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Scaling up: A guide to high-throughput genomic approaches for biodiversity analysis

DOI: 10.1111/mec.14478 Molecular Ecology, 2018, 27, 313-338.

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219	[Regular Paper] Decision Theory-Based DNA Barcoding Through Quick Response Code Representation. 2018 ,	
218	Historical DNA Metabarcoding of the Prey and Microbiome of Trematomid Fishes Using Museum Samples. 2018 , 6,	6
217	Advances in DNA Barcoding of Toxic Marine Organisms. 2018 , 19,	6
216	Metabarcoding of marine environmental DNA based on mitochondrial and nuclear genes. 2018 , 8, 14822	33
215	Shotgun metagenomics of honey DNA: Evaluation of a methodological approach to describe a multi-kingdom honey bee derived environmental DNA signature. 2018 , 13, e0205575	23
214	Over 2.5 million COI sequences in GenBank and growing. 2018 , 13, e0200177	66
213	Phylogenetic Diversity and Conservation Evaluation: Perspectives on Multiple Values, Indices, and Scales of Application. 2018 , 1-26	14
212	Advancing DNA Barcoding and Metabarcoding Applications for Plants Requires Systematic Analysis of Herbarium Collections An Australian Perspective. 2018 , 6,	33
211	Advantages and Limitations of Environmental DNA/RNA Tools for Marine Biosecurity: Management and Surveillance of Non-indigenous Species. 2018 , 5,	43
210	Recent progress in biohydrometallurgy and microbial characterisation. 2018, 180, 7-25	82
209	Uses and Misuses of Environmental DNA in Biodiversity Science and Conservation. 2018 , 49, 209-230	113
208	Testing clustering strategies for metabarcoding-based investigation of community-environment interactions. 2018 , 18, 1326-1338	18
207	Entomological signatures in honey: an environmental DNA metabarcoding approach can disclose information on plant-sucking insects in agricultural and forest landscapes. 2018 , 8, 9996	18
206	Cryfa: a secure encryption tool for genomic data. 2019 , 35, 146-148	15
205	Quantitative and qualitative assessment of pollen DNA metabarcoding using constructed species mixtures. <i>Molecular Ecology</i> , 2019 , 28, 431-455	65

(2019-2019)

204	Not just a migration problem: Metapopulations, habitat shifts, and gene flow are also important for fishway science and management. 2019 , 35, 1688-1696		26
203	Establishing arthropod community composition using metabarcoding: Surprising inconsistencies between soil samples and preservative ethanol and homogenate from Malaise trap catches. 2019 , 19, 1516-1530		30
202	DAIRYdb: a manually curated reference database for improved taxonomy annotation of 16S rRNA gene sequences from dairy products. 2019 , 20, 560		20
201	Prospects and challenges of implementing DNA metabarcoding for high-throughput insect surveillance. 2019 , 8,		56
200	Diatom DNA Metabarcoding for Biomonitoring: Strategies to Avoid Major Taxonomical and Bioinformatical Biases Limiting Molecular Indices Capacities. 2019 , 7,		27
199	Studying Ecosystems With DNA Metabarcoding: Lessons From Biomonitoring of Aquatic Macroinvertebrates. 2019 , 7,		41
198	Monitoring of marine nematode communities through 18S rRNA metabarcoding as a sensitive alternative to morphology. 2019 , 107, 105554		8
197	Gaps in DNA-Based Biomonitoring Across the Globe. 2019 , 7,		32
196	COI metabarcoding primer choice affects richness and recovery of indicator taxa in freshwater systems. 2019 , 14, e0220953		38
195	Editorial 2019. <i>Molecular Ecology</i> , 2019 , 28, 1-28	5.7	7
195 194	Editorial 2019. <i>Molecular Ecology</i> , 2019 , 28, 1-28 Rapid alignment-free phylogenetic identification of metagenomic sequences. 2019 , 35, 3303-3312	5-7	7
		5-7	
194	Rapid alignment-free phylogenetic identification of metagenomic sequences. 2019 , 35, 3303-3312	5-7	12
194	Rapid alignment-free phylogenetic identification of metagenomic sequences. 2019 , 35, 3303-3312 Estimating belowground plant abundance with DNA metabarcoding. 2019 , 19, 1265-1277	5-7	12
194 193 192	Rapid alignment-free phylogenetic identification of metagenomic sequences. 2019 , 35, 3303-3312 Estimating belowground plant abundance with DNA metabarcoding. 2019 , 19, 1265-1277 Biodiversity of Reef-Building, Scleractinian Corals. 2019 , 589-620 Bioinformatics matters: The accuracy of plant and soil fungal community data is highly dependent	5-7	12 15 7
194 193 192	Rapid alignment-free phylogenetic identification of metagenomic sequences. 2019 , 35, 3303-3312 Estimating belowground plant abundance with DNA metabarcoding. 2019 , 19, 1265-1277 Biodiversity of Reef-Building, Scleractinian Corals. 2019 , 589-620 Bioinformatics matters: The accuracy of plant and soil fungal community data is highly dependent on the metabarcoding pipeline. 2019 , 41, 23-33 Evaluation of denaturing gradient gel electrophoresis (DGGE) and next generation sequencing (NGS) in combination with enrichment culture techniques to identify bacteria in commercial	5-7	12 15 7 82
194 193 192 191	Rapid alignment-free phylogenetic identification of metagenomic sequences. 2019, 35, 3303-3312 Estimating belowground plant abundance with DNA metabarcoding. 2019, 19, 1265-1277 Biodiversity of Reef-Building, Scleractinian Corals. 2019, 589-620 Bioinformatics matters: The accuracy of plant and soil fungal community data is highly dependent on the metabarcoding pipeline. 2019, 41, 23-33 Evaluation of denaturing gradient gel electrophoresis (DGGE) and next generation sequencing (NGS) in combination with enrichment culture techniques to identify bacteria in commercial microbial-based products. 2019, 161, 118-130 Wood-rotting basidiomycetes are a minor component of fungal communities associated with	5-7	12 15 7 82 3

