

Mehrdad Hajibabaei

List of Publications by Year in descending order

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Version: 2024-02-01

110
papers

14,514
citations

36303

51
h-index

27406

106
g-index

132
all docs

132
docs citations

132
times ranked

13542
citing authors

#	ARTICLE	IF	CITATIONS
1	LANDMark: an ensemble approach to the supervised selection of biomarkers in high-throughput sequencing data. <i>BMC Bioinformatics</i> , 2022, 23, 110.	2.6	5
2	Multi-marker DNA metabarcoding detects suites of environmental gradients from an urban harbour. <i>Scientific Reports</i> , 2022, 12, .	3.3	4
3	Comparison of traditional and DNA metabarcoding samples for monitoring tropical soil arthropods (Formicidae, Collembola and Isoptera). <i>Scientific Reports</i> , 2022, 12, .	3.3	7
4	Propylene glycol-based antifreeze is an effective preservative for DNA metabarcoding of benthic arthropods. <i>Freshwater Science</i> , 2021, 40, 77-87.	1.8	14
5	Biotic signals associated with benthic impacts of salmon farms from eDNA metabarcoding of sediments. <i>Molecular Ecology</i> , 2021, 30, 3158-3174.	3.9	12
6	Profile hidden Markov model sequence analysis can help remove putative pseudogenes from DNA barcoding and metabarcoding datasets. <i>BMC Bioinformatics</i> , 2021, 22, 256.	2.6	15
7	Towards reproducible metabarcoding data: Lessons from an international cross-laboratory experiment. <i>Molecular Ecology Resources</i> , 2021, , .	4.8	25
8	The impacts of a logging road on the soil microbial communities, and carbon and nitrogen components in a Northern Zone Costa Rican forest. <i>Applied Soil Ecology</i> , 2021, 164, 103937.	4.3	4
9	Editorial: Stressors Acting on Aquatic Ecosystems: High-Throughput Sequencing Approaches to Shed Light on Human-Nature Interactions. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	2.2	3
10	eDNA and Bioassessment of Rivers. , 2021, , .		0
11	Key Questions for Next-Generation Biomonitoring. <i>Frontiers in Environmental Science</i> , 2020, 7, .	3.3	68
12	Influence of Two Important Leguminous Trees on Their Soil Microbiomes and Nitrogen Cycle Activities in a Primary and Recovering Secondary Forest in the Northern Zone of Costa Rica. <i>Soil Systems</i> , 2020, 4, 65.	2.6	3
13	Increase in abundance and decrease in richness of soil microbes following Hurricane Otto in three primary forest types in the Northern Zone of Costa Rica. <i>PLoS ONE</i> , 2020, 15, e0231187.	2.5	6
14	Putting COI Metabarcoding in Context: The Utility of Exact Sequence Variants (ESVs) in Biodiversity Analysis. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	2.2	37
15	Drivers of tropical soil invertebrate community composition and richness across tropical secondary forests using DNA metasystematics. <i>Scientific Reports</i> , 2020, 10, 18429.	3.3	5
16	Metabarcoding From Microbes to Mammals: Comprehensive Bioassessment on a Global Scale. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	2.2	49
17	Differences in the soil microbiomes of <i>Pentaclethra macroloba</i> across tree size and in contrasting land use histories. <i>Plant and Soil</i> , 2020, 452, 329-345.	3.7	3
18	Small-scale spatial variation of meiofaunal communities in Lima estuary (NW Portugal) assessed through metabarcoding. <i>Estuarine, Coastal and Shelf Science</i> , 2020, 238, 106683.	2.1	20

