Luisa Orsini

List of Publications by Year in descending order

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		218662	197805
50	2,639	26	49
papers	citations	h-index	g-index
			0000
53	53	53	3899
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	The Time Machine framework: monitoring and prediction of biodiversity loss. Trends in Ecology and Evolution, 2022, 37, 138-146.	8.7	13
2	Historical exposure to chemicals reduces tolerance to novel chemical stress in <i>Daphnia</i> (waterflea). Molecular Ecology, 2022, 31, 3098-3111.	3.9	12
3	Protocol for assay of transposase accessible chromatin sequencing in non-model species. STAR Protocols, 2021, 2, 100341.	1.2	6
4	Evolutionary mechanisms underpinning fitness response to multiple stressors in $\langle i \rangle$ Daphnia $\langle i \rangle$. Evolutionary Applications, 2021, 14, 2457-2469.	3.1	12
5	Extensive standing genetic variation from a small number of founders enables rapid adaptation in Daphnia. Nature Communications, 2021, 12, 4306.	12.8	27
6	Roundup causes embryonic development failure and alters metabolic pathways and gut microbiota functionality in non-target species. Microbiome, 2020, 8, 170.	11.1	27
7	Adaptive responses along a depth and a latitudinal gradient in the endemic seagrass Posidonia oceanica. Heredity, 2019, 122, 233-243.	2.6	18
8	Transgenerational response to early spring warming in Daphnia. Scientific Reports, 2019, 9, 4449.	3.3	21
9	Remasking of Candida albicans \hat{I}^2 -Glucan in Response to Environmental pH Is Regulated by Quorum Sensing. MBio, 2019, 10, .	4.1	37
10	Spatial and temporal variation in river corridor exchange across a 5th-order mountain stream network. Hydrology and Earth System Sciences, 2019, 23, 5199-5225.	4.9	23
11	Co-located contemporaneous mapping of morphological, hydrological, chemical, and biological conditions in a 5th-order mountain stream network, Oregon, USA. Earth System Science Data, 2019, 11, 1567-1581.	9.9	14
12	Resurrection of Dormant Daphnia magna : Protocol and Applications. Journal of Visualized Experiments, 2018, , .	0.3	8
13	Early transcriptional response pathways in <i>Daphnia magna</i> are coordinated in networks of crustaceanâ€specific genes. Molecular Ecology, 2018, 27, 886-897.	3.9	38
14	Haemoglobinâ€mediated response to hyperâ€thermal stress in the keystone species <i>Daphnia magna</i> Evolutionary Applications, 2018, 11, 112-120.	3.1	26
15	Founder effects determine the genetic structure of the water flea <i>Daphnia</i> in Ethiopian reservoirs. Limnology and Oceanography, 2018, 63, 915-926.	3.1	11
16	Predictability of the impact of multiple stressors on the keystone species Daphnia. Scientific Reports, 2018, 8, 17572.	3.3	32
17	Evolution of thermal tolerance in multifarious environments. Molecular Ecology, 2018, 27, 4529-4541.	3.9	26
18	Cracking the Code of Biodiversity Responses to Past Climate Change. Trends in Ecology and Evolution, 2018, 33, 765-776.	8.7	119

