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Weighted neighbor joining: a likelihood-based approach to distance-based phylogeny reconstruction

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#	Paper	IF	Citations
391	NJML: a hybrid algorithm for the neighbor-joining and maximum-likelihood methods. <i>Molecular Biology and Evolution</i> , 2000 , 17, 1401-9	8.3	43
390	Rapid evolution of the family of CONSTANS LIKE genes in plants. <i>Molecular Biology and Evolution</i> , 2000 , 17, 1499-507	8.3	72
389	Comparison of papillomavirus and immunodeficiency virus evolutionary patterns in the context of a papillomavirus vaccine. 2000 , 19, 43-56		27
388	Designing fast converging phylogenetic methods. 2001 , 17 Suppl 1, S190-8		27
387	Nitrogen fixation by symbiotic and free-living spirochetes. 2001 , 292, 2495-8		202
386	High guanine-cytosine content is not an adaptation to high temperature: a comparative analysis amongst prokaryotes. 2001 , 268, 493-7		139
385	A comparative test of a theory for the evolution of anisogamy. 2001 , 268, 879-84		34
384	Sponge homologs of vertebrate protein tyrosine kinases and frequent domain shufflings in the early evolution of animals before the parazoan-eumetazoan split. 2001 , 280, 195-201		39
383	References. 2001 , 328-342		
382	Foraminifera and Cercozoa are related in actin phylogeny: two orphans find a home?. <i>Molecular Biology and Evolution</i> , 2001 , 18, 1551-7	8.3	108
381	Dinoflagellate nuclear SSU rRNA phylogeny suggests multiple plastid losses and replacements. 2001 , 53, 204-13		275
380	Genetic algorithm-based maximum-likelihood analysis for molecular phylogeny. 2001 , 53, 477-84		65
379	Phylogeny and evolution of African shrews (Mammalia: Soricidae) inferred from 16s rRNA sequences. 2001 , 20, 185-95		62
378	Alpha and beta subunits of pyruvate dehydrogenase E1 from the microsporidian <i>Nosema locustae</i> : mitochondrion-derived carbon metabolism in microsporidia. 2001 , 117, 201-9		50
377	Molecular phylogenetics: state-of-the-art methods for looking into the past. 2001 , 17, 262-72		311
376	Lateral transfer at the gene and subgenic levels in the evolution of eukaryotic enolase. 2001 , 98, 10745-50		73
375	Strengths and limitations of the minimum evolution principle. 2001 , 50, 621-7		22

374	Exploring Among-Site Rate Variation Models in a Maximum Likelihood Framework Using Empirical Data: Effects of Model Assumptions on Estimates of Topology, Branch Lengths, and Bootstrap Support. 2001 , 50, 67-86		59
373	The RDP-II (Ribosomal Database Project). 2001 , 29, 173-4		1082
372	Exploring Among-Site Rate Variation Models in a Maximum Likelihood Framework Using Empirical Data: Effects of Model Assumptions on Estimates of Topology, Branch Lengths, and Bootstrap Support. 2001 , 50, 67-86		102
371	Evolutionary HMMs: a Bayesian approach to multiple alignment. 2001 , 17, 803-20		133
370	Fast recovery of evolutionary trees with thousands of nodes. 2002 , 9, 277-97		21
369	Improvement of distance-based phylogenetic methods by a local maximum likelihood approach using triplets. <i>Molecular Biology and Evolution</i> , 2002 , 19, 1952-63	8.3	29
368	Hyaloraphidium curvatum: a linear mitochondrial genome, tRNA editing, and an evolutionary link to lower fungi. <i>Molecular Biology and Evolution</i> , 2002 , 19, 310-9	8.3	98
367	Kinesin-related genes from diplomonad, sponge, amphioxus, and cyclostomes: divergence pattern of kinesin family and evolution of giardial membrane-bounded organella. <i>Molecular Biology and Evolution</i> , 2002 , 19, 1524-33	8.3	9
366	Algorithms in Bioinformatics. <i>Lecture Notes in Computer Science</i> , 2002 ,	0.9	3
365	Fast and accurate phylogeny reconstruction algorithms based on the minimum-evolution principle. 2002 , 9, 687-705		315
364	The protein kinase ERK3 is encoded by a single functional gene: genomic analysis of the ERK3 gene family. 2002 , 80, 673-80		16
363	Are Microsporidia really related to Fungi?: a reappraisal based on additional gene sequences from basal fungi. 2002 , 106, 1380-1391		35
362	Nitrogen-assimilating enzymes in land plants and algae: phylogenic and physiological perspectives. 2002 , 116, 1-11		55
361	The phylogeny of colpodellids (Alveolata) using small subunit rRNA gene sequences suggests they are the free-living sister group to apicomplexans. 2002 , 49, 498-504		78
360	Re-examining alveolate evolution using multiple protein molecular phylogenies. 2002 , 49, 30-7		136
359	Molecular DNA Markers in Phylogeny and Systematics. 2002 , 38, 851-868		28
358	On the origin of family 1 plant glycosyltransferases. 2003 , 62, 399-413		221
357	LESSARDIA ELONGATA GEN. ET SP. NOV. (DINOFLAGELLATA, PERIDINIALES, PODOLAMPACEAE) AND THE TAXONOMIC POSITION OF THE GENUS ROSCOFFIA1. 2003 , 39, 368-378		23

356	Molecular phylogeny and surface morphology of <i>Colpodella edax</i> (Alveolata): insights into the phagotrophic ancestry of apicomplexans. 2003 , 50, 334-40		58
355	Cryptic organelles in parasitic protists and fungi. 2003 , 54, 9-68		58
354	Neighbor-net: an agglomerative method for the construction of phylogenetic networks. <i>Molecular Biology and Evolution</i> , 2004 , 21, 255-65	8.3	1318
353	A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. 2003 , 52, 696-704		13613
352	Characterisation of a non-canonical genetic code in the oxymonad <i>Streblomastix strix</i> . 2003 , 326, 1337-49		58
351	Phylogenetic relationships of non-mitochondrial nucleotide transport proteins in bacteria and eukaryotes. 2003 , 306, 27-35		77
350	Plastid-derived Type II fatty acid biosynthetic enzymes in chromists. 2003 , 313, 139-48		33
349	Congruent evidence from alpha-tubulin and beta-tubulin gene phylogenies for a zygomycete origin of microsporidia. 2003 , 38, 298-309		171
348	Phylogeny of gregarines (Apicomplexa) as inferred from small-subunit rDNA and beta-tubulin. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003 , 53, 345-354	2.2	130
347	The Ribosomal Database Project (RDP-II): previewing a new autoaligner that allows regular updates and the new prokaryotic taxonomy. 2003 , 31, 442-3		1089
346	Multiple protein phylogenies show that <i>Oxyrrhis marina</i> and <i>Perkinsus marinus</i> are early branches of the dinoflagellate lineage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003 , 53, 355-365	2.2	164
345	18S ribosomal RNA and tetrapod phylogeny. 2003 , 52, 283-95		79
344	A comparison of three fission yeast mitochondrial genomes. 2003 , 31, 759-68		100
343	Recently duplicated maize R2R3 Myb genes provide evidence for distinct mechanisms of evolutionary divergence after duplication. 2003 , 131, 610-20		127
342	Theoretical foundation of the balanced minimum evolution method of phylogenetic inference and its relationship to weighted least-squares tree fitting. <i>Molecular Biology and Evolution</i> , 2004 , 21, 587-98	8.3	147
341	Evolution of the Fungi and their Mitochondrial Genomes. 2003 , 3, 133-159		9
340	Bacterial catalase in the microsporidian <i>Nosema locustae</i> : implications for microsporidian metabolism and genome evolution. 2003 , 2, 1069-75		41
339	Nucleus-encoded, plastid-targeted glyceraldehyde-3-phosphate dehydrogenase (GAPDH) indicates a single origin for chromalveolate plastids. <i>Molecular Biology and Evolution</i> , 2003 , 20, 1730-5	8.3	170

