

Rebecca B Dikow

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

1,874
citations

394421

19
h-index

434195

31
g-index

38
all docs

38
docs citations

38
times ranked

3109
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep learning as a tool for ecology and evolution. <i>Methods in Ecology and Evolution</i> , 2022, 13, 1640-1660.	5.2	55
2	Confronting Sources of Systematic Error to Resolve Historically Contentious Relationships: A Case Study Using Gadiform Fishes (Teleostei, Paracanthopterygii, Gadiformes). <i>Systematic Biology</i> , 2021, 70, 739-755.	5.6	14
3	Draft Genome Assemblies and Annotations of <i>Agrypnia vestita</i> Walker, and <i>Hesperophylax magnus</i> Banks Reveal Substantial Repetitive Element Expansion in Tube Case-Making Caddisflies (Insecta: Trichoptera). <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	14
4	First Annotated Genome of a Mandibulate Moth, <i>Neomicropteryx cornuta</i> , Generated Using PacBio HiFi Sequencing. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	7
5	Generating segmentation masks of herbarium specimens and a data set for training segmentation models using deep learning. <i>Applications in Plant Sciences</i> , 2020, 8, e11352.	2.1	25
6	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	27.8	251
7	Genomic architecture of endogenous ichnoviruses reveals distinct evolutionary pathways leading to virus domestication in parasitic wasps. <i>BMC Biology</i> , 2020, 18, 89.	3.8	24
8	First Genome Sequence of the Gunnisonâ€™s Prairie Dog (<i>Cynomys gunnisoni</i>), a Keystone Species and Player in the Transmission of Sylvatic Plague. <i>Genome Biology and Evolution</i> , 2020, 12, 618-625.	2.5	6
9	Genomic architecture and introgression shape a butterfly radiation. <i>Science</i> , 2019, 366, 594-599.	12.6	365
10	A fully resolved backbone phylogeny reveals numerous dispersals and explosive diversifications throughout the history of Asteraceae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14083-14088.	7.1	195
11	Congruent phylogenetic relationships of Melaphidina aphids (Aphididae: Eriosomatinae: Fordini) according to nuclear and mitochondrial DNA data with taxonomic implications on generic limits. <i>PLoS ONE</i> , 2019, 14, e0213181.	2.5	17
12	Population Genomics and Structure of the Critically Endangered Mariana Crow (<i>Corvus kubaryi</i>). <i>Genes</i> , 2019, 10, 187.	2.4	11
13	An empirical assessment of a single family-wide hybrid capture locus set at multiple evolutionary timescales in Asteraceae. <i>Applications in Plant Sciences</i> , 2019, 7, e11295.	2.1	28
14	Another look at the phylogenetic relationships and intercontinental biogeography of eastern Asian â€™ North American <i>Rhus</i> gall aphids (Hemiptera: Aphididae: Eriosomatinae): Evidence from mitogenome sequences via genome skimming. <i>Molecular Phylogenetics and Evolution</i> , 2017, 117, 102-110.	2.7	32
15	Developing integrative systematics in the informatics and genomic era, and calling for a global Biodiversity Cyberbank. <i>Journal of Systematics and Evolution</i> , 2017, 55, 308-321.	3.1	43
16	The Compositae Tree of Life in the age of phylogenomics. <i>Journal of Systematics and Evolution</i> , 2017, 55, 405-410.	3.1	61
17	Applications of deep convolutional neural networks to digitized natural history collections. <i>Biodiversity Data Journal</i> , 2017, 5, e21139.	0.8	40
18	Genomic and transcriptomic resources for assassin flies including the complete genome sequence of <i>Proctacanthus coquilletti</i> (Insecta: Diptera: Asilidae) and 16 representative transcriptomes. <i>PeerJ</i> , 2017, 5, e2951.	2.0	23

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19	Reciprocal genomic evolution in the ant-fungus agricultural symbiosis. <i>Nature Communications</i> , 2016, 7, 12233.	12.8	106
20	Using phylogenomics to resolve mega-families: An example from Compositae. <i>Journal of Systematics and Evolution</i> , 2015, 53, 391-402.	3.1	76
21	A target enrichment method for gathering phylogenetic information from hundreds of loci: An example from the Compositae. <i>Applications in Plant Sciences</i> , 2014, 2, 1300085.	2.1	178
22	Genomic resources for the endangered Hawaiian honeycreepers. <i>BMC Genomics</i> , 2014, 15, 1098.	2.8	21
23	Genome-level homology and phylogeny of Vibrionaceae (Gammaproteobacteria: Vibrionales) with three new complete genome sequences. <i>BMC Microbiology</i> , 2013, 13, 80.	3.3	11
24	Complete genome sequences provide a case study for the evaluation of gene-tree thinking. <i>Cladistics</i> , 2013, 29, 672-682.	3.3	5
25	Systematic relationships within the Vibrionaceae (Bacteria: Gammaproteobacteria): steps toward a phylogenetic taxonomy. <i>Cladistics</i> , 2011, 27, 9-28.	3.3	12
26	Genome-level homology and phylogeny of <i>Shewanella</i> (Gammaproteobacteria: Iteromonadales: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4	2.8	40
27	Phylogenetic analysis of the endemic New Caledonian cockroach <i>Lauraesilpha</i> . Testing competing hypotheses of diversification. <i>Cladistics</i> , 2008, 24, 802-812.	3.3	34
28	DNA-barcoding evidence for widespread introductions of a leech from the South American <i>Helobdella triserialis</i> complex. <i>Conservation Genetics</i> , 2005, 6, 467-472.	1.5	41
29	New Gammaproteobacteria Associated with Blood-Feeding Leeches and a Broad Phylogenetic Analysis of Leech Endosymbionts. <i>Applied and Environmental Microbiology</i> , 2005, 71, 5219-5224.	3.1	26
30	Phylogenetic evaluation of systematics and biogeography of the leech family Glossiphoniidae. <i>Invertebrate Systematics</i> , 2005, 19, 105.	1.3	90
31	Twelve variable microsatellite loci for the North American medicinal leech, <i>Macrobdella decora</i> . <i>Molecular Ecology Notes</i> , 2004, 4, 491-493.	1.7	4
32	Generating Masks for Image Segmentation in Digitized Herbarium Specimens. <i>Biodiversity Information Science and Standards</i> , 0, 3, .	0.0	0
33	Discovering Patterns of Biodiversity in Insects Using Deep Machine Learning. <i>Biodiversity Information Science and Standards</i> , 0, 3, .	0.0	1
34	Evaluating Geographic Patterns of Morphological Diversity in Ferns and Lycophytes Using Deep Neural Networks. <i>Biodiversity Information Science and Standards</i> , 0, 3, .	0.0	3