Alfried P Vogler

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3574523/publications.pdf

Version: 2024-02-01

176 papers	15,662 citations	20817 60 h-index	19749 117 g-index
183 all docs	183 docs citations	183 times ranked	13633 citing authors

#	Article	IF	Citations
1	Sequence-Based Species Delimitation for the DNA Taxonomy of Undescribed Insects. Systematic Biology, 2006, 55, 595-609.	5.6	2,257
2	A plea for DNA taxonomy. Trends in Ecology and Evolution, 2003, 18, 70-74.	8.7	781
3	A Comprehensive Phylogeny of Beetles Reveals the Evolutionary Origins of a Superradiation. Science, 2007, 318, 1913-1916.	12.6	729
4	Revisiting the Insect Mitochondrial Molecular Clock: The Mid-Aegean Trench Calibration. Molecular Biology and Evolution, 2010, 27, 1659-1672.	8.9	729
5	Accelerated Species Inventory on Madagascar Using Coalescent-Based Models of Species Delineation. Systematic Biology, 2009, 58, 298-311.	5.6	641
6	The Effect of Geographical Scale of Sampling on DNA Barcoding. Systematic Biology, 2012, 61, 851-869.	5.6	386
7	A comprehensive phylogenetic analysis of termites (Isoptera) illuminates key aspects of their evolutionary biology. Molecular Phylogenetics and Evolution, 2007, 44, 953-967.	2.7	341
8	Diagnosing Units of Conservation Management. Conservation Biology, 1994, 8, 354-363.	4.7	333
9	Implementation options for DNA-based identification into ecological status assessment under the European Water Framework Directive. Water Research, 2018, 138, 192-205.	11.3	275
10	Bulk De Novo Mitogenome Assembly from Pooled Total DNA Elucidates the Phylogeny of Weevils (Coleoptera: Curculionoidea). Molecular Biology and Evolution, 2014, 31, 2223-2237.	8.9	195
11	Building the <scp>C</scp>oleoptera treeâ€ofâ€life for >8000 species: composition of public <scp>DNA</scp> data and fit with <scp>L</scp>innaean classification. Systematic Entomology, 2014, 39, 97-110.	3.9	195
12	Revealing the factors that promote speciation. Philosophical Transactions of the Royal Society B: Biological Sciences, 1998, 353, 241-249.	4.0	182
13	DNA barcoding insectâ€"host plant associations. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 639-648.	2.6	174
14	Conservation Genetics at the Species Boundary. Conservation Biology, 2000, 14, 120-131.	4.7	168
15	Soup to Tree: The Phylogeny of Beetles Inferred by Mitochondrial Metagenomics of a Bornean Rainforest Sample. Molecular Biology and Evolution, 2015, 32, 2302-2316.	8.9	163
16	Family-Level Sampling of Mitochondrial Genomes in Coleoptera: Compositional Heterogeneity and Phylogenetics. Genome Biology and Evolution, 2016, 8, 161-175.	2.5	157
17	Connecting Earth observation to high-throughput biodiversity data. Nature Ecology and Evolution, 2017, 1, 176.	7.8	156
18	Capturing the Phylogeny of Holometabola with Mitochondrial Genome Data and Bayesian Site-Heterogeneous Mixture Models. Genome Biology and Evolution, 2016, 8, 1411-1426.	2.5	154

#	Article	IF	Citations
19	DNAqua-Net: Developing new genetic tools for bioassessment and monitoring of aquatic ecosystems in Europe. Research Ideas and Outcomes, 0, 2, e11321.	1.0	154
20	The towering orogeny of New Guinea as a trigger for arthropod megadiversity. Nature Communications, 2014, 5, 4001.	12.8	152
21	Sequence Alignment of 18S Ribosomal RNA and the Basal Relationships of Adephagan Beetles: Evidence for Monophyly of Aquatic Families and the Placement of Trachypachidae. Systematic Biology, 2001, 50, 945-969.	5.6	150
22	Exploring Data Interaction and Nucleotide Alignment in a Multiple Gene Analysis of Ips (Coleoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	5.6	141
23	Rarity and Incomplete Sampling in DNA-Based Species Delimitation. Systematic Biology, 2016, 65, 478-494.	5.6	138
