

Xin Zhou

List of Publications by Year in descending order

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Version: 2024-02-01

131
papers

11,470
citations

61687

45
h-index

39744

98
g-index

168
all docs

168
docs citations

168
times ranked

14506
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic features underlying the evolutionary transitions of <i>Apibacter</i> to honey bee gut symbionts. <i>Insect Science</i> , 2022, 29, 259-275.	1.5	13
2	Researching on the fine structure and admixture of the worldwide chicken population reveal connections between populations and important events in breeding history. <i>Evolutionary Applications</i> , 2022, 15, 553-564.	1.5	16
3	Tracing the origin of honey products based on metagenomics and machine learning. <i>Food Chemistry</i> , 2022, 371, 131066.	4.2	15
4	Amplicon Sequencing of Single-Copy Protein-Coding Genes Reveals Accurate Diversity for Sequence-Discrete Microbiome Populations. <i>Microbiology Spectrum</i> , 2022, 10, e0210521.	1.2	0
5	Geographical resistome profiling in the honeybee microbiome reveals resistance gene transfer conferred by mobilizable plasmids. <i>Microbiome</i> , 2022, 10, 69.	4.9	13
6	Diversity and functional analysis of Chinese bumblebee gut microbiota reveal the metabolic niche and antibiotic resistance variation of <i>Gilliamella</i> . <i>Insect Science</i> , 2021, 28, 302-314.	1.5	26
7	Taxonomy must engage with new technologies and evolve to face future challenges. <i>Nature Ecology and Evolution</i> , 2021, 5, 3-4.	3.4	25
8	Comparative transcriptomics of ice-crawlers demonstrates cold specialization constrains niche evolution in a relict lineage. <i>Evolutionary Applications</i> , 2021, 14, 360-382.	1.5	5
9	Analysis of RNA-Seq, DNA Target Enrichment, and Sanger Nucleotide Sequence Data Resolves Deep Splits in the Phylogeny of Cuckoo Wasps (Hymenoptera: Chrysididae). <i>Insect Systematics and Diversity</i> , 2021, 5, .	0.7	8
10	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, .	1.1	14
11	Viromics of extant insect orders unveil the evolution of the flavi-like superfamily. <i>Virus Evolution</i> , 2021, 7, veab030.	2.2	35
12	Beyond <i>Drosophila</i> : resolving the rapid radiation of schizophoran flies with phylotranscriptomics. <i>BMC Biology</i> , 2021, 19, 23.	1.7	22
13	The larvae of Chinese Hydropsychidae (Insecta: Trichoptera), Part II: <i>Potamyia chinensis</i> and <i>Cheumatopsyche trifascia</i> . <i>Zootaxa</i> , 2021, 4926, 547-558.	0.2	1
14	Combining molecular datasets with strongly heterogeneous taxon coverage enlightens the peculiar biogeographic history of stoneflies (Insecta: Plecoptera). <i>Systematic Entomology</i> , 2021, 46, 952-967.	1.7	13
15	The larvae of Chinese Hydropsychidae (Insecta: Trichoptera), Part III: <i>Hydromanicus melli</i> Complex, <i>H. canaliculatus</i> , and <i>H. umbonatus</i> . <i>Zootaxa</i> , 2021, 5026, 527-540.	0.2	0
16	Evolutionary history and divergence times of Odonata (dragonflies and damselflies) revealed through transcriptomics. <i>IScience</i> , 2021, 24, 103324.	1.9	25
17	<i>Enterococcus faecium</i> Regulates Honey Bee Developmental Genes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12105.	1.8	12
18	Multifunctional cellulase enzymes are ancestral in Polyneoptera. <i>Insect Molecular Biology</i> , 2020, 29, 124-135.	1.0	21

