

Michael Bunce

List of Publications by Year in descending order

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Version: 2024-02-01

109
papers

9,304
citations

71102

41
h-index

46799

89
g-index

116
all docs

116
docs citations

116
times ranked

11148
citing authors

#	ARTICLE	IF	CITATIONS
1	Coral monitoring in northwest Australia with environmental DNA metabarcoding using a curated reference database for optimized detection. <i>Environmental DNA</i> , 2022, 4, 63-76.	5.8	25
2	Strategies for sample labelling and library preparation in DNA metabarcoding studies. <i>Molecular Ecology Resources</i> , 2022, 22, 1231-1246.	4.8	40
3	Environmental DNA reveals a multi-taxa biogeographic break across the Arabian Sea and Sea of Oman. <i>Environmental DNA</i> , 2022, 4, 206-221.	5.8	17
4	Evaluating restoration trajectories using DNA metabarcoding of ground-dwelling and airborne invertebrates and associated plant communities. <i>Molecular Ecology</i> , 2022, 31, 2172-2188.	3.9	5
5	Phylogeography of recent <i>Plesiastrea</i> (Scleractinia: Plesiastreidae) based on an integrated taxonomic approach. <i>Molecular Phylogenetics and Evolution</i> , 2022, 172, 107469.	2.7	6
6	Ancient proteins resolve controversy over the identity of <i>Genyornis</i> eggshell. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	14
7	Complementary molecular and visual sampling of fish on oil and gas platforms provides superior biodiversity characterisation. <i>Marine Environmental Research</i> , 2022, 179, 105692.	2.5	5
8	Unlocking the phylogenetic diversity, primary habitats, and abundances of free-living Symbiodiniaceae on a coral reef. <i>Molecular Ecology</i> , 2021, 30, 343-360.	3.9	33
9	Comprehensive evidence for subspecies designations in Cook's Petrel <i>Pterodroma cookii</i> with implications for conservation management. <i>Bird Conservation International</i> , 2021, 31, 1-13.	1.3	2
10	Ancient DNA preserved in small bone fragments from the P.W. Lund collection. <i>Ecology and Evolution</i> , 2021, 11, 2064-2071.	1.9	9
11	eDNAFlow, an automated, reproducible and scalable workflow for analysis of environmental DNA sequences exploiting Nextflow and Singularity. <i>Molecular Ecology Resources</i> , 2021, 21, 1697-1704.	4.8	39
12	Ancient plant DNA reveals High Arctic greening during the Last Interglacial. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	29
13	Ancient DNA from bulk bone reveals past genetic diversity of vertebrate fauna on Kangaroo Island, Australia. <i>Quaternary Science Reviews</i> , 2021, 262, 106962.	3.0	6
14	Towards reproducible metabarcoding data: Lessons from an international cross-laboratory experiment. <i>Molecular Ecology Resources</i> , 2021, , .	4.8	25
15	Development of a 16S metabarcoding assay for the environmental DNA (eDNA) detection of aquatic reptiles across northern Australia. <i>Marine and Freshwater Research</i> , 2021, , .	1.3	11
16	Large-scale eDNA metabarcoding survey reveals marine biogeographic break and transitions over tropical north-western Australia. <i>Diversity and Distributions</i> , 2021, 27, 1942-1957.	4.1	45
17	Making environmental DNA (eDNA) biodiversity records globally accessible. <i>Environmental DNA</i> , 2021, 3, 699-705.	5.8	38
18	Climate-assisted persistence of tropical fish vagrants in temperate marine ecosystems. <i>Communications Biology</i> , 2021, 4, 1231.	4.4	5

