

David Posada

List of Publications by Citations

Source: <https://exaly.com/author-pdf/7854501/david-posada-publications-by-citations.pdf>

Version: 2024-04-23

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

174
papers

67,863
citations

55
h-index

201
g-index

201
ext. papers

75,070
ext. citations

6.6
avg, IF

8.53
L-index

#	Paper	IF	Citations
174	MODELTEST: testing the model of DNA substitution. <i>Bioinformatics</i> , 1998 , 14, 817-8	7.2	17513
173	jModelTest 2: more models, new heuristics and parallel computing. <i>Nature Methods</i> , 2012 , 9, 772	21.6	9965
172	jModelTest: phylogenetic model averaging. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1253-6	8.3	8077
171	TCS: a computer program to estimate gene genealogies. <i>Molecular Ecology</i> , 2000 , 9, 1657-9	5.7	7618
170	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	8.4	2994
169	ProtTest: selection of best-fit models of protein evolution. <i>Bioinformatics</i> , 2005 , 21, 2104-5	7.2	2556
168	ProtTest 3: fast selection of best-fit models of protein evolution. <i>Bioinformatics</i> , 2011 , 27, 1164-5	7.2	1864
167	RDP3: a flexible and fast computer program for analyzing recombination. <i>Bioinformatics</i> , 2010 , 26, 2462-3	7.2	1392
166	Intraspecific gene genealogies: trees grafting into networks. <i>Trends in Ecology and Evolution</i> , 2001 , 16, 37-45	10.9	1240
165	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, 13757-62	11.5	1104
164	GeoDis: a program for the cladistic nested analysis of the geographical distribution of genetic haplotypes. <i>Molecular Ecology</i> , 2000 , 9, 487-8	5.7	1094
163	RDP2: recombination detection and analysis from sequence alignments. <i>Bioinformatics</i> , 2005 , 21, 260-2	7.2	863
162	Automated phylogenetic detection of recombination using a genetic algorithm. <i>Molecular Biology and Evolution</i> , 2006 , 23, 1891-901	8.3	679
161	Selecting the Best-Fit Model of Nucleotide Substitution. <i>Systematic Biology</i> , 2001 , 50, 580-601	8.4	669
160	A modified bootscan algorithm for automated identification of recombinant sequences and recombination breakpoints. <i>AIDS Research and Human Retroviruses</i> , 2005 , 21, 98-102	1.6	615
159	GARD: a genetic algorithm for recombination detection. <i>Bioinformatics</i> , 2006 , 22, 3096-8	7.2	581
158	An exact nonparametric method for inferring mosaic structure in sequence triplets. <i>Genetics</i> , 2007 , 176, 1035-47	4	565

