

Edward L Braun

List of Publications by Year in descending order

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129
papers

13,994
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47409

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25983

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times ranked

15462
citing authors

#	ARTICLE	IF	CITATIONS
1	A novel exome probe set captures phototransduction genes across birds (Aves) enabling efficient analysis of vision evolution. <i>Molecular Ecology Resources</i> , 2022, 22, 587-601.	2.2	3
2	Dynamic Patterns of Sex Chromosome Evolution in Neognath Birds: Many Independent Barriers to Recombination at the ATP5F1A Locus. <i>Birds</i> , 2022, 3, 51-70.	0.6	3
3	Phylogenetic definitions for 25 higher-level clade names of birds. <i>Avian Research</i> , 2022, 13, 100027.	0.5	15
4	Categorical edge-based analyses of phylogenomic data reveal conflicting signals for difficult relationships in the avian tree. <i>Molecular Phylogenetics and Evolution</i> , 2022, 174, 107550.	1.2	1
5	Historical specimens and the limits of subspecies phylogenomics in the New World quails (Odontophoridae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 175, 107559.	1.2	10
6	Phylogenomics of manakins (Aves: Pipridae) using alternative locus filtering strategies based on informativeness. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 107013.	1.2	20
7	Data Types and the Phylogeny of Neoaves. <i>Birds</i> , 2021, 2, 1-22.	0.6	46
8	The Roles of Protein Structure, Taxon Sampling, and Model Complexity in Phylogenomics: A Case Study Focused on Early Animal Divergences. <i>Biophysica</i> , 2021, 1, 87-105.	0.6	2
9	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. <i>Genome Biology</i> , 2021, 22, 120.	3.8	69
10	A phylogenomic supermatrix of Galliformes (Landfowl) reveals biased branch lengths. <i>Molecular Phylogenetics and Evolution</i> , 2021, 158, 107091.	1.2	26
11	TAPER: Pinpointing errors in multiple sequence alignments despite varying rates of evolution. <i>Methods in Ecology and Evolution</i> , 2021, 12, 2145-2158.	2.2	13
12	When good mitochondria go bad: Cyto-nuclear discordance in landfowl (Aves: Galliformes). <i>Gene</i> , 2021, 801, 145841.	1.0	17
13	Protein Structure, Models of Sequence Evolution, and Data Type Effects in Phylogenetic Analyses of Mitochondrial Data: A Case Study in Birds. <i>Diversity</i> , 2021, 13, 555.	0.7	3
14	Divergence time estimation of Galliformes based on the best gene shopping scheme of ultraconserved elements. <i>Bmc Ecology and Evolution</i> , 2021, 21, 209.	0.7	17
15	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	13.7	251
16	Phylogeny and diversification of the gallopheasants (Aves: Galliformes): Testing roles of sexual selection and environmental niche divergence. <i>Zoologica Scripta</i> , 2020, 49, 549-562.	0.7	5
17	Tempo and Pattern of Avian Brain Size Evolution. <i>Current Biology</i> , 2020, 30, 2026-2036.e3.	1.8	72
18	Whole genome phylogeny of Gallus: introgression and data-type effects. <i>Avian Research</i> , 2020, 11, .	0.5	17

