

# Rob DeSalle

## List of Publications by Year in descending order

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Version: 2024-02-01

205  
papers

14,039  
citations

20759

60  
h-index

24179

110  
g-index

214  
all docs

214  
docs citations

214  
times ranked

17374  
citing authors

#	ARTICLE	IF	CITATIONS
1	A kiosk survey of perception, attitudes and knowledge (PAK) of Australians concerning microbes, antibiotics, probiotics and hygiene. <i>Health Promotion Journal of Australia</i> , 2022, 33, 838-851.	0.6	4
2	Morphological Characters Can Strongly Influence Early Animal Relationships Inferred from Phylogenomic Data Sets. <i>Systematic Biology</i> , 2021, 70, 360-375.	2.7	21
3	Scale-dependent patterns of metacommunity structuring in aquatic organisms across floodplain systems. <i>Journal of Biogeography</i> , 2021, 48, 872-885.	1.4	32
4	Can public online databases serve as a source of phenotypic information for Cannabis genetic association studies?. <i>PLoS ONE</i> , 2021, 16, e0247607.	1.1	1
5	A natural history museum visitor survey of perception, attitude and knowledge (PAK) of microbes and antibiotics. <i>PLoS ONE</i> , 2021, 16, e0257085.	1.1	2
6	K-Mer Analyses Reveal Different Evolutionary Histories of Alpha, Beta, and Gamma Papillomaviruses. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9657.	1.8	7
7	The enigmatic Placozoa part 1: Exploring evolutionary controversies and poor ecological knowledge. <i>BioEssays</i> , 2021, 43, e2100080.	1.2	17
8	The enigmatic Placozoa part 2: Exploring evolutionary controversies and promising questions on earth and in space. <i>BioEssays</i> , 2021, 43, 2100083.	1.2	3
9	Distinguishing Extinction and Natural Selection in the Anthropocene: Preventing the Panda Paradox through Practical Education Measures. <i>BioEssays</i> , 2020, 42, e1900206.	1.2	9
10	Whole Genome Sequencing and Assembly of the Asian Honey Bee <i>Apis dorsata</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 3677-3683.	1.1	21
11	NIH must confront the use of race in science. <i>Science</i> , 2020, 369, 1313-1314.	6.0	53
12	Should Networks Supplant Tree Building?. <i>Microorganisms</i> , 2020, 8, 1179.	1.6	7
13	An Investigation of How Environmental Science Textbooks Link Human Environmental Impact to Ecology and Daily Life. <i>CBE Life Sciences Education</i> , 2020, 19, ar54.	1.1	2
14	Review and Interpretation of Trends in DNA Barcoding. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	171
15	Mitochondrial lipid droplet formation as a detoxification mechanism to sequester and degrade excessive urothelial membranes. <i>Molecular Biology of the Cell</i> , 2019, 30, 2969-2984.	0.9	18
16	Genome analyses of a placozoan rickettsial endosymbiont show a combination of mutualistic and parasitic traits. <i>Scientific Reports</i> , 2019, 9, 17561.	1.6	11
17	Innate immunity in the simplest animals – placozoans. <i>BMC Genomics</i> , 2019, 20, 5.	1.2	28
18	Tough Luck. <i>Inference</i> , 2019, 4, .	0.0	0

