

Barbara R Holland

List of Publications by Year in descending order

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84
papers

3,023
citations

201674

27
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175258

52
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85
all docs

85
docs citations

85
times ranked

4102
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparing Partitioned Models to Mixture Models: Do Information Criteria Apply?. <i>Systematic Biology</i> , 2022, 71, 1541-1548.	5.6	11
2	Unattained geometric configurations of secondary structure elements in protein structural space. <i>Journal of Structural Biology</i> , 2022, 214, 107870.	2.8	1
3	A subfunctionalisation model of gene family evolution predicts balanced tree shapes. <i>Molecular Phylogenetics and Evolution</i> , 2022, 176, 107566.	2.7	4
4	GHOST: Recovering Historical Signal from Heterotachously Evolved Sequence Alignments. <i>Systematic Biology</i> , 2020, 69, 249-264.	5.6	75
5	The Ancient Operational Code is Embedded in the Amino Acid Substitution Matrix and aaRS Phylogenies. <i>Journal of Molecular Evolution</i> , 2020, 88, 136-150.	1.8	9
6	Level-dependent QBD models for the evolution of a family of gene duplicates. <i>Stochastic Models</i> , 2020, 36, 285-311.	0.5	6
7	Accuracy of ancestral state reconstruction for non-neutral traits. <i>Scientific Reports</i> , 2020, 10, 7644.	3.3	32
8	Benchmarking Methods of Protein Structure Alignment. <i>Journal of Molecular Evolution</i> , 2020, 88, 575-597.	1.8	4
9	The impracticalities of multiplicatively-closed codon models: a retreat to linear alternatives. <i>Journal of Mathematical Biology</i> , 2020, 81, 549-573.	1.9	0
10	A new phylogenetic protocol: dealing with model misspecification and confirmation bias in molecular phylogenetics. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa041.	3.2	15
11	Links between environment and stomatal size through evolutionary time in Proteaceae. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192876.	2.6	9
12	<sc>hyperoverlap</sc>: Detecting biological overlap in n -dimensional space. <i>Methods in Ecology and Evolution</i> , 2020, 11, 513-523.	5.2	15
13	On the decision support model for the patient admission scheduling problem with random arrivals and departures: A solution approach. <i>Stochastic Models</i> , 2020, 36, 312-336.	0.5	3
14	Mitogenomic diversity in Sacred Ibis Mummies sheds light on early Egyptian practices. <i>PLoS ONE</i> , 2019, 14, e0223964.	2.5	14
15	Ancient <sc>DNA</sc> tracks the mainland extinction and island survival of the Tasmanian devil. <i>Journal of Biogeography</i> , 2018, 45, 963-976.	3.0	22
16	Distinguishing Between Convergent Evolution and Violation of the Molecular Clock for Three Taxa. <i>Systematic Biology</i> , 2018, 67, 905-915.	5.6	3
17	Maximum likelihood estimates of pairwise rearrangement distances. <i>Journal of Theoretical Biology</i> , 2017, 423, 31-40.	1.7	15
18	Developing a statistically powerful measure for quartet tree inference using phylogenetic identities and Markov invariants. <i>Journal of Mathematical Biology</i> , 2017, 75, 1619-1654.	1.9	4

