

# David Posada

## List of Publications by Year in descending order

Source: [//exaly.com/author-pdf/7854501/publications.pdf](https://exaly.com/author-pdf/7854501/publications.pdf)

Version: 2024-02-01

180  
papers

83,860  
citations

18677

59  
h-index

4798

163  
g-index

216  
all docs

216  
docs citations

216  
times ranked

53211  
citing authors

#	ARTICLE	IF	CITATIONS
1	MODELTEST: testing the model of DNA substitution.. <i>Bioinformatics</i> , 1998, 14, 817-818.	4.2	18,840
2	jModelTest 2: more models, new heuristics and parallel computing. <i>Nature Methods</i> , 2012, 9, 772-772.	19.2	13,908
3	jModelTest: Phylogenetic Model Averaging. <i>Molecular Biology and Evolution</i> , 2008, 25, 1253-1256.	9.0	9,494
4	TCS: a computer program to estimate gene genealogies. <i>Molecular Ecology</i> , 2000, 9, 1657-1659.	3.5	8,734
5	Model Selection and Model Averaging in Phylogenetics: Advantages of Akaike Information Criterion and Bayesian Approaches Over Likelihood Ratio Tests. <i>Systematic Biology</i> , 2004, 53, 793-808.	5.9	3,555
6	ProtTest: selection of best-fit models of protein evolution. <i>Bioinformatics</i> , 2005, 21, 2104-2105.	4.2	2,825
7	ProtTest 3: fast selection of best-fit models of protein evolution. <i>Bioinformatics</i> , 2011, 27, 1164-1165.	4.2	2,488
8	GeoDis: a program for the cladistic nested analysis of the geographical distribution of genetic haplotypes. <i>Molecular Ecology</i> , 2000, 9, 487-488.	3.5	1,610
9	RDP3: a flexible and fast computer program for analyzing recombination. <i>Bioinformatics</i> , 2010, 26, 2462-2463.	4.2	1,536
10	PHYLOGEOGRAPHIC HISTORY OF THE LAND SNAIL CANDIDULA UNIFASCIATA (HELICELLINAE,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 387 <i>International Journal of Organic Evolution</i> , 2002, 56, 1776-1788.	2.2	1,376
11	Intraspecific gene genealogies: trees grafting into networks. <i>Trends in Ecology and Evolution</i> , 2001, 16, 37-45.	8.6	1,374
12	Evaluation of methods for detecting recombination from DNA sequences: Computer simulations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 13757-13762.	7.4	1,361
13	ModelTest-NG: A New and Scalable Tool for the Selection of DNA and Protein Evolutionary Models. <i>Molecular Biology and Evolution</i> , 2020, 37, 291-294.	9.0	1,182
14	RDP2: recombination detection and analysis from sequence alignments. <i>Bioinformatics</i> , 2005, 21, 260-262.	4.2	910
15	Automated Phylogenetic Detection of Recombination Using a Genetic Algorithm. <i>Molecular Biology and Evolution</i> , 2006, 23, 1891-1901.	9.0	885
16	GARD: a genetic algorithm for recombination detection. <i>Bioinformatics</i> , 2006, 22, 3096-3098.	4.2	764
17	A Modified Bootscan Algorithm for Automated Identification of Recombinant Sequences and Recombination Breakpoints. <i>AIDS Research and Human Retroviruses</i> , 2005, 21, 98-102.	1.2	762
18	Selecting the Best-Fit Model of Nucleotide Substitution. <i>Systematic Biology</i> , 2001, 50, 580-601.	5.9	727