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19	The mitochondrial genome of <i>Apis mellifera simensis</i> (Hymenoptera: Apidae), an Ethiopian honey bee. Mitochondrial DNA Part B: Resources, 2020, 5, 9-10.	0.2	13
20	The mitochondrial genome of the Spanish honey bee, <i>Apis mellifera iberiensis</i> (Insecta: Hymenoptera: Apidae). Mitochondrial DNA Part B: Resources, 2020, 5, 11-12.	0.2	7
21	The mitochondrial genome of the Maltese honey bee, <i>Apis mellifera ruttneri</i> (Insecta: Hymenoptera: Apidae). Mitochondrial DNA Part B: Resources, 2020, 5, 875-876.	0.2	4
22	The complete mitochondrial genome of the West African honey bee <i>Apis mellifera adansonii</i> (Insecta: Hymenoptera: Apidae). Mitochondrial DNA Part B: Resources, 2020, 5, 11-12.	0.2	6
23	The complete mitochondrial genome of <i>Apis mellifera jemenitica</i> (Insecta: Hymenoptera: Apidae), the Arabian honey bee. Mitochondrial DNA Part B: Resources, 2020, 5, 875-876.	0.2	8
24	Mitochondrial genome of <i>Apis mellifera anatoliaca</i> (Hymenoptera: Apidae) – the Anatolian honey bee. Mitochondrial DNA Part B: Resources, 2020, 5, 1876-1877.	0.2	2
25	Deep-Time Demographic Inference Suggests Ecological Release as Driver of Neoavian Adaptive Radiation. Diversity, 2020, 12, 164.	0.7	11
26	Phylogenetic Analyses of Sites in Different Protein Structural Environments Result in Distinct Placements of the Metazoan Root. Biology, 2020, 9, 64.	1.3	20
27	Protein evolution is structure dependent and non-homogeneous across the tree of life. , 2020, , .		4
28	A Phylogenomic Supertree of Birds. Diversity, 2019, 11, 109.	0.7	93
29	Resolving the Avian Tree of Life from Top to Bottom: The Promise and Potential Boundaries of the Phylogenomic Era. , 2019, , 151-210.		27
30	Phylogenetic Signal of Indels and the Neoavian Radiation. Diversity, 2019, 11, 108.	0.7	33
31	The complete mitochondrial genome of <i>Apis mellifera unicolor</i> (Insecta: Hymenoptera: Apidae), the Malagasy honey bee. Mitochondrial DNA Part B: Resources, 2019, 4, 3286-3287.	0.2	10
32	The mitochondrial genome of the Carniolan honey bee, <i>Apis mellifera carnica</i> (Insecta: Hymenoptera: Apidae). Mitochondrial DNA Part B: Resources, 2019, 4, 3286-3287.	0.2	9
33	Earth history and the passerine superradiation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7916-7925.	3.3	238
34	What are the roles of taxon sampling and model fit in tests of cyto-nuclear discordance using avian mitochondrial data?. Molecular Phylogenetics and Evolution, 2019, 130, 132-142.	1.2	30
35	Mitochondrial genome diversity and population structure of two western honey bee subspecies in the Republic of South Africa. Scientific Reports, 2018, 8, 1333.	1.6	23
36	A simple strategy for recovering ultraconserved elements, exons, and introns from low coverage shotgun sequencing of museum specimens: Placement of the partridge genus <i>Tropicoperdix</i> within the galliformes. Molecular Phylogenetics and Evolution, 2018, 129, 304-314.	1.2	13