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19	Water stratification in the marine biome restricts vertical environmental DNA (eDNA) signal dispersal. <i>Environmental DNA</i> , 2020, 2, 99-111.	5.8	74
20	Combined Liquid Chromatography-mass Spectrometry and Next-generation DNA Sequencing Detection of Adulterants and Contaminants in Analgesic and Anti-inflammatory Herbal Medicines. <i>Pharmaceutical Medicine</i> , 2020, 34, 49-61.	1.9	8
21	Development of a multi-assay approach for monitoring coral diversity using eDNA metabarcoding. <i>Coral Reefs</i> , 2020, 39, 159-171.	2.2	42
22	eDNA metabarcoding survey reveals fine-scale coral reef community variation across a remote, tropical island ecosystem. <i>Molecular Ecology</i> , 2020, 29, 1069-1086.	3.9	125
23	Crop-Zone Weed Mycobiomes of the South-Western Australian Grain Belt. <i>Frontiers in Microbiology</i> , 2020, 11, 581592.	3.5	4
24	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	27.8	251
25	Under the karst: detecting hidden subterranean assemblages using eDNA metabarcoding in the caves of Christmas Island, Australia. <i>Scientific Reports</i> , 2020, 10, 21479.	3.3	12
26	Detection of the rare Australian endemic blind cave eel (<i>Ophisternon candidum</i>) with environmental DNA: implications for threatened species management in subterranean environments. <i>Hydrobiologia</i> , 2020, 847, 3201-3211.	2.0	16
27	Rapid range shifts and megafaunal extinctions associated with late Pleistocene climate change. <i>Nature Communications</i> , 2020, 11, 2770.	12.8	46
28	Environmental DNA can act as a biodiversity barometer of anthropogenic pressures in coastal ecosystems. <i>Scientific Reports</i> , 2020, 10, 8365.	3.3	66
29	Development and evaluation of fish eDNA metabarcoding assays facilitate the detection of cryptic seahorse taxa (family: Syngnathidae). <i>Environmental DNA</i> , 2020, 2, 614-626.	5.8	48
30	Partitioning of diet between species and life history stages of sympatric and cryptic snappers (<i>Lutjanidae</i>) based on DNA metabarcoding. <i>Scientific Reports</i> , 2020, 10, 4319.	3.3	20
31	Maximizing fish detection with eDNA metabarcoding. <i>Environmental DNA</i> , 2020, 2, 493-504.	5.8	99
32	Testing multiple substrates for terrestrial biodiversity monitoring using environmental DNA metabarcoding. <i>Molecular Ecology Resources</i> , 2020, 20, 732-745.	4.8	60
33	Early Pastoral Economies and Herding Transitions in Eastern Eurasia. <i>Scientific Reports</i> , 2020, 10, 1001.	3.3	29
34	Combined use of eDNA metabarcoding and video surveillance for the assessment of fish biodiversity. <i>Conservation Biology</i> , 2019, 33, 196-205.	4.7	178
35	Protein and carbohydrate intakes alter gut microbial community structure in crickets: a Geometric Framework approach. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	2
36	Arctic shrub colonization lagged peak postglacial warmth: Molecular evidence in lake sediment from Arctic Canada. <i>Global Change Biology</i> , 2019, 25, 4244-4256.	9.5	43

