

Christopher M Austin

List of Publications by Year in descending order

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papers

2,718
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186265

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126
docs citations

126
times ranked

3066
citing authors

#	ARTICLE	IF	CITATIONS
1	More from less: Genome skimming for nuclear markers for animal phylogenomics, a case study using decapod crustaceans. <i>Journal of Crustacean Biology</i> , 2021, 41, .	0.8	7
2	The NGS Magic Pudding: A Nanopore-Led Long-Read Genome Assembly for the Commercial Australian Freshwater Crayfish, <i>Cherax destructor</i> . <i>Frontiers in Genetics</i> , 2021, 12, 695763.	2.3	1
3	Dataset for genome sequencing and de novo assembly of the Vietnamese bighead catfish (<i>Clarias</i>) Tj ETQq1 1 0.784314 rgBT ₅ /Overlo	1.0	5
4	A Giant Genome for a Giant Crayfish (<i>Cherax quadricarinatus</i>) With Insights Into <i>cox1</i> Pseudogenes in Decapod Genomes. <i>Frontiers in Genetics</i> , 2020, 11, 201.	2.3	23
5	Improved genomic resources for the black tiger prawn (<i>Penaeus monodon</i>). <i>Marine Genomics</i> , 2020, 52, 100751.	1.1	31
6	Dataset for sequencing and de novo assembly of the European endangered white-clawed crayfish (<i>Austropotamobius pallipes</i>) abdominal muscle transcriptome. <i>Data in Brief</i> , 2020, 29, 105166.	1.0	3
7	The <i>Pontastacus leptodactylus</i> (Astacidae) Repeatome Provides Insight Into Genome Evolution and Reveals Remarkable Diversity of Satellite DNA. <i>Frontiers in Genetics</i> , 2020, 11, 611745.	2.3	15
8	Genotypic characterization and genome comparison reveal insights into potential vaccine coverage and genealogy of <i>Neisseria meningitidis</i> in military camps in Vietnam. <i>PeerJ</i> , 2020, 8, e9502.	2.0	2
9	Comparative mitogenomics of the Decapoda reveals evolutionary heterogeneity in architecture and composition. <i>Scientific Reports</i> , 2019, 9, 10756.	3.3	57
10	Genomic characterization of <i>Vibrio parahaemolyticus</i> from Pacific white shrimp and rearing water in Malaysia reveals novel sequence types and structural variation in genomic regions containing the <i>Photorhabdus</i> insect-related (Pir) toxin-like genes. <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	6
11	Whole Genome Assembly of the Snout Otter Clam, <i>Lutraria rhynchaena</i> , Using Nanopore and Illumina Data, Benchmarked Against Bivalve Genome Assemblies. <i>Frontiers in Genetics</i> , 2019, 10, 1158.	2.3	16
12	Genomic evidence of neo-sex chromosomes in the eastern yellow robin. <i>GigaScience</i> , 2019, 8, .	6.4	35
13	Whole-genome sequencing and characterization of an antibiotic resistant <i>Neisseria meningitidis</i> B isolate from a military unit in Vietnam. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2019, 18, 16.	3.8	6
14	Absence of evidence is not evidence of absence: Nanopore sequencing and complete assembly of the European lobster (<i>Homarus gammarus</i>) mitogenome uncovers the missing <i>nad2</i> and a new major gene cluster duplication. <i>BMC Genomics</i> , 2019, 20, 335.	2.8	20
15	Two reads to rule them all: Nanopore long read-guided assembly of the iconic Christmas Island red crab, <i>Gecarcoidea natalis</i> (Pocock, 1888), mitochondrial genome and the challenges of AT-rich mitogenomes. <i>Marine Genomics</i> , 2019, 45, 64-71.	1.1	14
16	Best Foot Forward: Nanopore Long Reads, Hybrid Meta-Assembly, and Haplotig Purging Optimizes the First Genome Assembly for the Southern Hemisphere Blacklip Abalone (<i>Haliotis rubra</i>). <i>Frontiers in Genetics</i> , 2019, 10, 889.	2.3	25
17	Finding Nemo: hybrid assembly with Oxford Nanopore and Illumina reads greatly improves the clownfish (<i>Amphiprion ocellaris</i>) genome assembly. <i>GigaScience</i> , 2018, 7, 1-6.	6.4	90
18	More evolution underground: Accelerated mitochondrial substitution rate in Australian burrowing freshwater crayfishes (Decapoda: Parastacidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 88-98.	2.7	19

