

# Melania E Cristescu

## List of Publications by Year in descending order

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Version: 2024-02-01

80  
papers

4,409  
citations

87888

38  
h-index

118850

62  
g-index

89  
all docs

89  
docs citations

89  
times ranked

5498  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genotype diversity promotes the persistence of <i>Daphnia</i> populations exposed to severe copper stress. <i>Journal of Evolutionary Biology</i> , 2022, 35, 265-277.	1.7	7
2	Environmental RNA degrades more rapidly than environmental DNA across a broad range of pH conditions. <i>Molecular Ecology Resources</i> , 2022, 22, 2640-2650.	4.8	17
3	Environmental nucleic acids: A field-based comparison for monitoring freshwater habitats using eDNA and eRNA. <i>Molecular Ecology Resources</i> , 2022, 22, 2928-2940.	4.8	14
4	Thermal stratification and fish thermal preference explain vertical eDNA distributions in lakes. <i>Molecular Ecology</i> , 2021, 30, 3083-3096.	3.9	55
5	Freshwater zooplankton metapopulations and metacommunities respond differently to environmental and spatial variation. <i>Ecology</i> , 2021, 102, e03224.	3.2	8
6	Speciation in <i>Daphnia</i> . <i>Molecular Ecology</i> , 2021, 30, 1398-1418.	3.9	7
7	Assessment of current taxonomic assignment strategies for metabarcoding eukaryotes. <i>Molecular Ecology Resources</i> , 2021, 21, 2190-2203.	4.8	35
8	Environmental RNA: A Revolution in Ecological Resolution?. <i>Trends in Ecology and Evolution</i> , 2021, 36, 601-609.	8.7	84
9	Towards reproducible metabarcoding data: Lessons from an international cross-laboratory experiment. <i>Molecular Ecology Resources</i> , 2021, , .	4.8	25
10	Integrating physiology and environmental dynamics to operationalize environmental DNA (eDNA) as a means to monitor freshwater macroorganism abundance. <i>Molecular Ecology</i> , 2021, 30, 6531-6550.	3.9	38
11	Release and degradation of environmental DNA and RNA in a marine system. <i>Science of the Total Environment</i> , 2020, 704, 135314.	8.0	126
12	Horizon scan of conservation issues for inland waters in Canada. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2020, 77, 869-881.	1.4	10
13	Breaking ecological barriers: Anthropogenic disturbance leads to habitat transitions, hybridization, and high genetic diversity. <i>Science of the Total Environment</i> , 2020, 740, 140046.	8.0	13
14	Alternative splicing is highly variable among <i>Daphnia pulex</i> lineages in response to acute copper exposure. <i>BMC Genomics</i> , 2020, 21, 433.	2.8	15
15	Metal exposure causes rDNA copy number to fluctuate in mutation accumulation lines of <i>Daphnia pulex</i> . <i>Aquatic Toxicology</i> , 2020, 226, 105556.	4.0	5
16	Benefits of increased colonist quantity and genetic diversity for colonization depend on colonist identity. <i>Oikos</i> , 2019, 128, 1761-1771.	2.7	5
17	Can Environmental RNA Revolutionize Biodiversity Science?. <i>Trends in Ecology and Evolution</i> , 2019, 34, 694-697.	8.7	130
18	Trophic structure modulates community rescue following acidification. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190856.	2.6	22

