Michael C Fontaine

List of Publications by Year
in descending order

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60 papers	3,255 citations	201674 27 h-index	182427 51 g-index
72 all docs	72 docs citations	72 times ranked	5035 citing authors

#	Article	IF	Citations
1	Global flyway evolution in red knots Calidris canutus and genetic evidence for a Nearctic refugium. Molecular Ecology, 2022, 31, 2124-2139.	3.9	7
2	Evolutionary history of Plasmodium vivax and Plasmodium simium in the Americas. Malaria Journal, 2022, 21, 141.	2.3	2
3	The critically endangered vaquita is not doomed to extinction by inbreeding depression. Science, 2022, 376, 635-639.	12.6	49
4	Population structure in a continuously distributed coastal marine species, the harbor porpoise, based on microhaplotypes derived from poorâ€quality samples. Molecular Ecology, 2021, 30, 1457-1476.	3.9	10
5	Population genomic evidence of Plasmodium vivax Southeast Asian origin. Science Advances, 2021, 7, .	10.3	21
6	No leadingâ€edge effect in North Atlantic harbor porpoises: Evolutionary and conservation implications. Evolutionary Applications, 2021, 14, 1588-1611.	3.1	3
7	Europe as a bridgehead in the worldwide invasion history of grapevine downy mildew, Plasmopara viticola. Current Biology, 2021, 31, 2155-2166.e4.	3.9	36
8	Habitat segregation of plate phenotypes in a rapidly expanding population of threeâ€spined stickleback. Ecosphere, 2021, 12, e03561.	2.2	7
9	Predator biomass and vegetation influence the coastal distribution of threespine stickleback morphotypes. Ecology and Evolution, 2021, 11, 12485-12496.	1.9	3
10	Selection on ancestral genetic variation fuels repeated ecotype formation in bottlenose dolphins. Science Advances, 2021, 7, eabg1245.	10.3	27
11	Genetic homogeneity in the face of morphological heterogeneity in the harbor porpoise from the Black Sea and adjacent waters (Phocoena phocoena relicta). Heredity, 2020, 124, 469-484.	2.6	5
12	Mitochondrial genomics reveals the evolutionary history of the porpoises (Phocoenidae) across the speciation continuum. Scientific Reports, 2020, 10, 15190.	3.3	13
13	Building genomic infrastructure: Sequencing platinumâ€standard referenceâ€quality genomes of all cetacean species. Marine Mammal Science, 2020, 36, 1356-1366.	1.8	10
14	Assessing connectivity despite high diversity in island populations of a malaria mosquito. Evolutionary Applications, 2020, 13, 417-431.	3.1	11
15	Radiation with reticulation marks the origin of a major malaria vector. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31583-31590.	7.1	29
16	Population structure, connectivity, and demographic history of an apex marine predator, the bull shark Carcharhinus leucas. Ecology and Evolution, 2019, 9, 12980-13000.	1.9	18
17	Host, Symbionts, and the Microbiome: The Missing Tripartite Interaction. Trends in Microbiology, 2019, 27, 480-488.	7.7	70
18	Resilience of harbor porpoises to anthropogenic disturbance: Must they really feed continuously?. Marine Mammal Science, 2018, 34, 258-264.	1.8	28

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19	A genomic perspective timely needed for re-evaluating the species delimitations, evolutionary trajectories, and conservation strategies of the Galapagos giant tortoises. Peer Community in Evolutionary Biology, 2018, , 100031.	0.0	0
20	Genomic and proteomic identification of Late Holocene remains: Setting baselines for Black Sea odontocetes. Journal of Archaeological Science: Reports, 2017, 15, 262-271.	0.5	6
21	Genetic signatures of variation in population size in a native fungal pathogen after the recent massive plantation of its host tree. Heredity, 2017, 119, 402-410.	2.6	10
22	Patterns of divergence across the geographic and genomic landscape of a butterfly hybrid zone associated with a climatic gradient. Molecular Ecology, 2017, 26, 4725-4742.	3.9	44
23	Mixing of porpoise ecotypes in southwestern UK waters revealed by genetic profiling. Royal Society Open Science, 2017, 4, 160992.	2.4	40
24	Genetic diversity of the African malaria vector Anopheles gambiae. Nature, 2017, 552, 96-100.	27.8	288
25	Genetic footprint of population fragmentation and contemporary collapse in a freshwater cetacean. Scientific Reports, 2017, 7, 14449.	3.3	9
26	Spatial variation in the accumulation of POPs and mercury in bottlenose dolphins of the Lower Florida Keys and the coastal Everglades (South Florida). Environmental Pollution, 2017, 220, 577-587.	7.5	27
27	Harbour Porpoises, Phocoena phocoena, in the Mediterranean Sea and Adjacent Regions. Advances in Marine Biology, 2016, 75, 333-358.	1.4	22
28	Chromosomal inversions and ecotypic differentiation in Anopheles gambiae: the perspective from wholeâ€genome sequencing. Molecular Ecology, 2016, 25, 5889-5906.	3.9	35
29	Enhanced computational methods for quantifying the effect of geographic and environmental isolation on genetic differentiation. Methods in Ecology and Evolution, 2015, 6, 1270-1277.	5.2	13
30	Scaffold assembly based on genome rearrangement analysis. Computational Biology and Chemistry, 2015, 57, 46-53.	2.3	12
31	Extensive introgression in a malaria vector species complex revealed by phylogenomics. Science, 2015, 347, 1258524.	12.6	527
32	Highly evolvable malaria vectors: The genomes of 16 Anopheles mosquitoes. Science, 2015, 347, 1258522.	12.6	492
33	Ecological opportunities and specializations shaped genetic divergence in a highly mobile marine top predator. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20141558.	2.6	51
34	Postglacial climate changes and rise of three ecotypes of harbour porpoises, <scp>P</scp>hocoena phocoena, in western <scp>P</scp>alearctic waters. Molecular Ecology, 2014, 23, 3306-3321.	3.9	67
35	Polymorphism pattern at a miniature invertedâ€repeat transposable element locus downstream of the domestication gene Teosinteâ€branched1 in wild and domesticated pearl millet. Molecular Ecology, 2013, 22, 327-340.	3.9	7
36	History of the invasion of the anther smut pathogen on S ilene latifolia in N orth A merica. New Phytologist, 2013, 198, 946-956.	7.3	33