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19	Population mitogenomics provides insights into evolutionary history, source of invasions and diversifying selection in the House Crow (<i>Corvus splendens</i>). <i>Heredity</i> , 2018, 120, 296-309.	2.6	6
20	Microbiome analysis of Pacific white shrimp gut and rearing water from Malaysia and Vietnam: implications for aquaculture research and management. <i>PeerJ</i> , 2018, 6, e5826.	2.0	71
21	ORDER within the chaos: Insights into phylogenetic relationships within the Anomura (Crustacea: Tj ETQq1 1 0.784314 rgBT /Overlock and Evolution, 2018, 127, 320-331.	2.7	83
22	More limbs on the tree: mitogenome characterisation and systematic position of "living fossil" species <i>Neoglyphea inopinata</i> and <i>Laurentaeglyphea neocaledonica</i> (Decapoda : Glypheidea : Glypheidae). <i>Invertebrate Systematics</i> , 2018, 32, 448.	1.3	17
23	Transcriptome-Guided Identification of Carbohydrate Active Enzymes (CAZy) from the Christmas Island Red Crab, <i>Gecarcoidea natalis</i> and a Vote for the Inclusion of Transcriptome-Derived Crustacean CAZys in Comparative Studies. <i>Marine Biotechnology</i> , 2018, 20, 654-665.	2.4	21
24	Mitochondrial genomes and phylogenetic relationships of <i>Lates japonicus</i> , <i>Lates niloticus</i> , and <i>Psammoperca waigiensis</i> (Perciformes: Latidae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 73-75.	0.4	2
25	Rapid recovery of nuclear and mitochondrial genes by genome skimming from Northern Hemisphere freshwater crayfish. <i>Zoologica Scripta</i> , 2017, 46, 718-728.	1.7	40
26	Purifying selection and genetic drift shaped Pleistocene evolution of the mitochondrial genome in an endangered Australian freshwater fish. <i>Heredity</i> , 2017, 118, 466-476.	2.6	39
27	Signatures of polygenic adaptation associated with climate across the range of a threatened fish species with high genetic connectivity. <i>Molecular Ecology</i> , 2017, 26, 6253-6269.	3.9	34
28	De novo genome assembly and annotation of Australia's largest freshwater fish, the Murray cod (<i>Maccullochella peelii</i>), from Illumina and Nanopore sequencing read. <i>GigaScience</i> , 2017, 6, 1-6.	6.4	57
29	iDNA at Sea: Recovery of Whale Shark (<i>Rhincodon typus</i>) Mitochondrial DNA Sequences from the Whale Shark Copepod (<i>Pandarus rhincodonicus</i>) Confirms Global Population Structure. <i>Frontiers in Marine Science</i> , 2017, 4, .	2.5	20
30	Nanopore Long-Read Guided Complete Genome Assembly of <i>Hydrogenophaga intermedia</i> , and Genomic Insights into 4-Aminobenzenesulfonate, p-Aminobenzoic Acid and Hydrogen Metabolism in the Genus <i>Hydrogenophaga</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1880.	3.5	24
31	Digging deeper: new gene order rearrangements and distinct patterns of codons usage in mitochondrial genomes among shrimps from the Axiidea, Gebiidea and Caridea (Crustacea: Decapoda). <i>PeerJ</i> , 2017, 5, e2982.	2.0	43
32	The complete mitogenome of the river blackfish, <i>Gadopsis marmoratus</i> (Richardson, 1848) (Teleostei: Percichthyidae). <i>Mitochondrial DNA</i> , 2016, 27, 1-2.	0.6	1
33	The complete mitogenome of the soldier crab <i>Mictyris longicarpus</i> (Latreille, 1806) (Crustacea: Tj ETQq1 1 0.784314 rgBT /Overlock	0.6	3
34	The complete mitogenome of the red claw crayfish <i>Cherax quadricarinatus</i> (Von Martens, 1868) (Crustacea: Decapoda: Parastacidae). <i>Mitochondrial DNA</i> , 2016, 27, 385-386.	0.6	17
35	The complete mitochondrial genome of the invasive house crow <i>Corvus splendens</i> (Passeriformes: Tj ETQq1 1 0.784314 rgBT /Overlock	0.6	11
36	The complete mitogenome of the freshwater crayfish <i>Cherax cainii</i> (Crustacea: Decapoda: Tj ETQq0 0 0 rgBT /Overlock	0.6	10

