David Posada

List of Publications by Year in Descending Order

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	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data.. *Genome Biology*, **2022**, 23, 37	18.3	1
173	Mitochondrial genome sequencing of marine leukaemias reveals cancer contagion between clam species in the Seas of Southern Europe.. *ELife*, **2022**, 11,	8.9	2
172	SARS-CoV-2 Evolution and Spike-Specific CD4+ T-Cell Response in Persistent COVID-19 with Severe HIV Immune Suppression.. *Microorganisms*, **2022**, 10,	4.9	3
171	Limited genomic reconstruction of SARS-CoV-2 transmission history within local epidemiological clusters.. *Virus Evolution*, **2022**, 8, veac008	3.7	0
170	Single-cell mtDNA heteroplasmy in colorectal cancer.. *Genomics*, **2022**, 114, 110315	4.3	
169	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. *Genome Research*, **2021**, 31, 635-644	9.7	20
168	OmniSARS2: A Highly Sensitive and Specific RT-qPCR-Based COVID-19 Diagnostic Method Designed to Withstand SARS-CoV-2 Lineage Evolution. *Biomedicines*, **2021**, 9,	4.8	1
167	Coalescent models derived from birth-death processes. *Theoretical Population Biology*, **2021**, 142, 1-11	1.2	0
166	Felsenstein Phylogenetic Likelihood. *Journal of Molecular Evolution*, **2021**, 89, 134-145	3.1	0
165	CellCoal: Coalescent Simulation of Single-Cell Sequencing Samples. *Molecular Biology and Evolution*, **2020**, 37, 1535-1542	8.3	8
164	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. *Genome Biology*, **2020**, 21, 275	18.3	42
163	Malignant transformation and genetic alterations are uncoupled in early colorectal cancer progression. *BMC Biology*, **2020**, 18, 116	7.3	3
162	ModelTest-NG: A New and Scalable Tool for the Selection of DNA and Protein Evolutionary Models. *Molecular Biology and Evolution*, **2020**, 37, 291-294	8.3	372
161	Phylogenomics suggests oxygen availability as a driving force in Thaumarchaeota evolution. *ISME Journal*, **2019**, 13, 2150-2161	11.9	48
160	Rapid evolution and biogeographic spread in a colorectal cancer. *Nature Communications*, **2019**, 10, 5139	17.4	20
159	NGSphy: phylogenomic simulation of next-generation sequencing data. *Bioinformatics*, **2018**, 34, 2506-2507	7.9	3
158	Sensitivity to sequencing depth in single-cell cancer genomics. *Genome Medicine*, **2018**, 10, 29	14.4	11

157	Selective Pressures on Human Cancer Genes along the Evolution of Mammals. *Genes*, **2018**, 9,	4.2	16
156	RecPhyloXML: a format for reconciled gene trees. *Bioinformatics*, **2018**, 34, 3646-3652	7.2	8
155	Species Tree Estimation from Genome-Wide Data with guenomu. *Methods in Molecular Biology*, **2017**, 1525, 461-478	1.4	11
154	Classifying the evolutionary and ecological features of neoplasms. *Nature Reviews Cancer*, **2017**, 17, 605-619	31.3	208
153	Multiregional Tumor Trees Are Not Phylogenies. *Trends in Cancer*, **2017**, 3, 546-550	12.5	37
152	Multilocus inference of species trees and DNA barcoding. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2016**, 371,	5.8	48
151	A comparison of tools for the simulation of genomic next-generation sequencing data. *Nature Reviews Genetics*, **2016**, 17, 459-69	30.1	97
150	Infinitely long branches and an informal test of common ancestry. *Biology Direct*, **2016**, 11, 19	7.2	4
149	A Bayesian Supertree Model for Genome-Wide Species Tree Reconstruction. *Systematic Biology*, **2016**, 65, 397-416	8.4	27
148	SimPhy: Phylogenomic Simulation of Gene, Locus, and Species Trees. *Systematic Biology*, **2016**, 65, 334-48	8.4	76
147	A First Insight into the Genome of the Filter-Feeder Mussel Mytilus galloprovincialis. *PLoS ONE*, **2016**, 11, e0151561	3.7	90
146	Adapting Reproducible Research Capabilities to Resilient Distributed Calculations. *International Journal of Grid and High Performance Computing*, **2016**, 8, 58-69	0.7	