24	DNA-based taxonomy for associating adults and larvae in multi-species assemblages of chafers (Coleoptera: Scarabaeidae). Molecular Phylogenetics and Evolution, 2007, 44, 436-449.	2.7	137
25	Molecular phylogenetics of Elateriformia (Coleoptera): evolution of bioluminescence and neoteny. Cladistics, 2007, 23, 477-496.	3.3	134
26	Speciation of Iberian diving beetles in Pleistocene refugia (Coleoptera, Dytiscidae). Molecular Ecology, 2004, 13, 179-193.	3.9	131
27	The evolution of scarab beetles tracks the sequential rise of angiosperms and mammals. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20141470.	2.6	131
28	Why the COI barcode should be the community <scp>DNA</scp> metabarcode for the metazoa. Molecular Ecology, 2018, 27, 3968-3975.	3.9	131
29	Recalibrated Tree of Leaf Beetles (Chrysomelidae) Indicates Independent Diversification of Angiosperms and Their Insect Herbivores. PLoS ONE, 2007, 2, e360.	2.5	124
30	Recent Diversification Rates in North American Tiger Beetles Estimated from a Dated mtDNA Phylogenetic Tree. Molecular Biology and Evolution, 2002, 19, 1706-1716.	8.9	121
31	A molecular phylogenetic analysis of the Scarabaeinae (dung beetles). Molecular Phylogenetics and Evolution, 2007, 45, 674-692.	2.7	121
32	Molecular Population Genetics of the Endangered Tiger Beetle Cicindela dorsalis (Coleoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222	2.5	120
33	Comparative phylogeography of tenebrionid beetles in the Aegean archipelago: the effect of dispersal ability and habitat preference. Molecular Ecology, 2009, 18, 2503-2517.	3.9	119
34	Comparing the effectiveness of metagenomics and metabarcoding for diet analysis of a leafâ€feeding monkey (<scp>P</scp>ygathrix nemaeus). Molecular Ecology Resources, 2015, 15, 250-261.	4.8	119
35	Protecting an Ecosystem Service. Advances in Ecological Research, 2016, 54, 135-206.	2.7	115
36	Does habitat use explain large scale species richness patterns of aquatic beetles in Europe?. Ecography, 2003, 26, 145-152.	4.5	104

#	Article	IF	Citations
37	Speciation and DNA barcodes: testing the effects of dispersal on the formation of discrete sequence clusters. Philosophical Transactions of the Royal Society B: Biological Sciences, 2008, 363, 2987-2996.	4.0	104
38	Mitochondrial phylogenomics of the Hymenoptera. Molecular Phylogenetics and Evolution, 2019, 131, 8-18.	2.7	104
39	Mitochondrial metagenomics: letting the genes out of the bottle. GigaScience, 2016, 5, 15.	6.4	103
40	Phylogenetically informative rearrangements in mitochondrial genomes of Coleoptera, and monophyly of aquatic elateriform beetles (Dryopoidea). Molecular Phylogenetics and Evolution, 2012, 63, 299-304.	2.7	100
41	Phylogenetic community ecology of soil biodiversity using mitochondrial metagenomics. Molecular Ecology, 2015, 24, 3603-3617.	3.9	93
42	Beyond barcodes: complex DNA taxonomy of a South Pacific Island radiation. Proceedings of the Royal Society B: Biological Sciences, 2006, 273, 887-893.	2.6	87
43	Multiple ancient origins of neoteny in Lycidae (Coleoptera): consequences for ecology and macroevolution. Proceedings of the Royal Society B: Biological Sciences, 2008, 275, 2015-2023.	2.6	87
44	Dense Taxonomic EST Sampling and Its Applications for Molecular Systematics of the Coleoptera (Beetles). Molecular Biology and Evolution, 2006, 23, 268-278.	8.9	86
45	Testing the Speciesâ€“Genetic Diversity Correlation in the Aegean Archipelago: Toward a Haplotype-Based Macroecology?. American Naturalist, 2011, 178, 241-255.	2.1	86
46	Validating the power of mitochondrial metagenomics for community ecology and phylogenetics of complex assemblages. Methods in Ecology and Evolution, 2015, 6, 883-894.	5.2	86
47	Phylogeny and diversification of diving beetles (Coleoptera: Dytiscidae). Cladistics, 2008, 24, 563-590.	3.3	84