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19	Hawaiian <i>Drosophila</i> as an Evolutionary Model Clade: Days of Future Past. <i>BioEssays</i> , 2018, 40, e1700246.	1.2	17
20	Placozoa. <i>Current Biology</i> , 2018, 28, R97-R98.	1.8	39
21	What aDNA can (and cannot) tell us about the emergence of language and speech. <i>Journal of Language Evolution</i> , 2018, 3, 59-66.	0.4	27
22	Classification and evolution of human papillomavirus genome variants: Alpha-5 (HPV26, 51, 69, 82), Alpha-6 (HPV30, 53, 56, 66), Alpha-11 (HPV34, 73), Alpha-13 (HPV54) and Alpha-3 (HPV61). <i>Virology</i> , 2018, 516, 86-101.	1.1	35
23	Asymptomatic Summertime Shedding of Respiratory Viruses. <i>Journal of Infectious Diseases</i> , 2018, 217, 1074-1077.	1.9	33
24	Phylogeny of the Genus <i>Drosophila</i> . <i>Genetics</i> , 2018, 209, 1-25.	1.2	139
25	ICTV Virus Taxonomy Profile: Papillomaviridae. <i>Journal of General Virology</i> , 2018, 99, 989-990.	1.3	140
26	Niche adaptation and viral transmission of human papillomaviruses from archaic hominins to modern humans. <i>PLoS Pathogens</i> , 2018, 14, e1007352.	2.1	77
27	New Insights Into Beclin-1: Evolution and Pan-Malignancy Inhibitor Activity. <i>Advances in Cancer Research</i> , 2018, 137, 77-114.	1.9	19
28	Asymptomatic Shedding of Respiratory Virus among an Ambulatory Population across Seasons. <i>MSphere</i> , 2018, 3, .	1.3	42
29	Trichoplax genomes reveal profound admixture and suggest stable wild populations without bisexual reproduction. <i>Scientific Reports</i> , 2018, 8, 11168.	1.6	36
30	De Novo characterization of transcriptomes from two North American <i>Papaipema</i> stem-borers (Lepidoptera: Noctuidae). <i>PLoS ONE</i> , 2018, 13, e0191061.	1.1	6
31	Genome content analysis yields new insights into the relationship between the human malaria parasite <i>Plasmodium falciparum</i> and its anopheline vectors. <i>BMC Genomics</i> , 2017, 18, 205.	1.2	2
32	Comparative transcriptomics reveal developmental turning points during embryogenesis of a hemimetabolous insect, the damselfly <i>Ischnura elegans</i> . <i>Scientific Reports</i> , 2017, 7, 13547.	1.6	24
33	Large-scale differences in microbial biodiversity discovery between 16S amplicon and shotgun sequencing. <i>Scientific Reports</i> , 2017, 7, 6589.	1.6	174
34	Conservation Genetics, Precision Conservation, and De-extinction. <i>Hastings Center Report</i> , 2017, 47, S18-S23.	0.7	14
35	Ancient Evolution and Dispersion of Human Papillomavirus 58 Variants. <i>Journal of Virology</i> , 2017, 91, .	1.5	27
36	Colonization and diversification of aquatic insects on three Macaronesian archipelagos using 59 nuclear loci derived from a draft genome. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 27-38.	1.2	32

