

Rob DeSalle

List of Publications by Year in descending order

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205
papers

14,039
citations

20759

60
h-index

24179

110
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214
all docs

214
docs citations

214
times ranked

17374
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Multiple Sources of Character Information and the Phylogeny of Hawaiian <i>Drosophilids</i> . <i>Systematic Biology</i> , 1997, 46, 654-673.	2.7	533
3	Taking race out of human genetics. <i>Science</i> , 2016, 351, 564-565.	6.0	474
4	Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds. <i>Nature</i> , 2013, 500, 335-339.	13.7	468
5	Tempo and mode of sequence evolution in mitochondrial DNA of Hawaiian <i>Drosophila</i> . <i>Journal of Molecular Evolution</i> , 1987, 26, 157-164.	0.8	463
6	The expansion of conservation genetics. <i>Nature Reviews Genetics</i> , 2004, 5, 702-712.	7.7	354
7	Alignment-Ambiguous Nucleotide Sites and the Exclusion of Systematic Data. <i>Molecular Phylogenetics and Evolution</i> , 1993, 2, 152-157.	1.2	323
8	Integrating DNA barcode data and taxonomic practice: Determination, discovery, and description. <i>BioEssays</i> , 2011, 33, 135-147.	1.2	276
9	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
10	Assessing the Relative Contribution of Molecular and Morphological Characters in Simultaneous Analysis Trees. <i>Molecular Phylogenetics and Evolution</i> , 1998, 9, 427-436.	1.2	245
11	Concatenated Analysis Sheds Light on Early Metazoan Evolution and Fuels a Modern "Urmetazoan" Hypothesis. <i>PLoS Biology</i> , 2009, 7, e1000020.	2.6	235
12	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
13	Species Discovery versus Species Identification in DNA Barcoding Efforts: Response to Rubinoff. <i>Conservation Biology</i> , 2006, 20, 1545-1547.	2.4	198
14	Nonspecific Adherence by <i>Actinobacillus actinomycetemcomitans</i> Requires Genes Widespread in Bacteria and Archaea. <i>Journal of Bacteriology</i> , 2000, 182, 6169-6176.	1.0	194
15	Phylogeny of the Acipenseriformes: cytogenetic and molecular approaches. <i>Environmental Biology of Fishes</i> , 1997, 48, 127-155.	0.4	193
16	GENEFAMILYEVOLUTION ANDHOMOLOGY: Genomics Meets Phylogenetics. <i>Annual Review of Genomics and Human Genetics</i> , 2000, 1, 41-73.	2.5	193
17	Resolution of a Supertree/Supermatrix Paradox. <i>Systematic Biology</i> , 2002, 51, 652-664.	2.7	190
18	Molecular Phylogeny of Acipenserinae. <i>Molecular Phylogenetics and Evolution</i> , 1998, 9, 141-155.	1.2	185

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19	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
20	Taxonomic Impediment or Impediment to Taxonomy? A Commentary on Systematics and the Cybertaxonomic-Automation Paradigm. <i>Evolutionary Biology</i> , 2007, 34, 140-143.	0.5	179
21	Combined Support for Wholesale Taxic Atavism in Gavialine Crocodylians. <i>Systematic Biology</i> , 2003, 52, 403-422.	2.7	176
22	The Identity of Plant Glutamate Receptors. <i>Science</i> , 2001, 292, 1486b-1487.	6.0	175
23	Large-scale differences in microbial biodiversity discovery between 16S amplicon and shotgun sequencing. <i>Scientific Reports</i> , 2017, 7, 6589.	1.6	174
24	Review and Interpretation of Trends in DNA Barcoding. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	171
25	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
26	PCR identification of black caviar. <i>Nature</i> , 1996, 381, 197-198.	13.7	165
27	<scp>caos</scp> software for use in character-based DNA barcoding. <i>Molecular Ecology Resources</i> , 2008, 8, 1256-1259.	2.2	157
28	Elision: A Method for Accommodating Multiple Molecular Sequence Alignments with Alignment-Ambiguous Sites. <i>Molecular Phylogenetics and Evolution</i> , 1995, 4, 1-9.	1.2	145
29	ICTV Virus Taxonomy Profile: Papillomaviridae. <i>Journal of General Virology</i> , 2018, 99, 989-990.	1.3	140
30	Phylogeny of the Genus <i>Drosophila</i> . <i>Genetics</i> , 2018, 209, 1-25.	1.2	139
31	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
32	A Functional Phylogenomic View of the Seed Plants. <i>PLoS Genetics</i> , 2011, 7, e1002411.	1.5	134
33	Practical and Theoretical Considerations for Choice of a Dna Sequence Region in Insect Molecular Systematics, with a Short Review of Published Studies Using Nuclear Gene Regions. <i>Annals of the Entomological Society of America</i> , 1994, 87, 702-716.	1.3	133
34	The Widespread Colonization Island of <i>Actinobacillus actinomycetemcomitans</i> . <i>Nature Genetics</i> , 2003, 34, 193-198.	9.4	127
35	Molecular Population Genetics of the Endangered Tiger Beetle <i>Cicindela dorsalis</i> (Coleoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.5	120
36	Appearance of new tetraspanin genes during vertebrate evolution. <i>Genomics</i> , 2008, 91, 326-334.	1.3	115