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37	Comparative Genomics Reveals a Burst of Homoplasmy-Free Numt Insertions. <i>Molecular Biology and Evolution</i> , 2018, 35, 2060-2064.	3.5	32
38	An evolutionary model motivated by physicochemical properties of amino acids reveals variation among proteins. <i>Bioinformatics</i> , 2018, 34, i350-i356.	1.8	12
39	Historical relationships of three enigmatic phasianid genera (Aves: Galliformes) inferred using phylogenomic and mitogenomic data. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 217-225.	1.2	38
40	How do seemingly non-vagile clades accomplish trans-marine dispersal? Trait and dispersal evolution in the landfowl (Aves: Galliformes). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170210.	1.2	45
41	Phylogenomic analysis supports multiple instances of polyphyly in the oomycete peronosporalean lineage. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 199-211.	1.2	19
42	The complete mitochondrial genome of <i>Apis mellifera meda</i> (Insecta: Hymenoptera: Apidae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 268-269.	0.2	19
43	Why Do Phylogenomic Data Sets Yield Conflicting Trees? Data Type Influences the Avian Tree of Life more than Taxon Sampling. <i>Systematic Biology</i> , 2017, 66, 857-879.	2.7	242
44	The complete mitochondrial genome of <i>Apis nuluensis</i> Tingek, an Asian honey bee (Insecta: Hymenoptera: Apidae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 270-271.	0.2	1
45	The complete mitochondrial genome of an east African honey bee, <i>Apis mellifera monticola</i> Smith (Insecta: Hymenoptera: Apidae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 589-590.	0.2	9
46	The complete mitochondrial genome and phylogenetic placement of <i>Apis nigrocincta</i> Smith (Insecta: Hymenoptera: Apidae), an Asian, cavity-nesting honey bee. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 249-250.	0.2	9
47	The complete mitochondrial genome of the Egyptian honey bee, <i>Apis mellifera lamarckii</i> (Insecta: Hymenoptera: Apidae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 272-273.	0.2	17
48	Ancestral range reconstruction of Galliformes: the effects of topology and taxon sampling. <i>Journal of Biogeography</i> , 2017, 44, 122-135.	1.4	52
49	Evolution of the 3R-MYB Gene Family in Plants. <i>Genome Biology and Evolution</i> , 2017, 9, 1013-1029.	1.1	50
50	The complete mitochondrial genome of the Cape honey bee, <i>Apis mellifera capensis</i> Esch. (Insecta: Hymenoptera: Apidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 817-819.	0.2	19
51	Sorting out relationships among the grouse and ptarmigan using intron, mitochondrial, and ultra-conserved element sequences. <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 123-132.	1.2	32
52	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016, 26, 1577-1584.	1.8	175
53	The complete mitochondrial genome of the hybrid honey bee, <i>Apis mellifera capensis</i> × <i>Apis mellifera scutellata</i> , from South Africa. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 856-857.	0.2	5
54	Rapid and recent diversification of curassows, guans, and chachalacas (Galliformes: Cracidae) out of Mesoamerica: Phylogeny inferred from mitochondrial, intron, and ultraconserved element sequences. <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 320-330.	1.2	33

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55	Whole genome sequence of the emerging oomycete pathogen <i>Pythium insidiosum</i> strain CDC-B5653 isolated from an infected human in the USA. <i>Genomics Data</i> , 2016, 7, 60-61.	1.3	19
56	Analysis of a Rapid Evolutionary Radiation Using Ultraconserved Elements: Evidence for a Bias in Some Multispecies Coalescent Methods. <i>Systematic Biology</i> , 2016, 65, 612-627.	2.7	137
57	Avoiding Missing Data Biases in Phylogenomic Inference: An Empirical Study in the Landfowl (Aves: Tj ETQq1 1 0.784314 rgBT /Overl 3.5 208	3.5	208
58	Land connectivity changes and global cooling shaped the colonization history and diversification of New World quail (Aves: Galliformes: Odontophoridae). <i>Journal of Biogeography</i> , 2015, 42, 1883-1895.	1.4	42
59	Building the avian tree of life using a large-scale, sparse supermatrix. <i>Molecular Phylogenetics and Evolution</i> , 2015, 84, 53-63.	1.2	123
60	Multiple Lineages of Ancient CR1 Retroposons Shaped the Early Genome Evolution of Amniotes. <i>Genome Biology and Evolution</i> , 2015, 7, 205-217.	1.1	62
61	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015, 4, 4.	3.3	72
62	Response to Comment on "Whole-genome analyses resolve early branches in the tree of life of modern birds". <i>Science</i> , 2015, 349, 1460-1460.	6.0	53
63	Early Mesozoic Coexistence of Amniotes and Hepadnaviridae. <i>PLoS Genetics</i> , 2014, 10, e1004559.	1.5	61
64	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254449.	6.0	300
65	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	6.0	1,583
66	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	6.0	895
67	The evolution of peafowl and other taxa with ocelli (eyespot): a phylogenomic approach. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140823.	1.2	47
68	Incongruence among different mitochondrial regions: A case study using complete mitogenomes. <i>Molecular Phylogenetics and Evolution</i> , 2014, 78, 314-323.	1.2	75
69	Does more sequence data improve estimates of galliform phylogeny? Analyses of a rapid radiation using a complete data matrix. <i>PeerJ</i> , 2014, 2, e361.	0.9	44
70	Ratite Nonmonophyly: Independent Evidence from 40 Novel Loci. <i>Systematic Biology</i> , 2013, 62, 35-49.	2.7	73
71	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. <i>Genome Biology</i> , 2013, 14, R28.	13.9	276
72	Identifying localized biases in large datasets: A case study using the avian tree of life. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 1021-1032.	1.2	78