338	The mitochondrial genome of <i>Chara vulgaris</i> : insights into the mitochondrial DNA architecture of the last common ancestor of green algae and land plants. 2003 , 15, 1888-903		119
337	Polymorphism, shared functions and convergent evolution of genes with sequences coding for polyalanine domains. 2003 , 12, 2967-79		94
336	Lateral gene transfer and the evolution of plastid-targeted proteins in the secondary plastid-containing alga <i>Bigeloviella natans</i> . 2003 , 100, 7678-83		224
335	Foraminifera and Cercozoa share a common origin according to RNA polymerase II phylogenies. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003 , 53, 1735-9	2.2	44
334	Divergence in mycorrhizal specialization within <i>Hexalectris spicata</i> (Orchidaceae), a nonphotosynthetic desert orchid. 2003 , 90, 1168-79		125
333	Factors affecting the errors in the estimation of evolutionary distances between sequences. <i>Molecular Biology and Evolution</i> , 2003 , 20, 1-9	8.3	12
332	Molecular phylogeny and surface morphology of marine aseptate gregarines (Apicomplexa): <i>Selenidium</i> spp. and <i>Lecudina</i> spp. 2003 , 89, 1191-205		55
331	Getting a Tree Fast: Neighbor Joining and Distance-Based Methods. 2003 , 1, 6.3.1-6.3.23		
330	Comparative analysis of apicomplexa and genomic diversity in eukaryotes. 2004 , 14, 1686-95		149
329	Tracing the decay of the historical signal in biological sequence data. 2004 , 53, 623-37		127
328	The complete mitochondrial DNA sequence of the green alga <i>Pseudendoclonium akinetum</i> (Ulvophyceae) highlights distinctive evolutionary trends in the chlorophyta and suggests a sister-group relationship between the Ulvophyceae and Chlorophyceae. <i>Molecular Biology and Evolution</i> , 2004 , 21, 922-35	8.3	66
327	An evolutionary model for protein-coding regions with conserved RNA structure. <i>Molecular Biology and Evolution</i> , 2004 , 21, 1913-22	8.3	33
326	The evolution of SMC proteins: phylogenetic analysis and structural implications. <i>Molecular Biology and Evolution</i> , 2004 , 21, 332-47	8.3	116
325	The Omp85 family of proteins is essential for outer membrane biogenesis in mitochondria and bacteria. 2004 , 164, 19-24		322
324	Nucleus-encoded genes for plastid-targeted proteins in <i>Helicosporidium</i> : functional diversity of a cryptic plastid in a parasitic alga. 2004 , 3, 1198-205		36
323	Gene replacement of fructose-1,6-bisphosphate aldolase supports the hypothesis of a single photosynthetic ancestor of chromalveolates. 2004 , 3, 1169-75		129
322	A comparative method for finding and folding RNA secondary structures within protein-coding regions. 2004 , 32, 4925-36		70
321	Statistical and Combinatorial Aspects of Comparative Genomics*. 2004 , 31, 203-216		2

320	DESCRIPTION OF THECADINIUM MUCOSUM SP. NOV. (DINOPHYCEAE), A NEW SAND-DWELLING MARINE DINOFLAGELLATE, AND AN EMENDED DESCRIPTION OF THECADINIUM INCLINATUM BALECH1. 2004 , 40, 946-961	22
319	EARLY EVOLUTIONARY HISTORY OF DINOFLAGELLATES AND APICOMPLEXANS (ALVEOLATA) AS INFERRED FROM HSP90 AND ACTIN PHYLOGENIES1. 2004 , 40, 341-350	85
318	Actin and ubiquitin protein sequences support a cercozoan/foraminiferan ancestry for the plasmodiophorid plant pathogens. 2004 , 51, 113-8	56
317	HSP90, tubulin and actin are retained in the tertiary endosymbiont genome of <i>Kryptoperidinium foliaceum</i> . 2004 , 51, 651-9	31
316	Molecular cloning of the estrogen and progesterone receptors of the American alligator. 2004 , 136, 122-33	67
315	Accurate and robust phylogeny estimation based on profile distances: a study of the Chlorophyceae (Chlorophyta). 2004 , 4, 20	41
314	Reconstruction of ancestral protein sequences and its applications. 2004 , 4, 33	79
313	Novel conserved domains in proteins with predicted roles in eukaryotic cell-cycle regulation, decapping and RNA stability. 2004 , 5, 45	66
312	Molecular data and the evolutionary history of dinoflagellates. 2004 , 40, 85-111	185
311	Comparative morphology and molecular phylogeny of aplanochytrids (Labyrinthulomycota). 2004 , 40, 317-328	53
310	A fragment of chloroplast DNA was transferred horizontally, probably from non-eudicots, to mitochondrial genome of <i>Phaseolus</i> . 2004 , 56, 811-20	28
309	Minimal entropy probability paths between genome families. 2004 , 48, 563-90	1
308	Lateral transfer and re-compartmentalization of Calvin cycle enzymes of plants and algae. 2004 , 58, 367-75	62
307	The consistent phylogenetic signal in genome trees revealed by reducing the impact of noise. 2004 , 58, 527-39	60
306	Polymorphic insertions and deletions in parabasal enolase genes. 2004 , 58, 550-6	13
305	Molecular phylogeny of Zygomycota based on EF-1alpha and RPB1 sequences: limitations and utility of alternative markers to rDNA. 2004 , 30, 438-49	88
304	Reconstructing trees from subtree weights. 2004 , 17, 615-621	37
303	Molecular phylogenies of Parabasalia inferred from four protein genes and comparison with rRNA trees. 2004 , 31, 572-80	43

