

# Florian Leese

## List of Publications by Year in descending order

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Version: 2024-02-01

151  
papers

7,657  
citations

71061

41  
h-index

76872

74  
g-index

189  
all docs

189  
docs citations

189  
times ranked

7984  
citing authors

#	ARTICLE	IF	CITATIONS
1	Strategies for sample labelling and library preparation in DNA metabarcoding studies. <i>Molecular Ecology Resources</i> , 2022, 22, 1231-1246.	2.2	40
2	Fresh insights into Mediterranean biodiversity: environmental DNA reveals spatio-temporal patterns of stream invertebrate communities on Sicily. <i>Hydrobiologia</i> , 2022, 849, 155-173.	1.0	5
3	A global agenda for advancing freshwater biodiversity research. <i>Ecology Letters</i> , 2022, 25, 255-263.	3.0	95
4	Individual small in-stream barriers contribute little to strong local population genetic structure five strictly aquatic macroinvertebrate taxa. <i>Ecology and Evolution</i> , 2022, 12, e8807.	0.8	6
5	Morphological vs. DNA metabarcoding approaches for the evaluation of stream ecological status with benthic invertebrates: Testing different combinations of markers and strategies of data filtering. <i>Molecular Ecology</i> , 2021, 30, 3203-3220.	2.0	27
6	Ecosystems monitoring powered by environmental genomics: A review of current strategies with an implementation roadmap. <i>Molecular Ecology</i> , 2021, 30, 2937-2958.	2.0	149
7	DNA metabarcoding improves the detection of multiple stressor responses of stream invertebrates to increased salinity, fine sediment deposition and reduced flow velocity. <i>Science of the Total Environment</i> , 2021, 750, 141969.	3.9	14
8	Deep learning and computer vision will transform entomology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	203
9	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.	2.0	26
10	Revealing environmentally driven population dynamics of an Arctic diatom using a novel microsatellite <i>PoolSeq</i> barcoding approach. <i>Environmental Microbiology</i> , 2021, 23, 3809-3824.	1.8	6
11	TaxonTableTools: A comprehensive, platform-independent graphical user interface software to explore and visualise DNA metabarcoding data. <i>Molecular Ecology Resources</i> , 2021, 21, 1705-1714.	2.2	19
12	Social-ecological interactions in the Draa River Basin, southern Morocco: Towards nature conservation and human well-being using the IPBES framework. <i>Science of the Total Environment</i> , 2021, 769, 144492.	3.9	16
13	Cooking small and large portions of 'biodiversity soup': Miniaturized DNA metabarcoding PCRs perform as good as large-volume PCRs. <i>Ecology and Evolution</i> , 2021, 11, 9092-9099.	0.8	10
14	Unlocking our understanding of intermittent rivers and ephemeral streams with genomic tools. <i>Frontiers in Ecology and the Environment</i> , 2021, 19, 574-583.	1.9	9
15	Standardized high-throughput biomonitoring using DNA metabarcoding: Strategies for the adoption of automated liquid handlers. <i>Environmental Science and Ecotechnology</i> , 2021, 8, 100122.	6.7	19
16	Improved freshwater macroinvertebrate detection from environmental DNA through minimized nontarget amplification. <i>Environmental DNA</i> , 2021, 3, 261-276.	3.1	68
17	Revisiting global trends in freshwater insect biodiversity. <i>Wiley Interdisciplinary Reviews: Water</i> , 2021, 8, e1506.	2.8	34
18	A practical guide to DNA-based methods for biodiversity assessment. , 2021, , .		57