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37	A whole genome gene content phylogenetic analysis of anopheline mosquitoes. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 266-269.	1.2	6
38	A Global eDNA Comparison of Freshwater Bacterioplankton Assemblages Focusing on Large-River Floodplain Lakes of Brazil. <i>Microbial Ecology</i> , 2017, 73, 61-74.	1.4	19
39	MtDNA The small workhorse of evolutionary studies. <i>Frontiers in Bioscience - Landmark</i> , 2017, 22, 873-887.	3.0	55
40	Phosphotyrosine phosphatase R3 receptors: Origin, evolution and structural diversification. <i>PLoS ONE</i> , 2017, 12, e0172887.	1.1	9
41	The Tetraspanin-Associated Uroplakins Family (UPK2/3) Is Evolutionarily Related to PTPRQ, a Phosphotyrosine Phosphatase Receptor. <i>PLoS ONE</i> , 2017, 12, e0170196.	1.1	5
42	The marker choice: Unexpected resolving power of an unexplored CO1 region for layered DNA barcoding approaches. <i>PLoS ONE</i> , 2017, 12, e0174842.	1.1	30
43	Co-existence of <i>BRAF</i> and <i>NRAS</i> driver mutations in the same melanoma cells results in heterogeneity of targeted therapy resistance. <i>Oncotarget</i> , 2016, 7, 77163-77174.	0.8	73
44	Never Ending Analysis of a Century Old Evolutionary Debate: “Unringing” the Urmetazoon Bell. <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	1.1	15
45	Data for constructing insect genome content matrices for phylogenetic analysis and functional annotation. <i>Data in Brief</i> , 2016, 6, 279-281.	0.5	2
46	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. <i>Nature Genetics</i> , 2016, 48, 593-599.	9.4	273
47	The mitogenome of the bed bug <i>Cimex lectularius</i> (Hemiptera: Cimicidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 425-427.	0.2	5
48	Clusterflock: a flocking algorithm for isolating congruent phylogenomic datasets. <i>GigaScience</i> , 2016, 5, 44.	3.3	7
49	Insect genome content phylogeny and functional annotation of core insect genomes. <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 224-232.	1.2	11
50	Genome assembly and geospatial phylogenomics of the bed bug <i>Cimex lectularius</i> . <i>Nature Communications</i> , 2016, 7, 10164.	5.8	79
51	Taking race out of human genetics. <i>Science</i> , 2016, 351, 564-565.	6.0	474
52	Spermatogenesis Drives Rapid Gene Creation and Masculinization of the X Chromosome in Stalk-Eyed Flies (Diopsidae). <i>Genome Biology and Evolution</i> , 2016, 8, 896-914.	1.1	9
53	What do our genes tell us about our past?. <i>Journal of Anthropological Sciences</i> , 2016, 94, 193-200.	0.4	0
54	Degradation of Human PDZ-Proteins by Human Alphapapillomaviruses Represents an Evolutionary Adaptation to a Novel Cellular Niche. <i>PLoS Pathogens</i> , 2015, 11, e1004980.	2.1	20

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55	Changes in the Mitogenome Announcement manuscript category. Mitochondrial DNA, 2015, 26, 1-1.	0.6	24
56	Transcriptome sequencing and annotation of the polychaete <i>Hermodice carunculata</i> (Annelida, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 70	1.2	23
57	We can't all be supermodels: the value of comparative transcriptomics to the study of non-model insects. Insect Molecular Biology, 2015, 24, 139-154.	1.0	82
58	Adaptive Evolution of Eel Fluorescent Proteins from Fatty Acid Binding Proteins Produces Bright Fluorescence in the Marine Environment. PLoS ONE, 2015, 10, e0140972.	1.1	31
59	Generation of divergent uroplakin tetraspanins and their partners during vertebrate evolution: identification of novel uroplakins. BMC Evolutionary Biology, 2014, 14, 13.	3.2	20
60	Evolutionary dynamics of Polynucleotide phosphorylases. Molecular Phylogenetics and Evolution, 2014, 73, 77-86.	1.2	2
61	AEG-1/MTDH/LYRIC, the Beginning. Advances in Cancer Research, 2013, 120, 1-38.	1.9	55
62	Transcriptome deep-sequencing and clustering of expressed isoforms from <i>Favia</i> corals. BMC Genomics, 2013, 14, 546.	1.2	22
63	Global Diversity of the Placozoa. PLoS ONE, 2013, 8, e57131.	1.1	76
64	The Evolution of Tetraspanins Through a Phylogenetic Lens. , 2013, , 31-45.		2
65	Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds. Nature, 2013, 500, 335-339.	13.7	468
66	E value cutoff and eukaryotic genome content phylogenetics. Molecular Phylogenetics and Evolution, 2012, 63, 342-350.	1.2	14
67	DOR/Tp53inp2 and Tp53inp1 Constitute a Metazoan Gene Family Encoding Dual Regulators of Autophagy and Transcription. PLoS ONE, 2012, 7, e34034.	1.1	51
68	DNA barcoding of an invasive mammal species, the small Indian mongoose ( <i>Herpestes javanicus</i> ; E.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 70	0.6	10
69	Evolutionary relationships of the old world fruit bats (Chiroptera, Pteropodidae): Another star phylogeny?. BMC Evolutionary Biology, 2011, 11, 281.	3.2	50
70	Phylogenetic and ecological relationships of the Hawaiian <i>Drosophila</i> inferred by mitochondrial DNA analysis. Molecular Phylogenetics and Evolution, 2011, 58, 244-256.	1.2	56
71	The mega-matrix tree of life: using genome-scale horizontal gene transfer and sequence evolution data as information about the vertical history of life. Cladistics, 2011, 27, 417-427.	1.5	6
72	Mitochondrial DNA sequence variation in spiny lobsters: population expansion, panmixia, and divergence. Marine Biology, 2011, 158, 2027-2041.	0.7	51