302	Evolution of duplicated growth hormone genes in autotetraploid salmonid fishes. 2004 , 47, 714-23	33
301	Phylogenetic position of the Pentastomida and (pan)crustacean relationships. 2004 , 271, 537-44	172
300	Identification of the prokaryotic ligand-gated ion channels and their implications for the mechanisms and origins of animal Cys-loop ion channels. 2005 , 6, R4	190
299	A novel family of P-loop NTPases with an unusual phyletic distribution and transmembrane segments inserted within the NTPase domain. 2004 , 5, R30	43
298	Lateral gene transfer and the complex distribution of insertions in eukaryotic enolase. 2004 , 340, 227-35	24
297	Correlations between genomic GC levels and optimal growth temperatures in prokaryotes. 2004 , 573, 73-7	85
296	The molecular defect leading to Fabry disease: structure of human alpha-galactosidase. 2004 , 337, 319-35	276
295	Computational analysis of evolution and conservation in a protein superfamily. 2004 , 32, 73-92	8
294	Reconstruction of large phylogenetic trees: a parallel approach. 2005 , 29, 273-80	11
293	AtATG18a is required for the formation of autophagosomes during nutrient stress and senescence in <i>Arabidopsis thaliana</i> . 2005 , 42, 535-46	269
292	Systematics of African lowland rainforest <i>Praomys</i> (Rodentia, Muridae) based on molecular and craniometrical data. 2005 , 145, 539-553	19
291	Expressed sequence tag (EST) survey of the highly adapted green algal parasite, <i>Helicosporidium</i> . 2005 , 156, 181-90	11
290	Scoredist: a simple and robust protein sequence distance estimator. 2005 , 6, 108	89
289	Shortest triplet clustering: reconstructing large phylogenies using representative sets. 2005 , 6, 92	13
288	Explosive lineage-specific expansion of the orphan nuclear receptor HNF4 in nematodes. 2005 , 60, 577-86	90
287	On the Uniqueness of the Selection Criterion in Neighbor-Joining. 2005 , 22, 3-15	29
286	High-Performance Phylogeny Reconstruction Under Maximum Parsimony. 2005 , 369-394	
285	. 2005 ,	4

284	Assessment of protein distance measures and tree-building methods for phylogenetic tree reconstruction. <i>Molecular Biology and Evolution</i> , 2005 , 22, 2257-64	8.3	13
283	On the monophyly of chromalveolates using a six-protein phylogeny of eukaryotes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005 , 55, 487-496	2.2	147
282	Using evolutionary Expectation Maximization to estimate indel rates. 2005 , 21, 2294-300		30
281	Weighted genome trees: refinements and applications. 2005 , 187, 1305-16		43
280	Patterns that define the four domains conserved in known and novel isoforms of the protein import receptor Tom20. 2005 , 347, 81-93		50
279	Advances in phylogeny reconstruction from gene order and content data. 2005 , 395, 673-700		18
278	Mitochondrial genome of the homoscleromorph <i>Oscarella carmela</i> (Porifera, Demospongiae) reveals unexpected complexity in the common ancestor of sponges and other animals. <i>Molecular Biology and Evolution</i> , 2007 , 24, 363-73	8.3	55
277	Getting a tree fast: Neighbor Joining, FastME, and distance-based methods. 2006 , Chapter 6, Unit 6.3		18
276	Alveolate and chlorophycean mitochondrial <i>cox2</i> genes split twice independently. 2006 , 383, 33-7		38
275	Diversification of catalytic activities and ligand interactions in the protein fold shared by the sugar isomerases, eIF2B, DeoR transcription factors, acyl-CoA transferases and methenyltetrahydrofolate synthetase. 2006 , 356, 823-42		17
274	A tertiary plastid uses genes from two endosymbionts. 2006 , 357, 1373-82		132
273	Molecular clock and estimation of species divergence times. 2006 , 223-258		
272	Cellular identity of a novel small subunit rDNA sequence clade of apicomplexans: description of the marine parasite <i>Rhytidocystis polygordiae</i> n. sp. (host: <i>Polygordius</i> sp., Polychaeta). 2006 , 53, 280-91		17
271	Dinoflagellate, Euglenid, or Cercomonad? The ultrastructure and molecular phylogenetic position of <i>Protaspis grandis</i> n. sp. 2006 , 53, 327-42		39
270	Gene structure and expression pattern analysis of three monodehydroascorbate reductase (MdhAR) genes in <i>Physcomitrella patens</i> : implications for the evolution of the MDHAR family in plants. 2006 , 60, 259-75		46
269	Phylogenetic and biochemical studies reveal a potential evolutionary origin of small heat shock proteins of animals from bacterial class A. 2006 , 62, 257-66		39
268	Relaxed neighbor joining: a fast distance-based phylogenetic tree construction method. 2006 , 62, 785-92		110
267	Phylogeny of marine Gregarines (Apicomplexa)--Pterospira, Lithocystis and Lankesteria--and the origin(s) of coelomic parasitism. 2006 , 157, 45-60		57

266	Evidence from SSU rRNA phylogeny that Octomitus is a sister lineage to Giardia. 2006 , 157, 205-12		15
265	Ebriid phylogeny and the expansion of the Cercozoa. 2006 , 157, 279-90		27
264	EFL GTPase in cryptomonads and the distribution of EFL and EF-1alpha in chromalveolates. 2006 , 157, 435-44		25
263	Integrating protein structures and precomputed genealogies in the Magnum database: examples with cellular retinoid binding proteins. 2006 , 7, 89		1
262	The evolution of the histone methyltransferase gene Su(var)3-9 in metazoans includes a fusion with and a re-fission from a functionally unrelated gene. 2006 , 6, 18		16
261	PANDIT: an evolution-centric database of protein and associated nucleotide domains with inferred trees. 2006 , 34, D327-31		50
260	The NYN domains: novel predicted RNAses with a PIN domain-like fold. 2006 , 3, 18-27		97
259	Nucleus-to-nucleus gene transfer and protein retargeting into a remnant cytoplasm of cryptophytes and diatoms. <i>Molecular Biology and Evolution</i> , 2006 , 23, 2413-22	8.3	73
258	Proceedings of the SMBE Tri-National Young Investigators Workshop 2005. Insight into the diversity and evolution of the cryptomonad nucleomorph genome. <i>Molecular Biology and Evolution</i> , 2006 , 23, 856-65	8.3	39
257	Prediction of functional specificity determinants from protein sequences using log-likelihood ratios. 2006 , 22, 164-71		49
256	Lateral gene transfer of a multigene region from cyanobacteria to dinoflagellates resulting in a novel plastid-targeted fusion protein. <i>Molecular Biology and Evolution</i> , 2006 , 23, 1437-43	8.3	69
255	Genotype turnover by reassortment of replication complex genes from avian influenza A virus. 2006 , 87, 2803-2815		61
254	Inferring parameters shaping amino acid usage in prokaryotic genomes via Bayesian MCMC methods. <i>Molecular Biology and Evolution</i> , 2006 , 23, 203-11	8.3	14
253	Phylogenetic history of plastid-targeted proteins in the peridinin-containing dinoflagellate <i>Heterocapsa triquetra</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006 , 56, 1439-1447		31
252	STRAL: progressive alignment of non-coding RNA using base pairing probability vectors in quadratic time. 2006 , 22, 1593-9		57
251	Beyond pairwise distances: neighbor-joining with phylogenetic diversity estimates. <i>Molecular Biology and Evolution</i> , 2006 , 23, 491-8	8.3	19
250	References. 2007 , 238-257		
249	Naive Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. 2007 , 73, 5261-7		12136

