

Kyall R Zenger

List of Publications by Year in descending order

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Version: 2024-02-01

99
papers

3,856
citations

182225

30
h-index

162838

57
g-index

104
all docs

104
docs citations

104
times ranked

5439
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicted strong genetic gains from the application of genomic selection to improve growth related traits in barramundi (<i>Lates calcarifer</i>). <i>Aquaculture</i> , 2022, 549, 737761.	1.7	8
2	Genetic approaches for increasing fitness in endangered species. <i>Trends in Ecology and Evolution</i> , 2022, 37, 332-345.	4.2	14
3	Genome assembly of the Australian black tiger shrimp (<i>Penaeus monodon</i>) reveals a novel fragmented IHHNV EVE sequence. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	9
4	Non-invasive DNA collection for parentage analysis for bivalves: A case study from the silver-lipped pearl oyster (<i>Pinctada maxima</i>). <i>Aquaculture</i> , 2022, 552, 738036.	1.7	1
5	The interplay of fungal and bacterial microbiomes on rainforest frogs following a disease outbreak. <i>Ecosphere</i> , 2022, 13, .	1.0	4
6	The GIFT that keeps on giving? A genetic audit of the Fijian Genetically Improved Farmed Tilapia (GIFT) broodstock nucleus 20 years after introduction. <i>Aquaculture</i> , 2021, 537, 736524.	1.7	5
7	Population Structure, Genetic Connectivity, and Signatures of Local Adaptation of the Giant Black Tiger Shrimp (<i>Penaeus monodon</i>) throughout the Indo-Pacific Region. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	4
8	Fine-scale population structure and evidence for local adaptation in Australian giant black tiger shrimp (<i>Penaeus monodon</i>) using SNP analysis. <i>BMC Genomics</i> , 2020, 21, 669.	1.2	14
9	The identification of a major sex QTL in the white-leg shrimp, <i>Litopenaeus vannamei</i> . <i>Aquaculture</i> , 2020, 529, 735673.	1.7	6
10	Development and validation of a RAD-Seq target-capture based genotyping assay for routine application in advanced black tiger shrimp (<i>Penaeus monodon</i>) breeding programs. <i>BMC Genomics</i> , 2020, 21, 541.	1.2	17
11	Comparing Genomic Signatures of Selection Between the Abbassa Strain and Eight Wild Populations of Nile Tilapia (<i>Oreochromis niloticus</i>) in Egypt. <i>Frontiers in Genetics</i> , 2020, 11, 567969.	1.1	8
12	Infection dynamics, dispersal, and adaptation: understanding the lack of recovery in a remnant frog population following a disease outbreak. <i>Heredity</i> , 2020, 125, 110-123.	1.2	9
13	Pipette and paper: Combining molecular and genealogical methods to assess a Nile tilapia (<i>Oreochromis niloticus</i>) breeding program. <i>Aquaculture</i> , 2020, 523, 735171.	1.7	4
14	Microbiome diversity and composition varies across body areas in a freshwater turtle. <i>Microbiology (United Kingdom)</i> , 2020, 166, 440-452.	0.7	15
15	microDecon: A highly accurate read subtraction tool for the post-sequencing removal of contamination in metabarcoding studies. <i>Environmental DNA</i> , 2019, 1, 14-25.	3.1	115
16	The return of the frogs: The importance of habitat refugia in maintaining diversity during a disease outbreak. <i>Molecular Ecology</i> , 2019, 28, 2731-2745.	2.0	8
17	Dwarf minke whales from the South Pacific share a matrilineal lineage distinct from <i>Balaenoptera acutorostrata acutorostrata</i> and <i>B. a. scammoni</i> . <i>Australian Mammalogy</i> , 2019, 41, 231.	0.7	2
18	Considerations for Maintaining Family Diversity in Commercially Mass-Spawned Penaeid Shrimp: A Case Study on <i>Penaeus monodon</i> . <i>Frontiers in Genetics</i> , 2019, 10, 1127.	1.1	10

