## Alfried P Vogler

List of Publications by Year in descending order

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Version: 2024-02-01

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

| #  | Article   | IF  | Citations |
|----|---|-----|-----------|
| 1  | 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        |
| 2  | Coming of age for COI metabarcoding of whole organism community DNA: Towards bioinformatic harmonisation. Molecular Ecology Resources, 2022, 22, 847-861.   | 4.8 | 22        |
| 3  | Metabarcoding reveals massive species diversity of Diptera in a subtropical ecosystem. Ecology and Evolution, 2022, 12, e8535.  | 1.9 | 12        |
| 4  | 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         |
| 5  | 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         |
| 6  | <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         |
| 7  | 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         |
| 8  | 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         |
| 9  | Unveiling biogeographical patterns in the worldwide distributed <i>Ceratitis capitata</i> (medfly) using population genomics and microbiome composition. Molecular Ecology, 2022, 31, 4866-4883.  | 3.9 | 4         |
| 10 | The limited spatial scale of dispersal in soil arthropods revealed with wholeâ€community haplotypeâ€evel metabarcoding. Molecular Ecology, 2021, 30, 48-61.   | 3.9 | 49        |
| 11 | Higherâ€level phylogeny of longhorn beetles (Coleoptera: Chrysomeloidea) inferred from mitochondrial genomes. Systematic Entomology, 2021, 46, 56-70.   | 3.9 | 65        |
| 12 | 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         |
| 13 | 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        |
| 14 | Validated removal of nuclear pseudogenes and sequencing artefacts from mitochondrial metabarcode data. Molecular Ecology Resources, 2021, 21, 1772-1787.  | 4.8 | 32        |
| 15 | The diversity of soil mesofauna declines after bamboo invasion in subtropical China. Science of the Total Environment, 2021, 789, 147982.   | 8.0 | 14        |
| 16 | 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        |
| 17 | Vulnerability to climate change for two endemic highâ€elevation, lowâ€dispersive <i>Annitella</i> species (Trichoptera) in Sierra Nevada, the southernmost high mountain in Europe. Insect Conservation and Diversity, 2020, 13, 283-295. | 3.0 | 13        |
| 18 | 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        |

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|----|---|-------------------|---------------|
| 19 | The phylogeny of leaf beetles (Chrysomelidae) inferred from mitochondrial genomes. Systematic Entomology, 2020, 45, 188-204.  | 3.9               | 56            |
| 20 | Mimicry diversification in <i>Papilio dardanus</i> via a genomic inversion in the regulatory region of <i>engrailed</i> – <i>invected</i> . Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20200443.                             | 2.6               | 15            |
| 21 | New mitochondrial genomes of 39 soil dwelling Coleoptera from metagenome sequencing.<br>Mitochondrial DNA Part B: Resources, 2019, 4, 2447-2450.  | 0.4               | 4             |
| 22 | Diversification of mitogenomes in three sympatric <i>Altica</i> flea beetles (Insecta, Chrysomelidae). Zoologica Scripta, 2019, 48, 657-666.  | 1.7               | 11            |
| 23 | Predicting the unpredictable: How host specific is the mycobiota of bark and ambrosia beetles?. Fungal Ecology, 2019, 42, 100854.   | 1.6               | 17            |
| 24 | Incorporating older literature into genomic studies: A response to Zunino & Halffter. Molecular Phylogenetics and Evolution, 2019, 133, 164-165.  | 2.7               | 0             |
| 25 | Toward accurate speciesâ€level metabarcoding of arthropod communities from the tropical forest canopy. Ecology and Evolution, 2019, 9, 3105-3116.   | 1.9               | 45            |
| 26 | Mitochondrial phylogenomics of the Hymenoptera. Molecular Phylogenetics and Evolution, 2019, 131, 8-18.   | 2.7               | 104           |
| 27 | 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             |
| 28 | 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           |
| 29 | 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            |
| 30 | Ecological constraints from incumbent clades drive trait evolution across the treeâ€ofâ€life of freshwater macroinvertebrates. Ecography, 2018, 41, 1049-1063.  | 4.5               | 21            |
| 31 | Metabarcoding of freshwater invertebrates to detect the effects of a pesticide spill. Molecular Ecology, 2018, 27, 146-166.   | 3.9               | 54            |
| 32 | Re-evaluating conservation priorities of New World tarantulas (Araneae: Theraphosidae) in a molecular framework indicates non-monophyly of the genera, <i>Aphonopelma </i> and <i>Brachypelma </i> ). Systematics and Biodiversity, 2018, 16, 89-107. | 1.2               | 32            |
| 33 | 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            |
| 34 | 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            |
| 35 | Statistical Evaluation of Monophyly in the  Broad-Nosed Weevils' through Molecular Phylogenetic<br>Analysis Combining Mitochondrial Genome and Single-Locus Sequences (Curculionidae: Entiminae,) Tj ETQq1 1  | 0.7 <b>£4</b> 314 | rg&T /Overloo |
| 36 | Genome sequencing of Rhinorhipus Lawrence exposes an early branch of the Coleoptera. Frontiers in Zoology, 2018, 15, 21.  | 2.0               | 30            |