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19	Application of deep learning in aquatic bioassessment: Towards automated identification of non-biting midges. <i>Science of the Total Environment</i> , 2020, 711, 135160.	3.9	33
20	A Synthesis of Marine Monitoring Methods With the Potential to Enhance the Status Assessment of the Baltic Sea. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	12
21	Analyzing drivers of speciation in the Southern Ocean using the sea spider species complex <i>Colossendeis megalonyx</i> as a test case. <i>Polar Biology</i> , 2020, 43, 319-342.	0.5	5
22	Using Environmental DNA to Monitor the Reintroduction Success of the Rhine Sculpin ( <i>Cottus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62	1.1	13
23	DNA metabarcoding of stream invertebrates reveals spatio-temporal variation but consistent status class assessments in a natural and urban river. <i>Ecological Indicators</i> , 2020, 115, 106383.	2.6	23
24	Phylogenetic relationship within Cumacea (Crustacea: Peracarida) and genetic variability of two Antarctic species of the family Leuconidae. <i>Scientia Marina</i> , 2020, 84, 385-392.	0.3	3
25	Combining morphological and genomic evidence to resolve species diversity and study speciation processes of the <i>Pallenopsis patagonica</i> (Pycnogonida) species complex. <i>Frontiers in Zoology</i> , 2019, 16, 36.	0.9	12
26	DNA barcode reference libraries for the monitoring of aquatic biota in Europe: Gap-analysis and recommendations for future work. <i>Science of the Total Environment</i> , 2019, 678, 499-524.	3.9	336
27	Trends in DNA barcoding and metabarcoding. <i>Genome</i> , 2019, 62, v-viii.	0.9	21
28	Phylogenomics of the longitarsal Colossendeidae: The evolutionary history of an Antarctic sea spider radiation. <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 206-214.	1.2	23
29	Assessing the influence of sample tagging and library preparation on DNA metabarcoding. <i>Molecular Ecology Resources</i> , 2019, 19, 893-899.	2.2	46
30	Analysis of 13,312 benthic invertebrate samples from German streams reveals minor deviations in ecological status class between abundance and presence/absence data. <i>PLoS ONE</i> , 2019, 14, e0226547.	1.1	29
31	DNA metabarcoding from sample fixative as a quick and voucher-preserving biodiversity assessment method. <i>Genome</i> , 2019, 62, 122-136.	0.9	57
32	When barcoding fails: development of diagnostic nuclear markers for the sibling caddisfly species <i>Sericostoma personatum</i> (Spence in Kirby & Spence, 1826) and <i>Sericostoma flavicorne</i> Schneider, 1845. <i>ZooKeys</i> , 2019, 872, 57-68.	0.5	4
33	Title is missing!. , 2019, 14, e0226547.		0
34	Title is missing!. , 2019, 14, e0226547.		0
35	Title is missing!. , 2019, 14, e0226547.		0
36	Title is missing!. , 2019, 14, e0226547.		0

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37	Cryptic species and their utilization of indigenous and non-indigenous intermediate hosts in the acanthocephalan <i>Polymorphus minutus</i> sensu lato (Polymorphidae). <i>Parasitology</i> , 2018, 145, 1421-1429.	0.7	16
38	Detecting signatures of positive selection in non-model species using genomic data. <i>Zoological Journal of the Linnean Society</i> , 2018, 184, 528-583.	1.0	67
39	Responses of stream microbes to multiple anthropogenic stressors in a mesocosm study. <i>Science of the Total Environment</i> , 2018, 633, 1287-1301.	3.9	15
40	Genome-wide single-nucleotide polymorphism data reveal cryptic species within cryptic freshwater snail species – The case of the <i>Ancylus fluviatilis</i> species complex. <i>Ecology and Evolution</i> , 2018, 8, 1063-1072.	0.8	32
41	A simple centrifugation protocol for metagenomic studies increases mitochondrial <i>scpDNA</i> yield by two orders of magnitude. <i>Methods in Ecology and Evolution</i> , 2018, 9, 1070-1074.	2.2	9
42	Fishing in troubled waters: Revealing genomic signatures of local adaptation in response to freshwater pollutants in two macroinvertebrates. <i>Science of the Total Environment</i> , 2018, 633, 875-891.	3.9	15
43	Implementation options for DNA-based identification into ecological status assessment under the European Water Framework Directive. <i>Water Research</i> , 2018, 138, 192-205.	5.3	275
44	Multiple-stressor effects on stream macroinvertebrate communities: A mesocosm experiment manipulating salinity, fine sediment and flow velocity. <i>Science of the Total Environment</i> , 2018, 610-611, 961-971.	3.9	90
45	<i>ddrage</i> : A data set generator to evaluate <i>ddRADseq</i> analysis software. <i>Molecular Ecology Resources</i> , 2018, 18, 681-690.	2.2	7
46	Estimating intraspecific genetic diversity from community DNA metabarcoding data. <i>PeerJ</i> , 2018, 6, e4644.	0.9	132
47	DNA metabarcoding reveals the complex and hidden responses of chironomids to multiple stressors. <i>Environmental Sciences Europe</i> , 2018, 30, .	2.6	53
48	The future of biotic indices in the ecogenomic era: Integrating (e)DNA metabarcoding in biological assessment of aquatic ecosystems. <i>Science of the Total Environment</i> , 2018, 637-638, 1295-1310.	3.9	377
49	Why We Need Sustainable Networks Bridging Countries, Disciplines, Cultures and Generations for Aquatic Biomonitoring 2.0: A Perspective Derived From the DNAqua-Net COST Action. <i>Advances in Ecological Research</i> , 2018, 58, 63-99.	1.4	120
50	Feeding ecology in sea spiders (Arthropoda: Pycnogonida): what do we know?. <i>Frontiers in Zoology</i> , 2018, 15, 7.	0.9	17
51	Comparison of environmental DNA and bulk-sample metabarcoding using highly degenerate cytochrome <i>c</i> oxidase I primers. <i>Molecular Ecology Resources</i> , 2018, 18, 1456-1468.	2.2	93
52	Distinct sensitivity of fungal freshwater guilds to water quality. <i>Mycological Progress</i> , 2017, 16, 155-169.	0.5	24
53	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	13.7	332
54	RAD sequencing resolves fine-scale population structure in a benthic invertebrate: implications for understanding phenotypic plasticity. <i>Royal Society Open Science</i> , 2017, 4, 160548.	1.1	75

