

Going where traditional markers have not gone before:
<scp>RAD</scp> sequencing in marine invertebrate phylogenomics

Molecular Ecology

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Citation Report

#	ARTICLE	IF	CITATIONS
1	High-Throughput Genomic Data in Systematics and Phylogenetics. Annual Review of Ecology, Evolution, and Systematics, 2013, 44, 99-121.	3.8	434
2	High degree of genetic differentiation in marine three-spined sticklebacks (<i>Gasterosteus aculeatus</i>). <i>Evolution</i> , 2013, 67, 1073-1084.	2.0	30
3	Genotyping-by-sequencing in ecological and conservation genomics. <i>Molecular Ecology</i> , 2013, 22, 2841-2847.	2.0	469
4	ezRAD: a simplified method for genomic genotyping in non-model organisms. <i>PeerJ</i> , 2013, 1, e203.	0.9	184
5	Hundreds of SNPs vs. dozens of SSRs: which dataset better characterizes natural clonal lineages in a self-fertilizing fish?. <i>Frontiers in Ecology and Evolution</i> , 2014, 2, .	1.1	17
6	Development and application of genomic tools to the restoration of green abalone in southern California. <i>Conservation Genetics</i> , 2014, 15, 109-121.	0.8	30
7	Editorial 2014. <i>Molecular Ecology</i> , 2014, 23, 1-15.	2.0	1
8	Applicability of RAD-tag genotyping for interfamilial comparisons: empirical data from two cetaceans. <i>Molecular Ecology Resources</i> , 2014, 14, 597-605.	2.2	25
9	Seascape continuity plays an important role in determining patterns of spatial genetic structure in a coral reef fish. <i>Molecular Ecology</i> , 2014, 23, 2902-2913.	2.0	34
10	Identifying signatures of sexual selection using genomewide selection components analysis. <i>Ecology and Evolution</i> , 2015, 5, 2722-2744.	0.8	4
11	Using nuclear gene data for plant phylogenetics: Progress and prospects II. Next-generation approaches. <i>Journal of Systematics and Evolution</i> , 2015, 53, 371-379.	1.6	174
12	RAD genotyping reveals fine-scale genetic structuring and provides powerful population assignment in a widely distributed marine species, the American lobster (<i>Homarus americanus</i>). <i>Molecular Ecology</i> , 2015, 24, 3299-3315.	2.0	239
13	Species-specific responses to island connectivity cycles: refined models for testing phylogeographic concordance across a Mediterranean Pleistocene aggregate island complex. <i>Molecular Ecology</i> , 2015, 24, 4252-4268.	2.0	67
14	Genes mirror geography in <i>Daphnia magna</i> . <i>Molecular Ecology</i> , 2015, 24, 4521-4536.	2.0	41
15	Antarctic krill population genomics: apparent panmixia, but genome complexity and large population size muddy the water. <i>Molecular Ecology</i> , 2015, 24, 4943-4959.	2.0	46
16	Transition in sexual system and sex chromosome evolution in the tadpole shrimp <i>Triops cancriformis</i> . <i>Heredity</i> , 2015, 115, 37-46.	1.2	16
17	Predicting RAD-seq Marker Numbers across the Eukaryotic Tree of Life. <i>Genome Biology and Evolution</i> , 2015, 7, 3207-3225.	1.1	36
18	Evolutionary and biogeographical patterns of barnacles from deep-sea hydrothermal vents. <i>Molecular Ecology</i> , 2015, 24, 673-689.	2.0	92