48	Trans-oceanic and endemic origins of the small minnow mayflies (Ephemeroptera, Baetidae) of Madagascar. Proceedings of the Royal Society B: Biological Sciences, 2005, 272, 1829-1836.	2.6	83
49	Fecal metagenomics for the simultaneous assessment of diet, parasites, and population genetics of an understudied primate. Frontiers in Zoology, 2016, 13, 17.	2.0	79
50	New Guinea highland origin of a widespread arthropod supertramp. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 2359-2367.	2.6	78
51	Metabarcoding and mitochondrial metagenomics of endogean arthropods to unveil the mesofauna of the soil. Methods in Ecology and Evolution, 2016, 7, 1071-1081.	5.2	75
52	Phylogeny of Hydradephagan Water Beetles Inferred from 18S rRNA Sequences. Molecular Phylogenetics and Evolution, 2002, 23, 43-62.	2.7	72
53	Whole-community DNA barcoding reveals a spatio-temporal continuum of biodiversity at species and genetic levels. Nature Communications, 2013, 4, 1892.	12.8	71
54	Analysis of the nag regulon from Escberichia coli K12 and Klebsiella pneumoniae and of its regulation. Molecular Genetics and Genomics, 1989, 219, 97-105.	2.4	70

#	Article	IF	Citations
55	The mitogenome phylogeny of Adephaga (Coleoptera). Molecular Phylogenetics and Evolution, 2017, 114, 166-174.	2.7	70
56	Complex Pattern of Coalescence and Fast Evolution of a Mitochondrial rRNA Pseudogene in a Recent Radiation of Tiger Beetles. Molecular Biology and Evolution, 2005, 22, 991-1000.	8.9	69
57	Multilocus ribosomal RNA phylogeny of the leaf beetles (Chrysomelidae). Cladistics, 2008, 24, 34-50.	3.3	69
58	Mitogenome sequences stabilize the phylogenetics of weevils (Curculionoidea) and establish the monophyly of larval ectophagy. Molecular Phylogenetics and Evolution, 2013, 67, 156-166.	2.7	69
59	Basal relationships of Coleoptera inferred from 18S rDNA sequences. Zoologica Scripta, 2002, 31, 41-49.	1.7	68
60	On the constitution and phylogeny of Staphyliniformia (Insecta: Coleoptera). Molecular Phylogenetics and Evolution, 2005, 34, 655-672.	2.7	67
61	Higherâ€level phylogeny of longhorn beetles (Coleoptera: Chrysomeloidea) inferred from mitochondrial genomes. Systematic Entomology, 2021, 46, 56-70.	3.9	65
62	A Molecular Phylogeny of the Tiger Beetles (Cicindelidae): Congruence of Mitochondrial and Nuclear rDNA Data Sets. Molecular Phylogenetics and Evolution, 1996, 6, 321-338.	2.7	64
63	How Slippage-Derived Sequences Are Incorporated into rRNA Variable-Region Secondary Structure: Implications for Phylogeny Reconstruction. Molecular Phylogenetics and Evolution, 2000, 14, 366-374.	2.7	62
64	Reconstructing species phylogeny of the carabid beetles Ohomopterus using multiple nuclear DNA sequences: heterogeneous information content and the performance of simultaneous analyses. Molecular Phylogenetics and Evolution, 2003, 26, 139-154.	2.7	62
65	The phylogeny of Galerucinae (Coleoptera: Chrysomelidae) and the performance of mitochondrial genomes in phylogenetic inference compared to nuclear <scp>rRNA</scp> genes. Cladistics, 2018, 34, 113-130.	3.3	62
66	Sampling Error Does Not Invalidate the Yule-Coalescent Model for Species Delimitation. A Response to Lohse (2009). Systematic Biology, 2009, 58, 442-444.	5.6	59
67	Detection and decay rates of prey and prey symbionts in the gut of a predator through metagenomics. Molecular Ecology Resources, 2015, 15, 880-892.	4.8	59
68	MtDNA phylogeny and biogeography of Copelatinae, a highly diverse group of tropical diving beetles (Dytiscidae). Molecular Phylogenetics and Evolution, 2004, 32, 866-880.	2.7	58
69	Phylogenetics and biogeography of the dung beetle genus Onthophagus inferred from mitochondrial genomes. Molecular Phylogenetics and Evolution, 2016, 105, 86-95.	2.7	58