145	Evolutionary history ofTrachylepisskinks in the Seychelles islands: introgressive hybridization, morphological evolution and geographic structure. *Biological Journal of the Linnean Society*, **2016**, 119, 15-36	1.9	8
144	CodABC: a computational framework to coestimate recombination, substitution, and molecular adaptation rates by approximate Bayesian computation. *Molecular Biology and Evolution*, **2015**, 32, 1109-12	8.3	17
143	RNA-Seq in Mytilus galloprovincialis: comparative transcriptomics and expression profiles among different tissues. *BMC Genomics*, **2015**, 16, 728	4.5	70
142	Coestimation of recombination, substitution and molecular adaptation rates by approximate Bayesian computation. *Heredity*, **2014**, 112, 255-64	3.6	27
141	Unsorted homology within locus and species trees. *Systematic Biology*, **2014**, 63, 988-92	8.4	6
140	HIV epidemiology. The early spread and epidemic ignition of HIV-1 in human populations. *Science*, **2014**, 346, 56-61	33.3	370

139	High-performance computing selection of models of DNA substitution for multicore clusters. *International Journal of High Performance Computing Applications*, **2014**, 28, 112-125	1.8	6
138	Simulation of genome-wide evolution under heterogeneous substitution models and complex multispecies coalescent histories. *Molecular Biology and Evolution*, **2014**, 31, 1295-301	8.3	30
137	jmodeltest.org: selection of nucleotide substitution models on the cloud. *Bioinformatics*, **2014**, 30, 1310-1	4.2	55
136	A Fault Tolerant Workflow for Reproducible Research **2014**,		1
135	Origin and length distribution of unidirectional prokaryotic overlapping genes. *G3: Genes, Genomes, Genetics*, **2014**, 4, 19-27	3.2	8
134	Testing for universal common ancestry. *Systematic Biology*, **2014**, 63, 838-42	8.4	7
133	The Influence of Re combination on the Estimation of Selection from Coding Sequence Alignments **2014**, 112-125		10
132	The evolution and appearance of C3 duplications in fish originate an exclusive teleost c3 gene form with anti-inflammatory activity. *PLoS ONE*, **2014**, 9, e99673	3.7	35
131	The inversion of the Control Region in three mitogenomes provides further evidence for an asymmetric model of vertebrate mtDNA replication. *PLoS ONE*, **2014**, 9, e106654	3.7	30
130	Phylogeography and diversification history of the day-gecko genus Phelsuma in the Seychelles islands. *BMC Evolutionary Biology*, **2013**, 13, 3	3	17
129	Protein evolution along phylogenetic histories under structurally constrained substitution models. *Bioinformatics*, **2013**, 29, 3020-8	7.2	32
128	Gene expression analysis of clams Ruditapes philippinarum and Ruditapes decussatus following bacterial infection yields molecular insights into pathogen resistance and immunity. *Developmental and Comparative Immunology*, **2012**, 36, 140-9	3.2	45
127	jModelTest 2: more models, new heuristics and parallel computing. *Nature Methods*, **2012**, 9, 772	21.6	9965
126	Insights into origins of Human T-cell Lymphotropic Virus Type 1 based on new strains from aboriginal people of Canada. *Infection, Genetics and Evolution*, **2012**, 12, 1822-30	4.5	5
125	The evolution of the mitochondrial genetic code in arthropods revisited. *Mitochondrial DNA*, **2012**, 23, 84-91		25
124	Proving universal common ancestry with similar sequences. *Trends in Evolutionary Biology*, **2012**, 4,		3
123	Base-pairing versatility determines wobble sites in tRNA anticodons of vertebrate mitogenomes. *PLoS ONE*, **2012**, 7, e36605	3.7	2
122	Simulation of coding sequence evolution **2012**, 126-132		3

121	Individual sequence variability and functional activities of fibrinogen-related proteins (FREPs) in the Mediterranean mussel (Mytilus galloprovincialis) suggest ancient and complex immune recognition models in invertebrates. *Developmental and Comparative Immunology*, **2011**, 35, 334-44	3.2	81