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19	Mixed evidence for adaptation to environmental pollution. <i>Evolutionary Applications</i> , 2019, 12, 1259-1273.	3.1	28
20	Variation in transcriptional responses to copper exposure across <i>Daphnia pulex</i> lineages. <i>Aquatic Toxicology</i> , 2019, 210, 85-97.	4.0	23
21	The evolution of reproductive isolation in <i>Daphnia</i> . <i>BMC Evolutionary Biology</i> , 2019, 19, 216.	3.2	10
22	Accelerated rates of large-scale mutations in the presence of copper and nickel. <i>Genome Research</i> , 2019, 29, 64-73.	5.5	13
23	Fitness and Genomic Consequences of Chronic Exposure to Low Levels of Copper and Nickel in <i>Daphnia pulex</i> Mutation Accumulation Lines. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 61-71.	1.8	10
24	Optimization and performance testing of a sequence processing pipeline applied to detection of nonindigenous species. <i>Evolutionary Applications</i> , 2018, 11, 891-905.	3.1	23
25	Proteomic Profile of <i>Daphnia pulex</i> using Data-Independent Acquisition Mass Spectrometry and Ion Mobility Separation. <i>Proteomics</i> , 2018, 18, e1700460.	2.2	7
26	Bioinformatics for Biomonitoring: Species Detection and Diversity Estimates Across Next-Generation Sequencing Platforms. <i>Advances in Ecological Research</i> , 2018, , 1-32.	2.7	3
27	Uses and Misuses of Environmental DNA in Biodiversity Science and Conservation. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2018, 49, 209-230.	8.3	218
28	Metabarcoding using multiplexed markers increases species detection in complex zooplankton communities. <i>Evolutionary Applications</i> , 2018, 11, 1901-1914.	3.1	116
29	Selection Constrains High Rates of Tandem Repetitive DNA Mutation in <i>Daphnia pulex</i> . <i>Genetics</i> , 2017, 207, 697-710.	2.9	29
30	Spontaneous Mutation Accumulation in <i>Daphnia pulex</i> in Selection-Free vs. Competitive Environments. <i>Molecular Biology and Evolution</i> , 2017, 34, 160-173.	8.9	67
31	An Individual-Based Modeling Approach to Investigate Sympatric Speciation via Specialized Resource Usage. <i>Open Journal of Ecology</i> , 2017, 07, 222-269.	1.0	3
32	Population attenuation in zooplankton communities during transoceanic transfer in ballast water. <i>Ecology and Evolution</i> , 2016, 6, 6170-6177.	1.9	11
33	The effects of parameter choice on defining molecular operational taxonomic units and resulting ecological analyses of metabarcoding data. <i>Genome</i> , 2016, 59, 981-990.	2.0	73
34	Early detection of aquatic invaders using metabarcoding reveals a high number of nonindigenous species in Canadian ports. <i>Diversity and Distributions</i> , 2016, 22, 1045-1059.	4.1	82
35	Effect of shipping traffic on biofouling invasion success at population and community levels. <i>Biological Invasions</i> , 2016, 18, 3681-3695.	2.4	30
36	Metabarcoding reveals strong spatial structure and temporal turnover of zooplankton communities among marine and freshwater ports. <i>Diversity and Distributions</i> , 2016, 22, 493-504.	4.1	83

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37	Divergence thresholds and divergent biodiversity estimates: can metabarcoding reliably describe zooplankton communities?. <i>Ecology and Evolution</i> , 2015, 5, 2234-2251.	1.9	117
38	Toward accurate molecular identification of species in complex environmental samples: testing the performance of sequence filtering and clustering methods. <i>Ecology and Evolution</i> , 2015, 5, 2252-2266.	1.9	128
39	The contribution of Nicolae Botnariuc to evolutionary biology using systems theory. <i>Genome</i> , 2015, 58, iii-vi.	2.0	0
40	Genetic reconstructions of invasion history. <i>Molecular Ecology</i> , 2015, 24, 2212-2225.	3.9	190
41	Synergistic interactions of biotic and abiotic environmental stressors on gene expression. <i>Genome</i> , 2015, 58, 99-109.	2.0	17
42	Speciation without Pre-Defined Fitness Functions. <i>PLoS ONE</i> , 2015, 10, e0137838.	2.5	15
43	Reproducibility of pyrosequencing data for biodiversity assessment in complex communities. <i>Methods in Ecology and Evolution</i> , 2014, 5, 881-890.	5.2	40
44	From barcoding single individuals to metabarcoding biological communities: towards an integrative approach to the study of global biodiversity. <i>Trends in Ecology and Evolution</i> , 2014, 29, 566-571.	8.7	350
45	Morphological and genetic variability in an alien invasive mussel across an environmental gradient in South America. <i>Limnology and Oceanography</i> , 2014, 59, 400-412.	3.1	24
46	Gene Expression Variation in Duplicate Lactate dehydrogenase Genes: Do Ecological Species Show Distinct Responses?. <i>PLoS ONE</i> , 2014, 9, e103964.	2.5	4
47	Speciation patterns and processes in the zooplankton of the ancient lakes of <i>Sulawesi</i> , <i>Sri Lanka</i> , and <i>Indonesia</i> . <i>Ecology and Evolution</i> , 2013, 3, 3083-3094.	1.9	11
48	High sensitivity of 454 pyrosequencing for detection of rare species in aquatic communities. <i>Methods in Ecology and Evolution</i> , 2013, 4, 558-565.	5.2	208
49	The role of hybridization in the origin and spread of asexuality in <i>Daphnia</i> . <i>Molecular Ecology</i> , 2013, 22, 4549-4561.	3.9	48
50	Genetic Diversity in Introduced Golden Mussel Populations Corresponds to Vector Activity. <i>PLoS ONE</i> , 2013, 8, e59328.	2.5	26
51	Invasion Pathway of the Ctenophore <i>Mnemiopsis leidyi</i> in the Mediterranean Sea. <i>PLoS ONE</i> , 2013, 8, e81067.	2.5	44
52	Speciation with gene flow in a heterogeneous virtual world: can physical obstacles accelerate speciation?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 3055-3064.	2.6	23
53	Scale-dependent post-establishment spread and genetic diversity in an invading mollusc in South America. <i>Diversity and Distributions</i> , 2012, 18, 1042-1055.	4.1	43
54	Complex genetic patterns in closely related colonizing invasive species. <i>Ecology and Evolution</i> , 2012, 2, 1331-1346.	1.9	50

