Rui Faria

List of Publications by Year
in descending order

48 papers	2,533 citations	331670 21 h-index	233421 45 g-index
52 all docs	52 docs citations	52 times ranked	3739 citing authors

#	Article	IF	Citations
1	Ten years of demographic modelling of divergence and speciation in the sea. Evolutionary Applications, 2023, 16, 542-559.	3.1	11
2	An allozyme polymorphism is associated with a large chromosomal inversion in the marine snail<i>Littorina fabalis</i>. Evolutionary Applications, 2023, 16, 279-292.	3.1	7
3	Genetic structure, diversity, and connectivity in anadromous and freshwater Alosa alosa and A. fallax. Marine Biology, 2022, 169, 1.	1.5	3
4	Inversions and parallel evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, .	4.0	19
5	Genetic and morphological divergence between <i>Littorina fabalis</i> ecotypes in Northern Europe. Journal of Evolutionary Biology, 2021, 34, 97-113.	1.7	10
6	Accelerated Evolution of Tissue-Specific Genes Mediates Divergence Amidst Gene Flow in European Green Lizards. Genome Biology and Evolution, 2021, 13, .	2.5	1
7	Genetic variation for adaptive traits is associated with polymorphic inversions in<i>Littorina saxatilis</i>. Evolution Letters, 2021, 5, 196-213.	3.3	42
8	Inversions and genomic differentiation after secondary contact: When drift contributes to maintenance, not loss, of differentiation. Evolution; International Journal of Organic Evolution, 2021, 75, 1288-1303.	2.3	7
9	Using replicate hybrid zones to understand the genomic basis of adaptive divergence. Molecular Ecology, 2021, 30, 3797-3814.	3.9	37
10	Speciation in marine environments: Diving under the surface. Journal of Evolutionary Biology, 2021, 34, 4-15.	1.7	31
11	Is embryo abortion a postâ€zygotic barrier to gene flow between <i>Littorina</i> ecotypes?. Journal of Evolutionary Biology, 2020, 33, 342-351.	1.7	14
12	Mate Choice Contributes to the Maintenance of Shell Color Polymorphism in a Marine Snail via Frequency-Dependent Sexual Selection. Frontiers in Marine Science, 2020, 7, .	2.5	13
13	Transcriptomic resources for evolutionary studies in flat periwinkles and related species. Scientific Data, 2020, 7, 73.	5.3	1
14	Phylogeographic history of flat periwinkles, Littorina fabalis and L. obtusata. BMC Evolutionary Biology, 2020, 20, 23.	3.2	16
15	Hybridization patterns between two marine snails, <i>Littorina fabalis</i> and <i>L. obtusata</i>. Ecology and Evolution, 2020, 10, 1158-1179.	1.9	15
16	Evolutionary history of two cryptic species of northern African jerboas. BMC Evolutionary Biology, 2020, 20, 26.	3.2	16
17	Evolving Inversions. Trends in Ecology and Evolution, 2019, 34, 239-248.	8.7	179
18	Genomic architecture of parallel ecological divergence: Beyond a single environmental contrast. Science Advances, 2019, 5, eaav9963.	10.3	92