248	Neighbor joining algorithms for inferring phylogenies via LCA distances. 2007 , 14, 1-15	8
247	Statistics of the log-det estimator. <i>Molecular Biology and Evolution</i> , 2007 , 24, 2277-85	8,3 9
246	New approaches to phylogenetic tree search and their application to large numbers of protein alignments. 2007 , 56, 727-40	27
245	Avl9p, a member of a novel protein superfamily, functions in the late secretory pathway. 2007 , 18, 1203-19	36
244	The highly reduced and fragmented mitochondrial genome of the early-branching dinoflagellate <i>Oxyrrhis marina</i> shares characteristics with both apicomplexan and dinoflagellate mitochondrial genomes. 2007 , 372, 356-68	81
243	The ribosomal database project (RDP-II): introducing myRDP space and quality controlled public data. 2007 , 35, D169-72	898
242	Small but versatile: the extraordinary functional and structural diversity of the beta-grasp fold. 2007 , 2, 18	110
241	Bioinformatic Databases. 2007 ,	1
240	Multiple Sequence Alignment and Phylogenetic Inference. 123-155	
239	The Sorcerer II Global Ocean Sampling expedition: expanding the universe of protein families. 2007 , 5, e16	638
238	. 2007 ,	7
237	Evolution and diversification of lamprey antigen receptors: evidence for involvement of an AID-APOBEC family cytosine deaminase. 2007 , 8, 647-56	228
236	Molecular phylogeny and ultrastructure of <i>Selenidium serpulae</i> (Apicomplexa, Archigregarinia) from the calcareous tubeworm <i>Serpula vermicularis</i> (Annelida, Polychaeta, Sabellida). 2007 , 36, 213-227	27
235	Taxonomy, phylogeny, biogeography, and ecology of <i>Sabulodinium undulatum</i> (Dinophyceae), including an emended description of the species. 2007 , 55, 159-175	22
234	CHARACTER EVOLUTION IN POLYKRIKOID DINOFLAGELLATES1. 2007 , 43, 366-377	43
233	Phylogeny of phagotrophic euglenids (Euglenozoa) as inferred from hsp90 gene sequences. 2007 , 54, 86-92	35
232	Mitochondrial genome of a tertiary endosymbiont retains genes for electron transport proteins. 2007 , 54, 146-53	21
231	Morphology and phylogenetic position of <i>Eucomonympha imla</i> (Parabasalia: Hypermastigida). 2007 , 54, 325-32	29

230	BIRCH: a user-oriented, locally-customizable, bioinformatics system. 2007 , 8, 54		4
229	The dinoflagellates <i>Durinskia baltica</i> and <i>Kryptoperidinium foliaceum</i> retain functionally overlapping mitochondria from two evolutionarily distinct lineages. 2007 , 7, 172		48
228	Origin and distribution of epipolythiodioxopiperazine (ETP) gene clusters in filamentous ascomycetes. 2007 , 7, 174		134
227	Complex distribution of EFL and EF-1alpha proteins in the green algal lineage. 2007 , 7, 82		28
226	Morphology and phylogeny of the pseudocolonial dinoflagellates <i>Polykrikos lebourae</i> and <i>Polykrikos herdmanae</i> n. sp. 2007 , 158, 209-27		61
225	Random local neighbor joining: a new method for reconstructing phylogenetic trees. 2008 , 47, 117-28		63
224	Fast NJ-like algorithms to deal with incomplete distance matrices. 2008 , 9, 166		31
223	Accelerating the Neighbor-Joining Algorithm Using the Adaptive Bucket Data Structure. 2008 , 122-133		2
222	Encyclopedia of Algorithms. 2008 , 235-236		
221	The single mitochondrial porin of <i>Trypanosoma brucei</i> is the main metabolite transporter in the outer mitochondrial membrane. <i>Molecular Biology and Evolution</i> , 2009 , 26, 671-80	8,3	87
220	Performance comparison between k-tuple distance and four model-based distances in phylogenetic tree reconstruction. 2008 , 36, e33		33
219	Analysis of the genome of <i>Spodoptera frugiperda</i> nucleopolyhedrovirus (SfMNPV-19) and of the high genomic heterogeneity in group II nucleopolyhedroviruses. 2008 , 89, 1202-1211		42
218	Complete genome viral phylogenies suggests the concerted evolution of regulatory cores and accessory satellites. <i>PLoS ONE</i> , 2008 , 3, e3500	3,7	11
217	Phylogenetic analyses: A toolbox expanding towards Bayesian methods. 2008 , 2008, 683509		5
216	Maximum similarity: a new formulation of phylogenetic reconstruction. 2009 , 16, 887-96		
215	Pathogenic adaptation of intracellular bacteria by rewiring a cis-regulatory input function. 2009 , 106, 3982-7		48
214	Diets enriched in oat bran or wheat bran temporally and differentially alter the composition of the fecal community of rats. 2009 , 139, 2024-31		51
213	A fungal phylogeny based on 82 complete genomes using the composition vector method. 2009 , 9, 195		145

212	The minimum evolution problem: Overview and classification. 2009 , 53, 112-125	19
211	Why Neighbor-Joining Works. 2009 , 54, 1-24	59
210	Phylogenetic inference with weighted codon evolutionary distances. 2009 , 68, 377-92	5
209	Molecular phylogeography of European <i>Sciurus vulgaris</i> : refuge within refugia?. 2009 , 18, 2687-99	66
208	Morphology, phylogeny, and diversity of <i>Trichonympha</i> (Parabasalia: Hypermastigida) of the wood-feeding cockroach <i>Cryptocercus punctulatus</i> . 2009 , 56, 305-13	25
207	Type I polyketide synthases that require discrete acyltransferases. 2009 , 459, 165-86	35
206	Consistency of topological moves based on the balanced minimum evolution principle of phylogenetic inference. 2009 , 6, 110-7	18
205	Bacteriophages. <i>Methods in Molecular Biology</i> , 2009 ,	1.4 25
204	Alternative hierarchical clustering approach in construction of phylogenetic trees. 2009 ,	2
203	Phylogenetic Inference Using Molecular Data. 2009 , 67-88	1
202	Phylogenetic Trees in Bioinformatics. 2010 , 5, 40-52	4
201	Native granule associated short chain length polyhydroxyalkanoate synthase from a marine derived <i>Bacillus</i> sp. NQ-11/A2. 2010 , 97, 41-50	13
200	Diversity and antimicrobial activities of surface-attached marine bacteria from Sydney Harbour, Australia. 2010 , 165, 300-11	32
199	Role of Tob55 on mitochondrial protein biogenesis in <i>Trypanosoma brucei</i> . 2010 , 174, 89-100	23
198	Evolutionary ancestry and novel functions of the mammalian glucose transporter (GLUT) family. 2010 , 10, 152	32
197	A versatile palindromic amphipathic repeat coding sequence horizontally distributed among diverse bacterial and eucaryotic microbes. 2010 , 11, 430	9
196	INVESTIGATIONS INTO SOUTHERN AUSTRALIAN ULVA (ULVOPHYCEAE, CHLOROPHYTA) TAXONOMY AND MOLECULAR PHYLOGENY INDICATE BOTH COSMOPOLITANISM AND ENDEMIC CRYPTIC SPECIES1. 2010 , 46, 1257-1277	62
195	Characterization of glycolipid biosurfactant from <i>Pseudomonas aeruginosa</i> CPCL isolated from petroleum-contaminated soil. 2010 , 51, 75-82	35