120	Analysing recombination in nucleotide sequences. *Molecular Ecology Resources*, **2011**, 11, 943-55	8.4	85
119	Phylodynamics of HIV-1 from a phase III AIDS vaccine trial in Bangkok, Thailand. *PLoS ONE*, **2011**, 6, e16992	3.7	31
118	Genome-wide heterogeneity of nucleotide substitution model fit. *Genome Biology and Evolution*, **2011**, 3, 896-908	3.9	28
117	Cryptic diversity within the endemic prehensile-tailed gecko Urocotyledon inexpectata across the Seychelles Islands: patterns of phylogeographical structure and isolation at the multilocus level. *Biological Journal of the Linnean Society*, **2011**, 104, 177-191	1.9	17
116	HIV-1 infected monozygotic twins: a tale of two outcomes. *BMC Evolutionary Biology*, **2011**, 11, 62	3	10
115	HPC selection of models of DNA substitution **2011**,		2
114	ProtTest 3: fast selection of best-fit models of protein evolution. *Bioinformatics*, **2011**, 27, 1164-5	7.2	1864
113	ProtTest-HPC: Fast Selection of Best-Fit Models of Protein Evolution. *Lecture Notes in Computer Science*, **2011**, 177-184	0.9	18
112	Phylogenetic systematics of day geckos, genus Phelsuma, based on molecular and morphological data (Squamata: Gekkonidae). *Zootaxa*, **2010**, 2429, 1	0.5	28
111	Coalescent simulation of intracodon recombination. *Genetics*, **2010**, 184, 429-37	4	55
110	Phylodynamics of HIV-1 from a phase-III AIDS vaccine trial in North America. *Molecular Biology and Evolution*, **2010**, 27, 417-25	8.3	18
109	RDP3: a flexible and fast computer program for analyzing recombination. *Bioinformatics*, **2010**, 26, 2462-3	7.2	1392
108	The effect of recombination on the reconstruction of ancestral sequences. *Genetics*, **2010**, 184, 1133-9	4	54
107	ALTER: program-oriented conversion of DNA and protein alignments. *Nucleic Acids Research*, **2010**, 38, W14-8	20.1	265
106	The mussel Xenostrobus securis: a well-established alien invader in the Ria de Vigo (Spain, NE Atlantic). *Biological Invasions*, **2010**, 12, 2091-2103	2.7	39
105	Characterization of phylogenetic networks with NetTest. *BMC Bioinformatics*, **2010**, 11, 268	3.6	11
104	Grid selection of models of nucleotide substitution. *Studies in Health Technology and Informatics*, **2010**, 159, 244-8	0.5	

103	Computational design of centralized HIV-1 genes. *Current HIV Research*, **2010**, 8, 613-21	1.3	23
102	Accurate Selection of Models of Protein Evolution. *Advances in Intelligent and Soft Computing*, **2010**, 117-121		
101	An evolutionary model-based algorithm for accurate phylogenetic breakpoint mapping and subtype prediction in HIV-1. *PLoS Computational Biology*, **2009**, 5, e1000581	5	130
100	Are the sexual, somatic and genetic characters enough to solve nomenclatural problems in lumbricid taxonomy?. *Soil Biology and Biochemistry*, **2009**, 41, 2257-2271	7.5	42
99	Low-mitochondrial diversity and lack of structure in the velvet swimming crab Necora puber along the Galician coast. *Marine Biology*, **2009**, 156, 1039-1048	2.5	17
98	Widespread gene conversion of alpha-2-fucosyltransferase genes in mammals. *Journal of Molecular Evolution*, **2009**, 69, 22-31	3.1	22
97	Multigene phylogeny of Malagasy day geckos of the genus Phelsuma. *Molecular Phylogenetics and Evolution*, **2009**, 52, 530-7	4.1	40
96	Molecular phylogeny and biogeographic history of the European Maja spider crabs (Decapoda, Majidae). *Molecular Phylogenetics and Evolution*, **2009**, 53, 314-9	4.1	37
95	Bioinformatics for DNA sequence analysis. Preface. *Methods in Molecular Biology*, **2009**, 537, vii-viii	1.4	15
94	Selection of models of DNA evolution with jModelTest. *Methods in Molecular Biology*, **2009**, 537, 93-112	1.4	176