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37	An automated phylogenetic key for classifying homeoboxes. <i>Molecular Phylogenetics and Evolution</i> , 2002, 24, 388-399.	1.2	111
38	Molecular evolution of the synapsin gene family. , 1999, 285, 360-377.		105
39	Character Congruence of Multiple Data Partitions and the Origin of the Hawaiian Drosophilidae. <i>Molecular Phylogenetics and Evolution</i> , 1998, 9, 225-235.	1.2	101
40	Temporal and Spatial Heterogeneity of mtDNA Polymorphisms in Natural Populations of <i>Drosophila mercatorum</i> . <i>Genetics</i> , 1987, 116, 215-223.	1.2	101
41	Process Partitions, Congruence, and the Independence of Characters: Inferring Relationships among Closely Related Hawaiian <i>Drosophila</i> from Multiple Gene Regions. <i>Systematic Biology</i> , 1997, 46, 751-764.	2.7	100
42	Phylogenetic Incongruence among Oncogenic Genital Alpha Human Papillomaviruses. <i>Journal of Virology</i> , 2005, 79, 15503-15510.	1.5	94
43	Molluscan engrailed expression, serial organization, and shell evolution. <i>Evolution & Development</i> , 2000, 2, 340-347.	1.1	93
44	OrthologID: automation of genome-scale ortholog identification within a parsimony framework. <i>Bioinformatics</i> , 2006, 22, 699-707.	1.8	89
45	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
46	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
47	Calibrating phylogenetic species formation in a threatened insect using DNA from historical specimens. <i>Molecular Ecology</i> , 2003, 12, 1993-1998.	2.0	85
48	<i>Drosophila</i> Molecular Phylogenies and Their Uses. , 1995, , 87-138.		83
49	We can't all be supermodels: the value of comparative transcriptomics to the study of non-model insects. <i>Insect Molecular Biology</i> , 2015, 24, 139-154.	1.0	82
50	How Many Genes Should a Systematist Sample? Conflicting Insights from a Phylogenomic Matrix Characterized by Replicated Incongruence. <i>Systematic Biology</i> , 2007, 56, 355-363.	2.7	80
51	Genome assembly and geospatial phylogenomics of the bed bug <i>Cimex lectularius</i> . <i>Nature Communications</i> , 2016, 7, 10164.	5.8	79
52	Niche adaptation and viral transmission of human papillomaviruses from archaic hominins to modern humans. <i>PLoS Pathogens</i> , 2018, 14, e1007352.	2.1	77
53	Global Diversity of the Placozoa. <i>PLoS ONE</i> , 2013, 8, e57131.	1.1	76
54	Genetic Criteria for Establishing Evolutionarily Significant Units in <i>Cryan's</i> Buckmoth. <i>Conservation Biology</i> , 1996, 10, 85-98.	2.4	75

