Sarah J Helyar

List of Publications by Year
in descending order

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38	2,025	394421	276875
papers	citations	19 h-index	41 g-index

41	41	41	3179
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Application of SNPs for population genetics of nonmodel organisms: new opportunities and challenges. Molecular Ecology Resources, 2011, 11, 123-136.	4.8	391
2	Environmental selection on transcriptomeâ€derived SNPs in a high gene flow marine fish, the Atlantic herring (Clupea harengus). Molecular Ecology, 2012, 21, 3686-3703.	3.9	205
3	Gene-associated markers provide tools for tackling illegal fishing and false eco-certification. Nature Communications, 2012, 3, 851.	12.8	199
4	Outlier <scp>SNP</scp> markers reveal fineâ€scale genetic structuring across <scp>E</scp>uropean hake populations (<scp>M</scp>erluccius merluccius). Molecular Ecology, 2014, 23, 118-135.	3.9	171
5	A genomic island linked to ecotype divergence in <scp>A</scp>tlantic cod. Molecular Ecology, 2013, 22, 2653-2667.	3.9	137
6	Fish Product Mislabelling: Failings of Traceability in the Production Chain and Implications for Illegal, Unreported and Unregulated (IUU) Fishing. PLoS ONE, 2014, 9, e98691.	2.5	128
7	The future of NGS (Next Generation Sequencing) analysis in testing food authenticity. Food Control, 2019, 101, 134-143.	5.5	68
8	Detection of quantitative trait loci for androstenone, skatole and boar taint in a cross between Large White and Meishan pigs. Animal Genetics, 2005, 36, 14-22.	1.7	66
9	Tradeâ€offs between reducing complex terminology and producing accurate interpretations from environmental DNA: Comment on â€œEnvironmental DNA: What's behind the term?â€•by Pawlowski et al., (2020). Molecular Ecology, 2021, 30, 4601-4605.	3.9	60
10	Novel Tools for Conservation Genomics: Comparing Two High-Throughput Approaches for SNP Discovery in the Transcriptome of the European Hake. PLoS ONE, 2011, 6, e28008.	2.5	59
11	SNP Discovery Using Next Generation Transcriptomic Sequencing in Atlantic Herring (Clupea) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.5	53
12	Inbreeding uncovers fundamental differences in the genetic load affecting male and female fertility in a butterfly. Proceedings of the Royal Society B: Biological Sciences, 2005, 272, 39-46.	2.6	52
13	Life in a drop: Sampling environmental DNA for marine fishery management and ecosystem monitoring. Marine Policy, 2021, 124, 104331.	3.2	52
14	Gene-associated markers can assign origin in a weakly structured fish, Atlantic herring. ICES Journal of Marine Science, 2015, 72, 1790-1801.	2.5	50
15	ECOLOGICAL DIFFERENCES AND COEXISTENCE IN A GUILD OF MICROPARASITES:BARTONELLAIN WILD RODENTS. Ecology, 2007, 88, 1841-1849.	3.2	42
16	The effect of the â€˜Gait keeperâ€™ mutation in the DMRT3 gene on gaiting ability in Icelandic horses. Journal of Animal Breeding and Genetics, 2014, 131, 415-425.	2.0	34
17	Genetic structure of the lumpfish Cyclopterus lumpus across the North Atlantic. ICES Journal of Marine Science, 2014, 71, 2390-2397.	2.5	30
18	Outlier Loci Detect Intraspecific Biodiversity amongst Spring and Autumn Spawning Herring across Local Scales. PLoS ONE, 2016, 11, e0148499.	2.5	25

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19	Rhodopsin Gene Polymorphism Associated with Divergent Light Environments in Atlantic Cod. Behavior Genetics, 2015, 45, 236-244.	2.1	23
20	Stock structure of Atlantic herring Clupea harengus in the Norwegian Sea and adjacent waters. Marine Ecology - Progress Series, 2015, 522, 219-230.	1.9	21
21	THE DYNAMICS OF MURID GAMMAHERPESVIRUS 4 WITHIN WILD, SYMPATRIC POPULATIONS OF BANK VOLES AND WOOD MICE. Journal of Wildlife Diseases, 2007, 43, 32-39.	0.8	20
22	Evaluating genetic traceability methods for captiveâ€'bred marine fish and their applications in fisheries management and wildlife forensics. Aquaculture Environment Interactions, 2016, 8, 131-145.	1.8	18
23	Highly polymorphic microsatellite loci in the bank vole (Clethrionomys glareolus). Molecular Ecology Notes, 2005, 5, 311-313.	1.7	15
24	Natural history and molecular evolution of demersal Mediterranean sharks and skates inferred by comparative phylogeographic and demographic analyses. PeerJ, 2018, 6, e5560.	2.0	14
25	Chiridota hehevaâ€"the cosmopolitan holothurian. Marine Biodiversity, 2020, 50, 1.	1.0	13
26	Novel microsatellite loci for a deep sea fish (Macrourus berglax) and their amplification in other grenadiers (Gadiformes: Macrouridae). Conservation Genetics Resources, 2010, 2, 1-4.	0.8	9
27	Twenty-two novel microsatellite loci for lumpfish (Cyclopterus lumpus). Conservation Genetics Resources, 2013, 5, 177-179.	0.8	8
28	Validation of FASTFISH-ID: A new commercial platform for rapid fish species authentication via universal closed-tube barcoding. Food Research International, 2021, 141, 110035.	6.2	8
29	Life history of turbot in Icelandic waters: Intra- and inter-population genetic diversity and otolith tracking of environmental temperatures. Fisheries Research, 2014, 155, 185-193.	1.7	7
30	Rangeâ€wide genomic data synthesis reveals transatlantic vicariance and secondary contact in Atlantic cod. Ecology and Evolution, 2018, 8, 12140-12152.	1.9	7
31	Genomic Resources Notes Accepted 1 June 2015 - 31 July 2015. Molecular Ecology Resources, 2015, 15, 1510-1512.	4.8	6
32	The genetic composition of feeding aggregations of the Atlantic mackerel (Scomber scombrus) in the central north Atlantic: a microsatellite loci approach. ICES Journal of Marine Science, 2020, 77, 604-612.	2.5	6
33	Novel polymorphic microsatellite loci for the protogynous hermaphrodite slinger sea bream (Chrysoblephus puniceus, Sparidae). Molecular Ecology Resources, 2009, 9, 1223-1226.	4.8	5
34	Genetic homogeneity in the deep-sea grenadier Macrourus berglax across the North Atlantic Ocean. Deep-Sea Research Part I: Oceanographic Research Papers, 2018, 132, 60-67.	1.4	5
35	New microsatellite loci for the longnose velvet dogfish Centroselachus crepidater (Squaliformes:) Tj ETQq1 1 0.784314 rgBT /Overloc	0.8	4
36	Isolation and characterization of thirty microsatellite loci for Atlantic mackerel (Scomber scombrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.8	3

#	Article	IF	Citations
37	Combining spawn egg counts, individual photoâ€ID and genetic fingerprinting to estimate the population size and sex ratio of an endangered amphibian. Integrative Zoology, 2021, 16, 240-254.	2.6	2
38	Development and validation of a quantitative qPCR assay for detecting Natterjack toad (Epidalea) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	2