93	Automatic Prediction of the Genetic Code. *Lecture Notes in Computer Science*, **2009**, 1125-1129	0.9	1
92	Ethnic differences in the adaptation rate of HIV gp120 from a vaccine trial. *Retrovirology*, **2009**, 6, 67	3.6	22
91	Genetic code prediction for metazoan mitochondria with GenDecoder. *Methods in Molecular Biology*, **2009**, 537, 233-42	1.4	6
90	Genetic Identification of the Northeastern Atlantic Spiny Spider Crab as Maja Brachydactyla Balss, 1922. *Journal of Crustacean Biology*, **2008**, 28, 76-81	0.8	29
89	jModelTest: phylogenetic model averaging. *Molecular Biology and Evolution*, **2008**, 25, 1253-6	8.3	8077
88	Inverted replication of vertebrate mitochondria. *Molecular Biology and Evolution*, **2008**, 25, 805-8	8.3	37
87	Characterization of reticulate networks based on the coalescent with recombination. *Molecular Biology and Evolution*, **2008**, 25, 2517-20	8.3	19
86	A comparison of phylogenetic network methods using computer simulation. *PLoS ONE*, **2008**, 3, e1913	3.7	87

85	Introgression and genetic structure in northern Spanish Atlantic salmon (Salmo salar L.) populations according to mtDNA data. *Conservation Genetics*, **2008**, 9, 157-169	2.6	12
84	Disease progression and evolution of the HIV-1 env gene in 24 infected infants. *Infection, Genetics and Evolution*, **2008**, 8, 110-20	4.5	20
83	Genetic variation of the spiny spider crab Maja brachydactyla in the northeastern Atlantic. *Marine Ecology - Progress Series*, **2008**, 362, 211-223	2.6	20
82	Phylogenetic affinities of Comoroan and East African day geckos (genus Phelsuma): multiple natural colonisations, introductions and island radiations. *Molecular Phylogenetics and Evolution*, **2007**, 43, 685-92	4.1	26
81	Recombination favors the evolution of drug resistance in HIV-1 during antiretroviral therapy. *Infection, Genetics and Evolution*, **2007**, 7, 476-83	4.5	37
80	Spatio-temporal genetic variability in sea trout (Salmo trutta) populations from north-western Spain. *Freshwater Biology*, **2007**, 52, 510-524	3.1	12
79	Phylogenetic evidence for multiple sympatric ecological diversification in a marine snail. *Evolution; International Journal of Organic Evolution*, **2007**, 61, 1600-12	3.8	81
78	Recodon: coalescent simulation of coding DNA sequences with recombination, migration and demography. *BMC Bioinformatics*, **2007**, 8, 458	3.6	40
77	Lack of temporal structure in the short term HIV-1 evolution within asymptomatic naïve patients. *Virology*, **2007**, 362, 294-303	3.6	17
76	MtArt: a new model of amino acid replacement for Arthropoda. *Molecular Biology and Evolution*, **2007**, 24, 1-5	8.3	127
75	An exact nonparametric method for inferring mosaic structure in sequence triplets. *Genetics*, **2007**, 176, 1035-47	4	565
74	Identification of 3 phylogenetically related HIV-1 BG intersubtype circulating recombinant forms in Cuba. *Journal of Acquired Immune Deficiency Syndromes (1999)*, **2007**, 45, 151-60	3.1	21
73	GARD: a genetic algorithm for recombination detection. *Bioinformatics*, **2006**, 22, 3096-8	7.2	581
72	Recombination estimation under complex evolutionary models with the coalescent composite-likelihood method. *Molecular Biology and Evolution*, **2006**, 23, 817-27	8.3	35
71	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. *AIDS Research and Human Retroviruses*, **2006**, 22, 968-78	1.6	7
70	Automated phylogenetic detection of recombination using a genetic algorithm. *Molecular Biology and Evolution*, **2006**, 23, 1891-901	8.3	679
69	ModelTest Server: a web-based tool for the statistical selection of models of nucleotide substitution online. *Nucleic Acids Research*, **2006**, 34, W700-3	20.1	255
68	Parallel evolution of the genetic code in arthropod mitochondrial genomes. *PLoS Biology*, **2006**, 4, e127	9.7	73