#	ARTICLE	IF	CITATIONS
19	An Exact Nonparametric Method for Inferring Mosaic Structure in Sequence Triplets. <i>Genetics</i> , 2007, 176, 1035-1047.	2.9	712
20	The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , 2014, 346, 56-61.	19.6	539
21	The causes and consequences of HIV evolution. <i>Nature Reviews Genetics</i> , 2004, 5, 52-61.	16.4	450
22	Selecting the Best-Fit Model of Nucleotide Substitution. <i>Systematic Biology</i> , 2001, 50, 580-601.	5.9	446
23	The Effect of Recombination on the Accuracy of Phylogeny Estimation. <i>Journal of Molecular Evolution</i> , 2002, 54, 396-402.	1.8	426
24	Pharmacogenetic Study of Statin Therapy and Cholesterol Reduction. <i>JAMA - Journal of the American Medical Association</i> , 2004, 291, 2821.	6.9	411
25	ALTER: program-oriented conversion of DNA and protein alignments. <i>Nucleic Acids Research</i> , 2010, 38, W14-W18.	13.8	385
26	TCS: estimating gene genealogies. , 2002, , .		382
27	Evaluation of Methods for Detecting Recombination from DNA Sequences: Empirical Data. <i>Molecular Biology and Evolution</i> , 2002, 19, 708-717.	9.0	340
28	Mitochondrial DNA phylogeography and population history of the grey wolf <i>Canis lupus</i> . <i>Molecular Ecology</i> , 1999, 8, 2089-2103.	3.5	321
29	Classifying the evolutionary and ecological features of neoplasms. <i>Nature Reviews Cancer</i> , 2017, 17, 605-619.	28.2	315
30	ModelTest Server: a web-based tool for the statistical selection of models of nucleotide substitution online. <i>Nucleic Acids Research</i> , 2006, 34, W700-W703.	13.8	299
31	Recombination in Evolutionary Genomics. <i>Annual Review of Genetics</i> , 2002, 36, 75-97.	7.7	274
32	Selection of Models of DNA Evolution with jModelTest. <i>Methods in Molecular Biology</i> , 2009, 537, 93-112.	0.7	206
33	Using MODELTEST and PAUP * to Select a Model of Nucleotide Substitution. <i>Current Protocols in Bioinformatics</i> , 2003, 00, Unit 6.5.	2.7	204
34	Nested clade analysis statistics. <i>Molecular Ecology Notes</i> , 2006, 6, 590-593.	1.7	185
35	A comparison of tools for the simulation of genomic next-generation sequencing data. <i>Nature Reviews Genetics</i> , 2016, 17, 459-469.	16.4	169
36	MtArt: A New Model of Amino Acid Replacement for Arthropoda. <i>Molecular Biology and Evolution</i> , 2006, 24, 1-5.	9.0	161