194	Pyrosequencing reveals contrasting seasonal dynamics of taxa within Baltic Sea bacterioplankton communities. 2010 , 4, 171-81		227
193	Vibrio infections triggering mass mortality events in a warming Mediterranean Sea. <i>Environmental Microbiology</i> , 2010 , 12, 2007-19	5.2	165
192	A stochastic local search algorithm for distance-based phylogeny reconstruction. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2587-95	8.3	7
191	Unraveling Extensive Paraphyly in the Genus Hydrangea s. l. with Implications for the Systematics of Tribe Hydrangeeae. 2010 , 35, 593-600		20
190	Toward extracting all phylogenetic information from matrices of evolutionary distances. 2010 , 327, 1376-9		40
189	Adaptive distance measures for resolving K2P quartets: metric separation versus stochastic noise. 2010 , 17, 1509-18		3
188	[Toxicological effects of weapons of mass destruction and noxious agents in modern warfare and terrorism]. 2010 , 61, 247-56		2
187	A differentiation-based phylogeny of cancer subtypes. 2010 , 6, e1000777		30
186	Algorithms in Bioinformatics. <i>Lecture Notes in Computer Science</i> , 2010 ,	0.9	
185	Tool that integrates distance based programs for reconstructing phylogenetic trees. 2011 , 9, 895-901		
184	The Ribosomal Database Project: Sequences and Software for High-Throughput rRNA Analysis. 2011 , 313-324		19
183	<i>Deinobacterium chartae</i> gen. nov., sp. nov., an extremely radiation-resistant, biofilm-forming bacterium isolated from a Finnish paper mill. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011 , 61, 540-548	2.2	9
182	The Use of rRNA Gene Sequence Data in the Classification and Identification of Prokaryotes. 2011 , 349-384		4
181	Development and validation of a microbial source tracking marker for the detection of fecal pollution by muskrats. 2011 , 87, 82-8		16
180	Complete genome sequence of <i>Ferroglobus placidus</i> AEDII12DO. 2011 , 5, 50-60		27
179	Genome sequence of <i>Haemophilus parasuis</i> strain 29755. 2011 , 5, 61-8		15
178	Climate-driven genetic divergence of limpets with different life histories across a southeast African marine biogeographic disjunction: different processes, same outcome. 2011 , 20, 5025-41		36
177	Scaling properties of protein family phylogenies. 2011 , 11, 155		8

176	OWA-based linkage method in hierarchical clustering: Application on phylogenetic trees. 2011 , 38, 12684-12690		4
175	A resampling strategy for reliable network construction. 2011 , 60, 273-86		2
174	<i>Chryseobacterium piperi</i> sp. nov., isolated from a freshwater creek. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011 , 61, 2162-2166	2.2	26
173	Populations of select cultured and uncultured bacteria in the rumen of sheep and the effect of diets and ruminal fractions. 2011 , 2011, 750613		43
172	A Variance-Components Model for Distance-Matrix Phylogenetic Reconstruction. 2011 , 10,		78
171	Genome majority vote improves gene predictions. 2011 , 7, e1002284		11
170	Plasmid localization and organization of melamine degradation genes in <i>Rhodococcus</i> sp. strain Mel. 2012 , 78, 1397-403		21
169	Complete genome sequence of <i>Treponema pallidum</i> strain DAL-1. 2012 , 7, 12-21		32
168	Genome sequence of the halotolerant bacterium <i>Corynebacterium halotolerans</i> type strain YIM 70093(T) (= DSM 44683(T)). 2012 , 7, 284-93		5
167	Complete genome sequence of <i>Halopiger xanaduensis</i> type strain (SH-6(T)). 2012 , 6, 31-42		7
166	Monitoring microbial diversity of bioreactors using metagenomic approaches. 2012 , 64, 73-94		1
165	Clusters of genes encoding fructan biosynthesizing enzymes in wheat and barley. 2012 , 80, 299-314		23
164	Rapid phylogenetic and functional classification of short genomic fragments with signature peptides. 2012 , 5, 460		22
163	The essentials of computational molecular evolution. <i>Methods in Molecular Biology</i> , 2012 , 855, 111-52	1.4	23
162	Reprogramming Microbial Metabolic Pathways. 2012 ,		5
161	PHYRN: a robust method for phylogenetic analysis of highly divergent sequences. <i>PLoS ONE</i> , 2012 , 7, e34261	3.7	15
160	Molecular phylogenetics: principles and practice. 2012 , 13, 303-14		403
159	Evidence of a complex phylogeographic structure in the common dormouse, <i>Muscardinus avellanarius</i> (Rodentia: Gliridae). 2012 , 105, 648-664		16

158	Detection and characterization of bacterial symbionts in the Heteropteran, <i>Blissus insularis</i> . 2012 , 82, 629-41		35
157	An assessment of vertical inheritance versus endosymbiont transfer of nucleus-encoded genes for mitochondrial proteins following tertiary endosymbiosis in <i>Karlodinium micrum</i> . 2012 , 163, 76-90		9
156	Characterization of culturable <i>Paenibacillus</i> spp. from the snow surface on the high Antarctic Plateau (DOME C) and their dissemination in the Concordia research station. 2013 , 17, 565-73		5
155	Models and Algorithms for Genome Evolution. <i>Computational Biology</i> , 2013 ,	0.7	6
154	Introduction to Evolutionary Genomics. <i>Computational Biology</i> , 2013 ,	0.7	14
153	A phylogenetic analysis of the grape genus (<i>Vitis</i> L.) reveals broad reticulation and concurrent diversification during neogene and quaternary climate change. 2013 , 13, 141		83
152	Accuracy guarantees for phylogeny reconstruction algorithms based on balanced minimum evolution. 2013 , 10, 576-83		2
151	Application of the phylogenetic informativeness method to chloroplast markers: a test case of closely related species in tribe Hydrangeeae (<i>Hydrangeaceae</i>). 2013 , 66, 233-42		22
150	Bioinformatics Approaches in Studying Microbial Diversity. 2013 , 119-140		
149	Biological Sequence Analysis: Algorithms and Statistical Methods. 2013 , 303-333		
148	Testing evolutionary models to explain the process of nucleotide substitution in gut bacterial 16S rRNA gene sequences. 2013 , 346, 97-104		3
147	Assessment of a new Bacteroidales marker targeting North American beaver (<i>Castor canadensis</i>) fecal pollution by real-time PCR. 2013 , 95, 201-6		8
146	Properties and Evolutionary Implications of the Heliobacterial Genome. 2013 , 67-97		8
145	Identification of a Bacterial Consortium with Biotechnological Potential for Arsenic Bioremediation. 2013 , 825, 540-543		
144	Altered colonic function and microbiota profile in a mouse model of chronic depression. 2013 , 25, 733-e575		182
143	The Complete Genome Sequence of <i>Methanobrevibacter</i> sp. AbM4. 2013 , 8, 215-27		36
142	Genome sequence of the marine bacterium <i>Corynebacterium maris</i> type strain Coryn-1(T) (= DSM 45190(T)). 2013 , 8, 516-24		1
141	Genome sequence of the squalene-degrading bacterium <i>Corynebacterium terpenotabidum</i> type strain Y-11(T) (= DSM 44721(T)). 2014 , 9, 505-13		5