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19	The Future of Aquatic Protein: Implications for Protein Sources in Aquaculture Diets. <i>One Earth</i> , 2019, 1, 316-329.	3.6	433
20	Using Image Processing to Automatically Measure Pearl Oyster Size for Selective Breeding. , 2019, , .		5
21	Methods for normalizing microbiome data: An ecological perspective. <i>Methods in Ecology and Evolution</i> , 2019, 10, 389-400.	2.2	225
22	The evolution and origin of tetrodotoxin acquisition in the blue-ringed octopus (genus) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 Td (Ha</i>	1.9	18
23	Genomic comparisons reveal biogeographic and anthropogenic impacts in the koala (<i>Phascolarctos</i>) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 622 Td (Ha</i> 122, 525-544.	1.2	29
24	Genome-wide comparisons reveal evidence for a species complex in the black-lip pearl oyster <i>Pinctada margaritifera</i> (Bivalvia: Pteriidae). <i>Scientific Reports</i> , 2018, 8, 191.	1.6	7
25	Genome-wide comparisons reveal a clinal species pattern within a holobenthic octopodâ€”the Australian Southern blue-ringed octopus, <i>Hapalochlaena maculosa</i> (Cephalopoda: Octopodidae) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 622 Td (Ha</i>	1.2	29
26	Rapid and comprehensive discovery of unreported shellfish allergens using large-scale transcriptomic and proteomic resources. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 1501-1504.e8.	1.5	42
27	Mating behaviour and postcopulatory fertilization patterns in the southern blue-ringed octopus, <i>Hapalochlaena maculosa</i> . <i>Animal Behaviour</i> , 2018, 136, 41-51.	0.8	13
28	Genome-wide SNP analyses reveal high gene flow and signatures of local adaptation among the scalloped spiny lobster (<i>Panulirus homarus</i>) along the Omani coastline. <i>BMC Genomics</i> , 2018, 19, 690.	1.2	22
29	Sex-specific <i>dmrt1</i> and <i>cyp19a1</i> methylation and alternative splicing in gonads of the protandrous hermaphrodite <i>barramundi</i> . <i>PLoS ONE</i> , 2018, 13, e0204182.	1.1	48
30	De novo assembly, characterization, functional annotation and expression patterns of the black tiger shrimp (<i>Penaeus monodon</i>) transcriptome. <i>Scientific Reports</i> , 2018, 8, 13553.	1.6	48
31	The State of Omics Research for Farmed Penaeids: Advances in Research and Impediments to Industry Utilization. <i>Frontiers in Genetics</i> , 2018, 9, 282.	1.1	22
32	Gene flow and genetic structure in Nile perch, <i>Lates niloticus</i> , from African freshwater rivers and lakes. <i>PLoS ONE</i> , 2018, 13, e0200001.	1.1	10
33	Genomic Selection in Aquaculture: Application, Limitations and Opportunities With Special Reference to Marine Shrimp and Pearl Oysters. <i>Frontiers in Genetics</i> , 2018, 9, 693.	1.1	149
34	Effects of emerging infectious diseases on host population genetics: a review. <i>Conservation Genetics</i> , 2017, 18, 1235-1245.	0.8	39
35	Morphological changes and regulation of the genes <i>dmrt1</i> and <i>cyp11b</i> during the sex differentiation of <i>barramundi</i> (<i>Lates calcarifer</i> Bloch). <i>Aquaculture</i> , 2017, 479, 75-84.	1.7	14
36	Chemical cues correlate with agonistic behaviour and female mate choice in the southern blue-ringed octopus, <i>Hapalochlaena maculosa</i> (Hoyle, 1883) (Cephalopoda: Octopodidae). <i>Journal of Molluscan Studies</i> , 2017, 83, 79-87.	0.4	17