157	Phylogeographic history of the land snail <i>Candidula unifasciata</i> (Helicellinae, Stylommatophora): fragmentation, corridor migration, and secondary contact. <i>Evolution; International Journal of Organic Evolution</i> , 2002 , 56, 1776-88	3.8	447
156	The causes and consequences of HIV evolution. <i>Nature Reviews Genetics</i> , 2004 , 5, 52-61	30.1	372
155	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	8.3	372
154	HIV epidemiology. The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , 2014 , 346, 56-61	33.3	370
153	The effect of recombination on the accuracy of phylogeny estimation. <i>Journal of Molecular Evolution</i> , 2002 , 54, 396-402	3.1	335
152	Pharmacogenetic study of statin therapy and cholesterol reduction. <i>JAMA - Journal of the American Medical Association</i> , 2004 , 291, 2821-7	27.4	325
151	Evaluation of methods for detecting recombination from DNA sequences: empirical data. <i>Molecular Biology and Evolution</i> , 2002 , 19, 708-17	8.3	304
150	ALTER: program-oriented conversion of DNA and protein alignments. <i>Nucleic Acids Research</i> , 2010 , 38, W14-8	20.1	265
149	Mitochondrial DNA phylogeography and population history of the grey wolf <i>canis lupus</i> . <i>Molecular Ecology</i> , 1999 , 8, 2089-103	5.7	264
148	ModelTest Server: a web-based tool for the statistical selection of models of nucleotide substitution online. <i>Nucleic Acids Research</i> , 2006 , 34, W700-3	20.1	255
147	Selecting the Best-Fit Model of Nucleotide Substitution. <i>Systematic Biology</i> , 2001 , 50, 580-601	8.4	254
146	Recombination in evolutionary genomics. <i>Annual Review of Genetics</i> , 2002 , 36, 75-97	14.5	236
145	Classifying the evolutionary and ecological features of neoplasms. <i>Nature Reviews Cancer</i> , 2017 , 17, 605-619	31.9	208
144	TCS: estimating gene genealogies 2002 ,		178
143	Selection of models of DNA evolution with jModelTest. <i>Methods in Molecular Biology</i> , 2009 , 537, 93-112	1.4	176
142	Using MODELTEST and PAUP* to select a model of nucleotide substitution. <i>Current Protocols in Bioinformatics</i> , 2003 , Chapter 6, Unit 6.5	24.2	137
141	Widespread recombination in published animal mtDNA sequences. <i>Molecular Biology and Evolution</i> , 2005 , 22, 925-33	8.3	134
140	An evolutionary model-based algorithm for accurate phylogenetic breakpoint mapping and subtype prediction in HIV-1. <i>PLoS Computational Biology</i> , 2009 , 5, e1000581	5	130

139	MtArt: a new model of amino acid replacement for Arthropoda. <i>Molecular Biology and Evolution</i> , 2007 , 24, 1-5	8.3	127
138	Selecting models of nucleotide substitution: an application to human immunodeficiency virus 1 (HIV-1). <i>Molecular Biology and Evolution</i> , 2001 , 18, 897-906	8.3	127
137	A comparison of tools for the simulation of genomic next-generation sequencing data. <i>Nature Reviews Genetics</i> , 2016 , 17, 459-69	30.1	97
136	The evolutionary value of recombination is constrained by genome modularity. <i>PLoS Genetics</i> , 2005 , 1, e51	6	95
135	Molecular systematics of European Hyalodaphnia: the role of contemporary hybridization in ancient species. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000 , 267, 1833-42	4.4	91
134	A First Insight into the Genome of the Filter-Feeder Mussel <i>Mytilus galloprovincialis</i> . <i>PLoS ONE</i> , 2016 , 11, e0151561	3.7	90
133	A comparison of phylogenetic network methods using computer simulation. <i>PLoS ONE</i> , 2008 , 3, e1913	3.7	87
132	Analysing recombination in nucleotide sequences. <i>Molecular Ecology Resources</i> , 2011 , 11, 943-55	8.4	85
131	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, 334-44	3.2	81
130	Phylogenetic evidence for multiple sympatric ecological diversification in a marine snail. <i>Evolution; International Journal of Organic Evolution</i> , 2007 , 61, 1600-12	3.8	81
129	Effective population sizes: missing measures and missing concepts. <i>Animal Conservation</i> , 1999 , 2, 317-319	9.2	78
128	SimPhy: Phylogenomic Simulation of Gene, Locus, and Species Trees. <i>Systematic Biology</i> , 2016 , 65, 334-48	8.4	76
127	Parallel evolution of the genetic code in arthropod mitochondrial genomes. <i>PLoS Biology</i> , 2006 , 4, e127	9.7	73
126	Tree scanning: a method for using haplotype trees in phenotype/genotype association studies. <i>Genetics</i> , 2005 , 169, 441-53	4	72
125	RNA-Seq in <i>Mytilus galloprovincialis</i> : comparative transcriptomics and expression profiles among different tissues. <i>BMC Genomics</i> , 2015 , 16, 728	4.5	70
124	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	2.5	64
123	Nested clade analysis statistics. <i>Molecular Ecology Notes</i> , 2006 , 6, 590-593		61
122	Phylogeography and speciation of colour morphs in the colonial ascidian <i>Pseudodistoma crucigaster</i> . <i>Molecular Ecology</i> , 2004 , 13, 3125-36	5.7	60