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19	Validating metabarcoding-based biodiversity assessments with multi-species occupancy models: A case study using coastal marine eDNA. PLoS ONE, 2020, 15, e0224119.	2.5	33
20	DNA metabarcoding reveals metacommunity dynamics in a threatened boreal wetland wilderness. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 8539-8545.	7.1	50
21	Using DNA-barcoded Malaise trap samples to measure impact of a geothermal energy project on the biodiversity of a Costa Rican old-growth rain forest. Genome, 2020, 63, 407-436.	2.0	17
22	Harnessing the power of eDNA metabarcoding for the detection of deep-sea fishes. PLoS ONE, 2020, 15, e0236540.	2.5	46
23	Freshwater diatom biomonitoring through benthic kick-net metabarcoding. PLoS ONE, 2020, 15, e0242143.	2.5	9
24	Determinants of Soil Bacterial and Fungal Community Composition Toward Carbon-Use Efficiency Across Primary and Secondary Forests in a Costa Rican Conservation Area. Microbial Ecology, 2019, 77, 148-167.	2.8	38
25	Studying Ecosystems With DNA Metabarcoding: Lessons From Biomonitoring of Aquatic Macroinvertebrates. Frontiers in Ecology and Evolution, 2019, 7, .	2.2	85
26	Gaps in DNA-Based Biomonitoring Across the Globe. Frontiers in Ecology and Evolution, 2019, 7, .	2.2	75
27	COI metabarcoding primer choice affects richness and recovery of indicator taxa in freshwater systems. PLoS ONE, 2019, 14, e0220953.	2.5	86
28	Network-Based Biomonitoring: Exploring Freshwater Food Webs With Stable Isotope Analysis and DNA Metabarcoding. Frontiers in Ecology and Evolution, 2019, 7, .	2.2	31
29	Differences in the soil microbial community and carbon-use efficiency following development of Vochysia guatemalensis tree plantations in unproductive pastures in Costa Rica. Restoration Ecology, 2019, 27, 1263-1273.	2.9	9
30	Soil microbiomes associated with two dominant Costa Rican tree species, and implications for remediation: A case study from a Costa Rican conservation area. Applied Soil Ecology, 2019, 137, 139-153.	4.3	16
31	Interspecific competition in bats and diet shifts in response to white-nose syndrome. Ecosphere, 2019, 10, e02916.	2.2	12
32	Watered-down biodiversity? A comparison of metabarcoding results from DNA extracted from matched water and bulk tissue biomonitoring samples. PLoS ONE, 2019, 14, e0225409.	2.5	65
33	Variations in terrestrial arthropod DNA metabarcoding methods recovers robust beta diversity but variable richness and site indicators. Scientific Reports, 2019, 9, 18218.	3.3	23
34	Metabarcoding of storage ethanol vs. conventional morphometric identification in relation to the use of stream macroinvertebrates as ecological indicators in forest management. Ecological Indicators, 2019, 101, 173-184.	6.3	46
35	Bacterial diversity in the waterholes of the Kruger National Park: an eDNA metabarcoding approach. Genome, 2019, 62, 229-242.	2.0	11
36	Validation of COI metabarcoding primers for terrestrial arthropods. PeerJ, 2019, 7, e7745.	2.0	161

