

Naiara RodrÃ-iguez-Ezpeleta

List of Publications by Year in descending order

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66
papers

4,713
citations

136950

32
h-index

114465

63
g-index

75
all docs

75
docs citations

75
times ranked

7842
citing authors

#	ARTICLE	IF	CITATIONS
1	Population structure and geographic origin assignment of <i>Mytilus galloprovincialis</i> mussels using SNPs. <i>Aquaculture</i> , 2022, 550, 737836.	3.5	9
2	A review of the fisheries, life history and stock structure of tropical tuna (skipjack <i>Katsuwonus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 70 <i>Marine Biology</i> , 2021, 88, 39-89.	1.4	11
3	Life in a drop: Sampling environmental DNA for marine fishery management and ecosystem monitoring. <i>Marine Policy</i> , 2021, 124, 104331.	3.2	52
4	Sharing and reporting benefits from biodiversity research. <i>Molecular Ecology</i> , 2021, 30, 1103-1107.	3.9	19
5	Otolith chemical fingerprints of skipjack tuna (<i>Katsuwonus pelamis</i>) in the Indian Ocean: First insights into stock structure delineation. <i>PLoS ONE</i> , 2021, 16, e0249327.	2.5	5
6	Atlantic bluefin tuna (<i>Thunnus thynnus</i>) in Greenland " mixed-stock origin, diet, hydrographic conditions, and repeated catches in this new fringe area. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2021, 78, 400-408.	1.4	10
7	Trade-offs between reducing complex terminology and producing accurate interpretations from environmental DNA: Comment on "Environmental DNA: What's behind the term?" by Pawlowski et al., (2020). <i>Molecular Ecology</i> , 2021, 30, 4601-4605.	3.9	60
8	Biodiversity monitoring using environmental DNA. <i>Molecular Ecology Resources</i> , 2021, 21, 1405-1409.	4.8	15
9	Evidence of stock connectivity, hybridization, and misidentification in white anglerfish supports the need of a genetics-informed fisheries management framework. <i>Evolutionary Applications</i> , 2021, 14, 2221-2230.	3.1	4
10	Vertical stratification of environmental DNA in the open ocean captures ecological patterns and behavior of deep-sea fishes. <i>Limnology and Oceanography Letters</i> , 2021, 6, 339-347.	3.9	32
11	Pan-regional marine benthic cryptobiome biodiversity patterns revealed by metabarcoding Autonomous Reef Monitoring Structures. <i>Molecular Ecology</i> , 2020, 29, 4882-4897.	3.9	19
12	Marine water environmental DNA metabarcoding provides a comprehensive fish diversity assessment and reveals spatial patterns in a large oceanic area. <i>Ecology and Evolution</i> , 2020, 10, 7560-7584.	1.9	50
13	Combining genetic markers with stable isotopes in otoliths reveals complexity in the stock structure of Atlantic bluefin tuna (<i>Thunnus thynnus</i>). <i>Scientific Reports</i> , 2020, 10, 14675.	3.3	21
14	Considerations for metabarcoding-based port biological baseline surveys aimed at marine nonindigenous species monitoring and risk assessments. <i>Ecology and Evolution</i> , 2020, 10, 2452-2465.	1.9	32
15	Determining natal origin for improved management of Atlantic bluefin tuna. <i>Frontiers in Ecology and the Environment</i> , 2019, 17, 439-444.	4.0	46
16	Genome-wide SNP based population structure in European hake reveals the need for harmonizing biological and management units. <i>ICES Journal of Marine Science</i> , 2019, 76, 2260-2266.	2.5	13
17	Environmental DNA Metabarcoding: A Promising Tool for Ballast Water Monitoring. <i>Environmental Science & Technology</i> , 2019, 53, 11849-11859.	10.0	25
18	Selecting RAD-Seq Data Analysis Parameters for Population Genetics: The More the Better?. <i>Frontiers in Genetics</i> , 2019, 10, 533.	2.3	48