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55	FOUNDER EFFECTS AND THE RATE OF MITOCHONDRIAL DNA EVOLUTION IN HAWAIIAN DROSOPHILA. Evolution; International Journal of Organic Evolution, 1988, 42, 1076-1084.	1.1	74
56	DNA barcoding using chitons (genus Mopalia). Molecular Ecology Notes, 2007, 7, 177-183.	1.7	74
57	Co-existence of <i>BRAF</i> and <i>NRAS</i> driver mutations in the same melanoma cells results in heterogeneity of targeted therapy resistance. Oncotarget, 2016, 7, 77163-77174.	0.8	73
58	Phylogenetic Analysis of the repleta Species Group of the Genus Drosophila Using Multiple Sources of Characters. Molecular Phylogenetics and Evolution, 2000, 16, 296-307.	1.2	72
59	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
60	Population Aggregation Analysis of Three Caviar-Producing Species of Sturgeons and Implications for the Species Identification of Black Caviar. Conservation Biology, 1998, 12, 766-775.	2.4	71
61	The genus Drosophila as a model for testing tree- and character-based methods of species identification using DNA barcoding. Molecular Phylogenetics and Evolution, 2010, 57, 509-517.	1.2	70
62	Genomic diversity and interspecies host infection of 12 Macaca fascicularis papillomaviruses (MfPVs). Virology, 2009, 393, 304-310.	1.1	67
63	The Trichoplax PaxB Gene: A Putative Proto-PaxA/B/C Gene Predating the Origin of Nerve and Sensory Cells. Molecular Biology and Evolution, 2005, 22, 1569-1578.	3.5	60
64	The origin of polynucleotide phosphorylase domains. Molecular Phylogenetics and Evolution, 2004, 31, 123-130.	1.2	59
65	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
66	A New Method to Localize and Test the Significance of Incongruence: Detecting Domain Shuffling in the Nuclear Receptor Superfamily. Systematic Biology, 2000, 49, 183-201.	2.7	57
67	Mitochondrial DNA variability in natural populations of Hawaiian Drosophila. II. Genetic and phylogenetic relationships of natural populations of D. silvestris and D. heteroneura. Heredity, 1986, 56, 87-96.	1.2	56
68	Phylogenetic Species, Nested Hierarchies, and Character Fixation. Cladistics, 2000, 16, 364-384.	1.5	56
69	Lack of the canonical pRB-binding domain in the E7 ORF of artiodactyl papillomaviruses is associated with the development of fibropapillomas. Journal of General Virology, 2004, 85, 1243-1250.	1.3	56
70	Phylogenetic and ecological relationships of the Hawaiian Drosophila inferred by mitochondrial DNA analysis. Molecular Phylogenetics and Evolution, 2011, 58, 244-256.	1.2	56
71	PHYLOGEOGRAPHIC PATTERNS IN COASTAL NORTH AMERICAN TIGER BEETLES (<i>CICINDELA</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 of Organic Evolution, 1993, 47, 1192-1202.	1.1	55
72	Nanog Regulates Proliferation During Early Fish Development. Stem Cells, 2009, 27, 2081-2091.	1.4	55

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73	AEG-1/MTDH/LYRIC, the Beginning. <i>Advances in Cancer Research</i> , 2013, 120, 1-38.	1.9	55
74	MtDNA The small workhorse of evolutionary studies. <i>Frontiers in Bioscience - Landmark</i> , 2017, 22, 873-887.	3.0	55
75	Mitochondrial DNA variability in natural populations of Hawaiian <i>Drosophila</i> . I. Methods and levels of variability in <i>D. silvestris</i> and <i>D. heteroneura</i> populations. <i>Heredity</i> , 1986, 56, 75-85.	1.2	54
76	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
77	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
78	NIH must confront the use of race in science. <i>Science</i> , 2020, 369, 1313-1314.	6.0	53
79	THE EVOLUTION AND DEVELOPMENT OF DIPTERAN WING VEINS: A Systematic Approach. <i>Annual Review of Entomology</i> , 1999, 44, 97-129.	5.7	52
80	Mitochondrial DNA sequence variation in spiny lobsters: population expansion, panmixia, and divergence. <i>Marine Biology</i> , 2011, 158, 2027-2041.	0.7	51
81	DOR/Tp53inp2 and Tp53inp1 Constitute a Metazoan Gene Family Encoding Dual Regulators of Autophagy and Transcription. <i>PLoS ONE</i> , 2012, 7, e34034.	1.1	51
82	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
83	Evolutionary relationships of the old world fruit bats (Chiroptera, Pteropodidae): Another star phylogeny?. <i>BMC Evolutionary Biology</i> , 2011, 11, 281.	3.2	50
84	ON COMBINING PROTEIN SEQUENCES AND NUCLEIC ACID SEQUENCES IN PHYLOGENETIC ANALYSIS: THE HOMEBOX PROTEIN CASE. <i>Cladistics</i> , 1996, 12, 65-82.	1.5	49
85	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
86	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
87	Origin of the tetraspanin uroplakins and their co-evolution with associated proteins: Implications for uroplakin structure and function. <i>Molecular Phylogenetics and Evolution</i> , 2006, 41, 355-367.	1.2	46
88	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
89	Falsifications and corroborations: Karl Popper's influence on systematics. <i>Molecular Phylogenetics and Evolution</i> , 2005, 35, 271-280.	1.2	42
90	Asymptomatic Shedding of Respiratory Virus among an Ambulatory Population across Seasons. <i>MSphere</i> , 2018, 3, .	1.3	42