70	The phylogeny of the Histeroidea (Coleoptera: Staphyliniformia). Cladistics, 2002, 18, 394-415.	3.3	57
71	Towards the phylogeny of chafers (Sericini): Analysis of alignment-variable sequences and the evolution of segment numbers in the antennal club. Molecular Phylogenetics and Evolution, 2008, 47, 783-798.	2.7	57
72	Uncovering Trophic Interactions in Arthropod Predators through DNA Shotgun-Sequencing of Gut Contents. PLoS ONE, 2016, 11, e0161841.	2.5	56

#	Article	IF	Citations
73	The phylogeny of leaf beetles (Chrysomelidae) inferred from mitochondrial genomes. Systematic Entomology, 2020, 45, 188-204.	3.9	56
74	Metabarcoding of freshwater invertebrates to detect the effects of a pesticide spill. Molecular Ecology, 2018, 27, 146-166.	3.9	54
75	Habitat type as a determinant of species range sizes: the example of lotic-lentic differences in aquatic Coleoptera. Biological Journal of the Linnean Society, 2000, 71, 33-52.	1.6	52
76	Anti-predator defence drives parallel morphological evolution in flea beetles. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 2133-2141.	2.6	51
77	The founding charter of the Genomic Observatories Network. GigaScience, 2014, 3, 2.	6.4	51
78	Infrequent and unidirectional colonization of hyperdiverse Papuadytes diving beetles in New Caledonia and New Guinea. Molecular Phylogenetics and Evolution, 2007, 42, 505-516.	2.7	50
79	The limited spatial scale of dispersal in soil arthropods revealed with wholeâ€community haplotypeâ€level metabarcoding. Molecular Ecology, 2021, 30, 48-61.	3.9	49
80	A highly modified stygobiont diving beetle of the genus Copelatus (Coleoptera, Dytiscidae): taxonomy and cladistic analysis based on mitochondrial DNA sequences. Systematic Entomology, 2004, 29, 59-67.	3.9	48
81	Phylogeny and historical biogeography of Agabinae diving beetles (Coleoptera) inferred from mitochondrial DNA sequences. Molecular Phylogenetics and Evolution, 2004, 30, 545-562.	2.7	48
82	Evidence of non-neutral polymorphism in Plasmodium falciparum gamete surface protein genes Pfs47 and Pfs48/45. Molecular and Biochemical Parasitology, 2007, 156, 117-123.	1.1	48
83	Ancient associations of aquatic beetles and tank bromeliads in the Neotropical forest canopy. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6356-6361.	7.1	46
84	Utility of the DNA barcoding gene fragment for parasitic wasp phylogeny (Hymenoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 Td (Resources, 2012, 12, 676-685.	4.8	46
85	DNA profiling of hostâ€“herbivore interactions in tropical forests. Ecological Entomology, 2010, 35, 18-32.	2.2	45
86	Toward accurate speciesâ€level metabarcoding of arthropod communities from the tropical forest canopy. Ecology and Evolution, 2019, 9, 3105-3116.	1.9	45
87	THE EVOLUTION OF UNISEXUALITY IN CALLIGRAPHA LEAF BEETLES: MOLECULAR AND ECOLOGICAL INSIGHTS ON MULTIPLE ORIGINS VIA INTERSPECIFIC HYBRIDIZATION. Evolution; International Journal of Organic Evolution, 2006, 60, 328-347.	2.3	44
88	Using Exon and Intron Sequences of the Gene Mp20 to Resolve Basal Relationships in Cicindela (Coleoptera:Cicindelidae). Systematic Biology, 2004, 53, 554-570.	5.6	43
89	Phylogeny of North AmericanCicindelaTiger Beetles Inferred from Multiple Mitochondrial DNA Sequences. Molecular Phylogenetics and Evolution, 1997, 8, 225-235.	2.7	42
90	Metabarcoding of fungal communities associated with bark beetles. Ecology and Evolution, 2016, 6, 1590-1600.	1.9	42

#	Article	IF	Citations
91	Mitochondrial Metagenomics Reveals the Ancient Origin and Phylodiversity of Soil Mites and Provides a Phylogeny of the Acari. Molecular Biology and Evolution, 2020, 37, 683-694.	8.9	42
92	Local environment rather than past climate determines community composition of mountain stream macroinvertebrates across Europe. Molecular Ecology, 2017, 26, 6085-6099.	3.9	41