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19	Live bearing promotes the evolution of sociality in reptiles. <i>Nature Communications</i> , 2017, 8, 2030.	12.8	39
20	Analysis of a mechanistic Markov model for gene duplicates evolving under subfunctionalization. <i>BMC Evolutionary Biology</i> , 2017, 17, 38.	3.2	17
21	Genomic Scans across Three Eucalypts Suggest that Adaptation to Aridity is a Genome-Wide Phenomenon. <i>Genome Biology and Evolution</i> , 2017, 9, 253-265.	2.5	27
22	Detecting Selection on Temporal and Spatial Scales: A Genomic Time-Series Assessment of Selective Responses to Devil Facial Tumor Disease. <i>PLoS ONE</i> , 2016, 11, e0147875.	2.5	17
23	Comparison of Three Statistical Classification Techniques for Maser Identification. <i>Publications of the Astronomical Society of Australia</i> , 2016, 33, .	3.4	2
24	Simulating and Summarizing Sources of Gene Tree Incongruence. <i>Genome Biology and Evolution</i> , 2016, 8, 1299-1315.	2.5	12
25	Evaluation of Monitoring Schemes for Wastewater-Based Epidemiology to Identify Drug Use Trends Using Cocaine, Methamphetamine, MDMA and Methadone. <i>Environmental Science & Technology</i> , 2016, 50, 4760-4768.	10.0	18
26	Last hope for the doomed? Thoughts on the importance of a parasexual cycle for the yeast <i>Candida albicans</i> . <i>Current Genetics</i> , 2016, 62, 81-85.	1.7	7
27	Molecular Evolution: A Statistical Approach. " By Ziheng Yang.. <i>Systematic Biology</i> , 2015, 64, 545-546.	5.6	0
28	Patterns of Reproductive Isolation in <i>Eucalyptus</i> A Phylogenetic Perspective. <i>Molecular Biology and Evolution</i> , 2015, 32, 1833-1846.	8.9	56
29	Selective Advantages of a Parasexual Cycle for the Yeast <i>Candida albicans</i> . <i>Genetics</i> , 2015, 200, 1117-1132.	2.9	23
30	A tensorial approach to the inversion of group-based phylogenetic models. <i>BMC Evolutionary Biology</i> , 2014, 14, 236.	3.2	1
31	Extensive population decline in the Tasmanian devil predates European settlement and devil facial tumour disease. <i>Biology Letters</i> , 2014, 10, 20140619.	2.3	59
32	Reconstructing past changes in locus-specific recombination rates. <i>BMC Genetics</i> , 2013, 14, 11.	2.7	4
33	The Identification of Concerted Convergence in Insect Heads Corroborates Palaeoptera. <i>Systematic Biology</i> , 2013, 62, 250-263.	5.6	31
34	Missing Data and Influential Sites: Choice of Sites for Phylogenetic Analysis Can Be As Important As Taxon Sampling and Model Choice. <i>Genome Biology and Evolution</i> , 2013, 5, 681-687.	2.5	23
35	Low-Parameter Phylogenetic Inference Under the General Markov Model. <i>Systematic Biology</i> , 2013, 62, 78-92.	5.6	29
36	Novel Distances for Dollo Data. <i>Systematic Biology</i> , 2013, 62, 62-77.	5.6	25