67	GenDecoder: genetic code prediction for metazoan mitochondria. *Nucleic Acids Research*, **2006**, 34, W389-93	28.1	30
66	Perkinsoide chabelardi n. gen., a protozoan parasite with an intermediate evolutionary position: possible cause of the decrease of sardine fisheries?. *Environmental Microbiology*, **2006**, 8, 1105-14	5.2	21
65	Nested clade analysis statistics. *Molecular Ecology Notes*, **2006**, 6, 590-593		61
64	On the phylogenetic placement of human T cell leukemia virus type 1 sequences associated with an Andean mummy. *Infection, Genetics and Evolution*, **2006**, 6, 91-6	4.5	9
63	Genetic variation at MHC, mitochondrial and microsatellite loci in isolated populations of Brown trout (Salmo trutta). *Conservation Genetics*, **2006**, 7, 515-530	2.6	49
62	Identification and characterization of microsatellite loci in the spiny spider crab Maja brachydactyla. *Conservation Genetics*, **2006**, 8, 245-247	2.6	6
61	ProtTest: selection of best-fit models of protein evolution. *Bioinformatics*, **2005**, 21, 2104-5	7.2	2556
60	A modified bootscan algorithm for automated identification of recombinant sequences and recombination breakpoints. *AIDS Research and Human Retroviruses*, **2005**, 21, 98-102	1.6	615
59	Identification of a novel HIV-1 complex circulating recombinant form (CRF18_cpx) of Central African origin in Cuba. *Aids*, **2005**, 19, 1155-63	3.5	35
58	Using models of nucleotide evolution to build phylogenetic trees. *Developmental and Comparative Immunology*, **2005**, 29, 211-27	3.2	47
57	Polymorphisms in the sequences of Marteilia internal transcribed spacer region of the ribosomal RNA genes (ITS-1) in Spain: genetic types are not related with bivalve hosts. *Journal of Fish Diseases*, **2005**, 28, 331-8	2.6	24
56	Widespread recombination in published animal mtDNA sequences. *Molecular Biology and Evolution*, **2005**, 22, 925-33	8.3	134
55	The evolutionary value of recombination is constrained by genome modularity. *PLoS Genetics*, **2005**, 1, e51	6	95
54	TreeScan: a bioinformatic application to search for genotype/phenotype associations using haplotype trees. *Bioinformatics*, **2005**, 21, 2130-2	7.2	25
53	Tree scanning: a method for using haplotype trees in phenotype/genotype association studies. *Genetics*, **2005**, 169, 441-53	4	72
52	RDP2: recombination detection and analysis from sequence alignments. *Bioinformatics*, **2005**, 21, 260-2	7.2	863
51	Phylogeography and speciation of colour morphs in the colonial ascidian Pseudodistoma crucigaster. *Molecular Ecology*, **2004**, 13, 3125-36	5.7	60
50	The causes and consequences of HIV evolution. *Nature Reviews Genetics*, **2004**, 5, 52-61	30.1	372

49	Pharmacogenetic study of statin therapy and cholesterol reduction. *JAMA - Journal of the American Medical Association*, **2004**, 291, 2821-7	27.4	325
48	Model selection and model averaging in phylogenetics: advantages of akaike information criterion and bayesian approaches over likelihood ratio tests. *Systematic Biology*, **2004**, 53, 793-808	8.4	2994
47	Simulating haplotype blocks in the human genome. *Bioinformatics*, **2003**, 19, 289-90	7.2	21
46	New Approach to an Old Problem: Incorporating Signal from Gap-Rich Regions of ITS and rDNA Large Subunit into Phylogenetic Analyses to Resolve the Peltigera canina Species Complex. *Mycologia*, **2003**, 95, 1181	2.4	18
45	Evidence for survival of Pleistocene climatic changes in Northern refugia by the land snail Trochoidea geyeri (Soś 1926) (Helicellinae, Stylommatophora). *BMC Evolutionary Biology*, **2003**, 3, 8	3	44
44	Using MODELTEST and PAUP* to select a model of nucleotide substitution. *Current Protocols in Bioinformatics*, **2003**, Chapter 6, Unit 6.5	24.2	137
43	A coalescent model of recombination hotspots. *Genetics*, **2003**, 164, 407-17	4	16