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37	The complete mitogenome of the whale shark parasitic copepod <i>Pandarus rhincodonicus</i> norman, Newbound & Knott (Crustacea; Siphonostomatoida; Pandaridae) a new gene order for the copepoda. Mitochondrial DNA, 2016, 27, 694-695.	0.6	16
38	Social structure and landscape genetics of the endemic New Caledonian ant <i>Leptomymex pallens</i> Emery, 1883 (Hymenoptera: Formicidae: Dolichoderinae), in the context of fire-induced rainforest fragmentation. Conservation Genetics, 2016, 17, 931-947.	1.5	3
39	Genetic diversity of native and introduced populations of the invasive house crow (<i>Corvus splendens</i>) in Asia and Africa. Biological Invasions, 2016, 18, 1867-1881.	2.4	8
40	The complete mitogenome of the cow tail ray <i>Pastinachus atrus</i> (Macleay, 1883) (Elasmobranchii); Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.6	2
41	The complete mitogenome of the hermit crab <i>Clibanarius infraspinus</i> (Hilgendorf, 1869), (Crustacea; Decapoda; Diogenidae) a new gene order for the Decapoda. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4099-4100.	0.7	19
42	The complete mitogenome of the crayfish <i>Cherax glaber</i> (Crustacea: Decapoda: Parastacidae). Mitochondrial DNA, 2016, 27, 220-221.	0.6	7
43	The complete mitogenome of the endangered white-clawed freshwater crayfish <i>Austroptamobius pallipes</i> (Lereboullet, 1858) (Crustacea: Decapoda: Astacidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3329-3330.	0.7	5
44	The complete mitogenome of the giant clam <i>Tridacna squamosa</i> (Heterodonta: Bivalvia); Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 40	0.7	9
45	The complete mitogenome of the invasive spiny-cheek crayfish <i>Orconectes limosus</i> (Rafinesque,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 40 Analysis, 2016, 27, 3181-3183.	0.7	4
46	The complete mitogenome of the Norway lobster <i>Nephrops norvegicus</i> (Linnaeus, 1758) (Crustacea: Decapoda: Decapoda); Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3179-3180.	0.7	5
47	The complete mitochondrial genome of the bass yabby <i>Trypaea australiensis</i> Dana 1852, (Crustacea: Decapoda: Parastacidae); Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Mapping, Sequencing, and Analysis, 2016, 27, 3985-3986.	0.7	3
48	Pleistocene divergence across a mountain range and the influence of selection on mitogenome evolution in threatened Australian freshwater cod species. Heredity, 2016, 116, 506-515.	2.6	16
49	Characterisation of 12 microsatellite loci in the Vietnamese commercial clam <i>Lutraria rhynchaena</i> Jonas 1844 (Heterodonta: Bivalvia: Mactridae) through next-generation sequencing. Molecular Biology Reports, 2016, 43, 391-396.	2.3	7
50	The complete mitogenome of the Macquarie perch, <i>Macquaria australasica</i> Cuvier, 1830 (Teleostei); Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3983-3984.	0.6	4
51	The complete mitogenome of the porcelain crab <i>Petrolisthes haswelli</i> Miers, 1884 (Crustacea: Decapoda: Hippidae); Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 3983-3984.	0.7	6
52	The complete mitogenome of <i>Cherax monticola</i> (Crustacea: Decapoda: Parastacidae), a large highland crayfish from New Guinea.. Mitochondrial DNA, 2016, 27, 337-338.	0.6	15
53	The complete mitogenome of the Australian crayfish <i>Geocharax gracilis</i> Clark 1936 (Crustacea: Decapoda: Parastacidae); Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 3983-3984.	0.6	4
54	First comprehensive multi-tissue transcriptome of <i>Cherax quadricarinatus</i> (Decapoda: Parastacidae) reveals unexpected diversity of endogenous cellulase. Organisms Diversity and Evolution, 2016, 16, 185-200.	1.6	18