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37	Toxicological screening and DNA sequencing detects contamination and adulteration in regulated herbal medicines and supplements for diet, weight loss and cardiovascular health. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2019, 176, 112834.	2.8	22
38	Micro Methods for Megafauna: Novel Approaches to Late Quaternary Extinctions and Their Contributions to Faunal Conservation in the Anthropocene. <i>BioScience</i> , 2019, 69, 877-887.	4.9	11
39	Species-level biodiversity assessment using marine environmental DNA metabarcoding requires protocol optimization and standardization. <i>Ecology and Evolution</i> , 2019, 9, 1323-1335.	1.9	62
40	Evidence for fungi and gold redox interaction under Earth surface conditions. <i>Nature Communications</i> , 2019, 10, 2290.	12.8	25
41	Exploring the Application of the DSA-TOF, a Direct, High-resolution Time-of-Flight Mass Spectrometry Technique for the Screening of Potential Adulterated and Contaminated Herbal Medicines. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 1713-1719.	2.8	8
42	Invertebrate DNA metabarcoding reveals changes in communities across mine site restoration chronosequences. <i>Restoration Ecology</i> , 2019, 27, 1177-1186.	2.9	19
43	Beyond Biodiversity: Can Environmental DNA (eDNA) Cut It as a Population Genetics Tool?. <i>Genes</i> , 2019, 10, 192.	2.4	160
44	DNA metabarcoding assays reveal a diverse prey assemblage for <i>Mobula</i> rays in the Bohol Sea, Philippines. <i>Ecology and Evolution</i> , 2019, 9, 2459-2474.	1.9	20
45	Marine environmental DNA biomonitoring reveals seasonal patterns in biodiversity and identifies ecosystem responses to anomalous climatic events. <i>PLoS Genetics</i> , 2019, 15, e1007943.	3.5	112
46	Mitochondrial Genomes from New Zealand's Extinct Adzebills (Aves: Aptornithidae: Aptornis) Support a Sister-Taxon Relationship with the Afro-Madagascan Sarothruridae. <i>Diversity</i> , 2019, 11, 24.	1.7	22
47	Mitogenomic evidence of close relationships between New Zealand's extinct giant raptors and small-sized Australian sister-taxa. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 122-128.	2.7	17
48	Avian mitochondrial genomes retrieved from museum eggshell. <i>Molecular Ecology Resources</i> , 2019, 19, 1052-1062.	4.8	14
49	Towards a macroscope: Leveraging technology to transform the breadth, scale and resolution of macroecological data. <i>Global Ecology and Biogeography</i> , 2019, 28, 1937-1948.	5.8	20
50	MobiSeq: De novo SNP discovery in model and non-model species through sequencing the flanking region of transposable elements. <i>Molecular Ecology Resources</i> , 2019, 19, 512-525.	4.8	4
51	Environmental DNA (eDNA) metabarcoding reveals strong discrimination among diverse marine habitats connected by water movement. <i>Molecular Ecology Resources</i> , 2019, 19, 426-438.	4.8	180
52	Environmental DNA metabarcoding studies are critically affected by substrate selection. <i>Molecular Ecology Resources</i> , 2019, 19, 366-376.	4.8	105
53	Digging for DNA at depth: rapid universal metabarcoding surveys (RUMS) as a tool to detect coral reef biodiversity across a depth gradient. <i>PeerJ</i> , 2019, 7, e6379.	2.0	24
54	The influence of diet and environment on the gut microbial community of field crickets. <i>Ecology and Evolution</i> , 2018, 8, 4704-4720.	1.9	63

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55	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018, 2, 659-668.	7.8	124
56	Determination of the diet of the ghost bat (<i>Macroderma gigas</i>) in the Pilbara region of Western Australia from dried prey remains and DNA metabarcoding. <i>Australian Journal of Zoology</i> , 2018, 66, 195.	1.0	10
57	Adulterants and Contaminants in Psychotropic Herbal Medicines Detected with Mass Spectrometry and Next-Generation DNA Sequencing. <i>Pharmaceutical Medicine</i> , 2018, 32, 429-444.	1.9	13
58	Genomic and life-history discontinuity reveals a precinctive lineage for a deep-water grouper with gene flow from tropical to temperate waters on the west coast of Australia. <i>Ecological Genetics and Genomics</i> , 2018, 9, 23-33.	0.5	6
59	The value of environmental DNA biobanking for long-term biomonitoring. <i>Nature Ecology and Evolution</i> , 2018, 2, 1192-1193.	7.8	78
60	DNA metabarcoding—a new approach to fauna monitoring in mine site restoration. <i>Restoration Ecology</i> , 2018, 26, 1098-1107.	2.9	33
61	Subsistence practices, past biodiversity, and anthropogenic impacts revealed by New Zealand-wide ancient DNA survey. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7771-7776.	7.1	92
62	The Microbiome of the Gastrointestinal Tract of a Range-Shifting Marine Herbivorous Fish. <i>Frontiers in Microbiology</i> , 2018, 9, 2000.	3.5	67
63	Debugging diversity —a pancontinental exploration of the potential of terrestrial blood-feeding leeches as a vertebrate monitoring tool. <i>Molecular Ecology Resources</i> , 2018, 18, 1282-1298.	4.8	45
64	Eggshell palaeogenomics: Palaeognath evolutionary history revealed through ancient nuclear and mitochondrial DNA from Madagascan elephant bird (<i>Aepyornis</i> sp.) eggshell. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 151-163.	2.7	65
65	International workshop on advancing methods to overcome challenges associated with life history and stock assessments of data-poor deep-water snappers and groupers. <i>Marine Policy</i> , 2017, 79, 78-83.	3.2	18
66	Ecosystem biomonitoring with eDNA: metabarcoding across the tree of life in a tropical marine environment. <i>Scientific Reports</i> , 2017, 7, 12240.	3.3	355
67	<scp>DNA</scp> metabarcoding for diet analysis and biodiversity: A case study using the endangered Australian sea lion (<i>Neophoca cinerea</i>). <i>Ecology and Evolution</i> , 2017, 7, 5435-5453.	1.9	120
68	Assessing the utility of eDNA as a tool to survey reef-fish communities in the Red Sea. <i>Coral Reefs</i> , 2017, 36, 1245-1252.	2.2	84
69	Time to Spread Your Wings: A Review of the Avian Ancient DNA Field. <i>Genes</i> , 2017, 8, 184.	2.4	16
70	The application of metabolomics for herbal medicine pharmacovigilance: a case study on ginseng. <i>Essays in Biochemistry</i> , 2016, 60, 429-435.	4.7	6
71	Ancient DNA reveals complexity in the evolutionary history and taxonomy of the endangered Australian brush-tailed bettongs (<i>Bettongia</i> : Marsupialia: Macropodidae: Potoroinae). <i>Biodiversity and Conservation</i> , 2016, 25, 2907-2927.	2.6	14
72	Tropical ancient DNA from bulk archaeological fish bone reveals the subsistence practices of a historic coastal community in southwest Madagascar. <i>Journal of Archaeological Science</i> , 2016, 75, 82-88.	2.4	38