#	ARTICLE	IF	CITATIONS
37	Widespread Recombination in Published Animal mtDNA Sequences1. <i>Molecular Biology and Evolution</i> , 2005, 22, 925-933.	9.0	155
38	An Evolutionary Model-Based Algorithm for Accurate Phylogenetic Breakpoint Mapping and Subtype Prediction in HIV-1. <i>PLoS Computational Biology</i> , 2009, 5, e1000581.	3.0	155
39	Selecting Models of Nucleotide Substitution: An Application to Human Immunodeficiency Virus 1 (HIV-1). <i>Molecular Biology and Evolution</i> , 2001, 18, 897-906.	9.0	141
40	<i>SimPhy</i> : Phylogenomic Simulation of Gene, Locus, and Species Trees. <i>Systematic Biology</i> , 2016, 65, 334-344.	5.9	131
41	A First Insight into the Genome of the Filter-Feeder Mussel <i>Mytilus galloprovincialis</i> . <i>PLoS ONE</i> , 2016, 11, e0151561.	2.5	126
42	Phylogenomics suggests oxygen availability as a driving force in Thaumarchaeota evolution. <i>ISME Journal</i> , 2019, 13, 2150-2161.	9.8	116
43	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. <i>Genome Biology</i> , 2020, 21, 275.	9.1	114
44	Molecular systematics of European <i>Hyalodaphnia</i> : the role of contemporary hybridization in ancient species. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000, 267, 1833-1842.	2.7	113
45	Analysing recombination in nucleotide sequences. <i>Molecular Ecology Resources</i> , 2011, 11, 943-955.	4.9	111
46	The Evolutionary Value of Recombination Is Constrained by Genome Modularity. <i>PLoS Genetics</i> , 2005, 1, e51.	3.3	105
47	Tree Scanning. <i>Genetics</i> , 2005, 169, 441-453.	2.9	105
48	A Comparison of Phylogenetic Network Methods Using Computer Simulation. <i>PLoS ONE</i> , 2008, 3, e1913.	2.5	98
49	Individual sequence variability and functional activities of fibrinogen-related proteins (FREPs) in the Mediterranean mussel ( <i>Mytilus galloprovincialis</i> ) suggest ancient and complex immune recognition models in invertebrates. <i>Developmental and Comparative Immunology</i> , 2011, 35, 334-344.	2.2	94
50	PHYLOGENETIC EVIDENCE FOR MULTIPLE SYMPATRIC ECOLOGICAL DIVERSIFICATION IN A MARINE SNAIL. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 1600-1612.	2.2	93
51	RNA-Seq in <i>Mytilus galloprovincialis</i> : comparative transcriptomics and expression profiles among different tissues. <i>BMC Genomics</i> , 2015, 16, 728.	2.9	90
52	Parallel Evolution of the Genetic Code in Arthropod Mitochondrial Genomes. <i>PLoS Biology</i> , 2006, 4, e127.	5.3	88
53	<i>jmodeltest</i> .org: selection of nucleotide substitution models on the cloud. <i>Bioinformatics</i> , 2014, 30, 1310-1311.	4.2	86
54	Cryptic species of <i>Clavelina</i> (Asciacea) in two different habitats: harbours and rocky littoral zones in the northwestern Mediterranean. <i>Marine Biology</i> , 2001, 139, 455-462.	1.5	77

#	ARTICLE	IF	CITATIONS
55	The Effect of Recombination on the Reconstruction of Ancestral Sequences. <i>Genetics</i> , 2010, 184, 1133-1139.	2.9	75
56	Coalescent Simulation of Intracodon Recombination. <i>Genetics</i> , 2010, 184, 429-437.	2.9	73
57	Phylogeography and speciation of colour morphs in the colonial ascidian <i>Pseudodistoma crucigaster</i> . <i>Molecular Ecology</i> , 2004, 13, 3125-3136.	3.5	72
58	Multilocus inference of species trees and DNA barcoding. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150335.	4.1	70
59	SPERM COMPETITIVE ABILITY AND GENETIC RELATEDNESS IN <i>DROSOPHILA MELANOGASTER</i> : SIMILARITY BREEDS CONTEMPT. <i>Evolution; International Journal of Organic Evolution</i> , 2002, 56, 1789-1795.	2.2	69
60	PHYLOGEOGRAPHIC HISTORY OF THE LAND SNAIL <i>CANDIDULA UNIFASCIATA</i> (HELICELLINAE,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 547 <i>International Journal of Organic Evolution</i> , 2002, 56, 1776.	2.2	63
61	Multiregional Tumor Trees Are Not Phylogenies. <i>Trends in Cancer</i> , 2017, 3, 546-550.	7.7	61
62	Using models of nucleotide evolution to build phylogenetic trees. <i>Developmental and Comparative Immunology</i> , 2005, 29, 211-227.	2.2	59
63	The Evolution and Appearance of C3 Duplications in Fish Originate an Exclusive Teleost c3 Gene Form with Anti-Inflammatory Activity. <i>PLoS ONE</i> , 2014, 9, e99673.	2.5	56
64	Simple (Wrong) Models for Complex Trees: A Case from Retroviridae. <i>Molecular Biology and Evolution</i> , 2001, 18, 271-275.	9.0	55
65	The De Novo Transcriptome and Its Functional Annotation in the Seed Beetle <i>Callosobruchus maculatus</i> . <i>PLoS ONE</i> , 2016, 11, e0158565.	2.5	55
66	Rapid evolution and biogeographic spread in a colorectal cancer. <i>Nature Communications</i> , 2019, 10, 5139.	12.8	53
67	Genetic variation at MHC, mitochondrial and microsatellite loci in isolated populations of Brown trout ( <i>Salmo Årutta</i> ). <i>Conservation Genetics</i> , 2006, 7, 515-530.	1.5	52
68	Gene expression analysis of clams <i>Ruditapes philippinarum</i> and <i>Ruditapes decussatus</i> following bacterial infection yields molecular insights into pathogen resistance and immunity. <i>Developmental and Comparative Immunology</i> , 2012, 36, 140-149.	2.2	51
69	Recodon: Coalescent simulation of coding DNA sequences with recombination, migration and demography. <i>BMC Bioinformatics</i> , 2007, 8, 458.	2.6	49
70	Protein evolution along phylogenetic histories under structurally constrained substitution models. <i>Bioinformatics</i> , 2013, 29, 3020-3028.	4.2	49
71	Are the sexual, somatic and genetic characters enough to solve nomenclatural problems in lumbricid taxonomy?. <i>Soil Biology and Biochemistry</i> , 2009, 41, 2257-2271.	8.8	48
72	The mussel <i>Xenostrobus securis</i> : a well-established alien invader in the Ria de Vigo (Spain, NE Atlantic). <i>Biological Invasions</i> , 2010, 12, 2091-2103.	2.4	48