#	Article	IF	Citations
19	Thermal tolerance in the keystone species <i>Daphnia magna</i> â€"a candidate gene and an outlier analysis approach. Molecular Ecology, 2017, 26, 2291-2305.	3.9	28
20	Bisulfite Sequencing with <i>Daphnia</i> Highlights a Role for Epigenetics in Regulating Stress Response to <i>Microcystis</i> through Preferential Differential Methylation of Serine and Threonine Amino Acids. Environmental Science & Environmenta	10.0	57
21	Conserved Transcription Factors Steer Growth-Related Genomic Programs in Daphnia. Genome Biology and Evolution, 2017, 9, 1821-1842.	2.5	13
22	Temporal genetic stability in natural populations of the waterflea <i><scp>D</scp>aphnia magna</i> in response to strong selection pressure. Molecular Ecology, 2016, 25, 6024-6038.	3.9	35
23	Daphnia magna transcriptome by RNA-Seq across 12 environmental stressors. Scientific Data, 2016, 3, 160030.	5.3	89
24	Transcriptome characterisation and simple sequence repeat marker discovery in the seagrass Posidonia oceanica. Scientific Data, 2016, 3, 160115.	5.3	13
25	Rare interspecific breeding in Pseudo-nitzschia (Bacillariophyceae). Phytotaxa, 2015, 217, 145.	0.3	11
26	Drivers of population genetic differentiation in the wild: isolation by dispersal limitation, isolation by adaptation and isolation by colonization. Molecular Ecology, 2013, 22, 5983-5999.	3.9	398
27	Evolutionary Ecological Genomics. Molecular Ecology, 2013, 22, 527-531.	3.9	24
28	The evolutionary time machine: using dormant propagules to forecast how populations can adapt to changing environments. Trends in Ecology and Evolution, 2013, 28, 274-282.	8.7	123
29	The role of selection in driving landscape genomic structure of the waterflea <i>Daphnia magna</i> Molecular Ecology, 2013, 22, 583-601.	3.9	74
30	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 December 2012–31 January 2013. Molecular Ecology Resources, 2013, 13, 546-549.	4.8	36
31	Genomic signature of natural and anthropogenic stress in wild populations of the waterflea <i>Daphnia magna</i> : validation in space, time and experimental evolution. Molecular Ecology, 2012, 21, 2160-2175.	3.9	97
32	Single nucleotide polymorphism discovery from expressed sequence tags in the waterflea Daphnia magna. BMC Genomics, 2011, 12, 309.	2.8	18
33	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 October 2010-30 November 2010. Molecular Ecology Resources, 2011, 11, 418-421.	4.8	43
34	Thermal Genetic Adaptation in the Water Flea Daphnia and its Impact: An Evolving Metacommunity Approach. Integrative and Comparative Biology, 2011, 51, 703-718.	2.0	39
35	Three parallel radiations of Canthonini dung beetles in Madagascar. Molecular Phylogenetics and Evolution, 2010, 57, 710-727.	2.7	33
36	Fitness differences associated with <i>Pgi</i> SNP genotypes in the Glanville fritillary butterfly (<i>Melitaea cinxia</i>). Journal of Evolutionary Biology, 2009, 22, 367-375.	1.7	63

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37	An old adaptive radiation of forest dung beetles in Madagascar. Molecular Phylogenetics and Evolution, 2008, 47, 1076-1089.	2.7	66
38	Genetic spatial structure in a butterfly metapopulation correlates better with past than present demographic structure. Molecular Ecology, 2008, 17, 2629-2642.	3.9	82
39	SNP discovery by mismatch-targeting of Mu transposition. Nucleic Acids Research, 2007, 35, e44-e44.	14.5	17
40	Molecular evolution and radiation of dung beetles in Madagascar. Cladistics, 2007, 23, 145-168.	3.3	38
41	Phylogeographic patterns in Drosophila montana. Molecular Ecology, 2006, 16, 1085-1097.	3.9	31
42	Patterns of microsatellite variation through a transition zone of a chromosomal cline in Drosophila americana. Heredity, 2006, 97, 291-295.	2.6	19
43	LIFE CYCLE, SIZE REDUCTION PATTERNS, AND ULTRASTRUCTURE OF THE PENNATE PLANKTONIC DIATOM PSEUDO-NITZSCHIA DELICATISSIMA (BACILLARIOPHYCEAE)1. Journal of Phycology, 2005, 41, 542-556.	2.3	115
44	The alternation of different morphotypes in the seasonal cycle of the toxic diatom Pseudo-nitzschia galaxiae. Harmful Algae, 2005, 4, 33-48.	4.8	101
45	Isolation and characterization of microsatellites in Drosophila montana and their cross-species amplification in D. virilis. Molecular Ecology Notes, 2004, 4, 412-414.	1.7	6
46	A multilocus microsatellite phylogeny of the Drosophila virilis group. Heredity, 2004, 93, 161-165.	2.6	29
47	Multiple rDNA ITS-types within the diatom Pseudo-nitzschia delicatissima (Bacillariophyceae) and their relative abundances across a spring bloom in the Gulf of Naples. Marine Ecology - Progress Series, 2004, 271, 87-98.	1.9	127
48	Bipolar distribution of the cyst-forming dinoflagellate Polarella glacialis. Polar Biology, 2003, 26, 186-194.	1.2	120
49	Toxic Pseudo-nitzschia multistriata (Bacillariophyceae) from the Gulf of Naples: morphology, toxin analysis and phylogenetic relationships with other Pseudo-nitzschia species. European Journal of Phycology, 2002, 37, 247-257.	2.0	135
50	Spatial patterns of genetic diversity in Posidonia oceanica, an endemic Mediterranean seagrass. Molecular Ecology, 2001, 10, 1413-1421.	3.9	62