186	Variations in terrestrial arthropod DNA metabarcoding methods recovers robust beta diversity but variable richness and site indicators. 2019 , 9, 18218	9
185	Promises and pitfalls of using high-throughput sequencing for diet analysis. 2019 , 19, 327-348	77
184	Microbial Diversity of Thermophiles Through the Lens of Next Generation Sequencing. 2019, 217-226	2
183	Assembly processes of trophic guilds in the root mycobiome of temperate forests. <i>Molecular Ecology</i> , 2019 , 28, 348-364	22
182	Circumpolar terrestrial arthropod monitoring: A review of ongoing activities, opportunities and challenges, with a focus on spiders. 2020 , 49, 704-717	12
181	Status and trends of terrestrial arthropod abundance and diversity in the North Atlantic region of the Arctic. 2020 , 49, 718-731	23
180	Early Life Stages of a Common Broadcast Spawning Coral Associate with Specific Bacterial Communities Despite Lack of Internalized Bacteria. 2020 , 79, 706-719	16
179	SPIKEPIPE: A metagenomic pipeline for the accurate quantification of eukaryotic species occurrences and intraspecific abundance change using DNA barcodes or mitogenomes. 2020 , 20, 256-267	30
178	Mixed-mode bacterial transmission in the common brooding coral Pocillopora acuta. 2020 , 22, 397-412	17
177	Cyberinfrastructure and resources to enable an integrative approach to studying forest trees. 2020 , 13, 228-241	11
176	Enhancing DNA metabarcoding performance and applicability with bait capture enrichment and DNA from conservative ethanol. 2020 , 20, 79-96	6
175	Quantification of the paralytic shellfish poisoning dinoflagellate Alexandrium species using a digital PCR. 2020 , 92, 101726	14
174	Soil exposed to silver nanoparticles reveals significant changes in community structure and altered microbial transcriptional profiles. 2020 , 258, 113816	13
173	Key Questions for Next-Generation Biomonitoring. 2020 , 7,	30
172	Bacterial and algal symbiont dynamics in early recruits exposed to two adult coral species. 2020 , 39, 189-202	9
171	The Ecobiomics project: Advancing metagenomics assessment of soil health and freshwater quality in Canada. 2020 , 710, 135906	11
170	A practical guide to DNA metabarcoding for entomological ecologists. 2020 , 45, 373-385	32
169	Diet composition analysis provides new management insights for a highly specialized endangered small mammal. 2020 , 15, e0240136	2