#	ARTICLE	IF	CITATIONS
73	Evidence for survival of Pleistocene climatic changes in Northern refugia by the land snail <i>Trochoidea geyeri</i> (SoÅ³s 1926) (Helicellinae, Stylommatophora). <i>BMC Evolutionary Biology</i> , 2003, 3, 8.	3.1	47
74	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. <i>Genome Research</i> , 2021, 31, 635-644.	5.5	46
75	The Inversion of the Control Region in Three Mitogenomes Provides Further Evidence for an Asymmetric Model of Vertebrate mtDNA Replication. <i>PLoS ONE</i> , 2014, 9, e106654.	2.5	46
76	Multigene phylogeny of Malagasy day geckos of the genus <i>Phelsuma</i> . <i>Molecular Phylogenetics and Evolution</i> , 2009, 52, 530-537.	2.8	45
77	Recombination favors the evolution of drug resistance in HIV-1 during antiretroviral therapy. <i>Infection, Genetics and Evolution</i> , 2007, 7, 476-483.	2.3	44
78	Identification of a novel HIV-1 complex circulating recombinant form (CRF18_cpx) of Central African origin in Cuba. <i>Aids</i> , 2005, 19, 1155-1163.	2.1	43
79	A Bayesian Supertree Model for Genome-Wide Species Tree Reconstruction. <i>Systematic Biology</i> , 2016, 65, 397-416.	5.9	43
80	ProtTest-HPC: Fast Selection of Best-Fit Models of Protein Evolution. <i>Lecture Notes in Computer Science</i> , 2011, , 177-184.	2.0	42
81	Inverted Replication of Vertebrate Mitochondria. <i>Molecular Biology and Evolution</i> , 2008, 25, 805-808.	9.0	41
82	Simulation of Genome-Wide Evolution under Heterogeneous Substitution Models and Complex Multispecies Coalescent Histories. <i>Molecular Biology and Evolution</i> , 2014, 31, 1295-1301.	9.0	41
83	Phylogenomics for Systematic Biology. <i>Systematic Biology</i> , 2016, 65, 353-356.	5.9	41
84	Recombination Estimation Under Complex Evolutionary Models with the Coalescent Composite-Likelihood Method. <i>Molecular Biology and Evolution</i> , 2006, 23, 817-827.	9.0	40
85	Molecular phylogeny and biogeographic history of the European <i>Maja</i> spider crabs (Decapoda, Tj ETQq1 1 0.784314.rgBT /Overlock 1	2.8	40
86	Population Genetics of the <i>porB</i> Gene of <i>Neisseria gonorrhoeae</i> : Different Dynamics in Different Homology Groups. <i>Molecular Biology and Evolution</i> , 2000, 17, 423-436.	9.0	39
87	The Effect of Branch Length Variation on the Selection of Models of Molecular Evolution. <i>Journal of Molecular Evolution</i> , 2001, 52, 434-444.	1.8	36
88	GenDecoder: genetic code prediction for metazoan mitochondria. <i>Nucleic Acids Research</i> , 2006, 34, W389-W393.	13.8	36
89	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data. <i>Genome Biology</i> , 2022, 23, 37.	9.1	36
90	Phylogenetics of HIV-1 from a Phase III AIDS Vaccine Trial in Bangkok, Thailand. <i>PLoS ONE</i> , 2011, 6, e16902.	2.5	35