121	jmodeltest.org: selection of nucleotide substitution models on the cloud. <i>Bioinformatics</i> , 2014 , 30, 1310-1320	4.2	55
120	Coalescent simulation of intracodon recombination. <i>Genetics</i> , 2010 , 184, 429-37	4	55
119	The effect of recombination on the reconstruction of ancestral sequences. <i>Genetics</i> , 2010 , 184, 1133-9	4	54
118	Genetic variation at MHC, mitochondrial and microsatellite loci in isolated populations of Brown trout (<i>Salmo trutta</i>). <i>Conservation Genetics</i> , 2006 , 7, 515-530	2.6	49
117	Phylogenomics suggests oxygen availability as a driving force in Thaumarchaeota evolution. <i>ISME Journal</i> , 2019 , 13, 2150-2161	11.9	48
116	Multilocus inference of species trees and DNA barcoding. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016 , 371,	5.8	48
115	Using models of nucleotide evolution to build phylogenetic trees. <i>Developmental and Comparative Immunology</i> , 2005 , 29, 211-27	3.2	47
114	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, 140-9	3.2	45
113	Evidence for survival of Pleistocene climatic changes in Northern refugia by the land snail <i>Trochoidea geyeri</i> (Soß 1926) (Helicellinae, Stylommatophora). <i>BMC Evolutionary Biology</i> , 2003 , 3, 8	3	44
112	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	7.5	42
111	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. <i>Genome Biology</i> , 2020 , 21, 275	18.3	42
110	Multigene phylogeny of Malagasy day geckos of the genus <i>Phelsuma</i> . <i>Molecular Phylogenetics and Evolution</i> , 2009 , 52, 530-7	4.1	40
109	Recodon: coalescent simulation of coding DNA sequences with recombination, migration and demography. <i>BMC Bioinformatics</i> , 2007 , 8, 458	3.6	40
108	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	2.7	39
107	Multiregional Tumor Trees Are Not Phylogenies. <i>Trends in Cancer</i> , 2017 , 3, 546-550	12.5	37
106	Molecular phylogeny and biogeographic history of the European <i>Maja</i> spider crabs (Decapoda, Majidae). <i>Molecular Phylogenetics and Evolution</i> , 2009 , 53, 314-9	4.1	37
105	Inverted replication of vertebrate mitochondria. <i>Molecular Biology and Evolution</i> , 2008 , 25, 805-8	8.3	37
104	Recombination favors the evolution of drug resistance in HIV-1 during antiretroviral therapy. <i>Infection, Genetics and Evolution</i> , 2007 , 7, 476-83	4.5	37