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73	Changes in ectomycorrhizal fungal community composition and declining diversity along a 2â€millionâ€year soil chronosequence. <i>Molecular Ecology</i> , 2016, 25, 4919-4929.	3.9	35
74	An assessment of ancient DNA preservation in Holoceneâ€Pleistocene fossil bone excavated from the world heritage Naracoorte Caves, South Australia. <i>Journal of Quaternary Science</i> , 2016, 31, 33-45.	2.1	20
75	Combined DNA, toxicological and heavy metal analyses provides an auditing toolkit to improve pharmacovigilance of traditional Chinese medicine (TCM). <i>Scientific Reports</i> , 2015, 5, 17475.	3.3	99
76	Inhibition of the endosymbiont â€Candidatus Midichloria mitochondriiâ€ during 16S rRNA gene profiling reveals potential pathogens in Ixodes ticks from Australia. <i>Parasites and Vectors</i> , 2015, 8, 345.	2.5	95
77	The rise and fall of arbuscular mycorrhizal fungal diversity during ecosystem retrogression. <i>Molecular Ecology</i> , 2015, 24, 4912-4930.	3.9	51
78	Genetic diversity loss in a biodiversity hotspot: ancient <scp>DNA</scp> quantifies genetic decline and former connectivity in a critically endangered marsupial. <i>Molecular Ecology</i> , 2015, 24, 5813-5828.	3.9	48
79	From Benchtop to Desktop: Important Considerations when Designing Amplicon Sequencing Workflows. <i>PLoS ONE</i> , 2015, 10, e0124671.	2.5	177
80	A critical evaluation of how ancient DNA bulk bone metabarcoding complements traditional morphological analysis of fossil assemblages. <i>Quaternary Science Reviews</i> , 2015, 128, 37-47.	3.0	33
81	Comparison of Sanger and next generation sequencing performance for genotyping <i>Cryptosporidium</i> isolates at the 18S rRNA and actin loci. <i>Experimental Parasitology</i> , 2015, 151-152, 21-27.	1.2	32
82	Metagenomic analyses of bacteria on human hairs: a qualitative assessment for applications in forensic science. <i>Investigative Genetics</i> , 2014, 5, 16.	3.3	69
83	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	12.6	1,583
84	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	12.6	895
85	Interpreting biological degradative processes acting on mammalian hair in the living and the dead: which ones are taphonomic?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20141755.	2.6	18
86	Extinct New Zealand megafauna were not in decline before human colonization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4922-4927.	7.1	109
87	Identifying conservation units after large-scale land clearing: a spatio-temporal molecular survey of endangered white-tailed black cockatoos (<i>Calyptorhynchus</i> spp.). <i>Diversity and Distributions</i> , 2014, 20, 1208-1220.	4.1	15
88	Thorough assessment of DNA preservation from fossil bone and sediments excavated from a late Pleistoceneâ€Holocene cave deposit on Kangaroo Island, South Australia. <i>Quaternary Science Reviews</i> , 2014, 84, 56-64.	3.0	36
89	An extremely low-density human population exterminated New Zealand moa. <i>Nature Communications</i> , 2014, 5, 5436.	12.8	42
90	Scrapheap Challenge: A novel bulk-bone metabarcoding method to investigate ancient DNA in faunal assemblages. <i>Scientific Reports</i> , 2013, 3, 3371.	3.3	72