140	The Genomic Blueprint of <i>Salmonella enterica</i> subspecies <i>enterica</i> serovar Typhi P-stx-12. 2013 , 7, 483-96		4
139	Contrasting genetic structure among populations of two amphidromous fish species (Sicydiinae) in the Central West Pacific. <i>PLoS ONE</i> , 2013 , 8, e75465	3.7	20
138	Whole-proteome analysis of twelve species of alphaproteobacteria links four pathogens. 2013 , 2, 627-35		1
137	Influence of Methanogenic Populations in Holocene Lacustrine Sediments Revealed by Clone Libraries and Fatty Acid Biogeochemistry. 2014 , 31, 285-298		8
136	Models of nucleotide substitution. 2014 , 1-34		1
135	Complete genome sequence of the lignin-degrading bacterium <i>Klebsiella</i> sp. strain BRL6-2. 2014 , 9, 19		27
134	Nasopharyngeal colonization by potentially pathogenic bacteria found in healthy semi-captive wild-born chimpanzees in Uganda. 2014 , 76, 103-10		8
133	Ribosomal Database Project: data and tools for high throughput rRNA analysis. 2014 , 42, D633-42		2527
132	Predicting the emergence of H3N2 influenza viruses reveals contrasted modes of evolution of HA and NA antigens. 2014 , 78, 1-12		4
131	Population variation revealed high-altitude adaptation of Tibetan mastiffs. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1200-5	8.3	88
130	Multilocus sequence typing using mitochondrial genes (mtMLST) reveals geographic population structure of <i>Ixodes ricinus</i> ticks. 2014 , 5, 152-60		19
129	Distance-Based Phylogenetic Methods Around a Polytoomy. 2014 , 11, 325-35		3
128	STINGRAY: system for integrated genomic resources and analysis. 2014 , 7, 132		5
127	Comparative molecular analysis of bacterial communities inhabiting pristine and polluted with polycyclic aromatic hydrocarbons Black Sea coastal sediments. <i>Marine Pollution Bulletin</i> , 2014 , 83, 231-40	6.7	17
126	Draft genome sequence of <i>Dyadobacter tibetensis</i> type strain (Y620-1) isolated from glacial ice. 2014 , 9, 883-92		3
125	The Genome Sequence of a Type ST239 Methicillin-Resistant <i>Staphylococcus aureus</i> Isolate from a Malaysian Hospital. 2014 , 9, 933-9		2
124	Complete genome sequence of <i>Anabaena variabilis</i> ATCC 29413. 2014 , 9, 562-73		32
123	Histophagous ciliate <i>Pseudocollinia brintoni</i> and bacterial assemblage interaction with krill <i>Nyctiphanes simplex</i> . I. Transmission process. 2015 , 116, 213-25		8

122	Molecular Phylogenetics: A Tool for Elucidation of Evolutionary Processes from Biological Data. 2015 , 203-250		
121	Complete genome sequence of <i>Vibrio anguillarum</i> strain NB10, a virulent isolate from the Gulf of Bothnia. 2015 , 10, 60		14
120	Genome sequence of the soil bacterium <i>Corynebacterium callunae</i> type strain DSM 20147(T). 2015 , 10, 5		5
119	Complete genome sequence of <i>Actinobacillus equuli</i> subspecies <i>equuli</i> ATCC 19392(T). 2015 , 10, 32		6
118	Complete genome sequence of the thermophilic <i>Thermus</i> sp. CCB_US3_UF1 from a hot spring in Malaysia. 2015 , 10, 76		6
117	Impact of paleoclimate on the distribution of microbial communities in the subsurface sediment of the Dead Sea. 2015 , 13, 546-61		11
116	leBIBIQBPP: a set of databases and a webtool for automatic phylogenetic analysis of prokaryotic sequences. 2015 , 16, 251		42
115	Development of forensic assay signatures for ebolaviruses. 2015 , 60, 315-25		
114	A Primer to Molecular Phylogenetic Analysis in Plants. 2015 , 34, 454-468		4
113	Diversification of the cold-adapted butterfly genus <i>Oeneis</i> related to Holarctic biogeography and climatic niche shifts. 2015 , 92, 255-65		16
112	Fate of faecal indicator organisms and bacterial diversity dynamics in a series of continuously fed aerated tank reactors treating dairy manure. 2015 , 81, 363-372		
111	Genomic Analyses Reveal Potential Independent Adaptation to High Altitude in Tibetan Chickens. <i>Molecular Biology and Evolution</i> , 2015 , 32, 1880-9	8.3	114
110	A genome-scale mining strategy for recovering novel rapidly-evolving nuclear single-copy genes for addressing shallow-scale phylogenetics in <i>Hydrangea</i> . 2015 , 15, 132		19
109	Progressive alignment of genomic signals by multiple dynamic time warping. 2015 , 385, 20-30		15
108	Revisiting <i>Corynebacterium glyciniphilum</i> (ex Kubota et al., 1972) sp. nov., nom. rev., isolated from putrefied banana. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015 , 65, 177-182	2.2	3
107	Fundamentals of Bioinformatics and Computational Biology. <i>Modeling and Optimization in Science and Technologies</i> , 2015 ,	0.6	2
106	Multiple post-domestication origins of kabuli chickpea through allelic variation in a diversification-associated transcription factor. 2016 , 211, 1440-51		35
105	Complete genome sequence of an agr-dysfunctional variant of the ST239 lineage of the methicillin-resistant <i>Staphylococcus aureus</i> strain GV69 from Brazil. 2016 , 11, 34		3

