

Vasco Elbrecht

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

2,961
citations

279487

23
h-index

360668

35
g-index

90
all docs

90
docs citations

90
times ranked

2964
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Assessing strengths and weaknesses of DNA metabarcoding-based macroinvertebrate identification for routine stream monitoring. Methods in Ecology and Evolution, 2017, 8, 1265-1275.	2.2	245
3	Validation of COI metabarcoding primers for terrestrial arthropods. PeerJ, 2019, 7, e7745.	0.9	161
4	Validation and Development of COI Metabarcoding Primers for Freshwater Macroinvertebrate Bioassessment. Frontiers in Environmental Science, 2017, 5, .	1.5	145
5	Sorting things out: Assessing effects of unequal specimen biomass on <sc>DNA</sc> metabarcoding. Ecology and Evolution, 2017, 7, 6918-6926.	0.8	144
6	Estimating intraspecific genetic diversity from community DNA metabarcoding data. PeerJ, 2018, 6, e4644.	0.9	132
7	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. Advances in Ecological Research, 2018, 58, 63-99.	1.4	120
8	Testing the potential of a ribosomal 16S marker for DNA metabarcoding of insects. PeerJ, 2016, 4, e1966.	0.9	111
9	Short COI markers for freshwater macroinvertebrate metabarcoding. Metabarcoding and Metagenomics, 0, 1, e14625.	0.0	108
10	Metabarcoding a diverse arthropod mock community. Molecular Ecology Resources, 2019, 19, 711-727.	2.2	107
11	Multiple-stressor effects on stream invertebrates: a mesocosm experiment manipulating nutrients, fine sediment and flow velocity. Freshwater Biology, 2016, 61, 362-375.	1.2	90
12	Multiple-stressor effects on stream macroinvertebrate communities: A mesocosm experiment manipulating salinity, fine sediment and flow velocity. Science of the Total Environment, 2018, 610-611, 961-971.	3.9	90
13	<sc>PrimerMiner</sc>: an <sc>r</sc> package for development and <i>in silico</i> validation of <sc>DNA</sc> metabarcoding primers. Methods in Ecology and Evolution, 2017, 8, 622-626.	2.2	81
14	Scaling up <sc>DNA</sc> metabarcoding for freshwater macrozoobenthos monitoring. Freshwater Biology, 2019, 64, 380-387.	1.2	76
15	Improved freshwater macroinvertebrate detection from environmental DNA through minimized nontarget amplification. Environmental DNA, 2021, 3, 261-276.	3.1	68
16	A practical guide to DNA-based methods for biodiversity assessment. , 2021, , .		57
17	DNA metabarcoding reveals the complex and hidden responses of chironomids to multiple stressors. Environmental Sciences Europe, 2018, 30, .	2.6	53
18	Advancing the use of molecular methods for routine freshwater macroinvertebrate biomonitoring - the need for calibration experiments. Metabarcoding and Metagenomics, 0, 3, .	0.0	48

#	ARTICLE	IF	CITATIONS
19	Assessing the influence of sample tagging and library preparation on DNA metabarcoding. <i>Molecular Ecology Resources</i> , 2019, 19, 893-899.	2.2	46
20	Strategies for sample labelling and library preparation in DNA metabarcoding studies. <i>Molecular Ecology Resources</i> , 2022, 22, 1231-1246.	2.2	40
21	Genetic diversity and dispersal potential of the stonefly <i>Dinocras cephalotes</i> in a central European low mountain range. <i>Freshwater Science</i> , 2014, 33, 181-192.	0.9	39
22	Assessment of stream macroinvertebrate communities with eDNA is not congruent with tissue-based metabarcoding. <i>Molecular Ecology</i> , 2021, 30, 3239-3251.	2.0	38
23	Riparian forests can mitigate warming and ecological degradation of agricultural headwater streams. <i>Freshwater Biology</i> , 2021, 66, 785-798.	1.2	33
24	The complete mitochondrial genome of the stonefly <i>Dinocras cephalotes</i> (Plecoptera, Perlidae). <i>Mitochondrial DNA</i> , 2015, 26, 469-470.	0.6	28
25	A new primer for metabarcoding of spider gut contents. <i>Environmental DNA</i> , 2020, 2, 234-243.	3.1	26
26	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
27	Distinct sensitivity of fungal freshwater guilds to water quality. <i>Mycological Progress</i> , 2017, 16, 155-169.	0.5	24
28	A workflow for accurate metabarcoding using nanopore MinION sequencing. <i>Methods in Ecology and Evolution</i> , 2021, 12, 794-804.	2.2	23
29	Slippage of degenerate primers can cause variation in amplicon length. <i>Scientific Reports</i> , 2018, 8, 10999.	1.6	22
30	Effects of Malaise trap spacing on species richness and composition of terrestrial arthropod bulk samples. <i>Metabarcoding and Metagenomics</i> , 0, 5, .	0.0	21
31	Using DNA metabarcoding for assessing chironomid diversity and community change in mosquito controlled temporary wetlands. <i>Metabarcoding and Metagenomics</i> , 0, 2, e21060.	0.0	21
32	Metabarcoding unsorted kick samples facilitates macroinvertebrate-based biomonitoring with increased taxonomic resolution, while outperforming environmental DNA. <i>Environmental DNA</i> , 2021, 3, 353-371.	3.1	16
33	Pooling size sorted Malaise trap fractions to maximize taxon recovery with metabarcoding. <i>PeerJ</i> , 2021, 9, e12177.	0.9	16
34	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
35	Enhancing DNA metabarcoding performance and applicability with bait capture enrichment and DNA from conservative ethanol. <i>Molecular Ecology Resources</i> , 2020, 20, 79-96.	2.2	15
36	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

#	ARTICLE	IF	CITATIONS
37	Exploring the potential of metabarcoding to disentangle macroinvertebrate community dynamics in intermittent streams. <i>Metabarcoding and Metagenomics</i> , 0, 4, .	0.0	12
38	The mitochondrial genome of the Arizona Snowfly <i>Mesocapnia arizonensis</i> (Plecoptera, Capniidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3365-3366.	0.7	11
39	The power of metabarcoding: Can we improve bioassessment and biodiversity surveys of stream macroinvertebrate communities?. <i>Metabarcoding and Metagenomics</i> , 0, 5, .	0.0	7
40	Isolation, characterization and cross amplification of eleven novel microsatellite loci for the hydrozoan coral <i>Millepora</i> . <i>Conservation Genetics Resources</i> , 2015, 7, 215-217.	0.4	5
41	A bright ideaâ€”metabarcoding arthropods from light fixtures. <i>PeerJ</i> , 2021, 9, e11841.	0.9	3
42	Using DNA metabarcoding for assessing chironomid diversity and community change in mosquito controlled temporary wetlands. <i>Metabarcoding and Metagenomics</i> , 0, 1, e21060.	0.0	1
43	Technical challenges when scaling up macroinvertebrate DNA metabarcoding. <i>ARPHA Conference Abstracts</i> , 0, 4, .	0.0	0
44	Improved freshwater macroinvertebrate detection from environmental DNA through minimized nontarget amplification. <i>ARPHA Conference Abstracts</i> , 0, 4, .	0.0	0