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37	<i>Campylobacter jejuni</i> colonization and population structure in urban populations of ducks and starlings in New Zealand. <i>MicrobiologyOpen</i> , 2013, 2, 659-673.	3.0	28
38	The Rise of Statistical Phylogenetics. <i>Australian and New Zealand Journal of Statistics</i> , 2013, 55, 205-220.	0.9	5
39	Gaps: An Elusive Source of Phylogenetic Information. <i>Systematic Biology</i> , 2012, 61, 1075-1082.	5.6	15
40	Supermatrices, supertrees and serendipitous scaffolding: Inferring a well-resolved, genus-level phylogeny of Styphelioideae (Ericaceae) despite missing data. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 146-158.	2.7	20
41	Reconciling molecules and morphology: Molecular systematics and biogeography of Neotropical blennies (<i>Acanthemblemaria</i>). <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 159-173.	2.7	13
42	Is the General Time-Reversible Model Bad for Molecular Phylogenetics?. <i>Systematic Biology</i> , 2012, 61, 1069-1074.	5.6	41
43	Estimating the Relative Roles of Recombination and Point Mutation in the Generation of Single Locus Variants in <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> . <i>Journal of Molecular Evolution</i> , 2012, 74, 273-280.	1.8	9
44	The Algebra of the General Markov Model on Phylogenetic Trees and Networks. <i>Bulletin of Mathematical Biology</i> , 2012, 74, 858-880.	1.9	11
45	Faster exact maximum parsimony search with XMP. <i>Bioinformatics</i> , 2011, 27, 1359-1367.	4.1	13
46	Biogeography of circum-Antarctic springtails. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 48-58.	2.7	44
47	Identifying Cliques of Convergent Characters: Concerted Evolution in the Cormorants and Shags. <i>Systematic Biology</i> , 2010, 59, 433-445.	5.6	75
48	Phylogenetic Tree Reconstruction Accuracy and Model Fit when Proportions of Variable Sites Change across the Tree. <i>Systematic Biology</i> , 2010, 59, 288-297.	5.6	19
49	Impact of Genetic Background on Allele Selection in a Highly Mutable <i>Candida albicans</i> Gene, PNG2. <i>PLoS ONE</i> , 2010, 5, e9614.	2.5	9
50	Testing the Effect of Metabolic Rate on DNA Variability at the Intra-Specific Level. <i>PLoS ONE</i> , 2010, 5, e9686.	2.5	5
51	Molecular Epidemiology of <i>Campylobacter jejuni</i> Isolates from Wild-Bird Fecal Material in Children's Playgrounds. <i>Applied and Environmental Microbiology</i> , 2009, 75, 779-783.	3.1	120
52	LineageSpecificSeqgen: generating sequence data with lineage-specific variation in the proportion of variable sites. <i>BMC Evolutionary Biology</i> , 2009, 9, 200.	3.2	0
53	Distribution of mutations distinguishing the most prevalent disease-causing <i>Candida albicans</i> genotype from other genotypes. <i>Infection, Genetics and Evolution</i> , 2009, 9, 493-500.	2.3	11
54	The Emergence of Predators in Early Life: There was No Garden of Eden. <i>PLoS ONE</i> , 2009, 4, e5507.	2.5	17

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55	Conflict amongst chloroplast DNA sequences obscures the phylogeny of a group of Asplenium ferns. <i>Molecular Phylogenetics and Evolution</i> , 2008, 48, 176-187.	2.7	22
56	Using supernetworks to distinguish hybridization from lineage-sorting. <i>BMC Evolutionary Biology</i> , 2008, 8, 202.	3.2	104
57	LineageSpecificSeqgen: generating sequence data with lineage-specific variation in the proportion of variable sites. <i>BMC Evolutionary Biology</i> , 2008, 8, 317.	3.2	10
58	Optimizing Automated AFLP Scoring Parameters to Improve Phylogenetic Resolution. <i>Systematic Biology</i> , 2008, 57, 347-366.	5.6	111
59	Treeness Triangles: Visualizing the Loss of Phylogenetic Signal. <i>Molecular Biology and Evolution</i> , 2007, 24, 2029-2039.	8.9	24
60	The Problem of Rooting Rapid Radiations. <i>Molecular Biology and Evolution</i> , 2007, 24, 2400-2411.	8.9	72
61	Imputing Supertrees and Supernetworks from Quartets. <i>Systematic Biology</i> , 2007, 56, 57-67.	5.6	39
62	Analysis of Phylogenetics and Evolution with R. <i>Systematic Biology</i> , 2007, 56, 694-696.	5.6	3
63	Heterozygosity and functional allelic variation in the <i>Candida albicans</i> efflux pump genes CDR1 and CDR2. <i>Molecular Microbiology</i> , 2006, 62, 170-186.	2.5	61
64	Genome BLAST distance phylogenies inferred from whole plastid and whole mitochondrion genome sequences. <i>BMC Bioinformatics</i> , 2006, 7, 350.	2.6	76
65	Deciphering Past Human Population Movements in Oceania: Provably Optimal Trees of 127 mtDNA Genomes. <i>Molecular Biology and Evolution</i> , 2006, 23, 1966-1975.	8.9	62
66	Improved Consensus Network Techniques for Genome-Scale Phylogeny. <i>Molecular Biology and Evolution</i> , 2006, 23, 848-855.	8.9	34
67	xmlns:xs="http://www.w3.org/2001/XMLSchema" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" xmlns="http://www.elsevier.com/xml/ja/dtd" xmlns:ja="http://www.elsevier.com/xml/ja/dtd" xmlns:mml="http://www.w3.org/1998/Math/MathML" xmlns:tb="http://www.elsevier.com/xml/common/table/dtd" xmlns:tbl="http://www.elsevier.com/xml/common/struct-bib/dtd" xmlns:elsevier="http://www.elsevier.com/xml/elsevier-dtd"	0.9	16
68	Untangling Long Branches: Identifying Conflicting Phylogenetic Signals Using Spectral Analysis, Neighbor-Net, and Consensus Networks. <i>Systematic Biology</i> , 2005, 54, 620-633.	5.6	56
69	Visualizing Conflicting Evolutionary Hypotheses in Large Collections of Trees: Using Consensus Networks to Study the Origins of Placentals and Hexapods. <i>Systematic Biology</i> , 2005, 54, 66-76.	5.6	54
70	Analysis of <i>Acorus calamus</i> Chloroplast Genome and Its Phylogenetic Implications. <i>Molecular Biology and Evolution</i> , 2005, 22, 1813-1822.	8.9	136
71	A futile act? Thoughts on the reproductive biology of <i>Candida albicans</i> . <i>The Mycologist</i> , 2004, 18, 158-163.	0.4	5
72	Using Consensus Networks to Visualize Contradictory Evidence for Species Phylogeny. <i>Molecular Biology and Evolution</i> , 2004, 21, 1459-1461.	8.9	149