103	Recombination estimation under complex evolutionary models with the coalescent composite-likelihood method. <i>Molecular Biology and Evolution</i> , 2006 , 23, 817-27	8.3	35
102	Identification of a novel HIV-1 complex circulating recombinant form (CRF18_cpx) of Central African origin in Cuba. <i>Aids</i> , 2005 , 19, 1155-63	3.5	35
101	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	3.7	35
100	Population genetics of the porB gene of <i>Neisseria gonorrhoeae</i> : different dynamics in different homology groups. <i>Molecular Biology and Evolution</i> , 2000 , 17, 423-36	8.3	34
99	Protein evolution along phylogenetic histories under structurally constrained substitution models. <i>Bioinformatics</i> , 2013 , 29, 3020-8	7.2	32
98	Phylodynamics of HIV-1 from a phase III AIDS vaccine trial in Bangkok, Thailand. <i>PLoS ONE</i> , 2011 , 6, e16907	3.7	31
97	Simulation of genome-wide evolution under heterogeneous substitution models and complex multispecies coalescent histories. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1295-301	8.3	30
96	GenDecoder: genetic code prediction for metazoan mitochondria. <i>Nucleic Acids Research</i> , 2006 , 34, W389-93	3.9	30
95	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	3.7	30
94	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	0.8	29
93	The effect of branch length variation on the selection of models of molecular evolution. <i>Journal of Molecular Evolution</i> , 2001 , 52, 434-44	3.1	29
92	Genome-wide heterogeneity of nucleotide substitution model fit. <i>Genome Biology and Evolution</i> , 2011 , 3, 896-908	3.9	28
91	Phylogenetic systematics of day geckos, genus <i>Phelsuma</i> , based on molecular and morphological data (Squamata: Gekkonidae). <i>Zootaxa</i> , 2010 , 2429, 1	0.5	28
90	A Bayesian Supertree Model for Genome-Wide Species Tree Reconstruction. <i>Systematic Biology</i> , 2016 , 65, 397-416	8.4	27
89	Coestimation of recombination, substitution and molecular adaptation rates by approximate Bayesian computation. <i>Heredity</i> , 2014 , 112, 255-64	3.6	27
88	Unveiling the molecular clock in the presence of recombination. <i>Molecular Biology and Evolution</i> , 2001 , 18, 1976-8	8.3	27
87	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, 685-92	4.1	26
86	The evolution of the mitochondrial genetic code in arthropods revisited. <i>Mitochondrial DNA</i> , 2012 , 23, 84-91		25

85	TreeScan: a bioinformatic application to search for genotype/phenotype associations using haplotype trees. <i>Bioinformatics</i> , 2005 , 21, 2130-2	7.2	25
84	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, 331-8	2.6	24
83	Simple (wrong) models for complex trees: a case from retroviridae. <i>Molecular Biology and Evolution</i> , 2001 , 18, 271-5	8.3	23
82	Computational design of centralized HIV-1 genes. <i>Current HIV Research</i> , 2010 , 8, 613-21	1.3	23
81	Widespread gene conversion of alpha-2-fucosyltransferase genes in mammals. <i>Journal of Molecular Evolution</i> , 2009 , 69, 22-31	3.1	22
80	Ethnic differences in the adaptation rate of HIV gp120 from a vaccine trial. <i>Retrovirology</i> , 2009 , 6, 67	3.6	22
79	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, 151-60	3.1	21
78	Perkinsoide chabelardi n. gen., a protozoan parasite with an intermediate evolutionary position: possible cause of the decrease of sardine fisheries?. <i>Environmental Microbiology</i> , 2006 , 8, 1105-14	5.2	21
77	Simulating haplotype blocks in the human genome. <i>Bioinformatics</i> , 2003 , 19, 289-90	7.2	21
76	Rapid evolution and biogeographic spread in a colorectal cancer. <i>Nature Communications</i> , 2019 , 10, 5139	17.4	20
75	Disease progression and evolution of the HIV-1 env gene in 24 infected infants. <i>Infection, Genetics and Evolution</i> , 2008 , 8, 110-20	4.5	20
74	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	2.6	20
73	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. <i>Genome Research</i> , 2021 , 31, 635-644	9.7	20
72	Characterization of reticulate networks based on the coalescent with recombination. <i>Molecular Biology and Evolution</i> , 2008 , 25, 2517-20	8.3	19
71	Phylodynamics of HIV-1 from a phase-III AIDS vaccine trial in North America. <i>Molecular Biology and Evolution</i> , 2010 , 27, 417-25	8.3	18
70	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	2.4	18
69	ProtTest-HPC: Fast Selection of Best-Fit Models of Protein Evolution. <i>Lecture Notes in Computer Science</i> , 2011 , 177-184	0.9	18
68	CodABC: a computational framework to coestimate recombination, substitution, and molecular adaptation rates by approximate Bayesian computation. <i>Molecular Biology and Evolution</i> , 2015 , 32, 1109-12	8.3	17