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37	A comparative integrated gene-based linkage and locus ordering by linkage disequilibrium map for the Pacific white shrimp, <i>Litopenaeus vannamei</i> . <i>Scientific Reports</i> , 2017, 7, 10360.	1.6	55
38	Populations genetically rifted within a complex geological system: The case of strong structure and low genetic diversity in the migratory freshwater catfish, <i>Bagrus docmak</i> , in East Africa. <i>Ecology and Evolution</i> , 2017, 7, 6172-6187.	0.8	6
39	Fighting an uphill battle: the recovery of frogs in Australia's Wet Tropics. <i>Ecology</i> , 2017, 98, 3221-3223.	1.5	25
40	Swept away: ocean currents and seascape features influence genetic structure across the 18,000 Km Indo-Pacific distribution of a marine invertebrate, the black-lip pearl oyster <i>Pinctada margaritifera</i> . <i>BMC Genomics</i> , 2017, 18, 66.	1.2	50
41	Extensive genetic differentiation detected within a model marsupial, the tammar wallaby (<i>Notamacropus eugenii</i>). <i>PLoS ONE</i> , 2017, 12, e0172777.	1.1	6
42	Unravelling the effects of gene flow and selection in highly connected populations of the silver-lip pearl oyster (<i>Pinctada maxima</i>). <i>Marine Genomics</i> , 2016, 28, 99-106.	0.4	15
43	<sc>netview p</sc>: a network visualization tool to unravel complex population structure using genome-wide <sc>SNP</sc>s. <i>Molecular Ecology Resources</i> , 2016, 16, 216-227.	2.2	109
44	Genome-wide SNP loci reveal novel insights into koala (<i>Phascolarctos cinereus</i>) population variability across its range. <i>Conservation Genetics</i> , 2016, 17, 337-353.	0.8	50
45	Fishing for divergence in a sea of connectivity: The utility of ddRADseq genotyping in a marine invertebrate, the black-lip pearl oyster <i>Pinctada margaritifera</i> . <i>Marine Genomics</i> , 2016, 25, 57-68.	0.4	46
46	A Parallel Population Genomic and Hydrodynamic Approach to Fishery Management of Highly-Dispersive Marine Invertebrates: The Case of the Fijian Black-Lip Pearl Oyster <i>Pinctada margaritifera</i> . <i>PLoS ONE</i> , 2016, 11, e0161390.	1.1	18
47	Whole-genome shotgun sequence assembly enables rapid gene characterization in the tropical fish barramundi, <i>Lates calcarifer</i> . <i>Animal Genetics</i> , 2015, 46, 468-469.	0.6	15
48	Phylogenetic Analysis of Nucleus-Encoded Acetyl-CoA Carboxylases Targeted at the Cytosol and Plastid of Algae. <i>PLoS ONE</i> , 2015, 10, e0131099.	1.1	9
49	Nocturnal mating behaviour and dynamic male investment of copulation time in the southern blue-ringed octopus, <i>Hapalochlaena maculosa</i> (Cephalopoda: Octopodidae). <i>Behaviour</i> , 2015, 152, 1883-1910.	0.4	14
50	Development of genome-wide microsatellite genetic resources in a commercially important African freshwater fish species - the Nile perch, <i>Lates niloticus</i> . <i>Animal Genetics</i> , 2015, 46, 340-340.	0.6	4
51	Determining genetic contributions to host oyster shell growth: Quantitative trait loci and genetic association analysis for the silver-lipped pearl oyster, <i>Pinctada maxima</i> . <i>Aquaculture</i> , 2014, 434, 367-375.	1.7	20
52	The effect of nitrogen limitation on acetyl-CoA carboxylase expression and fatty acid content in <i>Chromera velia</i> and <i>Isochrysis aff. galbana</i> (TISO). <i>Gene</i> , 2014, 543, 204-211.	1.0	22
53	Quantitative trait loci and genetic association analysis reveals insights into complex pearl quality traits in donor silver-lipped pearl oysters. <i>Aquaculture</i> , 2014, 434, 476-485.	1.7	14
54	Effects of growth phase and nitrogen starvation on expression of fatty acid desaturases and fatty acid composition of <i>Isochrysis aff. galbana</i> (TISO). <i>Gene</i> , 2014, 545, 36-44.	1.0	24