93	The contribution of mitochondrial metagenomics to large-scale data mining and phylogenetic analysis of Coleoptera. Molecular Phylogenetics and Evolution, 2018, 128, 1-11.	2.7	41
94	Suprageneric systematics of flea beetles (Chrysomelidae: Alticinae) inferred from multilocus sequence data. Molecular Phylogenetics and Evolution, 2012, 62, 793-805.	2.7	40
95	Comparative genomics of the mimicry switch inPapilio dardanus. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20140465.	2.6	40
96	Rapid assembly of taxonomically validated mitochondrial genomes from historical insect collections. Biological Journal of the Linnean Society, 2016, 117, 83-95.	1.6	40
97	Complementation of a truncated membrane-bound enzyme IINag from Klebsiella pneumoniae with a soluble enzyme III in Escherichia coli K12. Molecular Genetics and Genomics, 1988, 213, 175-178.	2.4	39
98	The Origin of Multiple Sex Chromosomes in Tiger Beetles. Molecular Biology and Evolution, 2002, 19, 1792-1796.	8.9	37
99	Local and regional ecological morphology of dung beetle assemblages across four biogeographic regions. Journal of Biogeography, 2011, 38, 1668-1682.	3.0	37
100	Size, frequency, and phylogenetic signal of multiple-residue indels in sequence alignment of introns. Cladistics, 2006, 22, 144-156.	3.3	36
101	Deep mtDNA subdivision within Linnean species in an endemic radiation of tiger beetles from New Zealand (genus Neocicindela). Molecular Phylogenetics and Evolution, 2011, 59, 251-262.	2.7	36
102	The phylogeny of monkey beetles based on mitochondrial and ribosomal RNA genes (Coleoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.7	36
103	Colour pattern specification in the Mocker swallowtail Papilio dardanus : the transcription factor invected is a candidate for the mimicry locus H. Proceedings of the Royal Society B: Biological Sciences, 2008, 275, 1181-1188.	2.6	35
104	Multiâ€hierarchical macroecology at species and genetic levels to discern neutral and nonâ€neutral processes. Global Ecology and Biogeography, 2015, 24, 873-882.	5.8	35
105	Complex selection on life-history traits and the maintenance of variation in exaggerated rostrum length in acorn weevils. Oecologia, 2011, 167, 1053-1061.	2.0	34
106	Ribosomal protein genes of holometabolan insects reject the Halteria, instead revealing a close affinity of Strepsiptera with Coleoptera. Molecular Phylogenetics and Evolution, 2010, 55, 846-859.	2.7	33
107	Molecular systematics of Eumolpinae and the relationships with Spilopyrinae (Coleoptera,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	2.7	32
108	THE UTILITY OF MOLECULAR MARKERS FROM NON-LETHAL DNA SAMPLES OF THE CITES II PROTECTED â€œTARANTULAâ€•BRACHYPELMA VAGANS (ARANEAE, THERAPHOSIDAE). Journal of Arachnology, 2007, 35, 278-292.	0.5	32

#	Article	IF	Citations
109	Systematic placement of the recently discovered beetle family Meruidae (Coleoptera: Dytiscoidea) based on molecular data. Zoologica Scripta, 2008, 37, 647-650.	1.7	32
110	Metagenome Skimming of Insect Specimen Pools: Potential for Comparative Genomics. Genome Biology and Evolution, 2015, 7, 1474-1489.	2.5	32
111	Re-evaluating conservation priorities of New World tarantulas (Araneae: Theraphosidae) in a molecular framework indicates non-monophyly of the genera,AphonopelmaandBrachypelma. Systematics and Biodiversity, 2018, 16, 89-107.	1.2	32
112	Validated removal of nuclear pseudogenes and sequencing artefacts from mitochondrial metabarcode data. Molecular Ecology Resources, 2021, 21, 1772-1787.	4.8	32
113	Imprints of multiple glacial refugia in the Pyrenees revealed by phylogeography and palaeodistribution modelling of an endemic spider. Molecular Ecology, 2016, 25, 2046-2064.	3.9	31