104	Morphological, Physiological, and Taxonomic Characterization of Actinobacterial Isolates Living as Endophytes of Cacao Pods and Cacao Seeds. 2016 , 31, 56-62		15
103	Comparative population genomics reveals genetic basis underlying body size of domestic chickens. 2016 , 8, 542-552		15
102	Distance-Based Phylogenetic Inference. 2016 , 458-465		2
101	Genome-wide analysis reveals adaptation to high altitudes in Tibetan sheep. <i>Scientific Reports</i> , 2016 , 6, 26770	4.9	52
100	Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction. 2016 , 17, 783		12
99	Complete genome sequence of the actinomycete type strain HPA 177 isolated from a marine sponge. 2016 , 11, 91		3
98	Draft genome of CCAP 1490/1 (CALU1027), the chlorophyll containing filamentous cyanobacterium. 2016 , 11, 82		
97	Sulfide-oxidizing bacteria establishment in an innovative microaerobic reactor with an internal silicone membrane for sulfur recovery from wastewater. 2016 , 27, 119-30		9
96	Phylogenetic trees and Euclidean embeddings. 2017 , 74, 99-111		2
95	Rapid Evolution of Genes Involved in Learning and Energy Metabolism for Domestication of the Laboratory Rat. <i>Molecular Biology and Evolution</i> , 2017 , 34, 3148-3153	8.3	9
94	Characterization of , sp. nov., isolated from a human blood culture. 2017 , 19, 71-77		1
93	References. 339-375		
92	Evaluating Fast Maximum Likelihood-Based Phylogenetic Programs Using Empirical Phylogenomic Data Sets. <i>Molecular Biology and Evolution</i> , 2018 , 35, 486-503	8.3	82
91	On Multiple Virtual NICs in Cloud Computing: Performance Bottleneck and Enhancement. <i>IEEE Systems Journal</i> , 2018 , 12, 2417-2427	4.3	5
90	Phylogeny Construction. <i>Computational Biology</i> , 2018 , 395-466	0.7	
89	Study on Lipid Accumulation in Novel Oleaginous Yeast <i>Naganishia liquefaciens</i> NITTS2 Utilizing Pre-digested Municipal Waste Activated Sludge: a Low-cost Feedstock for Biodiesel Production. <i>Applied Biochemistry and Biotechnology</i> , 2018 , 186, 731-749	3.2	20
88	Fluid inclusions from the deep Dead Sea sediment provide new insights on Holocene extreme microbial life. <i>Quaternary Science Reviews</i> , 2019 , 212, 18-27	3.9	5
87	Estimation of Phylogenetic Tree using Gene Sequencing Data. 2019 ,		

86	Optimization of cultural factors of newly isolated microalga <i>Spirulina subsalsa</i> and its co-digestion with paddy straw for enhanced biogas production. <i>Bioresource Technology Reports</i> , 2019 , 5, 185-198	4.1	12
85	Whole genome sequence analysis to detect signatures of positive selection for high fecundity in sheep. <i>Reproduction in Domestic Animals</i> , 2019 , 54, 358-364	1.6	12
84	Antimicrobial efficacy of <i>Nocardiosis</i> sp. MK_MSt033 against selected multidrug resistant clinical microbial pathogens. <i>Journal of Infection and Public Health</i> , 2020 , 13, 1522-1532	7.4	5
83	Genetic Signatures of Selection for Cashmere Traits in Chinese Goats. <i>Animals</i> , 2020 , 10,	3.1	9
82	<i>Bacillus megaterium</i> -induced biocorrosion on mild steel and the effect of <i>Artemisia pallens</i> methanolic extract as a natural corrosion inhibitor. <i>Archives of Microbiology</i> , 2020 , 202, 2311-2323	3.1	12
81	Genetic diversity, SNP-trait associations and genomic selection accuracy in a west African collection of Kersting groundnut [<i>Macrotyloma geocarpum</i> (Harms) Marhal & Baudet]. <i>PLoS ONE</i> , 2020 , 15, e0234769	2.7	8
80	Analysis of the Complete Genome of the Alkaliphilic and Phototrophic Firmicute Strain HH. <i>Microorganisms</i> , 2020 , 8,	4.9	7
79	Fast clustering-based weighted twin support vector regression. <i>Soft Computing</i> , 2020 , 24, 6101-6117	3.5	2
78	ENJ algorithm can construct triple phylogenetic trees. <i>Molecular Therapy - Nucleic Acids</i> , 2021 , 23, 286-293	3.7	4
77	Integrating Genomic and Transcriptomic Data to Reveal Genetic Mechanisms Underlying Piao Chicken Rumpless Trait. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 ,	6.5	0
76	Realization problems on reachability sequences. <i>Theoretical Computer Science</i> , 2021 , 866, 1-13	1.1	
75	Enhancement of euryhaline biomass production for improving biogas generation through anaerobic co-digestion with carbon rich substrate. <i>3 Biotech</i> , 2021 , 11, 251	2.8	0
74	Genetic diversity and population structure of ridge gourd (<i>Luffa acutangula</i>) accessions in a Thailand collection using SNP markers. <i>Scientific Reports</i> , 2021 , 11, 15311	4.9	1
73	Function is a better predictor of plant rhizosphere community membership than 16S phylogeny. <i>Environmental Microbiology</i> , 2021 , 23, 6089-6103	5.2	1
72	Bioremediation of petroleum contaminated soil through biosurfactant and SA3 amended design treatments. <i>Current Research in Microbial Sciences</i> , 2021 , 2, 100031	3.3	4
71	Ancestral sequence reconstruction - An underused approach to understand the evolution of gene function in plants?. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 1579-1594	6.8	4
70	Identification and characterization of CONSTANS-like genes from <i>Curcuma alismatifolia</i> . <i>Horticulture Environment and Biotechnology</i> , 2021 , 62, 279-286	2	1
69	Robustness of Greedy Type Minimum Evolution Algorithms. <i>Lecture Notes in Computer Science</i> , 2006 , 815-821	0.9	3