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37	Performance of amplicon and shotgun sequencing for accurate biomass estimation in invertebrate community samples. <i>Molecular Ecology Resources</i> , 2018, 18, 1020-1034.	4.8	104
38	Identifying North American freshwater invertebrates using DNA barcodes: are existing COI sequence libraries fit for purpose?. <i>Freshwater Science</i> , 2018, 37, 178-189.	1.8	80
39	Scaling up: A guide to high-throughput genomic approaches for biodiversity analysis. <i>Molecular Ecology</i> , 2018, 27, 313-338.	3.9	248
40	Environmental DNA filtration techniques affect recovered biodiversity. <i>Scientific Reports</i> , 2018, 8, 4682.	3.3	93
41	Automated high throughput animal CO1 metabarcode classification. <i>Scientific Reports</i> , 2018, 8, 4226.	3.3	112
42	Fecal source tracking and eDNA profiling in an urban creek following an extreme rain event. <i>Scientific Reports</i> , 2018, 8, 14390.	3.3	28
43	Linking DNA Metabarcoding and Text Mining to Create Network-Based Biomonitoring Tools: A Case Study on Boreal Wetland Macroinvertebrate Communities. <i>Advances in Ecological Research</i> , 2018, 59, 33-74.	2.7	25
44	Over 2.5 million COI sequences in GenBank and growing. <i>PLoS ONE</i> , 2018, 13, e0200177.	2.5	125
45	Annual time-series analysis of aqueous eDNA reveals ecologically relevant dynamics of lake ecosystem biodiversity. <i>Nature Communications</i> , 2017, 8, 14087.	12.8	229
46	Integrative data helps the assessment of a butterfly within the <i>Udranomia kikkawai</i> species complex (Lepidoptera: HesperIIDae): Immature stages, natural history, and molecular evidence. <i>Zoologischer Anzeiger</i> , 2017, 266, 169-176.	0.9	4
47	DNA metabarcoding and morphological macroinvertebrate metrics reveal the same changes in boreal watersheds across an environmental gradient. <i>Scientific Reports</i> , 2017, 7, 12777.	3.3	80
48	Using metagenomics to show the efficacy of forest restoration in the New Jersey Pine Barrens. <i>Genome</i> , 2017, 60, 825-836.	2.0	15
49	Nuclear genomes distinguish cryptic species suggested by their DNA barcodes and ecology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8313-8318.	7.1	89
50	DNA metabarcoding for high-throughput monitoring of estuarine macrobenthic communities. <i>Scientific Reports</i> , 2017, 7, 15618.	3.3	65
51	A new way to contemplate Darwin's tangled bank: how DNA barcodes are reconnecting biodiversity science and biomonitoring. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150330.	4.0	67
52	From writing to reading the encyclopedia of life. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150321.	4.0	48
53	Altered intestinal microbiota-host mitochondria crosstalk in new onset Crohn's disease. <i>Nature Communications</i> , 2016, 7, 13419.	12.8	326
54	Reply to Garner et al.. <i>Trends in Ecology and Evolution</i> , 2016, 31, 83-84.	8.7	24

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55	DNA barcoding of earthworms (<i>Eisenia fetida/andrei</i> complex) from 28 ecotoxicological test laboratories. <i>Applied Soil Ecology</i> , 2016, 104, 3-11.	4.3	38
56	Ribosomal DNA and Plastid Markers Used to Sample Fungal and Plant Communities from Wetland Soils Reveals Complementary Biotas. <i>PLoS ONE</i> , 2016, 11, e0142759.	2.5	16
57	Large-Scale Monitoring of Plants through Environmental DNA Metabarcoding of Soil: Recovery, Resolution, and Annotation of Four DNA Markers. <i>PLoS ONE</i> , 2016, 11, e0157505.	2.5	113
58	Discrimination of grasshopper (<i>Orothoptera: Acrididae</i>) diet and niche overlap using next-generation sequencing of gut contents. <i>Ecology and Evolution</i> , 2015, 5, 3046-3055.	1.9	35
59	A DNA Mini-Barcoding System for Authentication of Processed Fish Products. <i>Scientific Reports</i> , 2015, 5, 15894.	3.3	170
60	Naphthenic Acid Mixtures from Oil Sands Process-Affected Water Enhance Differentiation of Mouse Embryonic Stem Cells and Affect Development of the Heart. <i>Environmental Science & Technology</i> , 2015, 49, 10165-10172.	10.0	19
61	Large-Scale Biomonitoring of Remote and Threatened Ecosystems via High-Throughput Sequencing. <i>PLoS ONE</i> , 2015, 10, e0138432.	2.5	154
62	Massively parallel multiplex DNA sequencing for specimen identification using an Illumina MiSeq platform. <i>Scientific Reports</i> , 2015, 5, 9687.	3.3	217
63	Genomics and the challenging translation into conservation practice. <i>Trends in Ecology and Evolution</i> , 2015, 30, 78-87.	8.7	469
64	A striking new genus and species of tiger-moth (Lepidoptera: Erebidae, Arctiinae.) <i>Taxonomy</i> , 2014, 3760, 289.	0.5	6
65	Review of <i>Apanteles</i> sensu stricto (Hymenoptera, Braconidae, Microgastrinae) from Area de Conservaci3n Guanacaste, northwestern Costa Rica, with keys to all described species from Mesoamerica. <i>ZooKeys</i> , 2014, 383, 1-565.	1.1	102
66	Rapid and accurate taxonomic classification of insect (class Insecta) cytochrome c oxidase subunit 1 (<i>COI</i>) using next-generation sequencing. <i>PLoS ONE</i> , 2014, 9, e929-942.	4.8	50
67	Simultaneous assessment of the macrobiome and microbiome in a bulk sample of tropical arthropods through DNA metasytematics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8007-8012.	7.1	252
68	Mitochondrial and nuclear phylogenetic analysis with Sanger and next-generation sequencing shows that, in Area de Conservaci3n Guanacaste, northwestern Costa Rica, the skipper butterfly named <i>Urbanus belli</i> (family Hesperiiidae) comprises three morphologically cryptic species. <i>BMC Evolutionary Biology</i> , 2014, 14, 153.	3.2	27
69	Next-generation DNA barcoding: using next-generation sequencing to enhance and accelerate DNA barcode capture from single specimens. <i>Molecular Ecology Resources</i> , 2014, 14, 892-901.	4.8	185
70	DNA Barcodes Reveal Yet Another New Species of <i>Venada</i> (Lepidoptera: Hesperiiidae) in Northwestern Costa Rica. <i>Proceedings of the Entomological Society of Washington</i> , 2013, 115, 37-47.	0.2	4
71	Cryptic species within cryptic moths: new species of <i>Dunama</i> Schaus (Notodontidae, Nystaleinae) in Costa Rica. <i>ZooKeys</i> , 2013, 264, 11-45.	1.1	12
72	Next-Generation DNA-Based Approaches for Comprehensive Assessment of Marine Communities. , 2012, , .		2