42	The effect of recombination on the accuracy of phylogeny estimation. *Journal of Molecular Evolution*, **2002**, 54, 396-402	3.1	335
41	Phylogeographic history of the land snail Candidula unifasciata (Helicellinae, Stylommatophora): fragmentation, corridor migration, and secondary contact. *Evolution; International Journal of Organic Evolution*, **2002**, 56, 1776-88	3.8	447
40	Evaluation of methods for detecting recombination from DNA sequences: empirical data. *Molecular Biology and Evolution*, **2002**, 19, 708-17	8.3	304
39	PHYLOGEOGRAPHIC HISTORY OF THE LAND SNAIL CANDIDULA UNIFASCIATA (HELICELLINAE, STYLOMMATOPHORA): FRAGMENTATION, CORRIDOR MIGRATION, AND SECONDARY CONTACT. *Evolution; International Journal of Organic Evolution*, **2002**, 56, 1776	3.8	16
38	Recombination in evolutionary genomics. *Annual Review of Genetics*, **2002**, 36, 75-97	14.5	236
37	TCS: estimating gene genealogies **2002**,		178
36	Phylogenetics of HIV **2002**, 121-160		1
35	Phylogenetic Approaches to Molecular Epidemiology **2002**, 25-40		3
34	Cryptic species of Clavelina (Ascidiacea) in two different habitats: harbours and rocky littoral zones in the northwestern Mediterranean. *Marine Biology*, **2001**, 139, 455-462	2.5	64
33	The effect of branch length variation on the selection of models of molecular evolution. *Journal of Molecular Evolution*, **2001**, 52, 434-44	3.1	29
32	Simple (wrong) models for complex trees: a case from retroviridae. *Molecular Biology and Evolution*, **2001**, 18, 271-5	8.3	23

31	Evaluation of methods for detecting recombination from DNA sequences: computer simulations. *Proceedings of the National Academy of Sciences of the United States of America*, **2001**, 98, 13757-62	11.5	1104
30	Selecting the Best-Fit Model of Nucleotide Substitution. *Systematic Biology*, **2001**, 50, 580-601	8.4	254
29	Selecting the Best-Fit Model of Nucleotide Substitution. *Systematic Biology*, **2001**, 50, 580-601	8.4	669
28	Intraspecific gene genealogies: trees grafting into networks. *Trends in Ecology and Evolution*, **2001**, 16, 37-45	10.9	1240
27	Nested clade phylogeographic analysis for conservation genetics **2001**, 80-103		1
26	Selecting models of nucleotide substitution: an application to human immunodeficiency virus 1 (HIV-1). *Molecular Biology and Evolution*, **2001**, 18, 897-906	8.3	127
25	Unveiling the molecular clock in the presence of recombination. *Molecular Biology and Evolution*, **2001**, 18, 1976-8	8.3	27
24	Population genetics of the porB gene of Neisseria gonorrhoeae: different dynamics in different homology groups. *Molecular Biology and Evolution*, **2000**, 17, 423-36	8.3	34
23	GeoDis: a program for the cladistic nested analysis of the geographical distribution of genetic haplotypes. *Molecular Ecology*, **2000**, 9, 487-8	5.7	1094
22	TCS: a computer program to estimate gene genealogies. *Molecular Ecology*, **2000**, 9, 1657-9	5.7	7618
21	Molecular systematics of European Hyalodaphnia: the role of contemporary hybridization in ancient species. *Proceedings of the Royal Society B: Biological Sciences*, **2000**, 267, 1833-42	4.4	91
20	How does recombination affect phylogeny estimation?. *Trends in Ecology and Evolution*, **2000**, 15, 489-490	10.9	10
19	Mitochondrial DNA phylogeography and population history of the grey wolf canis lupus. *Molecular Ecology*, **1999**, 8, 2089-103	5.7	264
18	Effective population sizes: missing measures and missing concepts. *Animal Conservation*, **1999**, 2, 317-319	3.2	78
17	Effective population sizes: missing measures and missing concepts **1999**, 2, 317		1
16	MODELTEST: testing the model of DNA substitution. *Bioinformatics*, **1998**, 14, 817-8	7.2	17513
15	Mytilus galloprovincialis Lmk. in northern Africa. *Journal of Experimental Marine Biology and Ecology* , **1998**, 223, 271-283	2.1	8
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