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55	Genome-Wide SNP Validation and Mantle Tissue Transcriptome Analysis in the Silver-Lipped Pearl Oyster, <i>Pinctada maxima</i> . <i>Marine Biotechnology</i> , 2013, 15, 647-658.	1.1	28
56	A high-density SNP genetic linkage map for the silver-lipped pearl oyster, <i>Pinctada maxima</i> : a valuable resource for gene localisation and marker-assisted selection. <i>BMC Genomics</i> , 2013, 14, 810.	1.2	56
57	Next-generation transcriptome profiling reveals insights into genetic factors contributing to growth differences and temperature adaptation in Australian populations of barramundi (<i>Lates Tj ETQq1 1 0.784304 rgBT / Overlock 10</i>)	0.4	10
58	Paternally inherited genetic markers reveal new insights into genetic structuring within <i>Macropus fuliginosus</i> and hybridisation with sympatric <i>Macropus giganteus</i> . <i>Australian Journal of Zoology</i> , 2013, 61, 58.	0.6	5
59	Genetic analysis reveals a distinct and highly diverse koala (<i>Phascolarctos cinereus</i>) population in South Gippsland, Victoria, Australia. <i>Australian Mammalogy</i> , 2012, 34, 68.	0.7	16
60	Transcriptome analysis of biomineralisation-related genes within the pearl sac: Host and donor oyster contribution. <i>Marine Genomics</i> , 2012, 5, 27-33.	0.4	57
61	Loss of genetic diversity in an outbreeding species: small population effects in the African wild dog (<i>Lycaon pictus</i>). <i>Conservation Genetics</i> , 2012, 13, 767-777.	0.8	15
62	Impact of Pleistocene aridity oscillations on the population history of a widespread, vagile Australian mammal, <i>Macropus fuliginosus</i> . <i>Journal of Biogeography</i> , 2012, 39, 1545-1563.	1.4	33
63	In silico whole-genome EST analysis reveals 2322 novel microsatellites for the silver-lipped pearl oyster, <i>Pinctada maxima</i> . <i>Marine Genomics</i> , 2011, 4, 287-290.	0.4	11
64	Genome sequence of an Australian kangaroo, <i>Macropus eugenii</i> , provides insight into the evolution of mammalian reproduction and development. <i>Genome Biology</i> , 2011, 12, 414.	13.9	22
65	Genome sequence of an Australian kangaroo, <i>Macropus eugenii</i> , provides insight into the evolution of mammalian reproduction and development. <i>Genome Biology</i> , 2011, 12, R81.	13.9	167
66	Diagnostic genetic markers unravel the interplay between host and donor oyster contribution in cultured pearl formation. <i>Aquaculture</i> , 2011, 316, 20-24.	1.7	24
67	Genetic consequences of isolation: island tammar wallaby (<i>Macropus eugenii</i>) populations and the conservation of threatened species. <i>Conservation Genetics</i> , 2011, 12, 1619-1631.	0.8	18
68	A second-generation anchored genetic linkage map of the tammar wallaby (<i>Macropus eugenii</i>). <i>BMC Genetics</i> , 2011, 12, 72.	2.7	15
69	A first-generation integrated tammar wallaby map and its use in creating a tammar wallaby first-generation virtual genome map. <i>BMC Genomics</i> , 2011, 12, 422.	1.2	19
70	Defining spatial genetic structure and management units for vulnerable koala (<i>Phascolarctos</i>) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 142	0.7	16
71	Molecular detection of hybridization between sympatric kangaroo species in south-eastern Australia. <i>Heredity</i> , 2010, 104, 502-512.	1.2	28
72	Mapping quantitative trait loci (QTL) in sheep. I. A new male framework linkage map and QTL for growth rate and body weight. <i>Genetics Selection Evolution</i> , 2009, 41, 34.	1.2	36