#	ARTICLE	IF	CITATIONS
91	Selective Pressures on Human Cancer Genes along the Evolution of Mammals. <i>Genes</i> , 2018, 9, 582.	2.4	35
92	Genome-Wide Heterogeneity of Nucleotide Substitution Model Fit. <i>Genome Biology and Evolution</i> , 2011, 3, 896-908.	2.6	34
93	Genetic Identification of the Northeastern Atlantic Spiny Spider Crab as <i>Maja Brachydactyla</i> Balss, 1922. <i>Journal of Crustacean Biology</i> , 2008, 28, 76-81.	0.7	33
94	Phylogenetic systematics of day geckos, genus <i>Phelsuma</i> , based on molecular and morphological data (Squamata: Gekkonidae). <i>Zootaxa</i> , 2010, 2429, .	0.6	32
95	Coestimation of recombination, substitution and molecular adaptation rates by approximate Bayesian computation. <i>Heredity</i> , 2014, 112, 255-264.	2.7	32
96	Unveiling the Molecular Clock in the Presence of Recombination. <i>Molecular Biology and Evolution</i> , 2001, 18, 1976-1978.	9.0	30
97	CellCoal: Coalescent Simulation of Single-Cell Sequencing Samples. <i>Molecular Biology and Evolution</i> , 2020, 37, 1535-1542.	9.0	30
98	Genetic variation of the spiny spider crab <i>Maja brachydactyla</i> in the northeastern Atlantic. <i>Marine Ecology - Progress Series</i> , 2008, 362, 211-223.	1.9	30
99	<i>Perkinsoide chabelardi</i> n. gen., a protozoan parasite with an intermediate evolutionary position: possible cause of the decrease of sardine fisheries?. <i>Environmental Microbiology</i> , 2006, 8, 1105-1114.	3.8	29
100	Phylogenetic affinities of Comoroan and East African day geckos (genus <i>Phelsuma</i> ): Multiple natural colonisations, introductions and island radiations. <i>Molecular Phylogenetics and Evolution</i> , 2007, 43, 685-692.	2.8	29
101	Polymorphisms in the sequences of <i>Marteilia</i> internal transcribed spacer region of the ribosomal RNA genes (ITS-1) in Spain: genetic types are not related with bivalve hosts. <i>Journal of Fish Diseases</i> , 2005, 28, 331-338.	1.9	28
102	The evolution of the mitochondrial genetic code in arthropods revisited. <i>Mitochondrial DNA</i> , 2012, 23, 84-91.	0.8	27
103	Computational Design of Centralized HIV-1 Genes. <i>Current HIV Research</i> , 2010, 8, 613-621.	0.5	27
104	Ethnic differences in the adaptation rate of HIV gp120 from a vaccine trial. <i>Retrovirology</i> , 2009, 6, 67.	2.2	26
105	Mitochondrial genome sequencing of marine leukaemias reveals cancer contagion between clam species in the Seas of Southern Europe. <i>ELife</i> , 2022, 11, .	5.8	26
106	TreeScan: a bioinformatic application to search for genotype/phenotype associations using haplotype trees. <i>Bioinformatics</i> , 2005, 21, 2130-2132.	4.2	25
107	Widespread Gene Conversion of Alpha-2-Fucosyltransferase Genes in Mammals. <i>Journal of Molecular Evolution</i> , 2009, 69, 22-31.	1.8	24
108	RecPhyloXML: a format for reconciled gene trees. <i>Bioinformatics</i> , 2018, 34, 3646-3652.	4.2	24