(2020-2020)

168	MARES, a replicable pipeline and curated reference database for marine eukaryote metabarcoding. 2020 , 7, 209		4	
167	Application of next generation sequencing for detection of protozoan pathogens in shellfish. 2020 , 21, e00096		5	
166	Decision-making and best practices for taxonomy-free environmental DNA metabarcoding in biomonitoring using Hill numbers. <i>Molecular Ecology</i> , 2021 , 30, 3326-3339	5.7	9	
165	Biases in bulk: DNA metabarcoding of marine communities and the methodology involved. <i>Molecular Ecology</i> , 2021 , 30, 3270-3288	5.7	23	
164	Putting COI Metabarcoding in Context: The Utility of Exact Sequence Variants (ESVs) in Biodiversity Analysis. 2020 , 8,		18	
163	Drivers of tropical soil invertebrate community composition and richness across tropical secondary forests using DNA metasystematics. 2020 , 10, 18429		2	
162	Greater topoclimatic control of above- versus below-ground communities. 2020 , 26, 6715-6728		3	
161	Marine biomonitoring with eDNA: Can metabarcoding of water samples cut it as a tool for surveying benthic communities?. <i>Molecular Ecology</i> , 2021 , 30, 3175-3188	5.7	15	
160	Hill-based dissimilarity indices and null models for analysis of microbial community assembly. 2020 , 8, 132		8	
159	Bacterial community assembly in Atlantic cod larvae (Gadus morhua): contributions of ecological processes and metacommunity structure. 2020 , 96,		7	
158	Molecular identification and geographic origin of a post-Medieval elephant finding from southwestern Portugal using high-throughput sequencing. 2020 , 10, 19252		2	
157	BIOCOM-PIPE: a new user-friendly metabarcoding pipeline for the characterization of microbial diversity from 16S, 18S and 23S rRNA gene amplicons. 2020 , 21, 492		4	
156	Development and evaluation of fish eDNA metabarcoding assays facilitate the detection of cryptic seahorse taxa (family: Syngnathidae). 2020 , 2, 614-626		16	
155	Shotgun sequencing of honey DNA can describe honey bee derived environmental signatures and the honey bee hologenome complexity. 2020 , 10, 9279		15	
154	Climate change impacts on Australia's eucalypt and coral species: Comparing and sharing knowledge across disciplines. 2020 , 11, e657		5	
153	Consistency of Targeted Metatranscriptomics and Morphological Characterization of Phytoplankton Communities. 2020 , 11, 96		2	
152	Broad and Fine Scale Variability in Bacterial Diversity and Cyanotoxin Quotas in Benthic Cyanobacterial Mats. 2020 , 11, 129		6	
151	DNA metabarcoding for biodiversity monitoring in a national park: Screening for invasive and pest species. 2020 , 20, 1542-1557		11	

150	Reappraising plastid markers of the red algae for phylogenetic community ecology in the genomic era. 2020 , 10, 1299-1310		4
149	Informing marine spatial planning decisions with environmental DNA. 2020 , 62, 375-407		9
148	Comparing environmental metabarcoding and trawling survey of demersal fish communities in the Gulf of St. Lawrence, Canada. 2021 , 3, 22-42		19
147	Propylene glycol-based antifreeze is an effective preservative for DNA metabarcoding of benthic arthropods. 2021 , 40, 77-87		7
146	Stirring up the relationship between quantified environmental DNA concentrations and exoskeleton-shedding invertebrate densities. 2021 , 3, 605-618		1
145	High-throughput sequencing of 5S-IGS in oaks: Exploring intragenomic variation and algorithms to recognize target species in pure and mixed samples. 2021 , 21, 495-510		5
144	Reanalysis of the Mars500 experiment reveals common gut microbiome alterations in astronauts induced by long-duration confinement. 2021 , 19, 2223-2235		3
143	Metagenomics Approaches for the Detection and Surveillance of Emerging and Recurrent Plant Pathogens. 2021 , 9,		19
142	Connecting high-throughput biodiversity inventories: Opportunities for a site-based genomic framework for global integration and synthesis. <i>Molecular Ecology</i> , 2021 , 30, 1120-1135	5.7	8
141	Extremely low nucleotide diversity among thirty-six new chloroplast genome sequences from (Heliantheae, Asteraceae) and comparative chloroplast genomics analyses with closely related genera. 2021 , 9, e10886		5
140	DNA Metabarcoding for the Characterization of Terrestrial Microbiota-Pitfalls and Solutions. 2021 , 9,		11
139	Quantitative assessment of fish larvae community composition in spawning areas using metabarcoding of bulk samples. 2021 , 31, e02284		O
138	eDNAFlow, an automated, reproducible and scalable workflow for analysis of environmental DNA sequences exploiting Nextflow and Singularity. 2021 , 21, 1697-1704		10
137	An Overview of DNA-Based Applications for the Assessment of Benthic Macroinvertebrates Biodiversity in Mediterranean Aquatic Ecosystems. 2021 , 13, 112		4
136	Developing a non-destructive metabarcoding protocol for detection of pest insects in bulk trap catches. 2021 , 11, 7946		5
135	The role of taxonomic expertise in interpretation of metabarcoding studies.		3
134	Assessments of Bacterial Community Shifts in Sediments along the Headwaters of SB Francisco River, Brazil. 2021 , 1, 91-105		1
133	Environmental DNA of preservative ethanol performed better than water samples in detecting macroinvertebrate diversity using metabarcoding. 2021 , 27, 1989-2002		O