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55	A <sc>DNA</sc> barcode library for Germany's mayflies, stoneflies and caddisflies (Ephemeroptera, Tj ETQq1,1,0.784314 rgBT 0	2.2	67
56	Assessing strengths and weaknesses of DNA metabarcoding-based macroinvertebrate identification for routine stream monitoring. <i>Methods in Ecology and Evolution</i> , 2017, 8, 1265-1275.	2.2	245
57	Sorting things out: Assessing effects of unequal specimen biomass on <sc>DNA</sc> metabarcoding. <i>Ecology and Evolution</i> , 2017, 7, 6918-6926.	0.8	144
58	Insights into species diversity of the genus <i>Hydropsyche</i> Pictet, 1834 (Hydropsychidae, Trichoptera) from the Lake Kinneret catchment (Israel). <i>Aquatic Insects</i> , 2017, 38, 125-140.	0.6	1
59	Deciphering the origin of mito-nuclear discordance in two sibling caddisfly species. <i>Molecular Ecology</i> , 2017, 26, 5705-5715.	2.0	25
60	The complete mitochondrial genome of a cryptic amphipod species from the <i>Gammarus fossarum</i> complex. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 17-18.	0.2	12
61	<sc>PrimerMiner</sc>: an <sc>r</sc> package for development and <i>in silico</i> validation of <sc>DNA</sc> metabarcoding primers. <i>Methods in Ecology and Evolution</i> , 2017, 8, 622-626.	2.2	81
62	Comparative study of bisected proboscides of Pycnogonida. <i>Organisms Diversity and Evolution</i> , 2017, 17, 121-135.	0.7	11
63	Validation and Development of COI Metabarcoding Primers for Freshwater Macroinvertebrate Bioassessment. <i>Frontiers in Environmental Science</i> , 2017, 5, .	1.5	145
64	Nuclear and Mitochondrial Gene Data Support Recent Radiation within the Sea Spider Species Complex <i>Pallenopsis patagonica</i> . <i>Frontiers in Ecology and Evolution</i> , 2017, 4, .	1.1	14
65	Digital gene expression analysis with sample multiplexing and PCR duplicate detection: A straightforward protocol. <i>BioTechniques</i> , 2016, 61, 26-32.	0.8	4
66	Cryptic diversity and population structure at small scales: the freshwater snail <i>Ancylus</i> (Planorbidae, Pulmonata) in the Montseny mountain range. <i>Annales De Limnologie</i> , 2016, 52, 387-399.	0.6	13
67	Multiple-stressor effects on stream invertebrates: a mesocosm experiment manipulating nutrients, fine sediment and flow velocity. <i>Freshwater Biology</i> , 2016, 61, 362-375.	1.2	90
68	Drastic underestimation of amphipod biodiversity in the endangered Irano-Anatolian and Caucasus biodiversity hotspots. <i>Scientific Reports</i> , 2016, 6, 22507.	1.6	48
69	Widely distributed and regionally isolated! Drivers of genetic structure in <i>Gammarus fossarum</i> in a human-impacted landscape. <i>BMC Evolutionary Biology</i> , 2016, 16, 153.	3.2	72
70	Ocean currents determine functional connectivity in an Antarctic deep-sea shrimp. <i>Marine Ecology</i> , 2016, 37, 1336-1344.	0.4	23
71	The mitochondrial genomes of the caddisflies <i>Sericostoma personatum</i> and <i>Thremma gallicum</i> (Insecta: Trichoptera). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3293-3294.	0.7	5
72	Multiple-stressor effects on stream invertebrates: DNA barcoding reveals contrasting responses of cryptic mayfly species. <i>Ecological Indicators</i> , 2016, 61, 159-169.	2.6	87