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73	The MinMax Squeeze: Guaranteeing a Minimal Tree for Population Data. <i>Molecular Biology and Evolution</i> , 2004, 22, 235-242.	8.9	13
74	Searching factors causing implausible non-monophyly: ssu rDNA phylogeny of Isopoda Asellota (Crustacea: Peracarida) and faster evolution in marine than in freshwater habitats. <i>Molecular Phylogenetics and Evolution</i> , 2003, 28, 536-551.	2.7	12
75	A novel exploratory method for visual recombination detection. <i>Genome Biology</i> , 2003, 4, R33.	9.6	19
76	Optimal alphabets for an RNA world. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003, 270, 1177-1182.	2.6	19
77	Sixty Alleles of the ALS7 Open Reading Frame in <i>Candida albicans</i> : ALS7 Is a Hypermutable Contingency Locus. <i>Genome Research</i> , 2003, 13, 2005-2017.	5.5	68
78	Mosaic Genomes of the Six Major Primate Lentivirus Lineages Revealed by Phylogenetic Analyses. <i>Journal of Virology</i> , 2003, 77, 7202-7213.	3.4	36
79	Upper bounds on maximum likelihood for phylogenetic trees. <i>Bioinformatics</i> , 2003, 19, ii66-ii72.	4.1	4
80	Outgroup Misplacement and Phylogenetic Inaccuracy Under a Molecular Clock—A Simulation Study. <i>Systematic Biology</i> , 2003, 52, 229-238.	5.6	132
81	Consensus Networks: A Method for Visualising Incompatibilities in Collections of Trees. <i>Lecture Notes in Computer Science</i> , 2003, , 165-176.	1.3	73
82	Rates of Evolution in Ancient DNA from Adelie Penguins. <i>Science</i> , 2002, 295, 2270-2273.	12.6	274
83	Ť Plots: A Tool for Analyzing Phylogenetic Distance Data. <i>Molecular Biology and Evolution</i> , 2002, 19, 2051-2059.	8.9	136
84	Multiple Maxima of Likelihood in Phylogenetic Trees: An Analytic Approach. <i>Molecular Biology and Evolution</i> , 2000, 17, 1529-1541.	8.9	115