#	ARTICLE	IF	CITATIONS
109	Pathway information extracted from 25 years of pathway figures. <i>Genome Biology</i> , 2020, 21, 273.	9.1	24
110	Selecting models of evolution. , 0, , 345-361.		23
111	Phylogeography and diversification history of the day-gecko genus <i>Phelsuma</i> in the Seychelles islands. <i>BMC Evolutionary Biology</i> , 2013, 13, 3.	3.1	23
112	Increased Hepatitis E Virus Seroprevalence Correlates with Lower CD4+ Cell Counts in HIV-Infected Persons in Argentina. <i>PLoS ONE</i> , 2016, 11, e0160082.	2.5	23
113	Simulating haplotype blocks in the human genome. <i>Bioinformatics</i> , 2003, 19, 289-290.	4.2	22
114	Identification of 3 Phylogenetically Related HIV-1 BG Intersubtype Circulating Recombinant Forms in Cuba. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2007, 45, 151-160.	2.1	22
115	Characterization of Reticulate Networks Based on the Coalescent with Recombination. <i>Molecular Biology and Evolution</i> , 2008, 25, 2517-2520.	9.0	22
116	Phylodynamics of HIV-1 from a Phase-III AIDS Vaccine Trial in North America. <i>Molecular Biology and Evolution</i> , 2010, 27, 417-425.	9.0	22
117	CodABC: A Computational Framework to Coestimate Recombination, Substitution, and Molecular Adaptation Rates by Approximate Bayesian Computation. <i>Molecular Biology and Evolution</i> , 2015, 32, 1109-1112.	9.0	22
118	Lack of temporal structure in the short term HIV-1 evolution within asymptomatic na <sup>+</sup> ve patients. <i>Virology</i> , 2007, 362, 294-303.	2.4	21
119	Disease progression and evolution of the HIV-1 env gene in 24 infected infants. <i>Infection, Genetics and Evolution</i> , 2008, 8, 110-120.	2.3	21
120	Cryptic diversity within the endemic prehensile-tailed gecko <i>Urocyon inexpectata</i> across the Seychelles Islands: patterns of phylogeographical structure and isolation at the multilocus level. <i>Biological Journal of the Linnean Society</i> , 2011, 104, 177-191.	1.6	21
121	Low-mitochondrial diversity and lack of structure in the velvet swimming crab <i>Necora puber</i> along the Galician coast. <i>Marine Biology</i> , 2009, 156, 1039-1048.	1.5	20
122	New Approach to an Old Problem: Incorporating Signal from Gap-Rich Regions of ITS and rDNA Large Subunit into Phylogenetic Analyses to Resolve the <i>Peltigera canina</i> Species Complex. <i>Mycologia</i> , 2003, 95, 1181.	1.9	19
123	A Coalescent Model of Recombination Hotspots. <i>Genetics</i> , 2003, 164, 407-417.	2.9	19
124	Introgression and genetic structure in northern Spanish Atlantic salmon ( <i>Salmo salar</i> L.) populations according to mtDNA data. <i>Conservation Genetics</i> , 2008, 9, 157-169.	1.5	18
125	Malignant transformation and genetic alterations are uncoupled in early colorectal cancer progression. <i>BMC Biology</i> , 2020, 18, 116.	3.8	18
126	How does recombination affect phylogeny estimation?. <i>Trends in Ecology and Evolution</i> , 2000, 15, 489-490.	8.6	17