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73	The mitochondrial genome of the Arizona Snowfly <i>Mesocapnia arizonensis</i> (Plecoptera, Capniidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3365-3366.	0.7	11
74	Testing the potential of a ribosomal 16S marker for DNA metabarcoding of insects. PeerJ, 2016, 4, e1966.	0.9	111
75	Transcriptional profiling of predator-induced phenotypic plasticity in <i>Daphnia pulex</i> . Frontiers in Zoology, 2015, 12, 18.	0.9	32
76	Can DNA-Based Ecosystem Assessments Quantify Species Abundance? Testing Primer Bias and Biomass-Sequence Relationships with an Innovative Metabarcoding Protocol. PLoS ONE, 2015, 10, e0130324.	1.1	540
77	Regional differentiation and extensive hybridization between mitochondrial clades of the Southern Ocean giant sea spider <i>Colossendeis megalonyx</i> . Royal Society Open Science, 2015, 2, 140424.	1.1	30
78	Genetic data support independent glacial refugia and open ocean barriers to dispersal for the Southern Ocean sea spider <i>Austropallene cornigera</i> (Mrbius, 1902). Journal of Crustacean Biology, 2015, 35, 480-490.	0.3	49
79	Assessing the phylogeographic history of the montane caddisfly <i>Tremma gallicum</i> using mitochondrial and restriction-associated DNA (RAD) markers. Ecology and Evolution, 2015, 5, 648-662.	0.8	25
80	A puzzle with many pieces: the genetic structure and diversity of <i>Phaeocystis antarctica</i> Karsten (Prymnesiophyta). European Journal of Phycology, 2015, 50, 112-124.	0.9	14
81	Dopamine is a key regulator in the signalling pathway underlying predator-induced defences in <i>Daphnia</i> . Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20151440.	1.2	40
82	Rapid evolution of chemosensory receptor genes in a pair of sibling species of orchid bees (Apidae: <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 56</i> )	3.2	56
83	Invaders, natives and their enemies: distribution patterns of amphipods and their microsporidian parasites in the Ruhr Metropolis, Germany. Parasites and Vectors, 2015, 8, 419.	1.0	66
84	Characterization of fossilized relatives of the White Spot Syndrome Virus in genomes of decapod crustaceans. BMC Evolutionary Biology, 2015, 15, 142.	3.2	14
85	The complete mitochondrial genome of the stonefly <i>Dinocras cephalotes</i> (Plecoptera, Perlidae). Mitochondrial DNA, 2015, 26, 469-470.	0.6	28
86	A new genus and new species of Desmosomatidae Sars, 1897 (Isopoda) from the eastern South Atlantic abyss described by means of integrative taxonomy. Marine Biodiversity, 2015, 45, 7-61.	0.3	36
87	A Multi-gene Analysis Reveals Multiple Highly Divergent Lineages of The Isopod Chelator <i>Insignis</i> (Hansen, 1916) South of Iceland. Polish Polar Research, 2014, 35, 225-242.	0.9	35
88	<i>Pallenopsis patagonica</i> (Hoek, 1881) - a species complex revealed by morphology and DNA barcoding, with description of a new species of <i>Pallenopsis</i> Wilson, 1881. Zoological Journal of the Linnean Society, 2014, 170, 110-131.	1.0	26
89	Integrating molecular tools into freshwater ecology: developments and opportunities. Freshwater Biology, 2014, 59, 1559-1576.	1.2	51
90	Genetic diversity and dispersal potential of the stonefly <i>Dinocras cephalotes</i> in a central European low mountain range. Freshwater Science, 2014, 33, 181-192.	0.9	39