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37	Genetic signature of a range expansion and leapâ€frog event after the recent invasion of Europe by the grapevine downy mildew pathogen Plasmopara viticola. Molecular Ecology, 2013, 22, 2771-2786.	3.9	86
38	The Evolution of the Anopheles 16 Genomes Project. G3: Genes, Genomes, Genetics, 2013, 3, 1191-1194.	1.8	49
39	Factors shaping gene flow in red deer (CervusÂelaphus) in seminatural landscapes ofÂcentral Europe. Canadian Journal of Zoology, 2012, 90, 150-162.	1.0	17
40	History of expansion and anthropogenic collapse in a top marine predator of the Black Sea estimated from genetic data. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2569-76.	7.1	54
41	A European Melting Pot of Harbour Porpoise in the French Atlantic Coasts Inferred from Mitochondrial and Nuclear Data. PLoS ONE, 2012, 7, e44425.	2.5	20
42	Barriers to Gene Flow in the Marine Environment: Insights from Two Common Intertidal Limpet Species of the Atlantic and Mediterranean. PLoS ONE, 2012, 7, e50330.	2.5	46
43	Genetic structure in a dynamic baboon hybrid zone corroborates behavioural observations in a hybrid population. Molecular Ecology, 2012, 21, 715-731.	3.9	114
44	Different biogeographic patterns of prokaryotes and microbial eukaryotes in epilithic biofilms. Molecular Ecology, 2012, 21, 3852-3868.	3.9	57
45	Cereal Domestication and Evolution of Branching: Evidence for Soft Selection in the Tb1 Orthologue of Pearl Millet (Pennisetum glaucum [L.] R. Br.). PLoS ONE, 2011, 6, e22404.	2.5	37
46	Temporal isolation explains hostâ€related genetic differentiation in a group of widespread mycoparasitic fungi. Molecular Ecology, 2011, 20, 1492-1507.	3.9	37
47	Cytochrome P450 1A1 expression in cetacean skin biopsies from the Indian Ocean. Marine Pollution Bulletin, 2011, 62, 1317-1319.	5.0	5
48	Maintenance of Fungal Pathogen Species That Are Specialized to Different Hosts: Allopatric Divergence and Introgression through Secondary Contact. Molecular Biology and Evolution, 2011, 28, 459-471.	8.9	79
49	Chromosomal Inversions, Natural Selection and Adaptation in the Malaria Vector Anopheles funestus. Molecular Biology and Evolution, 2011, 28, 745-758.	8.9	62
50	Finding candidate genes under positive selection in Non-model species: examples of genes involved in host specialization in pathogens. Molecular Ecology, 2010, 19, 292-306.	3.9	44
51	Glacial Refugia in Pathogens: European Genetic Structure of Anther Smut Pathogens on Silene latifolia and Silene dioica. PLoS Pathogens, 2010, 6, e1001229.	4.7	70
52	Genetic and historic evidence for climate-driven population fragmentation in a top cetacean predator: the harbour porpoises in European water. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 2829-2837.	2.6	61
53	A relict bank vole lineage highlights the biogeographic history of the Pyrenean region in Europe. Molecular Ecology, 2009, 18, 2489-2502.	3.9	36
54	Genetic pattern of the recent recovery of European otters in southern France. Ecography, 2008, 31, 176-186.	4.5	39

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55	Long-term feeding ecology and habitat use in harbour porpoises Phocoena phocoena from Scandinavian waters inferred from trace elements and stable isotopes. BMC Ecology, 2007, 7, 1.	3.0	37
56	Rise of oceanographic barriers in continuous populations of a cetacean: the genetic structure of harbour porpoises in Old World waters. BMC Biology, 2007, 5, 30.	3.8	161
57	Genetic pattern of the recent recovery of European otters in southern France. Ecography, 2007, .	4.5	2
58	Efficiency of Fluorescent Multiplex Polymerase Chain Reactions (PCRs) for Rapid Genotyping of Harbour Porpoises (<I>Phocoena phocoena</I>) with 11 Microsatellite Loci. Aquatic Mammals, 2006, 32, 301-304.	0.7	9
59	Ecological and pathological factors related to trace metal concentrations in harbour porpoises Phocoena phocoenaÂfrom the North Sea and adjacent areas. Marine Ecology - Progress Series, 2004, 281, 283-295.	1.9	59
60	Carbon and Nitrogen Isotopic Ratios of the Seagrass Posidonia oceanica: Depth-related Variations. Botanica Marina, 2003, 46, .	1.2	21