114	Genome sequencing of Rhinorhipus Lawrence exposes an early branch of the Coleoptera. Frontiers in Zoology, 2018, 15, 21.	2.0	30
115	A validated workflow for rapid taxonomic assignment and monitoring of a national fauna of bees (Apiformes) using high throughput DNA barcoding. Molecular Ecology Resources, 2020, 20, 40-53.	4.8	30
116	Gene expression in the gut of keratin-feeding clothes moths (Tineola) and keratin beetles (Trox) revealed by subtracted cDNA libraries. Insect Biochemistry and Molecular Biology, 2006, 36, 584-592.	2.7	29
117	DNA-based taxonomy of larval stages reveals huge unknown species diversity in neotropical seed weevils (genus Conotrachelus): relevance to evolutionary ecology. Molecular Phylogenetics and Evolution, 2010, 56, 281-293.	2.7	29
118	Species richness: Does flower power explain beetle-mania?. Current Biology, 1998, 8, R843-R845.	3.9	27
119	DNA taxonomy and phylogeography of beetles of the Falkland Islands (Islas Malvinas). Molecular Phylogenetics and Evolution, 2009, 53, 935-947.	2.7	27
120	DNA barcoding of endoparasitoid wasps in the genus Anicetus reveals high levels of host specificity (Hymenoptera: Encyrtidae). Biological Control, 2011, 58, 182-191.	3.0	26
121	Speciation: Don't Fly and Diversify?. Current Biology, 2012, 22, R284-R286.	3.9	26
122	Longâ€term isolation and endemicity of Neotropical aquatic insects limit the community responses to recent amphibian decline. Diversity and Distributions, 2015, 21, 938-949.	4.1	26
123	Connecting highâ€throughput biodiversity inventories: Opportunities for a siteâ€based genomic framework for global integration and synthesis. Molecular Ecology, 2021, 30, 1120-1135.	3.9	26
124	Exploring Rate Variation Among and Within Sites in a Densely Sampled Tree: Species Level Phylogenetics of North American Tiger Beetles (Genus Cicindela). Systematic Biology, 2005, 54, 4-20.	5.6	25
125	A protocol for large-scale rRNA sequence analysis: Towards a detailed phylogeny of Coleoptera. Molecular Phylogenetics and Evolution, 2008, 47, 289-301.	2.7	25
126	Ecology has contrasting effects on genetic variation within species versus rates of molecular evolution across species in water beetles. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20142476.	2.6	25

#	Article	IF	Citations
127	Gondwanian relicts and oceanic dispersal in a cosmopolitan radiation of euedaphic ground beetles. Molecular Phylogenetics and Evolution, 2016, 99, 235-246.	2.7	25
128	Arcticâ€Alpine Distributionsâ€”Metapopulations on a Continental Scale?. American Naturalist, 2009, 173, 313-326.	2.1	24
129	Comparison of the sequences of the nagE operons from Klebsiella pneumoniae and Escherichia colt K12: Enhanced variability of the enzyme IIN-acetylglucosamine in regions connecting functional domains. Molecular Genetics and Genomics, 1991, 230, 270-276.	2.4	23
130	Molecular Phylogeny of the Cicindela maritima (Coleoptera: Cicindelidae) Group Indicates Fast Radiation in Western North America. Annals of the Entomological Society of America, 1998, 91, 185-194.	2.5	22
131	Coming of age for COI metabarcoding of whole organism community DNA: Towards bioinformatic harmonisation. Molecular Ecology Resources, 2022, 22, 847-861.	4.8	22
132	Aposematism and mimicry in softâ€bodied beetles of the superfamily <scp>C</scp>leroidea (<scp>I</scp>nsecta). Zoologica Scripta, 2016, 45, 9-21.	1.7	21
133	Ecological constraints from incumbent clades drive trait evolution across the treeâ€ofâ€life of freshwater macroinvertebrates. Ecography, 2018, 41, 1049-1063.	4.5	21
134	Beta diversity at multiple hierarchical levels: explaining the high diversity of scarab beetles in tropical montane forests. Journal of Biogeography, 2013, 40, 2134-2145.	3.0	18