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73	Integrating DNA barcode data and taxonomic practice: Determination, discovery, and description. <i>BioEssays</i> , 2011, 33, 135-147.	1.2	276
74	A Functional Phylogenomic View of the Seed Plants. <i>PLoS Genetics</i> , 2011, 7, e1002411.	1.5	134
75	Using Phylogenomic Patterns and Gene Ontology to Identify Proteins of Importance in Plant Evolution. <i>Genome Biology and Evolution</i> , 2010, 2, 225-239.	1.1	27
76	Delineating geographic boundaries of the woolly mouse opossums, <i>Micoureus demerarae</i> and <i>Micoureus paraguayanus</i> (Didelphimorphia: Didelphidae). <i>Conservation Genetics</i> , 2010, 11, 1579-1585.	0.8	13
77	Molecular assessment of population differentiation and individual assignment potential of Nile crocodile ( <i>Crocodylus niloticus</i> ) populations. <i>Conservation Genetics</i> , 2010, 11, 1435-1443.	0.8	36
78	A whole-genome phylogeny of the family Pasteurellaceae. <i>Molecular Phylogenetics and Evolution</i> , 2010, 54, 950-956.	1.2	16
79	Evolution of cysteine patterns in the large extracellular loop of tetraspanins from animals, fungi, plants and single-celled eukaryotes. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 486-491.	1.2	29
80	The genus <i>Drosophila</i> as a model for testing tree- and character-based methods of species identification using DNA barcoding. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 509-517.	1.2	70
81	Catching the phylogenetic history through the ontogenetic hourglass: a phylogenomic analysis of <i>Drosophila</i> body segmentation genes. <i>Evolution &amp; Development</i> , 2010, 12, 288-295.	1.1	8
82	Is the microbial tree of life verificationist?. <i>Cladistics</i> , 2010, 26, 195-201.	1.5	9
83	DNA barcodes for globally threatened marine turtles: a registry approach to documenting biodiversity. <i>Molecular Ecology Resources</i> , 2010, 10, 252-263.	2.2	50
84	Trichoplax and Placozoa. , 2010, , 289-326.		17
85	Population genetic structuring in pacu ( <i>Piaractus mesopotamicus</i> ) across the Paraná-Paraguay basin: evidence from microsatellites. <i>Neotropical Ichthyology</i> , 2009, 7, 607-616.	0.5	26
86	The Impact of Outgroup Choice and Missing Data on Major Seed Plant Phylogenetics Using Genome-Wide EST Data. <i>PLoS ONE</i> , 2009, 4, e5764.	1.1	54
87	Testing taxonomic boundaries and the limit of DNA barcoding in the Siberian sturgeon, <i>Acipenser baerii</i> . <i>Mitochondrial DNA</i> , 2009, 20, 110-118.	0.6	18
88	The Diploblast-Bilateria sister hypothesis. <i>Communicative and Integrative Biology</i> , 2009, 2, 403-405.	0.6	23
89	Intron sliding in tetraspanins. <i>Communicative and Integrative Biology</i> , 2009, 2, 394-395.	0.6	9
90	Molecular Tooth Decay. <i>PLoS Genetics</i> , 2009, 5, e1000655.	1.5	2