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55	The complete mitogenome of the marine bivalve <i>Lutraria rhynchaena</i> Jonas 1844 (Heterodonta: Bivalvia.) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 13	0.6	13
56	The complete mitogenome of the Australian spiny crayfish <i>Euastacus yarraensis</i> (McCoy, 1888) (Crustacea: Decapoda: Parastacidae). Mitochondrial DNA, 2016, 27, 929-930.	0.6	5
57	The complete mitogenome of the swimming crab <i>Thalamita crenata</i> (Rappell, 1830) (Crustacea; Decapoda;) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 5	0.6	5
58	The complete mitogenome of the moon crab <i>Ashtoret lunaris</i> (Forsk., 1775), (Crustacea; Decapoda;) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 5	0.6	5
59	The complete mitogenome of the stone crab <i>Myomenippe fornasinii</i> (Bianconi, 1851) (Crustacea:) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 2	0.6	2
60	The complete mitogenome of purple mottled shore crab <i>Cyclograpsus granulatus</i> H. Milne-Edwards, 1853 (Crustacea: Decapoda: Grapsoidea). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3981-3982.	0.7	8
61	The complete mitogenome of the endangered freshwater crayfish <i>Cherax tenuimanus</i> (Smith) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 1	0.7	1
62	The complete mitogenome of the Murray Cod, <i>Maccullochella peelii</i> (Mitchell, 1838) (Teleostei:) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 46	0.6	3
63	The complete mitogenome of the minute mudskipper, <i>Periophthalmus minutus</i> Eggert, 1935 (Perciformes: Gobiidae: Oxudercinae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4187-4188.	0.7	2
64	The complete mitogenome of the rock pool prawn <i>Palaemon serenus</i> (Heller, 1862) (Crustacea:) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 7	0.7	7
65	The complete mitogenome of the Australian freshwater shrimp <i>Paratya australiensis</i> Kemp, 1917 (Crustacea: Decapoda: Atyidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3157-3158.	0.7	2
66	The complete mitogenome of the New Zealand freshwater crayfish <i>Paraneohrops planifrons</i> White 1842 (Crustacea: Decapoda: Parastacidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3333-3334.	0.7	2
67	Mitochondrial genomes of the jungle crow <i>Corvus macrorhynchos</i> (Passeriformes: Corvidae) from shed feathers and a phylogenetic analysis of genus <i>Corvus</i> using mitochondrial protein-coding genes. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 2668-2670.	0.7	6
68	The complete mitogenome of the bluespotted ribbontail ray <i>Taeniura lymma</i> (Forssk., 1775) (Elasmobranchii: Myliobatiformes: Dasyatidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3205-3207.	0.7	1
69	The complete mitogenome of the Morton Bay bug <i>Thenus orientalis</i> (Lund, 1793) (Crustacea: Decapoda:) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 3	0.6	3
70	The complete mitogenome of the Australian land crayfish <i>Engaeus lyelli</i> (Clark 1936) (Crustacea:) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 5	0.6	5
71	MitoPhAST, a new automated mitogenomic phylogeny tool in the post-genomic era with a case study of 89 decapod mitogenomes including eight new freshwater crayfish mitogenomes. Molecular Phylogenetics and Evolution, 2015, 85, 180-188.	2.7	71
72	Whole Genome Sequencing of the Asian Arowana (<i>Scleropages formosus</i>) Provides Insights into the Evolution of Ray-Finned Fishes. Genome Biology and Evolution, 2015, 7, 2885-2895.	2.5	43