132	Assessment of current taxonomic assignment strategies for metabarcoding eukaryotes. 2021 , 21, 2190-2203	7
131	eDNA metabarcoding outperforms traditional fisheries sampling and reveals fine-scale heterogeneity in a temperate freshwater lake. 2021 , 3, 912-929	3
130	Developing a monitoring program of genetic diversity: what do stakeholders say?. 2021, 22, 673-684	1
129	A metabarcoding approach for detecting protozoan pathogens in wild oysters from Prince Edward Island, Canada. 2021 , 360, 109315	
128	Scientific and budgetary trade-offs between morphological and molecular methods for deep-sea biodiversity assessment. 2021 ,	О
127	Community eDNA metabarcoding as a detection tool for documenting freshwater mussel (Unionidae) species assemblages. 2021 , 3, 1172	1
126	Environmental DNA and environmental RNA: Current and prospective applications for biological monitoring. 2021 , 782, 146891	8
125	High-Throughput Metabarcoding Characterizes Fungal Endophyte Diversity in the Phyllosphere of a Barley Crop. PBIOMES-09-20-0	3
124	Biological Ingredient Analysis of Traditional Herbal Patent Medicine Fuke Desheng Wan Using the Shotgun Metabarcoding Approach. 2021 , 12, 607197	1
123	Towards reproducible metabarcoding data: Lessons from an international cross-laboratory experiment. 2021 ,	6
122	Using unsorted sweep-net samples to rapidly assess macroinvertebrate biodiversity. 2021 , 40, 551-565	1
121	Extensive sex-specific and regional variations observed in the microbiome of Dermacentor reticulatus. 2021 , 12, 101767	1
120	Haplotype-level metabarcoding of freshwater macroinvertebrate species: a prospective tool for population genetic analysis.	O
119	Capture by hybridization for full-length barcode-based eukaryotic and prokaryotic biodiversity inventories of deep sea ecosystems. 2021 ,	O
118	Internal transcribed spacer primer evaluation for vascular plant metabarcoding. 5,	2
117	Plant biodiversity assessment through pollen DNA metabarcoding in Natura 2000 habitats (Italian Alps). 2021 , 11, 18226	1
116	Is it possible to understand a book missing a quarter of the letters? Unveiling the belowground species richness of grasslands. 2021 , 107683	O
115	Application of Next Generation Semiconductor-Based Sequencing for the Identification of () Alleles from Honey DNA. 2021 , 12,	1