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|----|---|-----|-----------|
| 37 | Why the COI barcode should be the community <scp>DNA</scp> metabarcode for the metazoa. Molecular Ecology, 2018, 27, 3968-3975.   | 3.9 | 131       |
| 38 | Population genetics and migration pathways of the Mediterranean fruit fly <i>Ceratitis capitata</i> inferred with coalescent methods. Peerl, 2018, 6, e5340.  | 2.0 | 6         |
| 39 | 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        |
| 40 | Evolution: Taking the Sting out of Wasp Phylogenetics. Current Biology, 2017, 27, R358-R360.  | 3.9 | 4         |
| 41 | The mitogenome phylogeny of Adephaga (Coleoptera). Molecular Phylogenetics and Evolution, 2017, 114, 166-174.   | 2.7 | 70        |
| 42 | Connecting Earth observation to high-throughput biodiversity data. Nature Ecology and Evolution, 2017, 1, 176.  | 7.8 | 156       |
| 43 | <i>Terra incognita</i> of soil biodiversity: unseen invasions under our feet. Molecular Ecology, 2017, 26, 3087-3089.   | 3.9 | 16        |
| 44 | Speciation below ground: Tempo and mode of diversification in a radiation of endogean ground beetles. Molecular Ecology, 2017, 26, 6053-6070.   | 3.9 | 17        |
| 45 | Local environment rather than past climate determines community composition of mountain stream macroinvertebrates across Europe. Molecular Ecology, 2017, 26, 6085-6099.  | 3.9 | 41        |
| 46 | 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        |
| 47 | 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        |
| 48 | Uncovering Trophic Interactions in Arthropod Predators through DNA Shotgun-Sequencing of Gut Contents. PLoS ONE, 2016, 11, e0161841.  | 2.5 | 56        |
| 49 | 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        |
| 50 | 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        |
| 51 | Gondwanian relicts and oceanic dispersal in a cosmopolitan radiation of euedaphic ground beetles.<br>Molecular Phylogenetics and Evolution, 2016, 99, 235-246.  | 2.7 | 25        |
| 52 | Metabarcoding of fungal communities associated with bark beetles. Ecology and Evolution, 2016, 6, 1590-1600.  | 1.9 | 42        |
| 53 | Protecting an Ecosystem Service. Advances in Ecological Research, 2016, 54, 135-206.  | 2.7 | 115       |
| 54 | 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        |

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|----|--|-----|-----------|
| 55 | Rapid assembly of taxonomically validated mitochondrial genomes from historical insect collections. Biological Journal of the Linnean Society, 2016, 117, 83-95.   | 1.6 | 40        |
| 56 | Phylogenetics and biogeography of the dung beetle genus Onthophagus inferred from mitochondrial genomes. Molecular Phylogenetics and Evolution, 2016, 105, 86-95.  | 2.7 | 58        |
| 57 | Family-Level Sampling of Mitochondrial Genomes in Coleoptera: Compositional Heterogeneity and Phylogenetics. Genome Biology and Evolution, 2016, 8, 161-175.   | 2.5 | 157       |
| 58 | 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       |
| 59 | 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        |
| 60 | Mitochondrial metagenomics: letting the genes out of the bottle. GigaScience, 2016, 5, 15.   | 6.4 | 103       |
| 61 | Rarity and Incomplete Sampling in DNA-Based Species Delimitation. Systematic Biology, 2016, 65, 478-494.   | 5.6 | 138       |
| 62 | 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        |
| 63 | 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       |
| 64 | 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        |
| 65 | Phylogenetic community ecology of soil biodiversity using mitochondrial metagenomics. Molecular Ecology, 2015, 24, 3603-3617.  | 3.9 | 93        |
| 66 | 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        |
| 67 | 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        |
| 68 | Metagenome Skimming of Insect Specimen Pools: Potential for Comparative Genomics. Genome Biology and Evolution, 2015, 7, 1474-1489.  | 2.5 | 32        |
| 69 | 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        |
| 70 | Comparing the effectiveness of metagenomics and metabarcoding for diet analysis of a leafâ€feeding monkey ( <i><scp>P</scp>ygathrix nemaeus</i> ). Molecular Ecology Resources, 2015, 15, 250-261.                     | 4.8 | 119       |
| 71 | The founding charter of the Genomic Observatories Network. GigaScience, 2014, 3, 2.  | 6.4 | 51        |
| 72 | 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        |