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73	Genome sequencing and annotation of <i>Aeromonas</i> sp. HZM. <i>Genomics Data</i> , 2015, 5, 38-39.	1.3	3
74	Genome sequencing and annotation of <i>Cellulomonas</i> sp. HZM. <i>Genomics Data</i> , 2015, 5, 40-41.	1.3	0
75	The complete mitogenome of the ghost crab <i>Ocyropsis ceratophthalmus</i> (Pallas, 1772) (Crustacea: Decapoda). <i>Genomics Data</i> , 2015, 5, 42-43.	0.6	5
76	Draft Genome Sequence of <i>Clostridium perfringens</i> Strain JJC, a Highly Efficient Hydrogen Producer Isolated from Landfill Leachate Sludge. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
77	Draft Genome Sequence of <i>Clostridium bifermentans</i> Strain WYM, a Promising Biohydrogen Producer Isolated from Landfill Leachate Sludge. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
78	Draft Genome Sequence of <i>Clostridium</i> sp. Strain Ade.TY, a New Biohydrogen- and Biochemical-Producing Bacterium Isolated from Landfill Leachate Sludge. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
79	Restricted movements of juvenile rays in the lagoon of Ningaloo Reef, Western Australia – evidence for the existence of a nursery. <i>Environmental Biology of Fishes</i> , 2014, 97, 371-383.	1.0	32
80	Integrated shotgun sequencing and bioinformatics pipeline allows ultra-fast mitogenome recovery and confirms substantial gene rearrangements in Australian freshwater crayfishes. <i>BMC Evolutionary Biology</i> , 2014, 14, 19.	3.2	94
81	Land cover and land use change related to shrimp farming in coastal areas of Quang Ninh, Vietnam using remotely sensed data. <i>Environmental Earth Sciences</i> , 2014, 72, 441-455.	2.7	27
82	The complete mitogenome of the Australian tadpole shrimp <i>Triops australiensis</i> (Spencer & Hall, 1895) (Crustacea: Branchiopoda: Notostraca). <i>Mitochondrial DNA</i> , 2014, 27, 1-2.	0.6	4
83	Two new species of <i>Eimeria</i> (Apicomplexa, Eimeriidae) from tree skinks, <i>Prasinohaema</i> spp. (Sauria). <i>Genomics Data</i> , 2015, 5, 44-45.	1.1	3
84	Assessment and monitoring of nutrient loading in the sediments of tidal creeks receiving shrimp farm effluent in Quang Ninh, Vietnam. <i>Environmental Monitoring and Assessment</i> , 2013, 185, 8715-8731.	2.7	13
85	Identification of Rays through DNA Barcoding: An Application for Ecologists. <i>PLoS ONE</i> , 2012, 7, e36479.	2.5	62
86	Why life history information matters: drought refuges and macroinvertebrate persistence in non-perennial streams subject to a drier climate. <i>Marine and Freshwater Research</i> , 2011, 62, 801.	1.3	120
87	Analysis of mitochondrial DNA clarifies the taxonomy and distribution of the Australian snubfin dolphin (<i>Orcaella heinsohni</i>) in northern Australian waters. <i>Marine and Freshwater Research</i> , 2011, 62, 1303.	1.3	6
88	Evolution underground: A molecular phylogenetic investigation of Australian burrowing freshwater crayfish (Decapoda: Parastacidae) with particular focus on <i>Engaeus</i> Erichson. <i>Molecular Phylogenetics and Evolution</i> , 2009, 50, 580-598.	2.7	38
89	Contrasting genetic structuring between colonies of the World's smallest penguin, <i>Eudyptula minor</i> (Aves: Spheniscidae). <i>Conservation Genetics</i> , 2008, 9, 893-905.	1.5	23
90	Sea-level changes and palaeo-ranges: reconstruction of ancient shorelines and river drainages and the phylogeography of the Australian land crayfish <i>Engaeus sericatus</i> Clark (Decapoda). <i>Genomics Data</i> , 2015, 5, 46-47.	0.0	56