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91	Concatenated Analysis Sheds Light on Early Metazoan Evolution and Fuels a Modern "Urmetazoon" Hypothesis. <i>PLoS Biology</i> , 2009, 7, e1000020.	2.6	235
92	Complete Genome Sequence of <i>Aggregatibacter</i> ( <i>Haemophilus</i> ) <i>aphrophilus</i> NJ8700. <i>Journal of Bacteriology</i> , 2009, 191, 4693-4694.	1.0	28
93	Genomic diversity and interspecies host infection of 12 <i>Macaca fascicularis</i> papillomaviruses (MfPVs). <i>Virology</i> , 2009, 393, 304-310.	1.1	67
94	Isolation, characterization and cross-species amplification of new microsatellite markers for three opossum species of the Didelphidae family. <i>Conservation Genetics Resources</i> , 2009, 1, 405-410.	0.4	4
95	Nanog Regulates Proliferation During Early Fish Development. <i>Stem Cells</i> , 2009, 27, 2081-2091.	1.4	55
96	The phylogenetic relationships of cynopterine fruit bats (Chiroptera: Pteropodidae: Cynopterinae). <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 772-783.	1.2	12
97	Placozoa and the evolution of Metazoa and intrasomatic cell differentiation. <i>International Journal of Biochemistry and Cell Biology</i> , 2009, 41, 370-379.	1.2	53
98	Mitochondrial DNA announces new fast-track manuscript category: Mitogenome Announcements. <i>Mitochondrial DNA</i> , 2009, 20, 1-1.	0.6	5
99	Intron Evolution: Testing Hypotheses of Intron Evolution Using the Phylogenomics of Tetraspanins. <i>PLoS ONE</i> , 2009, 4, e4680.	1.1	35
100	Development of EST-microsatellites from the cycad <i>Cycas rumphii</i> , and their use in the recently endangered <i>Cycas micronesica</i> . <i>Conservation Genetics</i> , 2008, 9, 1051-1054.	0.8	19
101	An even "newer" animal phylogeny. <i>BioEssays</i> , 2008, 30, 1043-1047.	1.2	22
102	Ten polymorphic STR loci in the cosmopolitan reef coral, <i>Pocillopora damicornis</i> . <i>Molecular Ecology Resources</i> , 2008, 8, 619-621.	2.2	31
103	Automated simultaneous analysis phylogenetics (ASAP): an enabling tool for phylogenomics. <i>BMC Bioinformatics</i> , 2008, 9, 103.	1.2	30
104	Out of Hawaii: the origin and biogeography of the genus <i>Scaptomyza</i> (Diptera: Drosophilidae). <i>Biology Letters</i> , 2008, 4, 195-199.	1.0	86
105	Appearance of new tetraspanin genes during vertebrate evolution. <i>Genomics</i> , 2008, 91, 326-334.	1.3	115
106	caos software for use in character-based DNA barcoding. <i>Molecular Ecology Resources</i> , 2008, 8, 1256-1259.	2.2	157
107	Mitochondrial DNA inaugural issue. <i>DNA Sequence</i> , 2008, 19, 371-372.	0.7	0
108	Using whole genome presence/absence data to untangle function in 12 <i>Drosophila</i> genomes. <i>Fly</i> , 2008, 2, 291-299.	0.9	10