135	Higher Î²â€and Î³â€diversity at species and genetic levels in headwaters than in midâ€order streams in <scp>H</scp>ydropsyche (<scp>T</scp>richoptera). Freshwater Biology, 2013, 58, 2226-2236.	2.4	17
136	Speciation below ground: Tempo and mode of diversification in a radiation of endogean ground beetles. Molecular Ecology, 2017, 26, 6053-6070.	3.9	17
137	Predicting the unpredictable: How host specific is the mycobiota of bark and ambrosia beetles?. Fungal Ecology, 2019, 42, 100854.	1.6	17
138	Shotgun mitogenomics across body size classes in a local assemblage of tropical Diptera: Phylogeny, species diversity and mitochondrial abundance spectrum. Molecular Ecology, 2017, 26, 5086-5098.	3.9	17
139	The mitochondrial genome of Iberobaenia (Coleoptera: Iberobaeniidae): first rearrangement of protein-coding genes in the beetles. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2017, 28, 156-158.	0.7	16
140	Terra incognita of soil biodiversity: unseen invasions under our feet. Molecular Ecology, 2017, 26, 3087-3089.	3.9	16
141	Mimicry diversification in Papilio dardanus via a genomic inversion in the regulatory region of engrailed â€“ invected. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20200443.	2.6	15
142	Community metabarcoding reveals the relative role of environmental filtering and spatial processes in metacommunity dynamics of soil microarthropods across a mosaic of montane forests. Molecular Ecology, 2023, 32, 6110-6128.	3.9	15
143	Mitogenomic data elucidate the phylogeny and evolution of life strategies in Dermestidae (Coleoptera). Systematic Entomology, 0, , .	3.9	14
144	The diversity of soil mesofauna declines after bamboo invasion in subtropical China. Science of the Total Environment, 2021, 789, 147982.	8.0	14

#	Article	IF	Citations
145	Phylogenetic and ecological structure of Mediterranean caddisfly communities at various spatioâ€temporal scales. Journal of Biogeography, 2012, 39, 1621-1632.	3.0	13
146	Vulnerability to climate change for two endemic highâ€elevation, lowâ€dispersive Annitella species (Trichoptera) in Sierra Nevada, the southernmost high mountain in Europe. Insect Conservation and Diversity, 2020, 13, 283-295.	3.0	13
147	The nematode?arthropod clade revisited: phylogenomic analyses from ribosomal protein genes misled by shared evolutionary biases. Cladistics, 2007, 23, 130-144.	3.3	12
148	A phylogenetic framework for wing pattern evolution in the mimetic Mocker Swallowtail Papilio dardanus. Molecular Ecology, 2009, 18, 3872-3884.	3.9	12
149	Distinct species or colour polymorphism? Life history, morphology and sequence data separate twoPyrrhaltaelm beetles (Coleoptera: Chrysomelidae). Systematics and Biodiversity, 2012, 10, 133-146.	1.2	12
150	Detection of the Acetylcholinesterase Insecticide Resistance Mutation (G328A) in Natural Populations of <I>Ceratitis capitata</I>. Journal of Economic Entomology, 2014, 107, 1965-1968.	1.8	12
151	Metabarcoding reveals massive species diversity of Diptera in a subtropical ecosystem. Ecology and Evolution, 2022, 12, e8535.	1.9	12
152	Intraspecific genetic variation in complex assemblages from mitochondrial metagenomics: comparison with DNA barcodes. Methods in Ecology and Evolution, 2017, 8, 248-256.	5.2	11
153	Diversification of mitogenomes in three sympatric Altica flea beetles (Insecta, Chrysomelidae). Zoologica Scripta, 2019, 48, 657-666.	1.7	11
154	Diagnosing an Overlooked North American Taxon: Biological Observations and Mitochondrial Insights on <I>Calligrapha suturella</I> Schaeffer, New Status (Coleoptera, Chrysomelidae). Annals of the Entomological Society of America, 2004, 97, 28-36.	2.5	10
155	Resolving Ambiguity of Species Limits and Concatenation in Multilocus Sequence Data for the Construction of Phylogenetic Supermatrices. Systematic Biology, 2013, 62, 456-466.	5.6	10