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19	Multiple chromosomal rearrangements in a hybrid zone between <i>Littorina saxatilis</i> ecotypes. Molecular Ecology, 2019, 28, 1375-1393.	3.9	103
20	Signatures of Selection on Standing Genetic Variation Underlie Athletic and Navigational Performance in Racing Pigeons. Molecular Biology and Evolution, 2018, 35, 1176-1189.	8.9	25
21	Divergent evolution in the genomes of closely-related lacertids, Lacerta viridis and L. bilineata and implications for speciation. GigaScience, 2018, 8, .	6.4	10
22	Karyotype Characterization of Nine Periwinkle Species (Gastropoda, Littorinidae). Genes, 2018, 9, 517.	2.4	10
23	Introducing evolutionary biologists to the analysis of big data: guidelines to organize extended bioinformatics training courses. Evolution: Education and Outreach, 2018, 11, .	0.8	3
24	Clines on the seashore: The genomic architecture underlying rapid divergence in the face of gene flow. Evolution Letters, 2018, 2, 297-309.	3.3	103
25	The complete mitochondrial genome of <i>Lacerta bilineata</i> and comparison with its closely related congener <i>L. Viridis</i>. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2017, 28, 116-118.	0.7	5
26	Interpreting the genomic landscape of speciation: a road map for finding barriers to gene flow. Journal of Evolutionary Biology, 2017, 30, 1450-1477.	1.7	399
27	Comparative mitogenomic analysis of three species of periwinkles: Littorina fabalis, L. obtusata and L. saxatilis. Marine Genomics, 2017, 32, 41-47.	1.1	12
28	Genetic characterization of flat periwinkles (Littorinidae) from the Iberian Peninsula reveals interspecific hybridization and different degrees of differentiation. Biological Journal of the Linnean Society, 2016, 118, 503-519.	1.6	12
29	Magadi tilapia ecological specialization: filling the early gap in the speciation continuum. Molecular Ecology, 2016, 25, 1420-1422.	3.9	2
30	De novoisolation of 17 microsatellite loci for flat periwinkles (Littorina fabalisandL. obtusata) and their application for species discrimination and hybridization studies. Journal of Molluscan Studies, 2015, 81, 421-425.	1.2	7
31	Pool and conquer: new tricks for (c)old problems. Molecular Ecology, 2014, 23, 1653-1655.	3.9	5
32	Advances in <scp>E</scp>cological <scp>S</scp>peciation: an integrative approach. Molecular Ecology, 2014, 23, 513-521.	3.9	63
33	The puzzling demographic history and genetic differentiation of the twaite shad (Alosa fallax) in the Ebro River. Conservation Genetics, 2014, 15, 1037-1052.	1.5	3
34	A prominent role of KRAB-ZNF transcription factors in mammalian speciation?. Trends in Genetics, 2013, 29, 130-139.	6.7	36
35	Comparative phylogeography and demographic history of European shads (Alosa alosa and A. fallax) inferred from mitochondrial DNA. BMC Evolutionary Biology, 2012, 12, 194.	3.2	27
36	Factors Influencing Progress toward Ecological Speciation. International Journal of Ecology, 2012, 2012, 1-7.	0.8	31

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37	Genetic tools for restoration of fish populations. Journal of Applied Ichthyology, 2011, 27, 5-15.	0.7	12
38	Molecular tools for species discrimination and detection of hybridization between two closely related Clupeid fishes Alosa alosa and A.Âfallax. Journal of Applied Ichthyology, 2011, 27, 16-20.	0.7	5
39	A preliminary genetic analysis of a recently rediscovered population of the Twaite shad (Alosa fallax) in the Ebro river, Spain (Western Mediterranean). Journal of Applied Ichthyology, 2011, 27, 21-23.	0.7	5
40	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	27.8	541
41	Recent human evolution has shaped geographical differences in susceptibility to disease. BMC Genomics, 2011, 12, 55.	2.8	27
42	Chromosomal speciation revisited: rearranging theory with pieces of evidence. Trends in Ecology and Evolution, 2010, 25, 660-669.	8.7	388
43	Interspecific differentiation and intraspecific substructure in two closely related clupeids with extensive hybridization, Alosa alosa and Alosa fallax. Journal of Fish Biology, 2006, 69, 242-259.	1.6	48
44	Evidence for genetic differentiation in the European conger eel Conger conger based on mitochondrial DNA analysis. Fisheries Science, 2006, 72, 20-27.	1.6	9
45	A molecular phylogenetic perspective on the evolutionary history of Alosa spp. (Clupeidae). Molecular Phylogenetics and Evolution, 2006, 40, 298-304.	2.7	34
46	Life on the Edge: The Long-Term Persistence and Contrasting Spatial Genetic Structure of Distinct Brown Trout Life Histories at Their Ecological Limits. Journal of Heredity, 2006, 97, 193-205.	2.4	30
47	Isolation and characterization of eight dinucleotide microsatellite loci from two closely related clupeid species (Alosa alosa and A. fallax). Molecular Ecology Notes, 2004, 4, 586-588.	1.7	25
48	Complex evolutionary history in the brown trout: Insights on the recognition of conservation units. Conservation Genetics, 2001, 2, 337-347.	1.5	30