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73	What happens to the traditional taxonomy when a well-known tropical saturniid moth fauna is DNA barcoded?. <i>Invertebrate Systematics</i> , 2012, 26, 478.	1.3	30
74	DNA barcodes for everyday life: Routine authentication of Natural Health Products. <i>Food Research International</i> , 2012, 49, 446-452.	6.2	117
75	Assessing biodiversity of a freshwater benthic macroinvertebrate community through non-destructive environmental barcoding of DNA from preservative ethanol. <i>BMC Ecology</i> , 2012, 12, 28.	3.0	185
76	The golden age of DNA metasystematics. <i>Trends in Genetics</i> , 2012, 28, 535-537.	6.7	65
77	DNA Mini-barcodes. <i>Methods in Molecular Biology</i> , 2012, 858, 339-353.	0.9	35
78	Biomonitoring 2.0: a new paradigm in ecosystem assessment made possible by next-generation DNA sequencing. <i>Molecular Ecology</i> , 2012, 21, 2039-2044.	3.9	375
79	Next-generation sequencing technologies for environmental DNA research. <i>Molecular Ecology</i> , 2012, 21, 1794-1805.	3.9	721
80	Environmental DNA. <i>Molecular Ecology</i> , 2012, 21, 1789-1793.	3.9	926
81	Wolbachia and DNA Barcoding Insects: Patterns, Potential, and Problems. <i>PLoS ONE</i> , 2012, 7, e36514.	2.5	148
82	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.	3.1	35
83	Discriminating plant species in a local temperate flora using the <i>rbcL</i> + <i>matK</i> DNA barcode. <i>Methods in Ecology and Evolution</i> , 2011, 2, 333-340.	5.2	154
84	The DNA Barcode Linker. <i>Molecular Ecology Resources</i> , 2011, 11, 84-88.	4.8	10
85	Reading the Complex Skipper Butterfly Fauna of One Tropical Place. <i>PLoS ONE</i> , 2011, 6, e19874.	2.5	45
86	Pyrosequencing for Mini-Barcoding of Fresh and Old Museum Specimens. <i>PLoS ONE</i> , 2011, 6, e21252.	2.5	66
87	Spatial patterns of plant diversity below-ground as revealed by DNA barcoding. <i>Molecular Ecology</i> , 2011, 20, 1289-1302.	3.9	96
88	Toward a knowledge infrastructure for traits-based ecological risk assessment. <i>Integrated Environmental Assessment and Management</i> , 2011, 7, 209-215.	2.9	37
89	Environmental Barcoding: A Next-Generation Sequencing Approach for Biomonitoring Applications Using River Benthos. <i>PLoS ONE</i> , 2011, 6, e17497.	2.5	459
90	Direct PCR amplification and sequencing of specimens' DNA from preservative ethanol. <i>BioTechniques</i> , 2010, 48, 305-306.	1.8	72