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73	Parsimony and Model-Based Analyses of Indels in Avian Nuclear Genes Reveal Congruent and Incongruent Phylogenetic Signals. <i>Biology</i> , 2013, 2, 419-444.	1.3	94
74	Assessing Phylogenetic Relationships among Galliformes: A Multigene Phylogeny with Expanded Taxon Sampling in Phasianidae. <i>PLoS ONE</i> , 2013, 8, e64312.	1.1	86
75	Assessing Parameter Identifiability in Phylogenetic Models Using Data Cloning. <i>Systematic Biology</i> , 2012, 61, 955-972.	2.7	41
76	Report from the First Snake Genomics and Integrative Biology Meeting. <i>Standards in Genomic Sciences</i> , 2012, 7, 150-152.	1.5	4
77	Testing Hypotheses about the Sister Group of the Passeriformes Using an Independent 30-Locus Data Set. <i>Molecular Biology and Evolution</i> , 2012, 29, 737-750.	3.5	62
78	An unbiased approach to identify genes involved in development in a turtle with temperature-dependent sex determination. <i>BMC Genomics</i> , 2012, 13, 308.	1.2	8
79	Evolutionary Genomics Implies a Specific Function of Ant4 in Mammalian and Anole Lizard Male Germ Cells. <i>PLoS ONE</i> , 2011, 6, e23122.	1.1	13
80	Evolutionary and comparative analysis of MYB and bHLH plant transcription factors. <i>Plant Journal</i> , 2011, 66, 94-116.	2.8	1,014
81	Are Transposable Element Insertions Homoplasy Free?: An Examination Using the Avian Tree of Life. <i>Systematic Biology</i> , 2011, 60, 375-386.	2.7	58
82	Homoplastic microinversions and the avian tree of life. <i>BMC Evolutionary Biology</i> , 2011, 11, 141.	3.2	33
83	A Macroevolutionary Perspective on Multiple Sexual Traits in the Phasianidae (Galliformes). <i>International Journal of Evolutionary Biology</i> , 2011, 2011, 1-16.	1.0	39
84	Comparative molecular evolution and phylogenetic utility of 3' UTRs and introns in Galliformes. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 536-542.	1.2	40
85	Phylogenomic Analyses Reveal the Evolutionary Origin of the Inhibin Î±-Subunit, a Unique TGFÎ² Superfamily Antagonist. <i>PLoS ONE</i> , 2010, 5, e9457.	1.1	11
86	A well-tested set of primers to amplify regions spread across the avian genome. <i>Molecular Phylogenetics and Evolution</i> , 2009, 50, 654-660.	1.2	170
87	From Reptilian Phylogenomics to Reptilian Genomes: Analyses of c-Myc, Jun, and DJ-1 Proto-Oncogenes. <i>Cytogenetic and Genome Research</i> , 2009, 127, 79-93.	0.6	18
88	A multigene phylogeny of Galliformes supports a single origin of erectile ability in nonfeathered facial traits. <i>Journal of Avian Biology</i> , 2008, 39, 438-445.	0.6	24
89	PHYLOGENOMICS AND SECONDARY PLASTIDS: A LOOK BACK AND A LOOK AHEAD. <i>Journal of Phycology</i> , 2008, 44, 2-6.	1.0	6
90	GENOMIC INSIGHTS INTO EVOLUTIONARY RELATIONSHIPS AMONG HETEROKONT LINEAGES EMPHASIZING THE PHAEOPHYCEAE. <i>Journal of Phycology</i> , 2008, 44, 15-18.	1.0	12