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91	A Molecular Phylogeny of Costaceae (Zingiberales). <i>Molecular Phylogenetics and Evolution</i> , 2001, 21, 333-345.	1.2	41
92	Multiple Sources of Character Information and the Phylogeny of Hawaiian <i>Drosophilids</i> . , 0, .		41
93	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
94	Placozoa. <i>Current Biology</i> , 2018, 28, R97-R98.	1.8	39
95	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
96	Trichoplax genomes reveal profound admixture and suggest stable wild populations without bisexual reproduction. <i>Scientific Reports</i> , 2018, 8, 11168.	1.6	36
97	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
98	Intron Evolution: Testing Hypotheses of Intron Evolution Using the Phylogenomics of Tetraspanins. <i>PLoS ONE</i> , 2009, 4, e4680.	1.1	35
99	THE MOLECULAR THROUGH ECOLOGICAL GENETICS OF ABNORMAL ABDOMEN. II. RIBOSOMAL DNA POLYMORPHISM IS ASSOCIATED WITH THE ABNORMAL ABDOMEN SYNDROME IN <i>DROSOPHILA MERCATORUM</i> . <i>Genetics</i> , 1986, 112, 861-875.	1.2	34
100	Asymptomatic Summertime Shedding of Respiratory Viruses. <i>Journal of Infectious Diseases</i> , 2018, 217, 1074-1077.	1.9	33
101	Nested areas of endemism analysis. <i>Journal of Biogeography</i> , 2006, 33, 1511-1526.	1.4	32
102	Phenetic and DNA taxonomy; a comment on Waugh. <i>BioEssays</i> , 2007, 29, 1289-1290.	1.2	32
103	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
104	Scale-dependent patterns of metacommunity structuring in aquatic organisms across floodplain systems. <i>Journal of Biogeography</i> , 2021, 48, 872-885.	1.4	32
105	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
106	Systematic Analysis of DNA Microarray Data: Ordering and Interpreting Patterns of Gene Expression. <i>Genome Research</i> , 2001, 11, 1149-1155.	2.4	31
107	ESTimating plant phylogeny: lessons from partitioning. <i>BMC Evolutionary Biology</i> , 2006, 6, 48.	3.2	31
108	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

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109	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
110	Automated simultaneous analysis phylogenetics (ASAP): an enabling tool for phylogenomics. BMC Bioinformatics, 2008, 9, 103.	1.2	30
111	Utility of North Atlantic Right Whale Museum Specimens for Assessing Changes in Genetic Diversity. Conservation Biology, 2000, 14, 1837-1842.	2.4	30
112	The marker choice: Unexpected resolving power of an unexplored CO1 region for layered DNA barcoding approaches. PLoS ONE, 2017, 12, e0174842.	1.1	30
113	Evolution of cysteine patterns in the large extracellular loop of tetraspanins from animals, fungi, plants and single-celled eukaryotes. Molecular Phylogenetics and Evolution, 2010, 56, 486-491.	1.2	29
114	Development, evolution, and corroboration. , 1999, 257, 6-14.		28
115	Complete Genome Sequence of <i>Aggregatibacter</i> (<i>Haemophilus</i>) <i>aphrophilus</i> NJ8700. Journal of Bacteriology, 2009, 191, 4693-4694.	1.0	28
116	Innate immunity in the simplest animals – placozoans. BMC Genomics, 2019, 20, 5.	1.2	28
117	Reciprocal Illumination in the Gene Content Tree of Life. Systematic Biology, 2006, 55, 441-453.	2.7	27
118	Using Phylogenomic Patterns and Gene Ontology to Identify Proteins of Importance in Plant Evolution. Genome Biology and Evolution, 2010, 2, 225-239.	1.1	27
119	Ancient Evolution and Dispersion of Human Papillomavirus 58 Variants. Journal of Virology, 2017, 91, .	1.5	27
120	What aDNA can (and cannot) tell us about the emergence of language and speech. Journal of Language Evolution, 2018, 3, 59-66.	0.4	27
121	Molecular evolution in Hawaiian drosophilids. Trends in Ecology and Evolution, 1987, 2, 212-216.	4.2	26
122	Captive breeding, reintroduction, and the conservation genetics of black and white ruffed lemurs, <i>Varecia variegata variegata</i> . Molecular Ecology, 1999, 8, S107-S115.	2.0	26
123	Population genetic structuring in pacu (<i>Piaractus mesopotamicus</i>) across the Paraná-Paraguay basin: evidence from microsatellites. Neotropical Ichthyology, 2009, 7, 607-616.	0.5	26
124	Phylogeny and Character Behavior in the Family Lemuridae. Molecular Phylogenetics and Evolution, 2000, 15, 124-134.	1.2	25
125	Changes in the Mitogenome Announcement manuscript category. Mitochondrial DNA, 2015, 26, 1-1.	0.6	24
126	Comparative transcriptomics reveal developmental turning points during embryogenesis of a hemimetabolous insect, the damselfly <i>Ischnura elegans</i> . Scientific Reports, 2017, 7, 13547.	1.6	24