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19	Phylogenomic analysis sheds light on the evolutionary pathways towards acoustic communication in Orthoptera. <i>Nature Communications</i> , 2020, 11, 4939.	5.8	82
20	The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest. <i>BMC Biology</i> , 2020, 18, 90.	1.7	40
21	Genomic architecture of endogenous ichnoviruses reveals distinct evolutionary pathways leading to virus domestication in parasitic wasps. <i>BMC Biology</i> , 2020, 18, 89.	1.7	24
22	Using full-length metabarcoding and DNA barcoding to infer community assembly for speciose taxonomic groups: a case study. <i>Evolutionary Ecology</i> , 2020, 34, 1063-1088.	0.5	2
23	Gene reuse facilitates rapid radiation and independent adaptation to diverse habitats in the Asian honeybee. <i>Science Advances</i> , 2020, 6, .	4.7	42
24	Four myriapod relatives “but who are sisters? No end to debates on relationships among the four major myriapod subgroups. <i>BMC Evolutionary Biology</i> , 2020, 20, 144.	3.2	13
25	An integrative phylogenomic approach to elucidate the evolutionary history and divergence times of Neuropterida (Insecta: Holometabola). <i>BMC Evolutionary Biology</i> , 2020, 20, 64.	3.2	48
26	Regional assemblages shaped by historical and contemporary factors: Evidence from a species-rich insect group. <i>Molecular Ecology</i> , 2020, 29, 2492-2510.	2.0	8
27	Analysis of the Chinese Alligator TCR α / β Loci Reveals the Evolutionary Pattern of Atypical TCR β /TCR γ in Tetrapods. <i>Journal of Immunology</i> , 2020, 205, 637-647.	0.4	6
28	Phylogenomics changes our understanding about earwig evolution. <i>Systematic Entomology</i> , 2020, 45, 516-526.	1.7	15
29	A multigene phylogeny and timeline for Trichoptera (Insecta). <i>Systematic Entomology</i> , 2020, 45, 670-686.	1.7	66
30	Chromosome-level genome assembly of an important pine defoliator, <i>Dendrolimus punctatus</i> (Lepidoptera; Lasiocampidae). <i>Molecular Ecology Resources</i> , 2020, 20, 1023-1037.	2.2	34
31	<i>Entomomonas moraniae</i> gen. nov., sp. nov., a member of the family Pseudomonadaceae isolated from Asian honey bee gut, possesses a highly reduced genome. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 165-171.	0.8	17
32	Verification of virus identity and host association using genomics technology. <i>Biodiversity Science</i> , 2020, 28, 587-595.	0.2	0
33	First mitochondrial genomes of five hoverfly species of the genus <i>Eristalinus</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.9	11
34	Genome-skimming provides accurate quantification for pollen mixtures. <i>Molecular Ecology Resources</i> , 2019, 19, 1433-1446.	2.2	31
35	Phylogenomics reveals the evolutionary timing and pattern of butterflies and moths. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22657-22663.	3.3	291
36	Alterations of the Gut Microbiota in Multiple System Atrophy Patients. <i>Frontiers in Neuroscience</i> , 2019, 13, 1102.	1.4	42