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109	Mito-communications. DNA Sequence, 2008, 19, 373-375.	0.7	1
110	Evolution of MDA-5/RIG-I-dependent innate immunity: Independent evolution by domain grafting. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17040-17045.	3.3	71
111	Examining Ancient Inter-domain Horizontal Gene Transfer. Evolutionary Bioinformatics, 2008, 4, 117693430800400.	0.6	7
112	Key transitions in animal evolution. Integrative and Comparative Biology, 2007, 47, 667-669.	0.9	10
113	How Many Genes Should a Systematist Sample? Conflicting Insights from a Phylogenomic Matrix Characterized by Replicated Incongruence. Systematic Biology, 2007, 56, 355-363.	2.7	80
114	Can we ever identify the Urmetazoan?. Integrative and Comparative Biology, 2007, 47, 670-676.	0.9	20
115	Phenetic and DNA taxonomy; a comment on Waugh. BioEssays, 2007, 29, 1289-1290.	1.2	32
116	DNA barcoding using chitons (genus Mopalia). Molecular Ecology Notes, 2007, 7, 177-183.	1.7	74
117	Human papillomavirus (HPV) types 101 and 103 isolated from cervicovaginal cells lack an E6 open reading frame (ORF) and are related to gamma-papillomaviruses. Virology, 2007, 360, 447-453.	1.1	58
118	Taxonomic Impediment or Impediment to Taxonomy? A Commentary on Systematics and the Cybertaxonomic-Automation Paradigm. Evolutionary Biology, 2007, 34, 140-143.	0.5	179
119	Species Discovery versus Species Identification in DNA Barcoding Efforts: Response to Rubinoff. Conservation Biology, 2006, 20, 1545-1547.	2.4	198
120	Nested areas of endemism analysis. Journal of Biogeography, 2006, 33, 1511-1526.	1.4	32
121	Origin of the tetraspanin uroplakins and their co-evolution with associated proteins: Implications for uroplakin structure and function. Molecular Phylogenetics and Evolution, 2006, 41, 355-367.	1.2	46
122	What are the limits of a character?. Journal of Biomedical Informatics, 2006, 39, 6-17.	2.5	14
123	ESTimating plant phylogeny: lessons from partitioning. BMC Evolutionary Biology, 2006, 6, 48.	3.2	31
124	Phylogenetic Relationships of the Enigmatic Harpy Fruit Bat, Harpyionycteris (Mammalia: Chiroptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.2	13
125	Reciprocal Illumination in the Gene Content Tree of Life. Systematic Biology, 2006, 55, 441-453.	2.7	27
126	OrthologID: automation of genome-scale ortholog identification within a parsimony framework. Bioinformatics, 2006, 22, 699-707.	1.8	89



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127	Falsifications and corroborations: Karl Popper's influence on systematics. <i>Molecular Phylogenetics and Evolution</i> , 2005, 35, 271-280.	1.2	42
128	Relationships among characiform fishes inferred from analysis of nuclear and mitochondrial gene sequences. <i>Molecular Phylogenetics and Evolution</i> , 2005, 36, 135-153.	1.2	201
129	Phylogeny and age of diversification of the planitibia species group of the Hawaiian <i>Drosophila</i> . <i>Molecular Phylogenetics and Evolution</i> , 2005, 37, 73-82.	1.2	46
130	Phylogenetic Incongruence among Oncogenic Genital Alpha Human Papillomaviruses. <i>Journal of Virology</i> , 2005, 79, 15503-15510.	1.5	94
131	The enigmatic Caspian Sea Russian sturgeon: How many cryptic forms does it contain?. <i>Systematics and Biodiversity</i> , 2005, 3, 203-218.	0.5	46
132	The Trichoplax PaxB Gene: A Putative Proto-PaxA/B/C Gene Predating the Origin of Nerve and Sensory Cells. <i>Molecular Biology and Evolution</i> , 2005, 22, 1569-1578.	3.5	60
133	Animal Phylogenomics: Multiple Interspecific Genome Comparisons. <i>Methods in Enzymology</i> , 2005, 395, 104-133.	0.4	6
134	The unholy trinity: taxonomy, species delimitation and DNA barcoding. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2005, 360, 1905-1916.	1.8	775
135	Preparation of Samples for Comparative Studies of Arthropod Chromosomes: Visualization, In Situ Hybridization, and Genome Size Estimation. <i>Methods in Enzymology</i> , 2005, 395, 460-488.	0.4	39
136	Lack of the canonical pRB-binding domain in the E7 ORF of artiodactyl papillomaviruses is associated with the development of fibropapillomas. <i>Journal of General Virology</i> , 2004, 85, 1243-1250.	1.3	56
137	The expansion of conservation genetics. <i>Nature Reviews Genetics</i> , 2004, 5, 702-712.	7.7	354
138	The origin of polynucleotide phosphorylase domains. <i>Molecular Phylogenetics and Evolution</i> , 2004, 31, 123-130.	1.2	59
139	The evolution of HOM-C homeoboxes in the Dipteran family Drosophilidae. <i>Insect Molecular Biology</i> , 2003, 12, 345-351.	1.0	1
140	Calibrating phylogenetic species formation in a threatened insect using DNA from historical specimens. <i>Molecular Ecology</i> , 2003, 12, 1993-1998.	2.0	85
141	The Widespread Colonization Island of <i>Actinobacillus actinomycetemcomitans</i> . <i>Nature Genetics</i> , 2003, 34, 193-198.	9.4	127
142	Combined Support for Wholesale Taxic Atavism in Gavialine Crocodylians. <i>Systematic Biology</i> , 2003, 52, 403-422.	2.7	176
143	Integrating gene flow, crop biology, and farm management in on-farm conservation of avocado ( <i>Persea americana</i> , Lauraceae). <i>American Journal of Botany</i> , 2003, 90, 1619-1627.	0.8	11
144	Phylogenetic and Expression Analysis of the Glutamate-Receptor-Like Gene Family in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2002, 19, 1066-1082.	3.5	167