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91	Duplications and functional divergence of ADP-glucose pyrophosphorylase genes in plants. <i>BMC Evolutionary Biology</i> , 2008, 8, 232.	3.2	34
92	A Phylogenomic Study of Birds Reveals Their Evolutionary History. <i>Science</i> , 2008, 320, 1763-1768.	6.0	1,767
93	Introns outperform exons in analyses of basal avian phylogeny using clathrin heavy chain genes. <i>Gene</i> , 2008, 410, 89-96.	1.0	77
94	Phylogenomic evidence for multiple losses of flight in ratite birds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13462-13467.	3.3	187
95	Duplication of Accelerated Evolution and Growth Hormone Gene in Passerine Birds. <i>Molecular Biology and Evolution</i> , 2008, 25, 795-795.	3.5	0
96	Duplication of Accelerated Evolution and Growth Hormone Gene in Passerine Birds. <i>Molecular Biology and Evolution</i> , 2008, 25, 352-361.	3.5	43
97	Turtle isochore structure is intermediate between amphibians and other amniotes. <i>Integrative and Comparative Biology</i> , 2008, 48, 454-462.	0.9	16
98	The Evolution of Seminal Ribonuclease: Pseudogene Reactivation or Multiple Gene Inactivation Events?. <i>Molecular Biology and Evolution</i> , 2007, 24, 1012-1024.	3.5	18
99	The Two AGPase Subunits Evolve at Different Rates in Angiosperms, yet They Are Equally Sensitive to Activity-Altering Amino Acid Changes When Expressed in Bacteria. <i>Plant Cell</i> , 2007, 19, 1458-1472.	3.1	56
100	PHYLOGENETIC POSITION OF THE NEW WORLD QUAIL (ODONTOPHORIDAE): EIGHT NUCLEAR LOCI AND THREE MITOCHONDRIAL REGIONS CONTRADICT MORPHOLOGY AND THE SIBLEY-AHLQUIST TAPESTRY. <i>Auk</i> , 2007, 124, 71.	0.7	29
101	Phylogenetic Position of the New World Quail (Odontophoridae): Eight Nuclear Loci and Three Mitochondrial Regions Contradict Morphology and the Sibley-Ahlquist Tapestry. <i>Auk</i> , 2007, 124, 71-84.	0.7	34
102	Patterns of Vertebrate Isochore Evolution Revealed by Comparison of Expressed Mammalian, Avian, and Crocodylian Genes. <i>Journal of Molecular Evolution</i> , 2007, 65, 259-266.	0.8	37
103	Mitochondrial Genomes and Avian Phylogeny: Complex Characters and Resolvability without Explosive Radiations. <i>Molecular Biology and Evolution</i> , 2006, 24, 269-280.	3.5	174
104	Molecular cloning of the estrogen and progesterone receptors of the American alligator. <i>General and Comparative Endocrinology</i> , 2004, 136, 122-133.	0.8	69
105	Genomics in <i>Neurospora crassa</i> : From One-Gene-One-Enzyme to 10,000 Genes. <i>Applied Mycology and Biotechnology</i> , 2004, , 295-313.	0.3	0
106	The genome sequence of the filamentous fungus <i>Neurospora crassa</i> . <i>Nature</i> , 2003, 422, 859-868.	13.7	1,528
107	Recently Duplicated Maize R2R3 Myb Genes Provide Evidence for Distinct Mechanisms of Evolutionary Divergence after Duplication. <i>Plant Physiology</i> , 2003, 131, 610-620.	2.3	151
108	Innovation from reduction: gene loss, domain loss and sequence divergence in genome evolution. <i>Applied Bioinformatics</i> , 2003, 2, 13-34.	1.7	13