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91	Metabarcoding avian diets at airports: implications for birdstrike hazard management planning. <i>Investigative Genetics</i> , 2013, 4, 27.	3.3	25
92	Deep Sequencing of Plant and Animal DNA Contained within Traditional Chinese Medicines Reveals Legality Issues and Health Safety Concerns. <i>PLoS Genetics</i> , 2012, 8, e1002657.	3.5	245
93	High-throughput sequencing of ancient plant and mammal DNA preserved in herbivore middens. <i>Quaternary Science Reviews</i> , 2012, 58, 135-145.	3.0	40
94	Application of STR markers in wildlife forensic casework involving Australian black-cockatoos (<i>Calyptrorhynchus</i> spp.). <i>Forensic Science International: Genetics</i> , 2012, 6, 664-670.	3.1	26
95	Ancient DNA analyses of early archaeological sites in New Zealand reveal extreme exploitation of moa (<i>Aves: Dinornithiformes</i>) at all life stages. <i>Quaternary Science Reviews</i> , 2012, 52, 41-48.	3.0	20
96	The half-life of DNA in bone: measuring decay kinetics in 158 dated fossils. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 4724-4733.	2.6	478
97	Quantitative Real-Time PCR in aDNA Research. <i>Methods in Molecular Biology</i> , 2012, 840, 121-132.	0.9	13
98	Profiling the Dead: Generating Microsatellite Data from Fossil Bones of Extinct Megafauna—Protocols, Problems, and Prospects. <i>PLoS ONE</i> , 2011, 6, e16670.	2.5	39
99	Molecular and morphological analyses of avian eggshell excavated from a late thirteenth century earth oven. <i>Journal of Archaeological Science</i> , 2011, , .	2.4	12
100	DNA-Based Faecal Dietary Analysis: A Comparison of qPCR and High Throughput Sequencing Approaches. <i>PLoS ONE</i> , 2011, 6, e25776.	2.5	124
101	Merging ancient and modern DNA: extinct seabird taxon rediscovered in the North Tasman Sea. <i>Biology Letters</i> , 2010, 6, 94-97.	2.3	17
102	Fossil avian eggshell preserves ancient DNA. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 1991-2000.	2.6	103
103	Identification of microsatellites from an extinct moa species using high-throughput (454) sequence data. <i>BioTechniques</i> , 2009, 46, 195-200.	1.8	94
104	“The Farm Beneath the Sand” an archaeological case study on ancient “dirty” DNA. <i>Antiquity</i> , 2009, 83, 430-444.	1.0	60
105	Ancient DNA Chronology within Sediment Deposits: Are Paleobiological Reconstructions Possible and Is DNA Leaching a Factor?. <i>Molecular Biology and Evolution</i> , 2007, 24, 982-989.	8.9	202
106	Cross-species amplification at microsatellite loci in Australian quolls including the description of five new markers from the Chuditch (<i>Dasyurus geoffroii</i>). <i>Molecular Ecology Notes</i> , 2007, 7, 1100-1103.	1.7	16
107	Ancient DNA Provides New Insights into the Evolutionary History of New Zealand's Extinct Giant Eagle. <i>PLoS Biology</i> , 2005, 3, e9.	5.6	77
108	Extreme reversed sexual size dimorphism in the extinct New Zealand moa <i>Dinornis</i> . <i>Nature</i> , 2003, 425, 172-175.	27.8	151

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109	Diverse Plant and Animal Genetic Records from Holocene and Pleistocene Sediments. Science, 2003, 300, 791-795.	12.6	571