67	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	17
66	Cryptic diversity within the endemic prehensile-tailed gecko <i>Urocytyledon 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	1.9	17
65	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	2.5	17
64	Lack of temporal structure in the short term HIV-1 evolution within asymptomatic naïve patients. <i>Virology</i> , 2007 , 362, 294-303	3.6	17
63	PHYLOGEOGRAPHIC HISTORY OF THE LAND SNAIL <i>CANDIDULA UNIFASCIATA</i> (HELICELLINAE, STYLOMMATOPHORA): FRAGMENTATION, CORRIDOR MIGRATION, AND SECONDARY CONTACT. <i>Evolution; International Journal of Organic Evolution</i> , 2002 , 56, 1776	3.8	16
62	A coalescent model of recombination hotspots. <i>Genetics</i> , 2003 , 164, 407-17	4	16
61	Selective Pressures on Human Cancer Genes along the Evolution of Mammals. <i>Genes</i> , 2018 , 9,	4.2	16
60	Bioinformatics for DNA sequence analysis. Preface. <i>Methods in Molecular Biology</i> , 2009 , 537, vii-viii	1.4	15
59	ModelTest-NG: a new and scalable tool for the selection of DNA and protein evolutionary models		15
58	Selecting models of evolution		13
57	Spatio-temporal genetic variability in sea trout (<i>Salmo trutta</i>) populations from north-western Spain. <i>Freshwater Biology</i> , 2007 , 52, 510-524	3.1	12
56	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	2.6	12
55	Species Tree Estimation from Genome-Wide Data with guenomu. <i>Methods in Molecular Biology</i> , 2017 , 1525, 461-478	1.4	11
54	Sensitivity to sequencing depth in single-cell cancer genomics. <i>Genome Medicine</i> , 2018 , 10, 29	14.4	11
53	Characterization of phylogenetic networks with NetTest. <i>BMC Bioinformatics</i> , 2010 , 11, 268	3.6	11
52	Massive gene presence/absence variation in the mussel genome as an adaptive strategy: first evidence of a pan-genome in Metazoa		11
51	HIV-1 infected monozygotic twins: a tale of two outcomes. <i>BMC Evolutionary Biology</i> , 2011 , 11, 62	3	10
50	How does recombination affect phylogeny estimation?. <i>Trends in Ecology and Evolution</i> , 2000 , 15, 489-490.	0.9	10

49	The Influence of Re combination on the Estimation of Selection from Coding Sequence Alignments 2014 , 112-125		10
48	Introduction to recombination detection493-518		9
47	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, 91-6	4.5	9
46	CellCoal: Coalescent Simulation of Single-Cell Sequencing Samples. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1535-1542	8.3	8
45	Origin and length distribution of unidirectional prokaryotic overlapping genes. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 19-27	3.2	8
44	<i>Mytilus galloprovincialis</i> Lmk. in northern Africa. <i>Journal of Experimental Marine Biology and Ecology</i> , 1998 , 223, 271-283	2.1	8
43	Evolutionary history of <i>Trachylepisskinks</i> in the Seychelles islands: introgressive hybridization, morphological evolution and geographic structure. <i>Biological Journal of the Linnean Society</i> , 2016 , 119, 15-36	1.9	8
42	RecPhyloXML: a format for reconciled gene trees. <i>Bioinformatics</i> , 2018 , 34, 3646-3652	7.2	8
41	Testing for universal common ancestry. <i>Systematic Biology</i> , 2014 , 63, 838-42	8.4	7
40	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, 968-78	1.6	7
39	Comparison of single-cell whole-genome amplification strategies		7
38	Unsorted homology within locus and species trees. <i>Systematic Biology</i> , 2014 , 63, 988-92	8.4	6
37	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	1.8	6
36	Identification and characterization of microsatellite loci in the spiny spider crab <i>Maja brachydactyla</i> . <i>Conservation Genetics</i> , 2006 , 8, 245-247	2.6	6
35	Genetic code prediction for metazoan mitochondria with GenDecoder. <i>Methods in Molecular Biology</i> , 2009 , 537, 233-42	1.4	6
34	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, 1822-30	4.5	5
33	Molecular clock analysis362-380		5
32	Infinitely long branches and an informal test of common ancestry. <i>Biology Direct</i> , 2016 , 11, 19	7.2	4