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37	Patterns and Constraints in the Evolution of Sperm Individualization Genes in Insects, with an Emphasis on Beetles. <i>Genes</i> , 2019, 10, 776.	1.0	1
38	Old World and New World Phasmatodea: Phylogenomics Resolve the Evolutionary History of Stick and Leaf Insects. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	80
39	Genomic signatures accompanying the dietary shift to phytophagy in polyphagan beetles. <i>Genome Biology</i> , 2019, 20, 98.	3.8	27
40	Trends in DNA barcoding and metabarcoding. <i>Genome</i> , 2019, 62, v-viii.	0.9	21
41	Phylogenomic analysis of Calyptratae: resolving the phylogenetic relationships within a major radiation of Diptera. <i>Cladistics</i> , 2019, 35, 605-622.	1.5	51
42	Phylogenomics of the superfamily Dytiscoidea (Coleoptera: Adephaga) with an evaluation of phylogenetic conflict and systematic error. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 270-285.	1.2	36
43	An integrative phylogenomic approach illuminates the evolutionary history of cockroaches and termites (Blattodea). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182076.	1.2	143
44	The evolution and genomic basis of beetle diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24729-24737.	3.3	372
45	Re-assessing the diversity of negative strand RNA viruses in insects. <i>PLoS Pathogens</i> , 2019, 15, e1008224.	2.1	101
46	Polymorphisms in DNA methylation-related genes are linked to the phenotype of Machado-Joseph disease. <i>Neurobiology of Aging</i> , 2019, 75, 225.e1-225.e8.	1.5	5
47	Phylogenomics from low-coverage whole-genome sequencing. <i>Methods in Ecology and Evolution</i> , 2019, 10, 507-517.	2.2	59
48	Evolutionary history of Polyneoptera and its implications for our understanding of early winged insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3024-3029.	3.3	150
49	Understanding biodiversity using genomics: Hooke's microscope in the era of big data. <i>Biodiversity Science</i> , 2019, 27, 475-479.	0.2	1
50	A new perspective on landscape impact in bee populations: Considering the bee gut microbiome. <i>Biodiversity Science</i> , 2019, 27, 516-525.	0.2	0
51	New data, same story: phylogenomics does not support Syrphoidea (Diptera: Syrphidae, Pipunculidae). <i>Systematic Entomology</i> , 2018, 43, 447-459.	1.7	53
52	Performance of amplicon and shotgun sequencing for accurate biomass estimation in invertebrate community samples. <i>Molecular Ecology Resources</i> , 2018, 18, 1020-1034.	2.2	104
53	Analysis of TCR β and TCR γ genes in Chinese alligator provides insights into the evolution of TCR genes in jawed vertebrates. <i>Developmental and Comparative Immunology</i> , 2018, 85, 31-43.	1.0	10
54	Updated frequency analysis of spinocerebellar ataxia in China. <i>Brain</i> , 2018, 141, e22-e22.	3.7	33

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55	Characterization of viral RNA splicing using whole-transcriptome datasets from host species. <i>Scientific Reports</i> , 2018, 8, 3273.	1.6	10
56	Association of <i>TNF-α</i> rs1799964 and <i>IL-1β</i> rs16944 polymorphisms with multiple system atrophy in Chinese Han population. <i>International Journal of Neuroscience</i> , 2018, 128, 761-764.	0.8	16
57	A phylogenomic analysis of lichen-feeding tiger moths uncovers evolutionary origins of host chemical sequestration. <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 23-34.	1.2	17
58	Epithelial Hes1 maintains gut homeostasis by preventing microbial dysbiosis. <i>Mucosal Immunology</i> , 2018, 11, 716-726.	2.7	35
59	Transcriptome sequence-based phylogeny of chalcidoid wasps (Hymenoptera: Chalcidoidea) reveals a history of rapid radiations, convergence, and evolutionary success. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 286-296.	1.2	83
60	Identifying SYNE1 Ataxia With Novel Mutations in a Chinese Population. <i>Frontiers in Neurology</i> , 2018, 9, 1111.	1.1	14
61	Phylogenomics and the evolution of hemipteroid insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12775-12780.	3.3	275
62	The genome of an underwater architect, the caddisfly <i>Stenopsyche tienmushanensis</i> Hwang (Insecta: Trichoptera). <i>GigaScience</i> , 2018, 7, .	3.3	41
63	Cerebellar lncRNA Expression Profile Analysis of SCA3/MJD Mice. <i>International Journal of Genomics</i> , 2018, 2018, 1-6.	0.8	5
64	Investigation on modulation of DNA repair pathways in Chinese MJD patients. <i>Neurobiology of Aging</i> , 2018, 71, 267.e5-267.e6.	1.5	5
65	Functional characterization of the <i>Hyles euphorbiae</i> hawkmoth transcriptome reveals strong expression of phorbol ester detoxification and seasonal cold hardiness genes. <i>Frontiers in Zoology</i> , 2018, 15, 20.	0.9	13
66	Anchored phylogenomics unravels the evolution of spider flies (Diptera, Acroceridae) and reveals discordance between nucleotides and amino acids. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 233-245.	1.2	35
67	Qualitative and quantitative molecular construction of plant-pollinator network: Application and prospective. <i>Biodiversity Science</i> , 2018, 26, 445-456.	0.2	3
68	Alteration of methylation status in the ATXN3 gene promoter region is linked to the SCA3/MJD. <i>Neurobiology of Aging</i> , 2017, 53, 192.e5-192.e10.	1.5	18
69	Advancing genomics through the Global Invertebrate Genomics Alliance (GIGA). <i>Invertebrate Systematics</i> , 2017, 31, 1.	0.5	22
70	Evolutionary History of the Hymenoptera. <i>Current Biology</i> , 2017, 27, 1013-1018.	1.8	611
71	Transcriptome and target DNA enrichment sequence data provide new insights into the phylogeny of vespid wasps (Hymenoptera: Aculeata: Vespidae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 213-226.	1.2	87
72	Positive and relaxed selection associated with flight evolution and loss in insect transcriptomes. <i>GigaScience</i> , 2017, 6, 1-14.	3.3	40