114	Coming of age for COI metabarcoding of whole organism community DNA: Towards bioinformatic harmonisation. 2021 ,	4
113	Connectivity, diversity, and hybridization between two endemic fish species (Percilia spp.) in a complex temperate landscape. 1	O
112	Viral quasispecies quantitative analysis: a novel approach for appraising the immune tolerant phase of chronic hepatitis B virus infection. 2021 , 10, 842-851	1
111	Linking Omics Approaches to Medicinal Plants and Human Health. 2019 , 31-57	2
110	Decision making and best practices for taxonomy-free eDNA metabarcoding in biomonitoring using Hill numbers.	4
109	Assessment of current taxonomic assignment strategies for metabarcoding eukaryotes.	2
108	Over 2.5 million COI sequences in GenBank and growing.	2
107	SPIKEPIPE: A metagenomic pipeline for the accurate quantification of eukaryotic species occurrences and abundances using DNA barcodes or mitogenomes.	2
106	Studying ecosystems with DNA metabarcoding: lessons from aquatic biomonitoring.	9
105	The current state of DNA barcoding of macroalgae in the Mediterranean Sea: presently lacking but urgently required. 2020 , 63, 253-272	13
105		13
	urgently required. 2020 , 63, 253-272 A flexible pipeline combining clustering and correction tools for prokaryotic and eukaryotic	
104	urgently required. 2020, 63, 253-272 A flexible pipeline combining clustering and correction tools for prokaryotic and eukaryotic metabarcoding. 100043 Towards conserving natural diversity: A biotic inventory by observations, specimens, DNA	1
104	A flexible pipeline combining clustering and correction tools for prokaryotic and eukaryotic metabarcoding. 100043 Towards conserving natural diversity: A biotic inventory by observations, specimens, DNA barcoding and high-throughput sequencing methods. 2020, 8, e50124 About Notiophilus Dumfil, 1806 (Coleoptera, Carabidae): Species delineation and phylogeny using	1
104	A flexible pipeline combining clustering and correction tools for prokaryotic and eukaryotic metabarcoding. 100043 Towards conserving natural diversity: A biotic inventory by observations, specimens, DNA barcoding and high-throughput sequencing methods. 2020, 8, e50124 About Notiophilus Dumfil, 1806 (Coleoptera, Carabidae): Species delineation and phylogeny using DNA barcodes. 2019, 66, 63-73 SoEM: a novel PCR-free biodiversity assessment method based on small-organelles enriched	1 1 5
104	A flexible pipeline combining clustering and correction tools for prokaryotic and eukaryotic metabarcoding. 100043 Towards conserving natural diversity: A biotic inventory by observations, specimens, DNA barcoding and high-throughput sequencing methods. 2020, 8, e50124 About Notiophilus Dumfil, 1806 (Coleoptera, Carabidae): Species delineation and phylogeny using DNA barcodes. 2019, 66, 63-73 SoEM: a novel PCR-free biodiversity assessment method based on small-organelles enriched metagenomics. 2019, 34, 57-70 Genome skimming is a low-cost and robust strategy to assemble complete mitochondrial genomes	1 1 5
104 103 102 101	A flexible pipeline combining clustering and correction tools for prokaryotic and eukaryotic metabarcoding. 100043 Towards conserving natural diversity: A biotic inventory by observations, specimens, DNA barcoding and high-throughput sequencing methods. 2020, 8, e50124 About Notiophilus Dumfil, 1806 (Coleoptera, Carabidae): Species delineation and phylogeny using DNA barcodes. 2019, 66, 63-73 SoEM: a novel PCR-free biodiversity assessment method based on small-organelles enriched metagenomics. 2019, 34, 57-70 Genome skimming is a low-cost and robust strategy to assemble complete mitochondrial genomes from ethanol preserved specimens in biodiversity studies. 2019, 7, e7543 The diet of otters () on the Agri river system, one of the most important presence sites in Italy: a	1 1 5 7 18