68	PhyNav: A Novel Approach to Reconstruct Large Phylogenies. <i>Studies in Classification, Data Analysis, and Knowledge Organization</i> , 2005 , 386-393	0.2	2
67	Sequence-Length Requirements for Phylogenetic Methods. <i>Lecture Notes in Computer Science</i> , 2002 , 343-356	0.9	18
66	Fast and Accurate Phylogeny Reconstruction Algorithms Based on the Minimum-Evolution Principle. <i>Lecture Notes in Computer Science</i> , 2002 , 357-374	0.9	8
65	Genome Rearrangement Phylogeny Using Weighbor. <i>Lecture Notes in Computer Science</i> , 2002 , 112-125	0.9	1
64	Large-Scale Multiple Sequence Alignment and Phylogeny Estimation. <i>Computational Biology</i> , 2013 , 85-146	0.7	11
63	A Not-So-Long Introduction to Computational Molecular Evolution. <i>Methods in Molecular Biology</i> , 2019 , 1910, 71-117	1.4	3
62	Accuracy Guarantees for Phylogeny Reconstruction Algorithms Based on Balanced Minimum Evolution. <i>Lecture Notes in Computer Science</i> , 2010 , 250-261	0.9	2
61	Computational Molecular Evolution. 2006 ,		547
60	Phylogeny reconstruction: overview. 2006 , 73-99		1
59	Maximum likelihood methods. 2006 , 100-144		2
58	Bayesian methods. 2006 , 145-184		1
57	Neutral and adaptive protein evolution. 2006 , 259-292		2
56	Molecular Evolution. 2014 ,		146
55	sp. nov., isolated from subsurface soil and leaf litter in a tropical peat swamp forest. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020 , 70, 6355-6363	2.2	1
54	Evaluating fast maximum likelihood-based phylogenetic programs using empirical phylogenomic data sets.		3
53	Molecular evolution and functional divergence of the Ca(2+) sensor protein in store-operated Ca(2+) entry: stromal interaction molecule. <i>PLoS ONE</i> , 2007 , 2, e609	3.7	38
52	Dichotomy in the NRT gene families of dicots and grass species. <i>PLoS ONE</i> , 2010 , 5, e15289	3.7	101
51	Genetic patterns of domestication in pigeonpea (<i>Cajanus cajan</i> (L.) Millsp.) and wild <i>Cajanus</i> relatives. <i>PLoS ONE</i> , 2012 , 7, e39563	3.7	72

50	The Relationship between Mating System and Genetic Diversity in Diploid Sexual Populations of <i>Cyrtomium falcatum</i> in Japan. <i>PLoS ONE</i> , 2016 , 11, e0163683	3.7	3
49	A fast alignment-free bioinformatics procedure to infer accurate distance-based phylogenetic trees from genome assemblies. <i>Research Ideas and Outcomes</i> , 5,	2.5	20
48	Microbial Observation in Bioaccumulation of Heavy Metals from the Ash Dyke of Thermal Power Plants of Chhattisgarh, India. <i>Advances in Bioscience and Biotechnology (Print)</i> , 2015 , 06, 131-138	0.9	20
47	Models of amino acid and codon substitution. 2006 , 40-70		1
46	Models of nucleotide substitution. 2006 , 3-39		
45	Simulating molecular evolution. 2006 , 293-307		4
44	Perspectives. 2006 , 308-310		
43	Comparison of methods and tests on trees. 2006 , 185-220		
42	A Covariance Matrix Inversion Problem arising from the Construction of Phylogenetic Trees. <i>LMS Journal of Computation and Mathematics</i> , 2007 , 10, 119-131		
41	Encyclopedia of Algorithms. 2008 , 253-256		1
40	Molecular phylogenetics: testing evolutionary hypotheses. <i>Methods in Molecular Biology</i> , 2009 , 502, 131-168		1
39	Phylogenetic Tree Reconstruction with Protein Linkage. <i>Lecture Notes in Computer Science</i> , 2012 , 315-327.9		
38	Tree and Network Building. <i>Computational Biology</i> , 2013 , 367-415	0.7	
37	Phylogeny reconstruction: overview. 2014 , 70-101		
36	Comparison of phylogenetic methods and tests on trees. 2014 , 153-181		
35	Molecular clock and estimation of species divergence times. 2014 , 361-389		
34	Models of amino acid and codon substitution. 2014 , 35-69		
33	Maximum likelihood methods. 2014 , 102-152		

32	Bayesian theory. 2014 , 182-213		
31	Simulating molecular evolution. 2014 , 418-441		0
30	Neutral and adaptive protein evolution. 2014 , 390-417		
29	Appendices. 2014 , 442-449		
28	Bayesian phylogenetics. 2014 , 263-307		
27	Coalescent theory and species trees. 2014 , 308-360		
26	Bayesian computation (MCMC). 2014 , 214-262		
25	Distance Based Methods. <i>Modeling and Optimization in Science and Technologies</i> , 2015 , 253-260	0.6	
24	Application of vacA Sequencing in Helicobacter pylori for Classification of Specimens from Healthy Persons, and from Hepatobiliary and Gastroduodenal Patients. <i>Journal of Pure and Applied Microbiology</i> , 2017 , 11, 01-07	0.9	1
23	Identification and Molecular Characterization of Microbial Isolates from Purified Water Used in Pharmaceutical Industry. <i>Journal of Pure and Applied Microbiology</i> , 2019 , 13, 1815-1821	0.9	
22	Integrating Genomic and Transcriptomic Data to Reveal Genetic Mechanisms Underlying Piao Chicken Rumpless Trait.		0
21	Genetic diversity and population structure of Luffa acutangula accessions in a Thailand collection using SNP markers.		
20	A New Algorithm for Reconstruction of Phylogenetic Tree. 2008 , 472-477		
19	Production of di-rhamnolipid with simultaneous distillery wastewater degradation and detoxification by newly isolated Pseudomonas aeruginosa SRRBL1. <i>Journal of Cleaner Production</i> , 2022 , 336, 130429	10.3	2
18	Role of gut microbial biofilm of anopheline mosquitoes to control its vectorial attribute: A study in some areas of West Bengal. <i>Biocatalysis and Agricultural Biotechnology</i> , 2022 , 102305	4.2	
17	Algorithms for Genomic Analysis. 2008 , 33-54		
16	Remediation and detoxification of oil contaminated marine intertidal sites through lipopeptide assisted washing strategy: An experimental and kinetic validation approach. <i>Marine Pollution Bulletin</i> , 2022 , 180, 113817	6.7	1
15	Editorial: Methods and Applications in Molecular Phylogenetics. <i>Frontiers in Genetics</i> , 13,	4.5	

14 Appendices. **2006**, 311-318

13 Preface. **2006**, vii-x

12 Dedication. **2006**, v-vi

11 Copyright Page. **2006**, iv-iv

10 Preface. **2014**, vii-viii

9 Copyright Page. **2014**, iv-iv

8 Foreword. **2014**, v-vi

7 Mining Candidate Genes and Favorable Haplotypes for Flag Leaf Shape in Rice (*Oryza sativa* L.) Based on a Genome-Wide Association Study. **2022**, 12, 1814 ○

6 Proteomic Analysis of Human Breast Cancer MCF-7 Cells to Identify Cellular Targets of the Anticancer Pigment OR3 from *Streptomyces coelicolor* JUACT03. ○

5 Production of Organic Liquid Biofertilizer from Fish Waste and Study of its Plant Growth Promoting Effect. ○

4 Report on Vincristine-Producing Endophytic Fungus *Nigrospora zimmermanii* from Leaves of *Catharanthus roseus*. **2022**, 12, 1119 ○

3 *Hominibacterium faecale* gen. nov., sp. nov., an anaerobic l-arginine-degrading bacterium isolated from human feces. **2023**, 205, ○

2 Comparative functional analysis of macrophage phagocytosis in Dagu chickens and Wenchang chickens. 14, ○

1 Investigating the Antibacterial Properties of Silver Nanoparticles Acquired using *Streptomyces* strain AK3 from Riverbank Soil. **2023**, 20, 351-358 ○