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73	Orthograph: a versatile tool for mapping coding nucleotide sequences to clusters of orthologous genes. <i>BMC Bioinformatics</i> , 2017, 18, 111.	1.2	146
74	Filling reference gaps via assembling DNA barcodes using high-throughput sequencing—moving toward barcoding the world. <i>GigaScience</i> , 2017, 6, 1-8.	3.3	18
75	The molecular evolutionary dynamics of oxidative phosphorylation (OXPHOS) genes in Hymenoptera. <i>BMC Evolutionary Biology</i> , 2017, 17, 269.	3.2	40
76	Earth BioGenome Project and Taxonomy. <i>Biodiversity Science</i> , 2017, 25, 1251-1254.	0.2	0
77	Effectiveness of physical, psychological, social, and spiritual intervention in breast cancer survivors: An integrative review. <i>Asia-Pacific Journal of Oncology Nursing</i> , 2016, 3, 226-232.	0.7	30
78	Networking Our Way to Better Ecosystem Service Provision. <i>Trends in Ecology and Evolution</i> , 2016, 31, 105-115.	4.2	72
79	The Trichoptera barcode initiative: a strategy for generating a species-level Tree of Life. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20160025.	1.8	62
80	<i>ATXN2</i> polymorphism modulates age at onset in Machado-Joseph disease. <i>Brain</i> , 2016, 139, aww176.	3.7	16
81	Horizontal Gene Transfer of Pectinases from Bacteria Preceded the Diversification of Stick and Leaf Insects. <i>Scientific Reports</i> , 2016, 6, 26388.	1.6	78
82	Transcriptomic data from panarthropods shed new light on the evolution of insulator binding proteins in insects. <i>BMC Genomics</i> , 2016, 17, 861.	1.2	23
83	The Global Genome Biodiversity Network (GGBN) Data Standard specification. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw125.	1.4	55
84	Evolution of neuropeptides in non-apterygote hexapods. <i>BMC Evolutionary Biology</i> , 2016, 16, 51.	3.2	63
85	Mitochondrial metagenomics: letting the genes out of the bottle. <i>GigaScience</i> , 2016, 5, 15.	3.3	103
86	Molecular phylogeny of the highly disjunct cliff water beetles from South Africa and China (Coleoptera: Aspidytidae). <i>Zoological Journal of the Linnean Society</i> , 2016, 176, 537-546.	1.0	19
87	The complete mitochondrial genome of the pumpkin fruit fly, <i>Bactrocera tau</i> (Diptera: Tephritidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2502-2503.	0.7	15
88	Mitochondrial capture enriches mitochondrial DNA 100 fold, enabling PCR-free mitogenomics biodiversity analysis. <i>Molecular Ecology Resources</i> , 2016, 16, 470-479.	2.2	74
89	The mitochondrial genome of the winter stonefly <i>Apteroperla tikumana</i> (Plecoptera, Capniidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3030-3032.	0.7	9
90	Mitochondrial genome of <i>Hylaeus dilatatus</i> (Hymenoptera: Colletidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3975-3976.	0.7	9