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19	The evolution of phylogeographic data sets. <i>Molecular Ecology</i> , 2015, 24, 1164-1171.	2.0	119
20	Assessing the phylogeographic history of the montane caddisfly <i>Tremma gallicum</i> using mitochondrial and restriction-associated DNA (RAD) markers. <i>Ecology and Evolution</i> , 2015, 5, 648-662.	0.8	25
21	AfrRAD: a pipeline for accurate and efficient <i>de novo</i> assembly of RAD-seq data. <i>Molecular Ecology Resources</i> , 2015, 15, 1163-1171.	2.2	34
22	Evolutionary patterns in Antarctic marine invertebrates: An update on molecular studies. <i>Marine Genomics</i> , 2015, 23, 1-13.	0.4	37
23	Genomic tests of the species-pump hypothesis: Recent island connectivity cycles drive population divergence but not speciation in Caribbean crickets across the Virgin Islands. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1501-1517.	1.1	88
24	Exploring the utility of cross-laboratory RAD-sequencing datasets for phylogenetic analysis. <i>BMC Research Notes</i> , 2015, 8, 299.	0.6	29
25	Population structure and connectivity in Indo-Pacific deep-sea mussels of the <i>Bathymodiolus septemdiarium</i> complex. <i>Conservation Genetics</i> , 2015, 16, 1415-1430.	0.8	41
27	Use of RAD sequencing for delimiting species. <i>Heredity</i> , 2015, 114, 450-459.	1.2	163
28	Marine invasion genetics: from spatio-temporal patterns to evolutionary outcomes. <i>Biological Invasions</i> , 2015, 17, 869-885.	1.2	92
29	Using <i>Nematostella vectensis</i> to Study the Interactions between Genome, Epigenome, and Bacteria in a Changing Environment. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	21
30	Genomic evidence for ecological divergence against a background of population homogeneity in the marine snail <i>Chlorostoma funebris</i> . <i>Molecular Ecology</i> , 2016, 25, 3557-3573.	2.0	39
31	Development of a universal double-digest RAD sequencing approach for a group of nonmodel, ecologically and economically important insect and fish taxa. <i>Molecular Ecology Resources</i> , 2016, 16, 1303-1314.	2.2	22
32	How to select networks of marine protected areas for multiple species with different dispersal strategies. <i>Diversity and Distributions</i> , 2016, 22, 161-173.	1.9	26
33	Effective application of next-generation sequencing (NGS) approaches in systematics and population genetics: case studies in <i>Eucalyptus</i> and <i>Acacia</i> . <i>Australian Systematic Botany</i> , 2016, 29, 235.	0.3	3
34	Genome-wide SNP discovery in the annual herb, <i>Lasthenia fremontii</i> (Asteraceae): genetic resources for the conservation and restoration of a California vernal pool endemic. <i>Conservation Genetics Resources</i> , 2016, 8, 145-158.	0.4	9
35	Beyond the Coral Triangle: high genetic diversity and near panmixia in Singapore's populations of the broadcast spawning sea star <i>Protoreaster nodosus</i> . <i>Royal Society Open Science</i> , 2016, 3, 160253.	1.1	16
36	A genomewide catalogue of single nucleotide polymorphisms in white-beaked and Atlantic white-sided dolphins. <i>Molecular Ecology Resources</i> , 2016, 16, 266-276.	2.2	16
37	Larval Dispersal and Population Connectivity in Anthozoans. , 2016, , 291-315.		7

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38	Evolutionary potential and adaptation of <i>Banksia attenuata</i> (Proteaceae) to climate and fire regime in southwestern Australia, a global biodiversity hotspot. <i>Scientific Reports</i> , 2016, 6, 26315.	1.6	8
39	Response of bacterial colonization in <i>Nematostella vectensis</i> to development, environment and biogeography. <i>Environmental Microbiology</i> , 2016, 18, 1764-1781.	1.8	109
40	Connectivity in the cold: the comparative population genetics of ventrâ€ndemic fauna in the Scotia Sea, Southern Ocean. <i>Molecular Ecology</i> , 2016, 25, 1073-1088.	2.0	23
41	Genome-wide polymorphism and signatures of selection in the symbiotic sea anemone <i>Aiptasia</i> . <i>BMC Genomics</i> , 2016, 17, 160.	1.2	22
42	New view of population genetics of zooplankton: RAD-seq analysis reveals population structure of the North Atlantic planktonic copepod <i>Centropages typicus</i> . <i>Molecular Ecology</i> , 2016, 25, 1566-1580.	2.0	56
43	Patterns of species range evolution in Indo-Pacific reef assemblages reveal the Coral Triangle as a net source of transoceanic diversity. <i>Biology Letters</i> , 2016, 12, 20160090.	1.0	17
44	An introduction to plant phylogenomics with a focus on palms. <i>Botanical Journal of the Linnean Society</i> , 2016, 182, 234-255.	0.8	42
45	RAD sequencing enables unprecedented phylogenetic resolution and objective species delimitation in recalcitrant divergent taxa. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 70-79.	1.2	125
46	Population genomics reveals that within-fungus polymorphism is common and maintained in populations of the mycorrhizal fungus <i>Rhizophagus irregularis</i> . <i>ISME Journal</i> , 2016, 10, 2514-2526.	4.4	54
47	Evaluation of genetic characteristics of wild and cultured populations of the Japanese pearl oyster <i>Pinctada fucata martensii</i> by using AFLP markers. <i>Aquaculture International</i> , 2016, 24, 537-548.	1.1	3
48	Genome-wide discovery of single nucleotide polymorphisms (SNPs) and single nucleotide variants (SNVs) in deep-sea mussels: Potential use in population genomics and cross-species application. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2017, 137, 318-326.	0.6	31
49	Potentially adaptive mitochondrial haplotypes as a tool to identify divergent nuclear loci. <i>Methods in Ecology and Evolution</i> , 2017, 8, 821-834.	2.2	10
50	Population genomics of an endemic Mediterranean fish: differentiation by fine scale dispersal and adaptation. <i>Scientific Reports</i> , 2017, 7, 43417.	1.6	83
51	RAD sequencing resolves fine-scale population structure in a benthic invertebrate: implications for understanding phenotypic plasticity. <i>Royal Society Open Science</i> , 2017, 4, 160548.	1.1	75
52	Species boundaries in the absence of morphological, ecological or geographical differentiation in the Red Sea octocoral genus <i>Ovabunda</i> (Alcyonacea: Xeniidae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 174-184.	1.2	53
53	Resolving interspecific relationships within evolutionarily young lineages using RNA-seq data: An example from <i>Pedicularis</i> section <i>Cyathophora</i> (Orobanchaceae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 345-355.	1.2	21
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55	Coral hybridization or phenotypic variation? Genomic data reveal gene flow between <i>Porites lobata</i> and <i>P. Compressa</i> . <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 132-148.	1.2	59