31	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data		4
30	NGSphy: phylogenomic simulation of next-generation sequencing data. <i>Bioinformatics</i> , 2018 , 34, 2506-2507		3
29	Proving universal common ancestry with similar sequences. <i>Trends in Evolutionary Biology</i> , 2012 , 4,		3
28	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,	4.9	3
27	Simulation of coding sequence evolution 2012 , 126-132		3
26	Accuracy of somatic variant detection in multiregional tumor sequencing data		3
25	Malignant transformation and genetic alterations are uncoupled in early colorectal cancer progression. <i>BMC Biology</i> , 2020 , 18, 116	7.3	3
24	Mitochondrial genome sequencing of marine leukemias reveals cancer contagion between clam species in the Seas of Southern Europe		3
23	Phylogenetic Approaches to Molecular Epidemiology 2002 , 25-40		3
22	HPC selection of models of DNA substitution 2011 ,		2
21	Mitochondrial genome sequencing of marine leukaemias reveals cancer contagion between clam species in the Seas of Southern Europe.. <i>ELife</i> , 2022 , 11,	8.9	2
20	Base-pairing versatility determines wobble sites in tRNA anticodons of vertebrate mitogenomes. <i>PLoS ONE</i> , 2012 , 7, e36605	3.7	2
19	SimPhy: Phylogenomic Simulation of Gene, Locus and Species Trees		2
18	Biased evolutionary inferences from bulk tumor samples		2
17	Rapid evolution and biogeographic spread in a colorectal cancer		2
16	Deciphering the Evolution of the Mitochondrial Genetic Code in Arthropods		2
15	A Fault Tolerant Workflow for Reproducible Research 2014 ,		1
14	Automatic Prediction of the Genetic Code. <i>Lecture Notes in Computer Science</i> , 2009 , 1125-1129	0.9	1

13	Nested clade phylogeographic analysis for conservation genetics 2001 , 80-103		1
12	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data.. <i>Genome Biology</i> , 2022 , 23, 37	18.3	1
11	Effective population sizes: missing measures and missing concepts 1999 , 2, 317		1
10	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,	4.8	1
9	Estimation of Species Trees		1
8	Phylogenetics of HIV 2002 , 121-160		1
7	Limited genomic reconstruction of SARS-CoV-2 transmission history within local epidemiological clusters.. <i>Virus Evolution</i> , 2022 , 8, veac008	3.7	0
6	Coalescent models derived from birth-death processes. <i>Theoretical Population Biology</i> , 2021 , 142, 1-11	1.2	0
5	Felsenstein Phylogenetic Likelihood. <i>Journal of Molecular Evolution</i> , 2021 , 89, 134-145	3.1	0
4	Grid selection of models of nucleotide substitution. <i>Studies in Health Technology and Informatics</i> , 2010 , 159, 244-8	0.5	
3	Adapting Reproducible Research Capabilities to Resilient Distributed Calculations. <i>International Journal of Grid and High Performance Computing</i> , 2016 , 8, 58-69	0.7	
2	Accurate Selection of Models of Protein Evolution. <i>Advances in Intelligent and Soft Computing</i> , 2010 , 117-121		
1	Single-cell mtDNA heteroplasmy in colorectal cancer.. <i>Genomics</i> , 2022 , 114, 110315	4.3	