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91	Phylogenetic Origin and Diversification of RNAi Pathway Genes in Insects. <i>Genome Biology and Evolution</i> , 2016, 8, evw281.	1.1	92
92	Progress on the phylogeny of caddisflies (Trichoptera). <i>Zoosymposia</i> , 2016, 10, 248-256.	0.3	17
93	Using DNA barcode data to add leaves to the Trichoptera tree of life. <i>Zoosymposia</i> , 2016, 10, 193-199.	0.3	4
94	High-throughput monitoring of wild bee diversity and abundance via mitogenomics. <i>Methods in Ecology and Evolution</i> , 2015, 6, 1034-1043.	2.2	119
95	Response to Comment on "Phylogenomics resolves the timing and pattern of insect evolution". <i>Science</i> , 2015, 349, 487-487.	6.0	17
96	Mitochondrial phylogenomics and genetic relationships of closely related pine moth (Lasiocampidae:). <i>Tj ETQq0 0 0,rgBT /Overlock 10 Tf</i>	1.2	53
97	Identification and distribution of SIFamide in the nervous system of the desert locust <i>Schistocerca gregaria</i>. <i>Journal of Comparative Neurology</i> , 2015, 523, 108-125.	0.9	28
98	Challenges in the early detection and intervention of the psychosis-risk syndrome. <i>Shanghai Archives of Psychiatry</i> , 2015, 27, 45-7.	0.7	0
99	Genomes of the rice pest brown planthopper and its endosymbionts reveal complex complementary contributions for host adaptation. <i>Genome Biology</i> , 2014, 15, 521.	3.8	404
100	Adaptations to a Subterranean Environment and Longevity Revealed by the Analysis of Mole Rat Genomes. <i>Cell Reports</i> , 2014, 8, 1354-1364.	2.9	162
101	The Global Invertebrate Genomics Alliance (GIGA): Developing Community Resources to Study Diverse Invertebrate Genomes. <i>Journal of Heredity</i> , 2014, 105, 1-18.	1.0	96
102	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014, 346, 763-767.	6.0	2,096
103	Multiplex sequencing of pooled mitochondrial genomes "a crucial step toward biodiversity analysis using mito-metagenomics. <i>Nucleic Acids Research</i> , 2014, 42, e166-e166.	6.5	230
104	SOAPdenovo-Trans: <i>de novo</i> transcriptome assembly with short RNA-Seq reads. <i>Bioinformatics</i> , 2014, 30, 1660-1666.	1.8	826
105	Genome-wide adaptive complexes to underground stresses in blind mole rats <i>Spalax</i> . <i>Nature Communications</i> , 2014, 5, 3966.	5.8	124
106	Omics-based interpretation of synergism in a soil-derived cellulose-degrading microbial community. <i>Scientific Reports</i> , 2014, 4, 5288.	1.6	39
107	Ultra-deep sequencing enables high-fidelity recovery of biodiversity for bulk arthropod samples without PCR amplification. <i>GigaScience</i> , 2013, 2, 4.	3.3	227
108	DNA barcoding facilitates associations and diagnoses for Trichoptera larvae of the Churchill (Manitoba, Canada) area. <i>BMC Ecology</i> , 2013, 13, 5.	3.0	54