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91	Detection of QTL for growth rate in the blacklip abalone (<i>Haliotis rubra</i> Leach) using selective DNA pooling. <i>Animal Genetics</i> , 2008, 39, 606-614.	1.7	19
92	Fossil evidence in Australia for oldest known freshwater crayfish of Gondwana. <i>Gondwana Research</i> , 2008, 14, 287-296.	6.0	46
93	Cryptic diversity in <i>Engaeus</i> Erichson, <i>Geocharax</i> Clark and <i>Gramastacus</i> Riek (Decapoda : Parastacidae) revealed by mitochondrial 16S rDNA sequences. <i>Invertebrate Systematics</i> , 2007, 21, 569.	1.3	26
94	Phylogenetic evaluation of subfamily classification of the Cyprinidae focusing on Vietnamese species. <i>Aquatic Living Resources</i> , 2007, 20, 143-153.	1.2	23
95	Genetic diversity of common carp (<i>Cyprinus carpio</i> L.) in Vietnam using four microsatellite loci. <i>Aquaculture</i> , 2007, 269, 174-186.	3.5	30
96	Genetic diversity of common carp in Vietnam using direct sequencing and SSCP analysis of the mitochondrial DNA control region. <i>Aquaculture</i> , 2006, 258, 228-240.	3.5	21
97	The molecular systematics of <i>Leiopotherapon unicolor</i> (Günther, 1859): testing for cryptic speciation in Australia's most widespread freshwater fish. <i>Biological Journal of the Linnean Society</i> , 2006, 87, 537-552.	1.6	24
98	Isolation and characterization of 125 microsatellite DNA markers in the blacklip abalone, <i>Haliotis rubra</i> . <i>Molecular Ecology Notes</i> , 2006, 6, 740-746.	1.7	16
99	A microsatellite linkage map of the blacklip abalone, <i>Haliotis rubra</i> . <i>Animal Genetics</i> , 2006, 37, 563-570.	1.7	35
100	The complete mitochondrial genome of the mantid shrimp <i>Harpisquilla harpax</i> , and a phylogenetic investigation of the Decapoda using mitochondrial sequences. <i>Molecular Phylogenetics and Evolution</i> , 2006, 38, 565-574.	2.7	39
101	Phylogeny of the Australian freshwater crayfish <i>Cherax destructor</i> -complex (Decapoda : Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 3	1.8	7
102	Phylogenetic relationships of the globally distributed freshwater prawn genus <i>Macrobrachium</i> (Crustacea: Decapoda: Palaemonidae): biogeography, taxonomy and the convergent evolution of abbreviated larval development. <i>Zoologica Scripta</i> , 2005, 34, 187-197.	1.7	133
103	Using mitochondrial nucleotide sequences to investigate diversity and genealogical relationships within common carp (<i>Cyprinus carpio</i> L.). <i>Animal Genetics</i> , 2005, 36, 23-28.	1.7	36
104	Biodegradation of Pyrene and Phenanthrene in Soil Using Immobilized Fungi <i>Fusarium</i> sp.. <i>Bulletin of Environmental Contamination and Toxicology</i> , 2005, 75, 443-450.	2.7	17
105	Complete Mitochondrial DNA Sequences of the Decapod Crustaceans <i>Pseudocarcinus gigas</i> (Menippidae) and <i>Macrobrachium rosenbergii</i> (Palaemonidae). <i>Marine Biotechnology</i> , 2005, 7, 339-349.	2.4	81
106	Degradation of Phenanthrene and Pyrene in Soil Slurry Reactors with Immobilized Bacteria <i>Zoogloeasp.</i> . <i>Environmental Engineering Science</i> , 2005, 22, 390-399.	1.6	30
107	Population genetic studies on the Australian freshwater crayfish, <i>Cherax destructor</i> (Crustacea:) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 3	1.2	13
108	Complete Mitochondrial DNA Sequences of the Decapod Crustaceans <i>Pseudocarcinus gigas</i> (Menippidae) and <i>Macrobrachium rosenbergii</i> (Palaemonidae). <i>Marine Biotechnology</i> , 2005, 7, 339.	2.4	6

