspecies Transmission of Human and Simian T-cell Leukemia/Lymphotropic Viruses. Genome Research, 1999, 9, 525-540.Independence of Evolutionary and Mutational Rates after Transmission of Avian Influenza Viruses to Swine. Journal of Virology, 1999, 73, 1878-1884.	2.9 2.9 2.9 5.5 3.4	6 2,064 23 507 180 63
307 309 310 311 315 316	Neutral and adaptive protein evolution., 2006, , 259-292.         Codon-Substitution Models for Heterogeneous Selection Pressure at Amino Acid Sites. Genetics, 2000, 155, 431-449.         Mutations as Missing Data: Inferences on the Ages and Distributions of Nonsynonymous and Synonymous Mutations. Genetics, 2001, 159, 401-411.         Effect of Recombination on the Accuracy of the Likelihood Method for Detecting Positive Selection at Amino Acid Sites. Genetics, 2003, 164, 1229-1236.         Genomic Evolution, Patterns of Global Dissemination, and Interspecies Transmission of Human and Simian T-cell Leukemia/Lymphotropic Viruses. Genome Research, 1999, 9, 525-540.         Independence of Evolutionary and Mutational Rates after Transmission of Avian Influenza Viruses to Swine. Journal of Virology, 1999, 73, 1878-1884.         Comparative Analysis of Evolutionary Mechanisms of the Hemagglutinin and Three Internal Protein Genes of Influenza B Virus: Multiple Cocirculating Lineages and Frequent Reassortment of the NP, M, and NS Genes. Journal of Virology, 1999, 73, 4413-4426.	2.9 2.9 2.9 5.5 3.4 3.4	6 2,064 23 507 180 63 107
<ul> <li>307</li> <li>309</li> <li>310</li> <li>311</li> <li>315</li> <li>316</li> <li>317</li> <li>318</li> </ul>	Neutral and adaptive protein evolution. , 2006, , 259-292.         Codon-Substitution Models for Heterogeneous Selection Pressure at Amino Acid Sites. Genetics, 2000, 155, 431-449.         Mutations as Missing Data: Inferences on the Ages and Distributions of Nonsynonymous and Synonymous Mutations. Genetics, 2001, 159, 401-411.         Effect of Recombination on the Accuracy of the Likelihood Method for Detecting Positive Selection at Amino Acid Sites. Genetics, 2003, 164, 1229-1236.         Genomic Evolution, Patterns of Global Dissemination, and Interspecies Transmission of Human and Simian T-cell Leukemia/Lymphotropic Viruses. Genome Research, 1999, 9, 525-540.         Independence of Evolutionary and Mutational Rates after Transmission of Avian Influenza Viruses to Swine. Journal of Virology, 1999, 73, 1878-1884.         Comparative Analysis of Evolutionary Mechanisms of the Hemagglutinin and Three Internal Protein Genes of Influenza B Virus: Multiple Cocirculating Lineages and Frequent Reassortment of the NP, M, and NS Genes. Journal of Virology, 1999, 73, 4413-4426.         The Persistent Circulation of Enterovirus 71 in People's Republic of China: Causing Emerging Nationwide Epidemics Since 2008. PLoS ONE, 2011, 6, e25662.	2.9 2.9 2.9 5.5 3.4 3.4 2.5	6 2,064 23 507 180 63 63 107 147

#	Article	IF	CITATIONS
320	Identification of Low- and High-Impact Hemagglutinin Amino Acid Substitutions That Drive Antigenic Drift of Influenza A(H1N1) Viruses. PLoS Pathogens, 2016, 12, e1005526.	4.7	58
321	The effective rate of influenza reassortment is limited during human infection. PLoS Pathogens, 2017, 13, e1006203.	4.7	42
322	Genetic and Antigenic Analysis of the First A/New Caledonia/20/99-like H1N1 Influenza Isolates Reported in the Americas. Emerging Infectious Diseases, 2002, 8, 408-412.	4.3	23
323	Virological surveillance in Africa can contribute to early detection of new genetic and antigenic lineages of influenza viruses. Journal of Infection in Developing Countries, 2011, 5, 270-277.	1.2	9
324	Selection of predicted siRNA as potential antiviral therapeutic agent against influenza virus. Bioinformation, 2011, 6, 340-343.	0.5	11
325	The contrasting phylodynamics of human influenza B viruses. ELife, 2015, 4, e05055.	6.0	166
326	The effects of a deleterious mutation load on patterns of influenza A/H3N2's antigenic evolution in humans. ELife, 2015, 4, e07361.	6.0	65
327	Phylodynamic theory of persistence, extinction and speciation of rapidly adapting pathogens. ELife, 2019, 8, .	6.0	30
328	A large effective population size for established within-host influenza virus infection. ELife, 2020, 9, .	6.0	15
329	Poor protective potential of influenza nucleoprotein antibodies despite wide prevalence. Immunology and Cell Biology, 2022, 100, 49-60.	2.3	9
330	A Mutation–Selection Model of Protein Evolution under Persistent Positive Selection. Molecular Biology and Evolution, 2022, 39, .	8.9	10
331	MAXIMUM LIKELIHOOD ANALYSIS OF ADAPTIVE EVOLUTION IN HIV-1 GP120 ENV GENE. , 2000, , .		15
332	Molecular Phylogenies and Virulence Evolution. , 2002, , 262-276.		0
333	Models of amino acid and codon substitution. , 2006, , 40-70.		1
334	Models of nucleotide substitution. , 2006, , 3-39.		0
335	Simulating molecular evolution. , 2006, , 293-307.		7
337	Comparison of methods and tests on trees. , 2006, , 185-220.		0
338	Viral bioinformatics. , 2008, , 429-452.		0