#	ARTICLE	IF	CITATIONS
127	Phylogenetic Models of Molecular Evolution: Next-Generation Data, Fit, and Performance. <i>Journal of Molecular Evolution</i> , 2013, 76, 351-352.	1.8	16
128	<i>Mytilus galloprovincialis</i> Lmk. in northern Africa. <i>Journal of Experimental Marine Biology and Ecology</i> , 1998, 223, 271-283.	1.5	15
129	Spatio-temporal genetic variability in sea trout ( <i>Salmo trutta</i> ) populations from north-western Spain. <i>Freshwater Biology</i> , 2007, 52, 510-524.	2.3	15
130	Species Tree Estimation from Genome-Wide Data with <i>guenomu</i> . <i>Methods in Molecular Biology</i> , 2017, 1525, 461-478.	0.7	15
131	Sensitivity to sequencing depth in single-cell cancer genomics. <i>Genome Medicine</i> , 2018, 10, 29.	8.4	13
132	The Influence of Re combination on the Estimation of Selection from Coding Sequence Alignments. , 2014, , 112-125.		12
133	SARS-CoV-2 Evolution and Spike-Specific CD4+ T-Cell Response in Persistent COVID-19 with Severe HIV Immune Suppression. <i>Microorganisms</i> , 2022, 10, 143.	3.6	12
134	Limited genomic reconstruction of SARS-CoV-2 transmission history within local epidemiological clusters. <i>Virus Evolution</i> , 2022, 8, veac008.	4.8	12
135	Joint analysis of species and genetic variation to quantify the role of dispersal and environmental constraints in community turnover. <i>Ecography</i> , 2022, 2022, .	4.6	12
136	On the phylogenetic placement of human T cell leukemia virus type 1 sequences associated with an Andean mummy. <i>Infection, Genetics and Evolution</i> , 2006, 6, 91-96.	2.3	11
137	Characterization of phylogenetic networks with <i>NetTest</i> . <i>BMC Bioinformatics</i> , 2010, 11, 268.	2.6	11
138	Origin and Length Distribution of Unidirectional Prokaryotic Overlapping Genes. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 19-27.	1.9	11
139	Felsenstein Phylogenetic Likelihood. <i>Journal of Molecular Evolution</i> , 2021, 89, 134-145.	1.8	11
140	Somatic variant calling from single-cell DNA sequencing data. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2978-2985.	4.1	11
141	Phylogenomic Analyses of 2,786 Genes in 158 Lineages Support a Root of the Eukaryotic Tree of Life between Opisthokonts and All Other Lineages. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.6	11
142	HIV-1 infected monozygotic twins: a tale of two outcomes. <i>BMC Evolutionary Biology</i> , 2011, 11, 62.	3.1	10
143	Testing for Universal Common Ancestry. <i>Systematic Biology</i> , 2014, 63, 838-842.	5.9	10
144	Clonality and timing of relapsing colorectal cancer metastasis revealed through whole-genome single-cell sequencing. <i>Cancer Letters</i> , 2022, 543, 215767.	7.2	10