96	Water quality and microbial load: a double-threshold identification procedure intended for space applications.	
95	DAIRYdb: A manually curated gold standard reference database for improved taxonomy annotation of 16S rRNA gene sequences from dairy products.	
94	Enhancing DNA metabarcoding performance and applicability with bait capture enrichment and DNA from conservative ethanol.	
93	COI metabarcoding primer choice affects richness and recovery of indicator taxa in freshwater systems.	1
92	Establishing insect community composition using metabarcoding of soil samples, and preservative ethanol and homogenate from Malaise trap catches: surprising inconsistencies between methods.	2
91	Variations in terrestrial arthropod DNA metabarcoding methods recovers robust beta diversity but variable richness and site indicators based on exact sequence variants.	
90	Editorial: Stressors Acting on Aquatic Ecosystems: High-Throughput Sequencing Approaches to Shed Light on Human-Nature Interactions. 2021 , 9,	О
89	Rapid quantitative assessment of fish larvae community composition using metabarcoding.	O
88	The utility of a metagenomics approach for marine biomonitoring.	4
87	METAWORKS: A flexible, scalable bioinformatic pipeline for multi-marker biodiversity assessments.	3
86	eDNA metabarcoding outperforms traditional fisheries sampling and reveals fine-scale heterogeneity in a temperate freshwater lake.	1
85	Environmental DNA for tracking waterhole visitation in savanna ecosystems.	О
84	ExTaxsI: an exploration tool of biodiversity molecular data.	О
83	Sampling of Plant Material to Study Endophytes in Small, Large, and Woody Plants. 2021 , 2232, 37-42	О
82	Full Issue PDF. 2021 , 5, 249-366	
81	Coupling ecological network analysis with high-throughput sequencing-based surveys: Lessons from the next-generation biomonitoring project. 2022 , 65, 367-430	1
80	Towards environmental DNA-based bioassessment of freshwater reservoirs with small volumes of water: robust molecular protocols.	O
79	MetaBARFcoding: DNA-barcoding of regurgitated prey yields insights into Christmas shearwater (Puffinus nativitatis) foraging ecology at H[anik[[Kure Atoll), Hawai?i.	1

78	eDNA and Bioassessment of Rivers. 2021 ,	
77	Environmental DNA Advancing Our Understanding and Conservation of Inland Waters. 2021,	1
76	Dealing with the promise of metabarcoding in mega-event biomonitoring: EXPO2015 unedited data.	
75	Inferring microbiota functions from taxonomic genes: a review 2022, 11,	3
74	ExTaxsI: an exploration tool of biodiversity molecular data 2022, 11,	1
73	ORTHOSKIM: in silico sequence capture from genomic and transcriptomic libraries for phylogenomic and barcoding applications 2022 ,	O
72	Organic matter and metal loadings influence the spatial gradient of the benthic bacterial community in a temperate estuary. 2022 ,	O
71	Assessment of the environmental distribution of the protozoan parasite Perkinsus olseni by next-generation sequencing, qPCR and histopathology allows the identification of alternative bivalve hosts. 2022 , 552, 737984	O
70	Differential gene expression and chemical patterns of an intertidal crab inhabiting a polluted port and an adjacent marine protected area 2022 , 153463	O
69	Diversity Patterns and Drivers of Soil Microbial Communities Along an Elevational Gradient in the Southern Himalayas, China.	
68	MOLECULAR INSIGHT REVEALS BROAD-SCALE SPATIAL PATTERNS IN FLOODPLAIN CILIATE COMMUNITIES, WHILE MORPHOLOGY REFLECTS LOCAL ENVIRONMENTAL CONTROLS.	
67	Fungal communities in feces of the frugivorous bat Ectophylla alba and its highly specialized Ficus colubrinae diet 2022 , 4, 24	
66	Deep selection shapes the intragenomic diversity of rRNA genes.	
65	Cattle manure application triggers short-term dominance of Acinetobacter in soil microbial communities. 2022 , 176, 104466	O
64	Table_1.XLSX. 2018 ,	
63	Data_Sheet_1.docx. 2018 ,	
62	Data_Sheet_1.CSV. 2019 ,	
61	Data_Sheet_2.CSV. 2019 ,	

(2020-2019)