#	Article	IF	Citations
339	Large-Scale Phylogenetic Analysis of Emerging Infectious Diseases. Lecture Notes in Mathematics, 2008, , 39-76.	0.2	0
340	VII.2 Mathematical Biology. , 2010, , 837-848.		1
341	Phylogeny reconstruction: overview. , 2014, , 70-101.		0
342	Comparison of phylogenetic methods and tests on trees. , 2014, , 153-181.		0
343	Molecular clock and estimation of species divergence times. , 2014, , 361-389.		0
344	Models of amino acid and codon substitution. , 2014, , 35-69.		0
345	Maximum likelihood methods. , 2014, , 102-152.		0
346	Bayesian theory. , 2014, , 182-213.		0
347	Simulating molecular evolution. , 2014, , 418-441.		2
348	Neutral and adaptive protein evolution. , 2014, , 390-417.		0
350	Bayesian phylogenetics. , 2014, , 263-307.		0
351	Coalescent theory and species trees. , 2014, , 308-360.		0
352	Bayesian computation (MCMC). , 2014, , 214-262.		0
353	Swine and Avian Influenza Outbreaks in Recent Times. , 2017, , 39-61.		0
354	Measuring Immunological Age: From T cell Repertoires to Populations. , 2018, , 1-60.		0
357	Measuring Immunological Age: From T Cell Repertoires to Populations. , 2019, , 63-124.		0
364	Application of neural network to predict mutations in proteins from influenza A viruses - A review of our approaches with implication for predicting mutations in coronaviruses. Journal of Physics: Conference Series, 2020, 1682, 012019.	0.4	4
370	Phylogenetic Comparison of Influenza Virus Isolates from Three Medical Centers in Tehran with the Vaccine Strains during 2008-2009. Iranian Journal of Medical Sciences, 2011, 36, 172-7.	0.4	2

		CITATION REPORT	Г
#	Article	IF	CITATIONS
371	A statistical analysis of antigenic similarity among influenza A (H3N2) viruses. Heliyon, 2021, 7, o	208384. 3.2	2
373	Intra- and inter-host evolution of H9N2 influenza A virus in Japanese quail. Virus Evolution, 2022, veac001.	8, 4.9	8
374	Molecular and Antigenic Characterization of Avian H9N2 Viruses in Southern China. Microbiolog Spectrum, 2022, 10, e0082221.	y 3.0	17
375	Antigenic characterization of influenza and SARS-CoV-2 viruses. Analytical and Bioanalytical Chemistry, 2022, 414, 2841-2881.	3.7	11
376	Molecular Detection of Avian Influenza Virus in Wild Birds in Morocco, 2016–2019. Avian Dise 2021, 66, .	ases, 1.0	4
381	Cenetic Analysis and Phylogenetic Characterization of Pandemic (H1N1) 2009 Influenza Viruses Found in Nagasaki, Japan. Japanese Journal of Infectious Diseases, 2011, 64, 195-203.	that 1.2	8
389	Evolutionary features of a prolific subtype of avian influenza A virus in European waterfowl. Virus Evolution, 2022, 8, .	4.9	6
390	Quantifying Mutational Response to Track the Evolution of SARS-CoV-2 Spike Variants: Introduc Statistical-Mechanics-Guided Machine Learning Method. Journal of Physical Chemistry B, 2022, 1 7895-7905.	ing a 26, 2.6	5
392	Next-generation development and application of codon model in evolution. Frontiers in Genetics	, 0, 14, 2.3	0
393	Spatial genetic structure of 2009 H1N1 pandemic influenza established as a result of interactior human populations in mainland China. PLoS ONE, 2023, 18, e0284716.	with 2.5	0
394	Have Diagnostics, Therapies, and Vaccines Made the Difference in the Pandemic Evolution of CC in Comparison with "Spanish Flu�. Pathogens, 2023, 12, 868.	VID-19 2.8	3