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19	Settlement and recruitment pattern variability of the mussel <i>Mytilus galloprovincialis</i> Lmk. from SE Bay of Biscay (Basque Country). <i>Regional Studies in Marine Science</i> , 2019, 27, 100523.	0.7	3
20	Spatial dynamics and mixing of bluefin tuna in the Atlantic Ocean and Mediterranean Sea revealed using next-generation sequencing. <i>Molecular Ecology Resources</i> , 2018, 18, 620-638.	4.8	34
21	Large-scale ocean connectivity and planktonic body size. <i>Nature Communications</i> , 2018, 9, 142.	12.8	102
22	Oceanographic variation influences spatial genomic structure in the sea scallop, <i>Placopecten magellanicus</i> . <i>Ecology and Evolution</i> , 2018, 8, 2824-2841.	1.9	12
23	The challenges and promises of genetic approaches for ballast water management. <i>Journal of Sea Research</i> , 2018, 133, 134-145.	1.6	26
24	Adapting metabarcoding-based benthic biomonitoring into routine marine ecological status assessment networks. <i>Ecological Indicators</i> , 2018, 95, 194-202.	6.3	103
25	A real-time PCR approach to detect predation on anchovy and sardine early life stages. <i>Journal of Sea Research</i> , 2017, 130, 204-209.	1.6	4
26	A bacterial community-based index to assess the ecological status of estuarine and coastal environments. <i>Marine Pollution Bulletin</i> , 2017, 114, 679-688.	5.0	120
27	Identifying patterns of dispersal, connectivity and selection in the sea scallop, <i>Placopecten magellanicus</i> , using RAD-seq derived SNPs. <i>Evolutionary Applications</i> , 2017, 10, 102-117.	3.1	82
28	Genetic Diversity and Connectivity in <i>Maurollicus muelleri</i> in the Bay of Biscay Inferred from Thousands of SNP Markers. <i>Frontiers in Genetics</i> , 2017, 8, 195.	2.3	14
29	Developing innovative methods to face aquatic invasions in Europe: the Aquainvad-ED project. <i>Management of Biological Invasions</i> , 2017, 8, 403-408.	1.2	2
30	Overview of Integrative Assessment of Marine Systems: The Ecosystem Approach in Practice. <i>Frontiers in Marine Science</i> , 2016, 3, .	2.5	215
31	Benchmarking DNA Metabarcoding for Biodiversity-Based Monitoring and Assessment. <i>Frontiers in Marine Science</i> , 2016, 3, .	2.5	157
32	Marine Sediment Sample Pre-processing for Macroinvertebrates Metabarcoding: Mechanical Enrichment and Homogenization. <i>Frontiers in Marine Science</i> , 2016, 3, .	2.5	25
33	Implementing and Innovating Marine Monitoring Approaches for Assessing Marine Environmental Status. <i>Frontiers in Marine Science</i> , 2016, 3, .	2.5	163
34	Population structure of Atlantic mackerel inferred from RAD-seq derived SNP markers: effects of sequence clustering parameters and hierarchical SNP selection. <i>Molecular Ecology Resources</i> , 2016, 16, 991-1001.	4.8	66
35	Metabarcoding of marine zooplankton: prospects, progress and pitfalls. <i>Journal of Plankton Research</i> , 2016, 38, 393-400.	1.8	160
36	Analysis of Illumina MiSeq Metabarcoding Data: Application to Benthic Indices for Environmental Monitoring. <i>Methods in Molecular Biology</i> , 2016, 1452, 237-249.	0.9	12

