

Martijn J T N Timmermans

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,814
citations

331670

21
h-index

477307

29
g-index

30
all docs

30
docs citations

30
times ranked

1777
citing authors

#	ARTICLE	IF	CITATIONS
1	Mimicry diversification in <i>Papilio dardanus</i> via a genomic inversion in the regulatory region of <i>engrailed</i> – <i>invested</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200443.	2.6	15
2	Phylogenomics resolves major relationships and reveals significant diversification rate shifts in the evolution of silk moths and relatives. <i>BMC Evolutionary Biology</i> , 2019, 19, 182.	3.2	49
3	Phylogeny of the Hawkmoth Tribe Ambulycini (Lepidoptera: Sphingidae): Mitogenomes from Museum Specimens Resolve Major Relationships. <i>Insect Systematics and Diversity</i> , 2019, 3, .	1.7	5
4	The phylogeny of Galerucinae (Coleoptera: Chrysomelidae) and the performance of mitochondrial genomes in phylogenetic inference compared to nuclear rRNA genes. <i>Cladistics</i> , 2018, 34, 113-130.	3.3	62
5	The contribution of mitochondrial metagenomics to large-scale data mining and phylogenetic analysis of Coleoptera. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 1-11.	2.7	41
6	Independent evolution of sexual dimorphism and female-limited mimicry in swallowtail butterflies (<i>Papilio dardanus</i> and <i>Papilio phorcas</i>). <i>Molecular Ecology</i> , 2017, 26, 1273-1284.	3.9	9
7	Intraspecific genetic variation in complex assemblages from mitochondrial metagenomics: comparison with DNA barcodes. <i>Methods in Ecology and Evolution</i> , 2017, 8, 248-256.	5.2	11
8	Rapid assembly of taxonomically validated mitochondrial genomes from historical insect collections. <i>Biological Journal of the Linnean Society</i> , 2016, 117, 83-95.	1.6	40
9	Family-Level Sampling of Mitochondrial Genomes in Coleoptera: Compositional Heterogeneity and Phylogenetics. <i>Genome Biology and Evolution</i> , 2016, 8, 161-175.	2.5	157
10	Mitogenomics of Old World Acraea butterflies reveals a highly divergent <i>Bematistes</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 233-241.	2.7	15
11	Soup to Tree: The Phylogeny of Beetles Inferred by Mitochondrial Metagenomics of a Bornean Rainforest Sample. <i>Molecular Biology and Evolution</i> , 2015, 32, 2302-2316.	8.9	163
12	Phylogenetic community ecology of soil biodiversity using mitochondrial metagenomics. <i>Molecular Ecology</i> , 2015, 24, 3603-3617.	3.9	93
13	Validating the power of mitochondrial metagenomics for community ecology and phylogenetics of complex assemblages. <i>Methods in Ecology and Evolution</i> , 2015, 6, 883-894.	5.2	86
14	Metagenome Skimming of Insect Specimen Pools: Potential for Comparative Genomics. <i>Genome Biology and Evolution</i> , 2015, 7, 1474-1489.	2.5	32
15	Characterising the Phenotypic Diversity of <i>Papilio dardanus</i> Wing Patterns Using an Extensive Museum Collection. <i>PLoS ONE</i> , 2014, 9, e96815.	2.5	11
16	The evolutionary genetics of highly divergent alleles of the mimicry locus in <i>Papilio dardanus</i> . <i>BMC Evolutionary Biology</i> , 2014, 14, 140.	3.2	12
17	Bulk De Novo Mitogenome Assembly from Pooled Total DNA Elucidates the Phylogeny of Weevils (Coleoptera: Curculionioidea). <i>Molecular Biology and Evolution</i> , 2014, 31, 2223-2237.	8.9	195
18	Comparative genomics of the mimicry switch in <i>Papilio dardanus</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140465.	2.6	40

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19	Towards a mitogenomic phylogeny of Lepidoptera. <i>Molecular Phylogenetics and Evolution</i> , 2014, 79, 169-178.	2.7	185
20	Mitogenome sequences stabilize the phylogenetics of weevils (Curculionoidea) and establish the monophyly of larval ectophagy. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 156-166.	2.7	69
21	Phylogenetically informative rearrangements in mitochondrial genomes of Coleoptera, and monophyly of aquatic elateriform beetles (Dryopoidea). <i>Molecular Phylogenetics and Evolution</i> , 2012, 63, 299-304.	2.7	100
22	Hybrid Origins: DNA Techniques Confirm that <i>Papilio nandina</i> is a Species Hybrid (Papilionidae). <i>Journal of the Lepidopterists' Society</i> , 2011, 65, 199-201.	0.2	3
23	Why barcode? High-throughput multiplex sequencing of mitochondrial genomes for molecular systematics. <i>Nucleic Acids Research</i> , 2010, 38, e197-e197.	14.5	152
24	Sugar sweet springtails: on the transcriptional response of <i>Folsomia candida</i> (Collembola) to desiccation stress. <i>Insect Molecular Biology</i> , 2009, 18, 737-746.	2.0	34
25	Revealing pancrustacean relationships: Phylogenetic analysis of ribosomal protein genes places Collembola (springtails) in a monophyletic Hexapoda and reinforces the discrepancy between mitochondrial and nuclear DNA markers. <i>BMC Evolutionary Biology</i> , 2008, 8, 83.	3.2	46
26	Allelic diversity of metallothionein in <i>Orchesella cincta</i> (L.): traces of natural selection by environmental pollution. <i>Heredity</i> , 2007, 98, 311-319.	2.6	26
27	Collembase: a repository for springtail genomics and soil quality assessment. <i>BMC Genomics</i> , 2007, 8, 341.	2.8	44
28	Genetic structure in <i>Orchesella cincta</i> (Collembola): strong subdivision of European populations inferred from mtDNA and AFLP markers. <i>Molecular Ecology</i> , 2005, 14, 2017-2024.	3.9	55
29	Metallothionein mRNA Expression and Cadmium Tolerance in Metal-stressed and Reference Populations of the Springtail <i>Orchesella cincta</i> . <i>Ecotoxicology</i> , 2005, 14, 727-739.	2.4	63
30	Mitochondrial genome divergence supports an ancient origin of circatidal behaviour in the <i>Anurida maritima</i> (Collembola: Neanuridae) species group. <i>Organisms Diversity and Evolution</i> , 0, , 1.	1.6	1