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56	Advances of genotyping-by-sequencing in fisheries and aquaculture. <i>Reviews in Fish Biology and Fisheries</i> , 2017, 27, 535-559.	2.4	34
57	Phylogenomic inferences from reference-mapped and de novo assembled short-read sequence data using RADseq sequencing of California white oaks (<i>Quercus</i> section <i>Quercus</i>). <i>Genome</i> , 2017, 60, 743-755.	0.9	50
58	Geographic structure in the Southern Ocean circumpolar brittle star <i>Ophionotus victoriae</i> (Ophiuridae) revealed from mt DNA and single nucleotide polymorphism data. <i>Ecology and Evolution</i> , 2017, 7, 475-485.	0.8	30
59	Invertebrate population genetics across Earth's largest habitat: The deep sea floor. <i>Molecular Ecology</i> , 2017, 26, 4872-4896.	2.0	87
60	More than meets the eye: The barrier effect of the Yangtze River outflow. <i>Molecular Ecology</i> , 2017, 26, 4591-4602.	2.0	28
61	Can asexuality confer a short-term advantage? Investigating apparent biogeographic success in the apomictic triploid fern <i>Myriopteris gracilis</i> . <i>American Journal of Botany</i> , 2017, 104, 1254-1265.	0.8	7
62	The Utility of Single Nucleotide Polymorphism (SNP) Data in Phylogenetics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2017, 48, 69-84.	3.8	141
63	Sex matters in massive parallel sequencing: Evidence for biases in genetic parameter estimation and investigation of sex determination systems. <i>Molecular Ecology</i> , 2017, 26, 6767-6783.	2.0	44
64	Swept away: ocean currents and seascape features influence genetic structure across the 18,000 Km Indo-Pacific distribution of a marine invertebrate, the black-lip pearl oyster <i>Pinctada margaritifera</i> . <i>BMC Genomics</i> , 2017, 18, 66.	1.2	50
65	Identifying patterns of dispersal, connectivity and selection in the sea scallop, <i>Placopecten magellanicus</i> , using RAD-seq derived SNP's. <i>Evolutionary Applications</i> , 2017, 10, 102-117.	1.5	82
66	Marine genomics: News and views. <i>Marine Genomics</i> , 2017, 31, 1-8.	0.4	12
67	Exploring the phylogeography of a hexaploid freshwater fish by RAD sequencing. <i>Ecology and Evolution</i> , 2018, 8, 2326-2342.	0.8	17
68	Metaorganisms in extreme environments: do microbes play a role in organismal adaptation?. <i>Zoology</i> , 2018, 127, 1-19.	0.6	194
69	Population Genomics of Early-Splitting Lineages of Metazoans. <i>Population Genomics</i> , 2018, , 103-137.	0.2	7
70	Population Genomics of Marine Zooplankton. <i>Population Genomics</i> , 2018, , 61-102.	0.2	24
71	Oceanographic variation influences spatial genomic structure in the sea scallop, <i>Placopecten magellanicus</i> . <i>Ecology and Evolution</i> , 2018, 8, 2824-2841.	0.8	12
72	Development and characterization of new polymorphic microsatellite markers in four sea anemones: <i>Entacmaea quadricolor</i> , <i>Heteractis magnifica</i> , <i>Stichodactyla gigantea</i> , and <i>Stichodactyla mertensii</i> . <i>Marine Biodiversity</i> , 2018, 48, 1283-1290.	0.3	2
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74	Population connectivity of the plating coral <i>Agaricia lamarcki</i> from southwest Puerto Rico. <i>Coral Reefs</i> , 2018, 37, 183-191.	0.9	23
75	Spatial patterns of genetic diversity among Australian alpine flora communities revealed by comparative phylogenomics. <i>Journal of Biogeography</i> , 2018, 45, 177-189.	1.4	8
76	Hierarchical biogeographical processes largely explain the genomic divergence pattern in a species complex of sea anemones (Metridioidea: Sagartiidae: Anthothoe). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 217-228.	1.2	8