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109	A heterozygous moth genome provides insights into herbivory and detoxification. <i>Nature Genetics</i> , 2013, 45, 220-225.	9.4	472
110	SOAP B barcode: revealing arthropod biodiversity through assembly of Illumina shotgun sequences of PCR amplicons. <i>Methods in Ecology and Evolution</i> , 2013, 4, 1142-1150.	2.2	45
111	The i5K Initiative: Advancing Arthropod Genomics for Knowledge, Human Health, Agriculture, and the Environment. <i>Journal of Heredity</i> , 2013, 104, 595-600.	1.0	358
112	The importance of biobanking in molecular taxonomy, with proposed definitions for vouchers in a molecular context. <i>ZooKeys</i> , 2013, 365, 67-70.	0.5	64
113	Suggestions for a molecular biodiversity assessment of South East Asian freshwater invertebrates. Lessons from the megadiverse beetles (Coleoptera). <i>Journal of Limnology</i> , 2013, 72, .	0.3	8
114	<i>Eupolybothrus cavernicolus</i> Komeri & Stoev sp. n. (Chilopoda: Lithobiomorpha: Lithobiidae): the first eukaryotic species description combining transcriptomic, DNA barcoding and micro-CT imaging data. <i>Biodiversity Data Journal</i> , 2013, 1, e1013.	0.4	46
115	Diversity of mitochondrial and larval morphology characters in the genus <i>Diplectronea</i> (Trichoptera: Tj ETQq1 1 0.784314 rgBT /Overl	0.8	4
116	A DNA Barcode Library for North American Ephemeroptera: Progress and Prospects. <i>PLoS ONE</i> , 2012, 7, e38063.	1.1	86
117	DNA barcodes reveal cryptic genetic diversity within the blackfly subgenus <i>Trichodagmia</i> Enderlein (Diptera: Simuliidae: Simulium) and related taxa in the New World. <i>Zootaxa</i> , 2012, 3514, 43.	0.2	40
118	Congruence of biodiversity measures among larval dragonflies and caddisflies from three Canadian rivers. <i>Freshwater Biology</i> , 2012, 57, 628-639.	1.2	14
119	<i>Wolbachia</i> and DNA Barcoding Insects: Patterns, Potential, and Problems. <i>PLoS ONE</i> , 2012, 7, e36514.	1.1	148
120	Building freshwater macroinvertebrate DNA-barcode libraries from reference collection material: formalin preservation vs specimen age. <i>Journal of the North American Benthological Society</i> , 2011, 30, 125-130.	3.0	35
121	DNA barcoding facilitates description of unknown faunas: a case study on Trichoptera in the headwaters of the Tigris River, Iraq. <i>Journal of the North American Benthological Society</i> , 2011, 30, 163-173.	3.0	18
122	Pyrosequencing for Mini-Barcoding of Fresh and Old Museum Specimens. <i>PLoS ONE</i> , 2011, 6, e21252.	1.1	66
123	Environmental Barcoding: A Next-Generation Sequencing Approach for Biomonitoring Applications Using River Benthos. <i>PLoS ONE</i> , 2011, 6, e17497.	1.1	459
124	Accelerated construction of a regional DNA-barcode reference library: caddisflies (Trichoptera) in the Great Smoky Mountains National Park. <i>Journal of the North American Benthological Society</i> , 2011, 30, 131-162.	3.0	58
125	DNA barcode data confirm new species and reveal cryptic diversity in Chilean <i>Smicridea</i> (<i>Smicridea</i>) (Trichoptera:Hydropsychidae). <i>Journal of the North American Benthological Society</i> , 2010, 29, 1058-1074.	3.0	72
126	Defining the genus <i>Hydropsyche</i> (Trichoptera:Hydropsychidae) based on DNA and morphological evidence. <i>Journal of the North American Benthological Society</i> , 2010, 29, 918-933.	3.0	27

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127	COI and ITS2 sequences delimit species, reveal cryptic taxa and host specificity of fig-associated <i>Sycophila</i> (Hymenoptera, Eurytomidae). <i>Molecular Ecology Resources</i> , 2010, 10, 31-40.	2.2	58
128	Ephemeroptera, Plecoptera, and Trichoptera fauna of Churchill (Manitoba, Canada): insights into biodiversity patterns from DNA barcoding. <i>Journal of the North American Benthological Society</i> , 2010, 29, 814-837.	3.0	95
129	Towards a comprehensive barcode library for arctic life - Ephemeroptera, Plecoptera, and Trichoptera of Churchill, Manitoba, Canada. <i>Frontiers in Zoology</i> , 2009, 6, 30.	0.9	112
130	The larvae of Chinese Hydropsychidae (Insecta: Trichoptera), Part I: <i>Arctopsyche shimianensis</i> , <i>Parapsyche</i> sp. A, and <i>Diplectrona obscura</i> . <i>Zootaxa</i> , 2009, 2174, 1-17.	0.2	9
131	Associating larvae and adults of Chinese Hydropsychidae caddisflies (Insecta:Trichoptera) using DNA sequences. <i>Journal of the North American Benthological Society</i> , 2007, 26, 719-742.	3.0	113