156	Host specificity of parasitoids (Encyrtidae) toward armored scale insects (Diaspididae): Untangling the effect of cryptic species on quantitative food webs. Ecology and Evolution, 2018, 8, 7879-7893.	1.9	10
157	Coalescence Models Reveal the Rise of the White-Bellied Rat (Niviventer confucianus) Following the Loss of Asian Megafauna. Journal of Mammalian Evolution, 2019, 26, 423-434.	1.8	9
158	Joint analysis of species and genetic variation to quantify the role of dispersal and environmental constraints in community turnover. Ecography, 2022, 2022, .	4.5	9
159	Community assembly and metaphylogeography of soil biodiversity: Insights from haplotypeâ€level community<scp>DNA</scp>metabarcoding within an oceanic island. Molecular Ecology, 2022, 31, 4078-4094.	3.9	9
160	Rare Failures of DNA Bar Codes to Separate Morphologically Distinct Species in a Biodiversity Survey of Iberian Leaf Beetles. PLoS ONE, 2013, 8, e74854.	2.5	8
161	Demographic History and Genomic Response to Environmental Changes in a Rapid Radiation of Wild Rats. Molecular Biology and Evolution, 2021, 38, 1905-1923.	8.9	7
162	Selection of auxotrophic and carbohydrate-negative mutants in penicillin-resistantKlebsiella pneumoniaeby nalidixic acid treatment. FEMS Microbiology Letters, 1986, 37, 299-304.	1.8	6

#	Article	IF	Citations
163	A New Subspecies of <I>Cicindela limbata</I> (Coleoptera: Cicindelidae) from Alaska, and Further Review of the <I>maritima</I> group by Using Mitochondrial DNA Analysis. Annals of the Entomological Society of America, 2008, 101, 277-288.	2.5	6
164	Statistical Evaluation of Monophyly in the â€˜Broad-Nosed Weevilsâ€™ through Molecular Phylogenetic Analysis Combining Mitochondrial Genome and Single-Locus Sequences (Curculionidae: Entiminae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.7	6
165	Distribution and habitat preferences of tiger beetles (Coleoptera: Cicindelidae) of the riverine ecosystems of Sri Lanka. Journal of Threatened Taxa, 2014, 6, 6195-6203.	0.3	6
166	Population genetics and migration pathways of the Mediterranean fruit flyCeratitis capitatainferred with coalescent methods. PeerJ, 2018, 6, e5340.	2.0	6
167	ï»¿Metabarcoding of insect-associated fungal communities: a comparison of internal transcribed spacer (ITS) and large-subunit (LSU) rRNA markers. MycoKeys, 2022, 88, 1-33.	1.9	6
168	The SITE-100 Project: Site-Based Biodiversity Genomics for Species Discovery, Community Ecology, and a Global Tree-of-Life. Frontiers in Ecology and Evolution, 2022, 10, .	2.2	6
169	Evolution: Taking the Sting out of Wasp Phylogenetics. Current Biology, 2017, 27, R358-R360.	3.9	4
170	New mitochondrial genomes of 39 soil dwelling Coleoptera from metagenome sequencing. Mitochondrial DNA Part B: Resources, 2019, 4, 2447-2450.	0.4	4
171	Unveiling biogeographical patterns in the worldwide distributed Ceratitis capitata (medfly) using population genomics and microbiome composition. Molecular Ecology, 2022, 31, 4866-4883.	3.9	4
172	Investigation of hormone activity in butterfly imaginal wing discs by protein expression pattern changes. Electrophoresis, 2007, 28, 535-544.	2.4	3
173	The phylogeny of the Histeroidea (Coleoptera: Staphyliniformia). Cladistics, 2002, 18, 394-415.	3.3	3
174	<scp>DNA</scp>â€based assessment of environmental degradation in an unknown fauna: The freshwater macroinvertebrates of the <scp>Indoâ€Burmese</scp> hotspot. Journal of Applied Ecology, 2022, 59, 1644-1658.	4.0	2
175	Metabarcoding to establish freshwater indicators of environmental degradation in the Indo-Burmese biodiversity hotspot. ARPHA Conference Abstracts, 0, 4, .	0.0	1
176	Incorporating older literature into genomic studies: A response to Zunino & Halffter. Molecular Phylogenetics and Evolution, 2019, 133, 164-165.	2.7	0