

# Vasco Elbrecht

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9418314/publications.pdf>

Version: 2024-02-01

44  
papers

2,961  
citations

279701

23  
h-index

360920

35  
g-index

90  
all docs

90  
docs citations

90  
times ranked

2964  
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	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
3	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
4	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
5	Riparian forests can mitigate warming and ecological degradation of agricultural headwater streams. <i>Freshwater Biology</i> , 2021, 66, 785-798.	1.2	33
6	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
7	A workflow for accurate metabarcoding using nanopore MinION sequencing. <i>Methods in Ecology and Evolution</i> , 2021, 12, 794-804.	2.2	23
8	A bright idea" metabarcoding arthropods from light fixtures. <i>PeerJ</i> , 2021, 9, e11841.	0.9	3
9	Improved freshwater macroinvertebrate detection from environmental DNA through minimized nontarget amplification. <i>Environmental DNA</i> , 2021, 3, 261-276.	3.1	68
10	Pooling size sorted Malaise trap fractions to maximize taxon recovery with metabarcoding. <i>PeerJ</i> , 2021, 9, e12177.	0.9	16
11	A practical guide to DNA-based methods for biodiversity assessment. , 2021, , .		57
12	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
13	A new primer for metabarcoding of spider gut contents. <i>Environmental DNA</i> , 2020, 2, 234-243.	3.1	26
14	Scaling up <sc>DNA</sc> metabarcoding for freshwater macrozoobenthos monitoring. <i>Freshwater Biology</i> , 2019, 64, 380-387.	1.2	76
15	Assessing the influence of sample tagging and library preparation on DNA metabarcoding. <i>Molecular Ecology Resources</i> , 2019, 19, 893-899.	2.2	46
16	Metabarcoding a diverse arthropod mock community. <i>Molecular Ecology Resources</i> , 2019, 19, 711-727.	2.2	107
17	Validation of COI metabarcoding primers for terrestrial arthropods. <i>PeerJ</i> , 2019, 7, e7745.	0.9	161
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	Estimating intraspecific genetic diversity from community DNA metabarcoding data. <i>PeerJ</i> , 2018, 6, e4644.	0.9	132
21	DNA metabarcoding reveals the complex and hidden responses of chironomids to multiple stressors. <i>Environmental Sciences Europe</i> , 2018, 30, .	2.6	53
22	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
23	Slippage of degenerate primers can cause variation in amplicon length. <i>Scientific Reports</i> , 2018, 8, 10999.	1.6	22
24	Distinct sensitivity of fungal freshwater guilds to water quality. <i>Mycological Progress</i> , 2017, 16, 155-169.	0.5	24
25	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
26	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
27	<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
28	Validation and Development of COI Metabarcoding Primers for Freshwater Macroinvertebrate Bioassessment. <i>Frontiers in Environmental Science</i> , 2017, 5, .	1.5	145
29	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
30	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
31	Testing the potential of a ribosomal 16S marker for DNA metabarcoding of insects. <i>PeerJ</i> , 2016, 4, e1966.	0.9	111
32	Can DNA-Based Ecosystem Assessments Quantify Species Abundance? Testing Primer Bias and Biomass-Sequence Relationships with an Innovative Metabarcoding Protocol. <i>PLoS ONE</i> , 2015, 10, e0130324.	1.1	540
33	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
34	The complete mitochondrial genome of the stonefly <i>Dinocras cephalotes</i> (Plecoptera, Perlidae). <i>Mitochondrial DNA</i> , 2015, 26, 469-470.	0.6	28
35	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
36	Technical challenges when scaling up macroinvertebrate DNA metabarcoding. <i>ARPHA Conference Abstracts</i> , 0, 4, .	0.0	0

#	ARTICLE	IF	CITATIONS
37	Improved freshwater macroinvertebrate detection from environmental DNA through minimized nontarget amplification. ARPHA Conference Abstracts, 0, 4, .	0.0	0
38	Effects of Malaise trap spacing on species richness and composition of terrestrial arthropod bulk samples. Metabarcoding and Metagenomics, 0, 5, .	0.0	21
39	The power of metabarcoding: Can we improve bioassessment and biodiversity surveys of stream macroinvertebrate communities?. Metabarcoding and Metagenomics, 0, 5, .	0.0	7
40	Short COI markers for freshwater macroinvertebrate metabarcoding. Metabarcoding and Metagenomics, 0, 1, e14625.	0.0	108
41	Using DNA metabarcoding for assessing chironomid diversity and community change in mosquito controlled temporary wetlands. Metabarcoding and Metagenomics, 0, 1, e21060.	0.0	1
42	Using DNA metabarcoding for assessing chironomid diversity and community change in mosquito controlled temporary wetlands. Metabarcoding and Metagenomics, 0, 2, e21060.	0.0	21
43	Advancing the use of molecular methods for routine freshwater macroinvertebrate biomonitoring – the need for calibration experiments. Metabarcoding and Metagenomics, 0, 3, .	0.0	48
44	Exploring the potential of metabarcoding to disentangle macroinvertebrate community dynamics in intermittent streams. Metabarcoding and Metagenomics, 0, 4, .	0.0	12