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91	Molecular evidence for further overlooked species within the <i>Gammarus fossarum</i> complex (Crustacea: Amphipoda). <i>Hydrobiologia</i> , 2014, 721, 165-184.	1.0	86
92	Phylogeographical analysis of <i>Ligia oceanica</i> (Crustacea: Isopoda) reveals two deeply divergent mitochondrial lineages. <i>Biological Journal of the Linnean Society</i> , 2014, 112, 16-30.	0.7	17
93	“Late” male sperm precedence in polyandrous wool-carder bees and the evolution of male resource defence in Hymenoptera. <i>Animal Behaviour</i> , 2014, 90, 211-217.	0.8	6
94	Detection and Removal of PCR Duplicates in Population Genomic ddRAD Studies by Addition of a Degenerate Base Region (DBR) in Sequencing Adapters. <i>Biological Bulletin</i> , 2014, 227, 146-160.	0.7	70
95	Isolation and characterization of nine polymorphic microsatellite markers for the deep-sea shrimp <i>Nematocarcinus lanceopes</i> (Crustacea: Decapoda: Caridea). <i>BMC Research Notes</i> , 2013, 6, 75.	0.6	7
96	Morphological and genetic analyses of xeniid soft coral diversity (Octocorallia; Alcyonacea). <i>Organisms Diversity and Evolution</i> , 2013, 13, 135-150.	0.7	16
97	Evidence from morphological and genetic data confirms that <i>Colossendeis tenera</i> Hilton, 1943 (Arthropoda: Pycnogonida), does not belong to the <i>Colossendeis megalonyx</i> Hoek, 1881 complex. <i>Organisms Diversity and Evolution</i> , 2013, 13, 151-162.	0.7	22
98	Patterns, processes and vulnerability of Southern Ocean benthos: a decadal leap in knowledge and understanding. <i>Marine Biology</i> , 2013, 160, 2295-2317.	0.7	79
99	Pan genome of the phytoplankton <i>Emiliania huxleyi</i> underpins its global distribution. <i>Nature</i> , 2013, 499, 209-213.	13.7	448
100	Isolation and characterization of 10 polymorphic loci for the giant Antarctic isopod, <i>Glyptonotus antarcticus</i> . <i>Conservation Genetics Resources</i> , 2013, 5, 963-965.	0.4	0
101	Exploring Pandora's Box: Potential and Pitfalls of Low Coverage Genome Surveys for Evolutionary Biology. <i>PLoS ONE</i> , 2012, 7, e49202.	1.1	31
102	Isolation and characterisation of nine microsatellite markers in the boring giant clam ( <i>Tridacna</i> ) <i>Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 30</i>	0.3	4
103	Are shoals of minnow <i>Phoxinus phoxinus</i> formed by close kin?. <i>Journal of Fish Biology</i> , 2012, 80, 713-721.	0.7	6
104	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 August 2010 – 30 September 2010. <i>Molecular Ecology Resources</i> , 2011, 11, 219-222.	2.2	48
105	Analyzing intraspecific genetic variation. <i>Crustacean Issues</i> , 2011, , 3-30.	0.9	6
106	Molecular evolution of a chordate specific family of G protein-coupled receptors. <i>BMC Evolutionary Biology</i> , 2011, 11, 234.	3.2	16
107	The mitochondrial genome of <i>Colossendeis megalonyx</i> supports a basal position of Colossendeidae within the Pycnogonida. <i>Molecular Phylogenetics and Evolution</i> , 2011, 58, 553-558.	1.2	20
108	First genetic data for species of the genus <i>Haploniscus</i> Richardson, 1908 (Isopoda: Asellota:) <i>Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 62 T</i>	0.2	39