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73	Landscape discontinuities influence gene flow and genetic structure in a large, vagile Australian mammal, <i>Macropus fuliginosus</i> . <i>Molecular Ecology</i> , 2009, 18, 3363-3378.	2.0	56
74	Rapid identification of maternal lineages in common carp (<i>Cyprinus carpio</i> L.) using real-time PCR and high resolution melt-curve analysis. <i>Aquaculture</i> , 2009, 287, 59-66.	1.7	8
75	Extent of genome-wide linkage disequilibrium in Australian Holstein-Friesian cattle based on a high-density SNP panel. <i>BMC Genomics</i> , 2008, 9, 187.	1.2	203
76	Predicting Genetic Merit for Mastitis and Fertility in Dairy Cattle using Genome Wide Selection and High Density SNP Screens. <i>Developments in Biologicals</i> , 2008, 132, 219-223.	0.4	9
77	A Primary Assembly of a Bovine Haplotype Block Map Based on a 15,036-Single-Nucleotide Polymorphism Panel Genotyped in Holstein-Friesian Cattle. <i>Genetics</i> , 2007, 176, 763-772.	1.2	77
78	Genome-wide genetic diversity of Holstein Friesian cattle reveals new insights into Australian and global population variability, including impact of selection. <i>Animal Genetics</i> , 2007, 38, 7-14.	0.6	52
79	Genetic structure of introduced European fallow deer (<i>Dama dama</i>) in Tasmania, Australia. <i>European Journal of Wildlife Research</i> , 2007, 53, 40-46.	0.7	14
80	Technical Note: Whole-Genome Amplification of DNA Extracted from Cattle Semen Samples. <i>Journal of Dairy Science</i> , 2006, 89, 2217-2221.	1.4	10
81	Isolation and genetic diversity of endangered grey nurse shark (<i>Carcharias taurus</i>) populations. <i>Biology Letters</i> , 2006, 2, 308-311.	1.0	64
82	Y chromosome microsatellite markers identified from the tammar wallaby (<i>Macropus eugenii</i>) and their amplification in three other macropod species. <i>Molecular Ecology Notes</i> , 2006, 6, 1202-1204.	1.7	17
83	Widespread Utility of Highly Informative AFLP Molecular Markers across Divergent Shark Species. <i>Journal of Heredity</i> , 2006, 97, 607-611.	1.0	15
84	A First-Generation Metric Linkage Disequilibrium Map of Bovine Chromosome 6. <i>Genetics</i> , 2006, 174, 79-85.	1.2	35
85	Phylogenetics, population structure and genetic diversity of the endangered southern brown bandicoot (<i>Isodon obesulus</i>) in south-eastern Australia. <i>Conservation Genetics</i> , 2005, 6, 193-204.	0.8	25
86	Genetic Diversity in Remnant Mainland and "Pristine" Island Populations of Three Endemic Australian Macropodids (Marsupialia): <i>Macropus eugenii</i> , <i>Lagorchestes hirsutus</i> and <i>Petrogale lateralis</i> . <i>Conservation Genetics</i> , 2004, 5, 325-338.	0.8	62
87	Low levels of genetic variation within introduced Javan rusa deer (<i>Cervus timorensis russa</i>) in Australia. <i>European Journal of Wildlife Research</i> , 2004, 50, 137.	0.7	12
88	Quantitative trait loci for steady-state platelet count in mice. <i>Mammalian Genome</i> , 2004, 15, 784-797.	1.0	15
89	Genetic analysis of a population crash in brush-tailed rock-wallabies (<i>Petrogale penicillata</i>) from Jenolan Caves, south-eastern Australia. <i>Wildlife Research</i> , 2004, 31, 229.	0.7	22
90	Title is missing!. <i>Conservation Genetics</i> , 2003, 4, 655-657.	0.8	2

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91	A rapid population expansion retains genetic diversity within European rabbits in Australia. <i>Molecular Ecology</i> , 2003, 12, 789-794.	2.0	103
92	Intraspecific variation, sex-biased dispersal and phylogeography of the eastern grey kangaroo (<i>Macropus giganteus</i>). <i>Heredity</i> , 2003, 91, 153-162.	1.2	52
93	Characterisation and cross-species utility of microsatellite markers within kangaroos, wallabies and rat kangaroos (<i>Macropodoidea</i> : <i>Marsupialia</i>). <i>Australian Journal of Zoology</i> , 2003, 51, 587.	0.6	19
94	Ontogeny of immunoglobulin expression in the brushtail possum (<i>Trichosurus vulpecula</i>). <i>Developmental and Comparative Immunology</i> , 2002, 26, 599-602.	1.0	12
95	Echidna IgA supports mammalian unity and traditional Therian relationship. <i>Mammalian Genome</i> , 2002, 13, 656-663.	1.0	33
96	The First Comprehensive Genetic Linkage Map of a Marsupial: The Tammar Wallaby (<i>Macropus</i>)	1.2	64
97	Characterization of 14 macropod microsatellite genetic markers. <i>Animal Genetics</i> , 2001, 32, 166-167.	0.6	25
98	Isolation and characterization of microsatellite loci in the southern brown bandicoot (<i>Isodon</i>)	1.7	12
99	SSCP is not so difficult: the application and utility of single-stranded conformation polymorphism in evolutionary biology and molecular ecology. <i>Molecular Ecology</i> , 2000, 9, 1699-1710.	2.0	327