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109	Multiple origins of the endemic Australian Macrobrachium (Decapoda : Palaemonidae) based on 16S rRNA mitochondrial sequences. Australian Journal of Zoology, 2004, 52, 549.	1.0	29
110	Phylogeography of the widespread Australian freshwater prawn, Macrobrachium australiense (Decapoda, Palaemonidae). Journal of Biogeography, 2004, 31, 1065-1072.	3.0	31
111	Inheritance of molecular markers and sex in the Australian freshwater crayfish, Cherax destructor Clark. Aquaculture Research, 2004, 35, 1328-1338.	1.8	11
112	Phylogeography of the freshwater crayfish Cherax destructor Clark (Parastacidae) in inland Australia: historical fragmentation and recent range expansion. Biological Journal of the Linnean Society, 2004, 83, 539-550.	1.6	45
113	Complete mitochondrial DNA sequence of the Australian freshwater crayfish, Cherax destructor (Crustacea: Decapoda: Parastacidae): a novel gene order revealed. Gene, 2004, 331, 65-72.	2.2	86
114	Re-examination of the taxonomy of the Macrobrachium australiense Holthuis (Decapoda : Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 547 Td 18, 227.	1.3	11
115	Mitochondrial 12S rRNA sequences support the existence of a third species of freshwater blackfish (Percichthyidae: Gadopsis) from south-eastern Australia. Memoirs of Museum Victoria, 2004, 61, 121-127.	0.6	18
116	MOLECULAR TAXONOMY AND PHYLOGENETICS OF SOME SPECIES OF AUSTRALIAN PALAEMONID SHRIMPS. Journal of Crustacean Biology, 2003, 23, 169-177.	0.8	19
117	Molecular Taxonomy and Phylogenetics of Some Species of Australian Palaemonid Shrimps. Journal of Crustacean Biology, 2003, 23, 169-177.	0.8	29
118	A preliminary study of primary sex ratios in the freshwater crayfish, Cherax destructor Clark. Aquaculture, 1999, 174, 43-50.	3.5	15
119	Phylogenetic relationships among the Australian and New Zealand genera of freshwater crayfishes (Decapoda : Parastacidae). Australian Journal of Zoology, 1999, 47, 199.	1.0	96
120	A Comparison of Natural and Artificial Diets for Juveniles of the Australian Freshwater Crayfish Cherax destructor. Journal of the World Aquaculture Society, 1998, 29, 243-248.	2.4	24
121	Nanopore long reads enable the first complete genome assembly of a Malaysian Vibrio parahaemolyticus isolate bearing the pVa plasmid associated with acute hepatopancreatic necrosis disease. F1000Research, 0, 8, 2108.	1.6	2