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55	Multilocus genetic analyses differentiate between widespread and spatially restricted cryptic species in a model ascidian. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 2377-2385.	2.6	71
56	Speciation with gene flow and the genetics of habitat transitions. <i>Molecular Ecology</i> , 2012, 21, 1411-1422.	3.9	61
57	Disentangling invasion processes in a dynamic shippingâ€“boating network. <i>Molecular Ecology</i> , 2012, 21, 4227-4241.	3.9	35
58	The Evolutionary History of Sarco(endo)plasmic Calcium ATPase (SERCA). <i>PLoS ONE</i> , 2012, 7, e52617.	2.5	44
59	An Integrated Multi-Disciplinary Approach for Studying Multiple Stressors in Freshwater Ecosystems: <i>Daphnia</i> as a Model Organism. <i>Integrative and Comparative Biology</i> , 2011, 51, 623-633.	2.0	142
60	Comparative phylogeography of two colonial ascidians reveals contrasting invasion histories in North America. <i>Biological Invasions</i> , 2011, 13, 635-650.	2.4	52
61	Multiple introductions and invasion pathways for the invasive ctenophore <i>Mnemiopsis leidyi</i> in Eurasia. <i>Biological Invasions</i> , 2011, 13, 679-690.	2.4	65
62	Use of DNA barcoding to detect invertebrate invasive species from diapausing eggs. <i>Biological Invasions</i> , 2011, 13, 1325-1340.	2.4	86
63	Evolutionary factors affecting Lactate dehydrogenase A and B variation in the <i>Daphnia pulex</i> species complex. <i>BMC Evolutionary Biology</i> , 2011, 11, 212.	3.2	20
64	High Rate of Large-Scale Hemizygous Deletions in Asexually Propagating <i>Daphnia</i> : Implications for the Evolution of Sex. <i>Molecular Biology and Evolution</i> , 2011, 28, 335-342.	8.9	33
65	The Ancient Lakes of Indonesia: Towards Integrated Research on Speciation. <i>Integrative and Comparative Biology</i> , 2011, 51, 634-643.	2.0	37
66	Pleistocene-driven diversification in freshwater zooplankton: Genetic patterns of refugial isolation and postglacial recolonization in <i>Leptodora kindtii</i> (Crustacea, Cladocera). <i>Limnology and Oceanography</i> , 2011, 56, 1725-1736.	3.1	32
67	Efficacy of â€“saltwater flushingâ€™ in protecting the Great Lakes from biological invasions by invertebrate eggs in shipsâ€™ ballast sediment. <i>Freshwater Biology</i> , 2010, 55, 2414-2424.	2.4	38
68	Ancient lakes revisited: from the ecology to the genetics of speciation. <i>Molecular Ecology</i> , 2010, 19, 4837-4851.	3.9	79
69	Invasion genetics of the <i>Ciona intestinalis</i> species complex: from regional endemism to global homogeneity. <i>Molecular Ecology</i> , 2010, 19, 4678-4694.	3.9	140
70	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 August 2009â€“30 September 2009. <i>Molecular Ecology Resources</i> , 2010, 10, 232-236.	4.8	71
71	Evolutionary History of d-Lactate Dehydrogenases: A Phylogenomic Perspective on Functional Diversity in the FAD Binding Oxidoreductase/Transferase Type 4 Family. <i>Journal of Molecular Evolution</i> , 2009, 69, 276-287.	1.8	19
72	D- and L-lactate dehydrogenases during invertebrate evolution. <i>BMC Evolutionary Biology</i> , 2008, 8, 268.	3.2	40

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73	A microsatellite-based genetic linkage map of the waterflea, <i>Daphnia pulex</i> : On the prospect of crustacean genomics. <i>Genomics</i> , 2006, 88, 415-430.	2.9	76
74	Probing the relationships of the branchiopod crustaceans. <i>Molecular Phylogenetics and Evolution</i> , 2006, 39, 491-502.	2.7	75
75	The "Crustacean Seas" — an evolutionary perspective on the Ponto-Caspian peracarids. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2005, 62, 505-517.	1.4	58
76	Phylogeography of Ponto-Caspian crustaceans: a benthic-planktonic comparison. <i>Molecular Ecology</i> , 2003, 12, 985-996.	3.9	63
77	Genetic perspectives on invasions: the case of the Cladocera. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2002, 59, 1229-1234.	1.4	61
78	Taxonomic resolution of the genus <i>Bythotrephes</i> Leydig using molecular markers and re-evaluation of its global distribution. <i>Diversity and Distributions</i> , 2002, 8, 67-84.	4.1	50
79	Distribution, Fecundity, and Genetics of <i>Cercopagis pengoi</i> (Ostroumov) (Crustacea, Cladocera) in Lake Ontario. <i>Journal of Great Lakes Research</i> , 2001, 27, 19-32.	1.9	52
80	An invasion history for <i>Cercopagis pengoi</i> based on mitochondrial gene sequences. <i>Limnology and Oceanography</i> , 2001, 46, 224-229.	3.1	115