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109	Diversification and Molecular Evolution of ATOH8, a Gene Encoding a bHLH Transcription Factor. PLoS ONE, 2011, 6, e23005.	1.1	24
110	Long-distance island hopping without dispersal stages: transportation across major zoogeographic barriers in a Southern Ocean isopod. Die Naturwissenschaften, 2010, 97, 583-594.	0.6	80
111	Genetic homogeneity and circum-Antarctic distribution of two benthic shrimp species of the Southern Ocean, <i>Chorismus antarcticus</i> and <i>Nematocarcinus lanceopes</i> . Marine Biology, 2010, 157, 1783-1797.	0.7	74
112	Cryptic mitochondrial lineages in the widespread pycnogonid <i>Colossendeis megalonyx</i> Hoek, 1881 from Antarctic and Subantarctic waters. Polar Biology, 2010, 33, 281-292.	0.5	95
113	Genome-wide analysis of tandem repeats in <i>Daphnia pulex</i> - a comparative approach. BMC Genomics, 2010, 11, 277.	1.2	87
114	Predator-induced defences in <i>Daphnia pulex</i> : Selection and evaluation of internal reference genes for gene expression studies with real-time PCR. BMC Molecular Biology, 2010, 11, 50.	3.0	52
115	Ecological genomics: steps towards unraveling the genetic basis of inducible defenses in <i>Daphnia</i> . BMC Biology, 2010, 8, 51.	1.7	38
116	Genetic variability, shell and sperm morphology suggest that the surf clams <i>Donax marincovichi</i> and <i>D. obesulus</i> are one species. Journal of Molluscan Studies, 2009, 75, 381-390.	0.4	19
117	STAMP: Extensions to the STADEN sequence analysis package for high throughput interactive microsatellite marker design. BMC Bioinformatics, 2009, 10, 41.	1.2	40
118	Identification and characterization of microsatellites from the Antarctic isopod <i>Ceratoserolis trilobitoides</i> : nuclear evidence for cryptic species. Conservation Genetics, 2008, 9, 1369-1372.	0.8	29
119	Cryptic speciation in a benthic isopod from Patagonian and Falkland Island waters and the impact of glaciations on its population structure. Frontiers in Zoology, 2008, 5, 19.	0.9	53
120	Isolation and characterization of microsatellite markers from the marine isopods <i>Serolis paradoxa</i> and <i>Septemserolis septemcarinata</i> (Crustacea: Peracarida). Molecular Ecology Resources, 2008, 8, 818-821.	2.2	6
121	Isolation of microsatellites from unknown genomes using known genomes as enrichment templates. Limnology and Oceanography: Methods, 2008, 6, 412-426.	1.0	31
122	The utility of fast evolving molecular markers for studying speciation in the Antarctic benthos. Polar Biology, 2007, 30, 513-521.	0.5	32
123	sp. nov., a new deep-sea species from the Angola Basin (Crustacea, Isopoda, Asellota, Janiroidea.) Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.7	2
124	Metadata standards and practical guidelines for specimen and DNA curation when building barcode reference libraries for aquatic life. Metabarcoding and Metagenomics, 0, 5, .	0.0	29
125	New insights into Danube's macroinvertebrate communities from DNA metabarcoding as part of the Joint Danube Survey 4 (JDS4). ARPHA Conference Abstracts, 0, 4, .	0.0	1
126	Technical challenges when scaling up macroinvertebrate DNA metabarcoding. ARPHA Conference Abstracts, 0, 4, .	0.0	0