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145	Resolution of a Supertree/Supermatrix Paradox. <i>Systematic Biology</i> , 2002, 51, 652-664.	2.7	190
146	An automated phylogenetic key for classifying homeoboxes. <i>Molecular Phylogenetics and Evolution</i> , 2002, 24, 388-399.	1.2	111
147	managedpop: a computer simulation to project allelic diversity in managed populations with overlapping generations. <i>Molecular Ecology Notes</i> , 2002, 2, 615-617.	1.7	2
148	Systematic Analysis of DNA Microarray Data: Ordering and Interpreting Patterns of Gene Expression. <i>Genome Research</i> , 2001, 11, 1149-1155.	2.4	31
149	flp-1, the first representative of a new pilin gene subfamily, is required for non-specific adherence of <i>Actinobacillus actinomycetemcomitans</i> . <i>Molecular Microbiology</i> , 2001, 40, 542-554.	1.2	179
150	Current problems with the zootype and the early evolution of Hox genes. <i>The Journal of Experimental Zoology</i> , 2001, 291, 169-174.	1.4	43
151	A Molecular Phylogeny of Costaceae (Zingiberales). <i>Molecular Phylogenetics and Evolution</i> , 2001, 21, 333-345.	1.2	41
152	Phylogenetic Utility of Different Types of Molecular Data Used to Infer Evolutionary Relationships among Stalk-Eyed Flies (Diopsidae). <i>Systematic Biology</i> , 2001, 50, 87-105.	2.7	85
153	Phylogenetic Utility of Different Types of Molecular Data Used to Infer Evolutionary Relationships among Stalk-Eyed Flies (Diopsidae). <i>Systematic Biology</i> , 2001, 50, 87-105.	2.7	136
154	The Identity of Plant Glutamate Receptors. <i>Science</i> , 2001, 292, 1486b-1487.	6.0	175
155	Phylogeny and Character Behavior in the Family Lemuridae. <i>Molecular Phylogenetics and Evolution</i> , 2000, 15, 124-134.	1.2	25
156	Phylogenetic Analysis of the repleta Species Group of the Genus <i>Drosophila</i> Using Multiple Sources of Characters. <i>Molecular Phylogenetics and Evolution</i> , 2000, 16, 296-307.	1.2	72
157	Molluscan engrailed expression, serial organization, and shell evolution. <i>Evolution &amp; Development</i> , 2000, 2, 340-347.	1.1	93
158	Phylogenetic Species, Nested Hierarchies, and Character Fixation. <i>Cladistics</i> , 2000, 16, 364-384.	1.5	56
159	Utility of North Atlantic Right Whale Museum Specimens for Assessing Changes in Genetic Diversity. <i>Conservation Biology</i> , 2000, 14, 1837-1842.	2.4	31
160	Insect evolution: How the fruit fly changed (some of) its spots. <i>Current Biology</i> , 2000, 10, R75-R77.	1.8	6
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