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| 73 | The towering orogeny of New Guinea as a trigger for arthropod megadiversity. Nature Communications, 2014, 5, 4001.  | 12.8 | 152       |
| 74 | 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       |
| 75 | 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       |
| 76 | Comparative genomics of the mimicry switch in <i>Papilio dardanus</i> . Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20140465.   | 2.6  | 40        |
| 77 | 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       |
| 78 | 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         |
| 79 | Higher β―and γâ€diversity at species and genetic levels in headwaters than in midâ€order streams in <i><scp>H</scp>ydropsyche</i> ( <scp>T</scp> richoptera). Freshwater Biology, 2013, 58, 2226-2236.      | 2.4  | 17        |
| 80 | 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        |
| 81 | Whole-community DNA barcoding reveals a spatio-temporal continuum of biodiversity at species and genetic levels. Nature Communications, 2013, 4, 1892.  | 12.8 | 71        |
| 82 | 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        |
| 83 | 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        |
| 84 | 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         |
| 85 | The Effect of Geographical Scale of Sampling on DNA Barcoding. Systematic Biology, 2012, 61, 851-869.   | 5.6  | 386       |
| 86 | Suprageneric systematics of flea beetles (Chrysomelidae: Alticinae) inferred from multilocus sequence data. Molecular Phylogenetics and Evolution, 2012, 62, 793-805.                                       | 2.7  | 40        |
| 87 | 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       |
| 88 | Distinct species or colour polymorphism? Life history, morphology and sequence data separate two <i>Pyrrhalta</i> elm beetles (Coleoptera: Chrysomelidae). Systematics and Biodiversity, 2012, 10, 133-146. | 1.2  | 12        |
| 89 | Speciation: Don't Fly and Diversify?. Current Biology, 2012, 22, R284-R286.   | 3.9  | 26        |
| 90 | Phylogenetic and ecological structure of Mediterranean caddisfly communities at various spatioâ€temporal scales. Journal of Biogeography, 2012, 39, 1621-1632.  | 3.0  | 13        |

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|-----|--|--------------------|-------------------|
| 91  | Utility of the DNA barcoding gene fragment for parasitic wasp phylogeny (Hymenoptera:) Tj ETQq1 1 0.784314 rgResources, 2012, 12, 676-685.   | gBT /Overlo<br>4.8 | ock 10 Tf 5<br>46 |
| 92  | Testing the Species–Genetic Diversity Correlation in the Aegean Archipelago: Toward a Haplotype-Based Macroecology?. American Naturalist, 2011, 178, 241-255.  | 2.1                | 86                |
| 93  | Local and regional ecological morphology of dung beetle assemblages across four biogeographic regions. Journal of Biogeography, 2011, 38, 1668-1682.   | 3.0                | 37                |
| 94  | 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                |
| 95  | 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                |
| 96  | 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                |
| 97  | The phylogeny of monkey beetles based on mitochondrial and ribosomal RNA genes (Coleoptera:) Tj ETQq1 1 0.7  | 84314 rgB<br>2.7   | 3T/Overlock       |
| 98  | 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                |
| 99  | DNA profiling of host–herbivore interactions in tropical forests. Ecological Entomology, 2010, 35, 18-32.  | 2.2                | 45                |
| 100 | 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                |
| 101 | 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                |
| 102 | Revisiting the Insect Mitochondrial Molecular Clock: The Mid-Aegean Trench Calibration. Molecular Biology and Evolution, 2010, 27, 1659-1672.  | 8.9                | 729               |
| 103 | DNA barcoding insect–host plant associations. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 639-648.   | 2.6                | 174               |
| 104 | New Guinea highland origin of a widespread arthropod supertramp. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 2359-2367.  | 2.6                | 78                |
| 105 | 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               |
| 106 | A phylogenetic framework for wing pattern evolution in the mimetic Mocker Swallowtail <i>Papilio dardanus</i> . Molecular Ecology, 2009, 18, 3872-3884.  | 3.9                | 12                |
| 107 | DNA taxonomy and phylogeography of beetles of the Falkland Islands (Islas Malvinas). Molecular Phylogenetics and Evolution, 2009, 53, 935-947.   | 2.7                | 27                |
| 108 | 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                |