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37	RAD-seq derived genome-wide nuclear markers resolve the phylogeny of tunas. <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 202-207.	2.7	75
38	The ocean sampling day consortium. <i>GigaScience</i> , 2015, 4, 27.	6.4	185
39	Environmental Status Assessment Using DNA Metabarcoding: Towards a Genetics Based Marine Biotic Index (gAMBI). <i>PLoS ONE</i> , 2014, 9, e90529.	2.5	147
40	The founding charter of the Genomic Observatories Network. <i>GigaScience</i> , 2014, 3, 2.	6.4	51
41	Long Distance Linkage Disequilibrium and Limited Hybridization Suggest Cryptic Speciation in Atlantic Cod. <i>PLoS ONE</i> , 2014, 9, e106380.	2.5	37
42	Genomics in marine monitoring: New opportunities for assessing marine health status. <i>Marine Pollution Bulletin</i> , 2013, 74, 19-31.	5.0	196
43	<i>Solute carrier family 2 member 1</i> is involved in the development of nonalcoholic fatty liver disease. <i>Hepatology</i> , 2013, 57, 505-514.	7.3	25
44	Whole Transcriptome Analysis of <i>Acinetobacter baumannii</i> Assessed by RNA-Sequencing Reveals Different mRNA Expression Profiles in Biofilm Compared to Planktonic Cells. <i>PLoS ONE</i> , 2013, 8, e72968.	2.5	127
45	A high density SNP genotyping approach within the 19q13 chromosome region identifies an association of a CNOT3 polymorphism with ankylosing spondylitis. <i>Annals of the Rheumatic Diseases</i> , 2012, 71, 714-717.	0.9	14
46	The RNA-Binding Protein Human Antigen R Controls Global Changes in Gene Expression during Schwann Cell Development. <i>Journal of Neuroscience</i> , 2012, 32, 4944-4958.	3.6	12
47	Comparison of methods to detect copy number alterations in cancer using simulated and real genotyping data. <i>BMC Bioinformatics</i> , 2012, 13, 192.	2.6	14
48	Whole transcriptome analysis of a reversible neurodegenerative process in <i>Drosophila</i> reveals potential neuroprotective genes. <i>BMC Genomics</i> , 2012, 13, 483.	2.8	10
49	A cytokine gene screen uncovers SOCS1 as genetic risk factor for multiple sclerosis. <i>Genes and Immunity</i> , 2012, 13, 21-28.	4.1	56
50	The SAR11 Group of Alpha-Proteobacteria Is Not Related to the Origin of Mitochondria. <i>PLoS ONE</i> , 2012, 7, e30520.	2.5	71
51	Fine mapping of a major histocompatibility complex in ankylosing spondylitis: Association of the <i>HLA-DPA1</i> and <i>HLA-DPB1</i> regions. <i>Arthritis and Rheumatism</i> , 2011, 63, 3305-3312.	6.7	17
52	miRanalyzer: an update on the detection and analysis of microRNAs in high-throughput sequencing experiments. <i>Nucleic Acids Research</i> , 2011, 39, W132-W138.	14.5	253
53	Phylogenomic Evidence for Separate Acquisition of Plastids in Cryptophytes, Haptophytes, and Stramenopiles. <i>Molecular Biology and Evolution</i> , 2010, 27, 1698-1709.	8.9	248
54	High-density SNP genotyping detects homogeneity of Spanish and French Basques, and confirms their genomic distinctiveness from other European populations. <i>Human Genetics</i> , 2010, 128, 113-117.	3.8	43

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55	Phylogenomic Analyses Support the Monophyly of Taphrinomycotina, including <i>Schizosaccharomyces</i> Fission Yeasts. <i>Molecular Biology and Evolution</i> , 2009, 26, 27-34.	8.9	91
56	Phylogenomics. , 2009, , 633-643.		0
57	Construction of cDNA Libraries: Focus on Protists and Fungi. <i>Methods in Molecular Biology</i> , 2009, 533, 33-47.	0.9	18
58	SCaFoS: a tool for Selection, Concatenation and Fusion of Sequences for phylogenomics. <i>BMC Evolutionary Biology</i> , 2007, 7, S2.	3.2	158
59	Toward Resolving the Eukaryotic Tree: The Phylogenetic Positions of Jakobids and Cercozoans. <i>Current Biology</i> , 2007, 17, 1420-1425.	3.9	170
60	Detecting and Overcoming Systematic Errors in Genome-Scale Phylogenies. <i>Systematic Biology</i> , 2007, 56, 389-399.	5.6	288
61	Plastid Origin: Replaying the Tape. <i>Current Biology</i> , 2006, 16, R53-R56.	3.9	36
62	Phylogenetic Analyses of Nuclear, Mitochondrial, and Plastid Multigene Data Sets Support the Placement of Mesostigma in the Streptophyta. <i>Molecular Biology and Evolution</i> , 2006, 24, 723-731.	8.9	84
63	Monophyly of Primary Photosynthetic Eukaryotes: Green Plants, Red Algae, and Glaucophytes. <i>Current Biology</i> , 2005, 15, 1325-1330.	3.9	502
64	Fungal Evolution Meets Fungal Genomics. <i>Mycology</i> , 2003, , .	0.5	5
65	Intraguild predation of Atlantic mackerel on early life stages of anchovy and sardine. <i>Frontiers in Marine Science</i> , 0, 3, .	2.5	0
66	Evaluation of the global marine mesozooplankton diversity using alternative metabarcoding approaches. <i>Frontiers in Marine Science</i> , 0, 3, .	2.5	0