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127	THE MOLECULAR THROUGH ECOLOGICAL GENETICS OF ABNORMAL ABDOMEN. III. TISSUE-SPECIFIC DIFFERENTIAL REPLICATION OF RIBOSOMAL GENES MODULATES THE ABNORMAL ABDOMEN PHENOTYPE IN <i>DROSOPHILA MERCATORUM</i> . <i>Genetics</i> , 1986, 112, 877-886.	1.2	24
128	The Diploblast-Bilateria sister hypothesis. <i>Communicative and Integrative Biology</i> , 2009, 2, 403-405.	0.6	23
129	Transcriptome sequencing and annotation of the polychaete <i>Hermodice carunculata</i> (Annelida.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	1.2	23
130	An even "newer" animal phylogeny. <i>BioEssays</i> , 2008, 30, 1043-1047.	1.2	22
131	Transcriptome deep-sequencing and clustering of expressed isoforms from <i>Favia</i> corals. <i>BMC Genomics</i> , 2013, 14, 546.	1.2	22
132	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
133	Morphological Characters Can Strongly Influence Early Animal Relationships Inferred from Phylogenomic Data Sets. <i>Systematic Biology</i> , 2021, 70, 360-375.	2.7	21
134	Phyletic phenocopy and the role of developmental genes in morphological evolution in the <i>Drosophilidae</i> . <i>Journal of Evolutionary Biology</i> , 1992, 5, 363-374.	0.8	20
135	Phylogenetic Pattern and Developmental Process in <i>Drosophila</i> . <i>Systematic Biology</i> , 1993, 42, 458-475.	2.7	20
136	Can we ever identify the Urmetazoan?. <i>Integrative and Comparative Biology</i> , 2007, 47, 670-676.	0.9	20
137	Generation of divergent uroplakin tetraspanins and their partners during vertebrate evolution: identification of novel uroplakins. <i>BMC Evolutionary Biology</i> , 2014, 14, 13.	3.2	20
138	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
139	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
140	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
141	New Insights Into Beclin-1: Evolution and Pan-Malignancy Inhibitor Activity. <i>Advances in Cancer Research</i> , 2018, 137, 77-114.	1.9	19
142	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
143	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
144	Hawaiian <i>Drosophila</i> as an Evolutionary Model Clade: Days of Future Past. <i>BioEssays</i> , 2018, 40, e1700246.	1.2	17

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145	The enigmatic Placozoa part 1: Exploring evolutionary controversies and poor ecological knowledge. <i>BioEssays</i> , 2021, 43, e2100080.	1.2	17
146	Trichoplax and Placozoa. , 2010, , 289-326.		17
147	A whole-genome phylogeny of the family Pasteurellaceae. <i>Molecular Phylogenetics and Evolution</i> , 2010, 54, 950-956.	1.2	16
148	Population Aggregation Analysis of Three Caviar-Producing Species of Sturgeons and Implications for the Species Identification of Black Caviar. <i>Conservation Biology</i> , 1998, 12, 766-775.	2.4	15
149	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
150	What's in a character?. <i>Journal of Biomedical Informatics</i> , 2006, 39, 6-17.	2.5	14
151	E value cutoff and eukaryotic genome content phylogenetics. <i>Molecular Phylogenetics and Evolution</i> , 2012, 63, 342-350.	1.2	14
152	Conservation Genetics, Precision Conservation, and De-extinction. <i>Hastings Center Report</i> , 2017, 47, S18-S23.	0.7	14
153	Phylogenetic Relationships of the Enigmatic Harpy Fruit Bat, <i>Harpyionycteris</i> (Mammalia: Chiroptera: Tj ETQq1 1 0.784314 rgBT / Overl	0.2	13
154	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
155	The phylogenetic relationships of cynopterine fruit bats (Chiroptera: Pteropodidae: Cynopterinae). <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 772-783.	1.2	12
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