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91	Googling DNA sequences on the World Wide Web. BMC Bioinformatics, 2009, 10, S4.	2.6	8
92	iBarcode.org: web-based molecular biodiversity analysis. BMC Bioinformatics, 2009, 10, S14.	2.6	19
93	Integration of DNA barcoding into an ongoing inventory of complex tropical biodiversity. Molecular Ecology Resources, 2009, 9, 1-26.	4.8	305
94	Are plant species inherently harder to discriminate than animal species using DNA barcoding markers?. Molecular Ecology Resources, 2009, 9, 130-139.	4.8	234
95	A universal DNA mini-barcode for biodiversity analysis. BMC Genomics, 2008, 9, 214.	2.8	535
96	DNA barcodes and cryptic species of skipper butterflies in the genus <i>Perichares</i> in Area de Conservaci3n Guanacaste, Costa Rica. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6350-6355.	7.1	212
97	Multiple Multilocus DNA Barcodes from the Plastid Genome Discriminate Plant Species Equally Well. PLoS ONE, 2008, 3, e2802.	2.5	526
98	Assembling DNA Barcodes. Methods in Molecular Biology, 2008, 410, 275-294.	0.9	276
99	Biological identifications through DNA barcodes: the case of the Crustacea. Canadian Journal of Fisheries and Aquatic Sciences, 2007, 64, 272-295.	1.4	419
100	Design and applicability of DNA arrays and DNA barcodes in biodiversity monitoring. BMC Biology, 2007, 5, 24.	3.8	141
101	DNA barcoding: how it complements taxonomy, molecular phylogenetics and population genetics. Trends in Genetics, 2007, 23, 167-172.	6.7	934
102	DNA barcodes distinguish species of tropical Lepidoptera. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 968-971.	7.1	1,160
103	A minimalist barcode can identify a specimen whose DNA is degraded. Molecular Ecology Notes, 2006, 6, 959-964.	1.7	466
104	Seed plant phylogeny: Gnetophytes are derived conifers and a sister group to Pinaceae. Molecular Phylogenetics and Evolution, 2006, 40, 208-217.	2.7	44
105	Benchmarking DNA barcodes: an assessment using available primate sequences. Genome, 2006, 49, 851-854.	2.0	68
106	Wedding biodiversity inventory of a large and complex Lepidoptera fauna with DNA barcoding. Philosophical Transactions of the Royal Society B: Biological Sciences, 2005, 360, 1835-1845.	4.0	285
107	Critical factors for assembling a high volume of DNA barcodes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2005, 360, 1959-1967.	4.0	430
108	Identity of the ailanthus webworm moth (Lepidoptera, Yponomeutidae), a complex of two species: evidence from DNA barcoding, morphology and ecology. ZooKeys, 0, 46, 41-60.	1.1	25

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109	Choice of DNA extraction method affects DNA metabarcoding of unsorted invertebrate bulk samples. <i>Metabarcoding and Metagenomics</i> , 0, 2, .	0.0	40
110	Methodological considerations for monitoring soil/litter arthropods in tropical rainforests using DNA metabarcoding, with a special emphasis on ants, springtails and termites. <i>Metabarcoding and Metagenomics</i> , 0, 4, .	0.0	6