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|-----|---|--------------|-----------|
| 109 | Accelerated Species Inventory on Madagascar Using Coalescent-Based Models of Species Delineation. Systematic Biology, 2009, 58, 298-311.  | 5 <b>.</b> 6 | 641       |
| 110 | Arcticâ€Alpine Distributionsâ€"Metapopulations on a Continental Scale?. American Naturalist, 2009, 173, 313-326.  | 2.1          | 24        |
| 111 | A protocol for large-scale rRNA sequence analysis: Towards a detailed phylogeny of Coleoptera.<br>Molecular Phylogenetics and Evolution, 2008, 47, 289-301.   | 2.7          | 25        |
| 112 | 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        |
| 113 | Multilocus ribosomal RNA phylogeny of the leaf beetles (Chrysomelidae). Cladistics, 2008, 24, 34-50.  | 3.3          | 69        |
| 114 | Phylogeny and diversification of diving beetles (Coleoptera: Dytiscidae). Cladistics, 2008, 24, 563-590.  | 3.3          | 84        |
| 115 | Systematic placement of the recently discovered beetle family Meruidae (Coleoptera: Dytiscoidea) based on molecular data. Zoologica Scripta, 2008, 37, 647-650.   | 1.7          | 32        |
| 116 | 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       |
| 117 | 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        |
| 118 | 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        |
| 119 | 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        |
| 120 | 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         |
| 121 | THE UTILITY OF MOLECULAR MARKERS FROM NON-LETHAL DNA SAMPLES OF THE CITES II PROTECTED "TARANTULA―BRACHYPELMA VAGANS (ARANEAE, THERAPHOSIDAE). Journal of Arachnology, 2007, 35, 278-292.   | 0.5          | 32        |
| 122 | A Comprehensive Phylogeny of Beetles Reveals the Evolutionary Origins of a Superradiation. Science, 2007, 318, 1913-1916.   | 12.6         | 729       |
| 123 | Investigation of hormone activity in butterfly imaginal wing discs by protein expression pattern changes. Electrophoresis, 2007, 28, 535-544.   | 2.4          | 3         |
| 124 | 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        |
| 125 | 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       |
| 126 | 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       |

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|-----|---|-----------|----------------|
| 127 | A molecular phylogenetic analysis of the Scarabaeinae (dung beetles). Molecular Phylogenetics and Evolution, 2007, 45, 674-692.   | 2.7       | 121            |
| 128 | The nematode?arthropod clade revisited: phylogenomic analyses from ribosomal protein genes misled by shared evolutionary biases. Cladistics, 2007, 23, 130-144.   | 3.3       | 12             |
| 129 | Molecular phylogenetics of Elateriformia (Coleoptera): evolution of bioluminescence and neoteny. Cladistics, 2007, 23, 477-496.   | 3.3       | 134            |
| 130 | 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             |
| 131 | Recalibrated Tree of Leaf Beetles (Chrysomelidae) Indicates Independent Diversification of Angiosperms and Their Insect Herbivores. PLoS ONE, 2007, 2, e360.  | 2.5       | 124            |
| 132 | Sequence-Based Species Delimitation for the DNA Taxonomy of Undescribed Insects. Systematic Biology, 2006, 55, 595-609.   | 5.6       | 2,257          |
| 133 | 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             |
| 134 | Size, frequency, and phylogenetic signal of multiple-residue indels in sequence alignment of introns. Cladistics, 2006, 22, 144-156.  | 3.3       | 36             |
| 135 | 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             |
| 136 | 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             |
| 137 | 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             |
| 138 | On the constitution and phylogeny of Staphyliniformia (Insecta: Coleoptera). Molecular Phylogenetics and Evolution, 2005, 34, 655-672.  | 2.7       | 67             |
| 139 | Molecular systematics of Eumolpinae and the relationships with Spilopyrinae (Coleoptera,) Tj ETQq1 1 0.784314   | rgBT /Ove | erlock 10 Tf 5 |
| 140 | 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             |
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