42	Data_Sheet_5.docx. 2020 ,	
41	Taxonomy Informed Clustering, an Optimized Method for Purer and More Informative Clusters in Diversity Analysis and Microbiome Profiling. 2022 , 2,	O
40	Environmental genomics applications for environmental management activities in the oil and gas industry: state-of-the-art review and future research needs. 2022 , 62, S310-S316	
39	DNA barcoding and metabarcoding of highly diverse aquatic mites (Acarina) can improve their use in routine biological monitoring. 2022 ,	
38	Implementation of Genetic Markers from Molecular Systematics to DNA Taxonomy and Field Application. 2022 , 339-358	
37	Sensitive and accurate DNA metabarcoding of parasitic helminth mock communities using the mitochondrial rRNA genes. 2022 , 12,	Ο
36	Comparison of traditional and DNA metabarcoding samples for monitoring tropical soil arthropods (Formicidae, Collembola and Isoptera). 2022 , 12,	О
35	Microbial Community Composition of the Antarctic Ecosystems: Review of the Bacteria, Fungi, and Archaea Identified through an NGS-Based Metagenomics Approach. 2022 , 12, 916	2
34	Diversity patterns and drivers of soil bacterial and fungal communities along elevational gradients in the Southern Himalayas, China. 2022 , 178, 104563	1
33	Environment biomonitoring with eDNAA new perspective to identify biodiversity. 2022, 109-164	
32	Potential of Meta-Omics to Provide Modern Microbial Indicators for Monitoring Soil Quality and Securing Food Production. 13,	О
31	Simultaneous compression of multiple error-corrected short-read sets for faster data transmission and better de novo assemblies.	
30	Changes in bovine milk bacterial microbiome from healthy and subclinical mastitis affected animals of the Girolando, Gyr, Guzera, and Holstein breeds.	O
29	The use of environmental DNA to monitor impacted coastal estuaries. 2022, 181, 113860	O
28	High-throughput degraded DNA sequencing of subfossil shells of a critically endangered stenoendemic land snail in the Aegean. 2022 , 175, 107561	О
27	Key factors to consider in the use of environmental DNA metabarcoding to monitor terrestrial ecological restoration. 2022 , 157617	
26	Demystifying eDNA validation. 2022,	
25	The protist community traces seasonality and mesoscale hydrographic features in the oligotrophic Sargasso Sea. 9,	O

24	Characterization of the Fungal Community in Fritillariae Cirrhosae Bulbus through DNA Metabarcoding. 2022 , 8, 876	
23	Metagenomic Insights into the Gut Microbiota of Eudrilus eugeniae (Kinberg) and Its Potential Roles in Agroecosystem. 2022 , 79,	O
22	Bridging a Gap in Metabarcoding Research: The ASV Table Registry. 6,	
21	DNA metabarcoding confirms primary targets and breadth of diet for coral reef butterflyfishes.	O
20	Environmental DNA as a management tool for tracking artificial waterhole use in savanna ecosystems. 2022 , 274, 109712	O
19	Toward global integration of biodiversity big data: a harmonized metabarcode data generation module for terrestrial arthropods. 2022 , 11,	O
18	DNA metabarcoding reveals that coyotes in New York City consume wide variety of native prey species and human food. 10, e13788	O
17	MetaWorks: A flexible, scalable bioinformatic pipeline for high-throughput multi-marker biodiversity assessments. 2022 , 17, e0274260	1
16	Plectus of the Prairie: A Case Study of Taxonomic Resolution from a Nematode Biodiversity Survey. 2022 , 54,	O
15	Towards more effective identification keys: A study of people identifying plant species characters.	O
14	Discovering marine biodiversity in the 21st century. 2022 ,	O
13	Comparative analysis of fish eDNA reveals higher sensitivity achieved through targeted sequence-based metabarcoding.	O
12	Boreal forest soil biotic communities are affected by harvesting, site preparation with no additional effects of higher biomass removal 5 years post-harvest. 2023 , 528, 120636	O
11	All boreal forest successional stages needed to maintain the full suite of soil biodiversity following natural wildfire in jack pine-dominated forest ecosites.	O
10	Varying strength of selection contributes to the intragenomic diversity of rRNA genes. 2022, 13,	O
9	General principles for assignments of communities from eDNA : Open versus closed taxonomic databases.	O
8	Toward eDNA-based bioassessment of freshwater reservoirs with small volumes of water: Robust molecular protocols.	O
7	Using Cyanobacteria and Other Phytoplankton to Assess Trophic Conditions: A qPCR-Based, Multi-Year Study in Twelve Large Rivers across the United States. 2023 , 119679	O

6	Bacterial diversity in the aquatic system in India based on metagenome analysis critical review.	О
5	Bacterial community structure in the alcyoniid Lobophytum pauciflorum.	O
4	Towards DNA-Based Methods Analysis for Honey: An Update. 2023 , 28, 2106	O
3	Environmental DNA (eDNA) applications in freshwater fisheries management and conservation in Canada: overview of current challenges and opportunities.	O
2	Applying molecular and genetic methods to trees and their fungal communities. 2023, 107, 2783-2830	O
1	Optimization of cacao beans fermentation by native species and electromagnetic fields. 2023 , 9, e15065	O