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109	Examining Basal Avian Divergences with Mitochondrial Sequences: Model Complexity, Taxon Sampling, and Sequence Length. <i>Systematic Biology</i> , 2002, 51, 614-625.	2.7	89
110	Phylogenetic Utility of Avian Ovomuroid Intron G: A Comparison of Nuclear and Mitochondrial Phylogenies in Galliformes. <i>Auk</i> , 2001, 118, 799-804.	0.7	61
111	Evolution of the Mitochondrial DNA Control Region and Cytochrome b Genes and the Inference of Phylogenetic Relationships in the Avian Genus <i>Lophura</i> (Galliformes). <i>Molecular Phylogenetics and Evolution</i> , 2001, 19, 187-201.	1.2	47
112	A molecular phylogeny of the peacock-pheasants (Galliformes: <i>Polyplectron</i> spp.) indicates loss and reduction of ornamental traits and display behaviours. <i>Biological Journal of the Linnean Society</i> , 2001, 73, 187-198.	0.7	39
113	POLYTOMIES, THE POWER OF PHYLOGENETIC INFERENCE, AND THE STOCHASTIC NATURE OF MOLECULAR EVOLUTION: A COMMENT ON WALSH ET AL. (1999). <i>Evolution; International Journal of Organic Evolution</i> , 2001, 55, 1261-1263.	1.1	35
114	Fungal Zuotin Proteins Evolved from MIDA1-like Factors by Lineage-Specific Loss of MYB Domains. <i>Molecular Biology and Evolution</i> , 2001, 18, 1401-1412.	3.5	26
115	Functional Conservation of Plant Secondary Metabolic Enzymes Revealed by Complementation of <i>Arabidopsis</i> Flavonoid Mutants with Maize Genes. <i>Plant Physiology</i> , 2001, 127, 46-57.	2.3	93
116	Chapter Five Transcription factors and metabolic engineering: Novel applications for ancient tools. <i>Recent Advances in Phytochemistry</i> , 2001, 35, 79-109.	0.5	14
117	Analysis of the <i>pxd-1</i> (<i>snz-1/sno-1</i>) Region of the <i>Neurospora crassa</i> Genome: Correlation of Pyridoxine-Requiring Phenotypes With Mutations in Two Structural Genes. <i>Genetics</i> , 2001, 157, 1067-1075.	1.2	32
118	Large-Scale Comparison of Fungal Sequence Information: Mechanisms of Innovation in <i>Neurospora crassa</i> and Gene Loss in <i>Saccharomyces cerevisiae</i> . <i>Genome Research</i> , 2000, 10, 416-430.	2.4	68
119	Newly Discovered Plant <i>c-myb</i> -Like Genes Rewrite the Evolution of the Plant <i>myb</i> Gene Family : Fig. 1.. <i>Plant Physiology</i> , 1999, 121, 21-24.	2.3	79
120	The <i>nop-1</i> gene of <i>Neurospora crassa</i> encodes a seven transmembrane helix retinal-binding protein homologous to archaeal rhodopsins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 8034-8039.	3.3	212
121	A Molecular Phylogeny of the Pheasants and Partridges Suggests That These Lineages Are Not Monophyletic. <i>Molecular Phylogenetics and Evolution</i> , 1999, 11, 38-54.	1.2	147
122	Maize R2R3 Myb Genes: Sequence Analysis Reveals Amplification in the Higher Plants. <i>Genetics</i> , 1999, 153, 427-444.	1.2	150
123	Identification of the First Fungal Annexin: Analysis of Annexin Gene Duplications and Implications for Eukaryotic Evolution. <i>Journal of Molecular Evolution</i> , 1998, 47, 531-543.	0.8	61
124	Resolution of the phylogenetic position of the Congo peafowl, <i>Afropavo congensis</i> : a biogeographic and evolutionary enigma. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1997, 264, 1517-1523.	1.2	35
125	Expressed Sequences from Conidial, Mycelial, and Sexual Stages of <i>Neurospora crassa</i> . <i>Fungal Genetics and Biology</i> , 1997, 21, 348-363.	0.9	151
126	A stationary-phase gene in <i>Saccharomyces cerevisiae</i> is a member of a novel, highly conserved gene family. <i>Journal of Bacteriology</i> , 1996, 178, 6865-6872.	1.0	79

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127	Stationary phase in <i>Saccharomyces cerevisiae</i> . <i>Molecular Microbiology</i> , 1996, 19, 1159-1166.	1.2	216
128	Protein synthesis in long-term stationary-phase cultures of <i>Saccharomyces cerevisiae</i> . <i>Journal of Bacteriology</i> , 1994, 176, 5802-5813.	1.0	156
129	Gene tree quality affects empirical coalescent branch length estimation. <i>Zoologica Scripta</i> , 0, , .	0.7	9