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127	Morphological features of larvae of <i>Drusus osogovicus</i> Kumanski, 1980 (Insecta, Trichoptera) from the Republic of North Macedonia, DNA barcoding of the species and notes on its ecology and distribution. ARPHA Conference Abstracts, 0, 4, .	0.0	2
128	Improved freshwater macroinvertebrate detection from environmental DNA through minimized nontarget amplification. ARPHA Conference Abstracts, 0, 4, .	0.0	0
129	Wet grinding of invertebrate bulk samples – a scalable and cost-efficient protocol for metabarcoding and metagenomics. ARPHA Conference Abstracts, 0, 4, .	0.0	0
130	TaxonTableTools - A comprehensive, platform-independent graphical user interface software to explore and visualise DNA metabarcoding data. ARPHA Conference Abstracts, 0, 4, .	0.0	0
131	Analyzing multiple stressor effects on EPT taxa in a mesocosm experiment with DNA metabarcoding. ARPHA Conference Abstracts, 0, 4, .	0.0	0
132	Application of eDNA method in the detection of <i>Cordulegaster</i> (Insecta: Odonata) species. ARPHA Conference Abstracts, 0, 4, .	0.0	0
133	Assessment of the macroinvertebrate community of the Vjosa river through non-destructive DNA metabarcoding of preservative ethanol. ARPHA Conference Abstracts, 0, 4, .	0.0	0
134	Beyond fish eDNA metabarcoding: Field replicates disproportionately improve the detection of stream-associated vertebrate species. ARPHA Conference Abstracts, 0, 4, .	0.0	0
135	Community metabarcoding uncovers vast diversity and a lack of barcode references for aquatic invertebrates in Carpathian spring fens. ARPHA Conference Abstracts, 0, 4, .	0.0	0
136	Welcome to DNAQUA2021 International Conference. ARPHA Conference Abstracts, 0, 4, .	0.0	1
137	Wet grinding of invertebrate bulk samples – a scalable and cost-efficient protocol for metabarcoding and metagenomics. Metabarcoding and Metagenomics, 0, 5, .	0.0	12
138	Beyond fish eDNA metabarcoding: Field replicates disproportionately improve the detection of stream associated vertebrate species. Metabarcoding and Metagenomics, 0, 5, .	0.0	16
139	DNAqua-Net or how to navigate on the stormy waters of standards and legislations. Biodiversity Information Science and Standards, 0, 2, e25953.	0.0	2
140	Taming the Wild West of Molecular Tools Application in Aquatic Research and Biomonitoring. Biodiversity Information Science and Standards, 0, 3, .	0.0	3
141	Short COI markers for freshwater macroinvertebrate metabarcoding. Metabarcoding and Metagenomics, 0, 1, e14625.	0.0	108
142	Using DNA metabarcoding for assessing chironomid diversity and community change in mosquito controlled temporary wetlands. Metabarcoding and Metagenomics, 0, 1, e21060.	0.0	1
143	Combining NCBI and BOLD databases for OTU assignment in metabarcoding and metagenomic datasets: The BOLD_NCBI_Merger. Metabarcoding and Metagenomics, 0, 1, e22262.	0.0	17
144	Using DNA metabarcoding for assessing chironomid diversity and community change in mosquito controlled temporary wetlands. Metabarcoding and Metagenomics, 0, 2, e21060.	0.0	21

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145	Advancing the use of molecular methods for routine freshwater macroinvertebrate biomonitoring – the need for calibration experiments. <i>Metabarcoding and Metagenomics</i> , 0, 3, .	0.0	48
146	Exploring the potential of metabarcoding to disentangle macroinvertebrate community dynamics in intermittent streams. <i>Metabarcoding and Metagenomics</i> , 0, 4, .	0.0	12
147	Can metabarcoding resolve intraspecific genetic diversity changes to environmental stressors? A test case using river macrozoobenthos. <i>Metabarcoding and Metagenomics</i> , 0, 4, .	0.0	18
148	BOLDigger – a Python package to identify and organise sequences with the Barcode of Life Data systems. <i>Metabarcoding and Metagenomics</i> , 0, 4, .	0.0	62
149	DNAqua-Net: Developing new genetic tools for bioassessment and monitoring of aquatic ecosystems in Europe. <i>Research Ideas and Outcomes</i> , 0, 2, e11321.	1.0	154
150	New molecular methods to assess biodiversity. Potentials and pitfalls of DNA metabarcoding: a workshop report. <i>Research Ideas and Outcomes</i> , 0, 5, .	1.0	2
151	Let me see your iD: Impacts of Environmental Stressors on Aquatic Ecosystems Assessed by (e)DNA Metabarcoding. <i>Biodiversity Information Science and Standards</i> , 0, 2, e25983.	0.0	0