#	ARTICLE	IF	CITATIONS
145	Introduction to recombination detection. , 2009, , 493-518.		9
146	Evolutionary history of <i>Trachylepis</i> skinks in the Seychelles islands: introgressive hybridization, morphological evolution and geographic structure. <i>Biological Journal of the Linnean Society</i> , 2016, 119, 15-36.	1.6	9
147	Identification and characterization of microsatellite loci in the spiny spider crab <i>Maja brachydactyla</i> . <i>Conservation Genetics</i> , 2006, 8, 245-247.	1.5	8
148	Longitudinal Population Analysis of Dual Infection with Recombination in Two Strains of HIV Type 1 Subtype B in an Individual from a Phase 3 HIV Vaccine Efficacy Trial. <i>AIDS Research and Human Retroviruses</i> , 2006, 22, 968-978.	1.2	8
149	Unsorted Homology within Locus and Species Trees. <i>Systematic Biology</i> , 2014, 63, 988-992.	5.9	8
150	Emerging Frontiers in the Study of Molecular Evolution. <i>Journal of Molecular Evolution</i> , 2020, 88, 211-226.	1.8	8
151	OmniSARS2: A Highly Sensitive and Specific RT-qPCR-Based COVID-19 Diagnostic Method Designed to Withstand SARS-CoV-2 Lineage Evolution. <i>Biomedicines</i> , 2021, 9, 1314.	3.2	8
152	Insights into origins of Human T-cell Lymphotropic Virus Type 1 based on new strains from aboriginal people of Canada. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1822-1830.	2.3	7
153	Cancer Molecular Evolution. <i>Journal of Molecular Evolution</i> , 2015, 81, 81-83.	1.8	7
154	Infinitely long branches and an informal test of common ancestry. <i>Biology Direct</i> , 2016, 11, 19.	4.6	7
155	NGSphy: phylogenomic simulation of next-generation sequencing data. <i>Bioinformatics</i> , 2018, 34, 2506-2507.	4.2	7
156	Simulation of coding sequence evolution. , 2012, , 126-132.		7
157	Molecular clock analysis. , 2009, , 362-380.		6
158	High-performance computing selection of models of DNA substitution for multicore clusters. <i>International Journal of High Performance Computing Applications</i> , 2014, 28, 112-125.	3.8	6
159	Genetic Code Prediction for Metazoan Mitochondria with GenDecoder. <i>Methods in Molecular Biology</i> , 2009, 537, 233-242.	0.7	6
160	Proving universal common ancestry with similar sequences. <i>Trends in Evolutionary Biology</i> , 2012, 4, 5.	0.4	5
161	Somatic evolution of marine transmissible leukemias in the common cockle, <i>Cerastoderma edule</i> . <i>Nature Cancer</i> , 2023, 4, 1575-1591.	12.0	5
162	Coalescent models derived from birth-death processes. <i>Theoretical Population Biology</i> , 2021, 142, 1-11.	1.0	3

#	ARTICLE	IF	CITATIONS
163	Phylogenetic Approaches to Molecular Epidemiology. , 2002, , 25-40.		3
164	Single-cell mtDNA heteroplasmy in colorectal cancer. Genomics, 2022, 114, 110315.	2.9	3
165	HPC selection of models of DNA substitution. , 2011, , .		2
166	Selection of Phylogenetic Models of Molecular Evolution. , 0, , .		2
167	Deciphering the Evolution of the Mitochondrial Genetic Code in Arthropods. , 0, , .		2
168	Estimation of Species Trees. , 0, , .		2
169	Phylogenetics of HIV. , 2002, , 121-160.		2
170	Base-Pairing Versatility Determines Wobble Sites in tRNA Anticodons of Vertebrate Mitogenomes. PLoS ONE, 2012, 7, e36605.	2.5	2
171	Nested clade phylogeographic analysis for conservation genetics. , 2001, , 80-103.		1
172	Automatic Prediction of the Genetic Code. Lecture Notes in Computer Science, 2009, , 1125-1129.	2.0	1
173	Phylogenetic Likelihood. , 0, , .		1
174	A Fault Tolerant Workflow for Reproducible Research. , 2014, , .		1
175	Characterization of Reticulate Networks Based on the Coalescent with Recombination. Molecular Biology and Evolution, 2009, 26, 951-951.	9.0	0
176	Accurate Selection of Models of Protein Evolution. Advances in Intelligent and Soft Computing, 2010, , 117-121.	0.0	0
177	Adapting Reproducible Research Capabilities to Resilient Distributed Calculations. International Journal of Grid and High Performance Computing, 2016, 8, 58-69.	0.9	0
178	Exploring the Solution Space of Cancer Evolution Inference Frameworks for Single-Cell Sequencing Data. Communications in Computer and Information Science, 2023, , 70-81.	0.0	0
179	Crykey: Rapid identification of SARS-CoV-2 cryptic mutations in wastewater. Nature Communications, 2024, 15, .	12.8	0
180	Dispersal history of SARS-CoV-2 in Galicia, Spain. Journal of Medical Virology, 2024, 96, .	4.9	0