77	Marine Invasion Genomics: Revealing Ecological and Evolutionary Consequences of Biological Invasions. <i>Population Genomics</i> , 2018, , 363-398.	0.2	11
78	Cryptic diversity, low connectivity and suspected human-mediated dispersal among 17 widespread Indo-Pacific hydroid species of the south-western Indian Ocean. <i>Journal of Biogeography</i> , 2018, 45, 2104-2117.	1.4	19
79	Population Genetic Structure in Glyphosate-Resistant and -Susceptible Palmer Amaranth (<i>Amaranthus</i>) Tj ETQq1 1 0.784314.rgBT/Over	1.7	31
80	Exploring the Ecology of Deep-Sea Hydrothermal Vents in a Metacommunity Framework. <i>Frontiers in Marine Science</i> , 2018, 5, .	1.2	79
81	Full mitochondrial genome sequences reveal new insights about post-glacial expansion and regional phylogeographic structure in the Atlantic silverside (<i>Menidia menidia</i>). <i>Marine Biology</i> , 2018, 165, 1.	0.7	16
82	Nonclonal coloniality: Genetically chimeric colonies through fusion of sexually produced polyps in the hydrozoan <i>Ectopleura larynx</i> . <i>Evolution Letters</i> , 2018, 2, 442-455.	1.6	32
83	Adaptation Without Boundaries: Population Genomics in Marine Systems. <i>Population Genomics</i> , 2018, , 587-612.	0.2	2
84	Complex signatures of genomic variation of two non-model marine species in a homogeneous environment. <i>BMC Genomics</i> , 2018, 19, 347.	1.2	21
85	A RAD-sequencing approach to genome-wide marker discovery, genotyping, and phylogenetic inference in a diverse radiation of primates. <i>PLoS ONE</i> , 2018, 13, e0201254.	1.1	19
86	Genome-wide analyses of the <i>Bemisia tabaci</i> species complex reveal contrasting patterns of admixture and complex demographic histories. <i>PLoS ONE</i> , 2018, 13, e0190555.	1.1	46
87	Maintenance of species boundaries in three sympatric <i>Ligularia</i> (Senecioneae, Asteraceae) species. <i>Journal of Integrative Plant Biology</i> , 2018, 60, 986-999.	4.1	7
88	31 Past, Present and Future Connectivity of Mediterranean Cold-Water Corals: Patterns, Drivers and Fate in a Technically and Environmentally Changing World. <i>Coral Reefs of the World</i> , 2019, , 357-372.	0.3	6
89	Strengths and potential pitfalls of hay transfer for ecological restoration revealed by RADseq analysis in floodplain <i>Arabis</i> species. <i>Molecular Ecology</i> , 2019, 28, 3887-3901.	2.0	14
90	The genetics and genomics of marine fish invasions: a global review. <i>Reviews in Fish Biology and Fisheries</i> , 2019, 29, 837-859.	2.4	7
91	Causes and analytical impacts of missing data in RADseq phylogenetics: Insights from an African frog (<i>Afraxalus</i>). <i>Zoologica Scripta</i> , 2019, 48, 157-167.	0.7	30

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92	Population structure, genetic connectivity, and adaptation in the Olympia oyster (<i>Ostrea</i>)	1.5	33
93	Population substructure and signals of divergent adaptive selection despite admixture in the sponge <i>Dendrilla antarctica</i> from shallow waters surrounding the Antarctic Peninsula. <i>Molecular Ecology</i> , 2019, 28, 3151-3170.	2.0	23
94	Role of SNPs in determining QTLs for major traits in cotton. <i>Journal of Cotton Research</i> , 2019, 2, .	1.0	18
95	Multiple spatially distinct introductions and not range expansion may explain colonization history in a non-native marine shrimp. <i>Marine Biology</i> , 2019, 166, 1.	0.7	1
96	Distribution of the highly toxic clinging jellyfish <i>Gonionemus</i> sp. around the island of Martha's Vineyard, Massachusetts, USA. <i>Marine Biodiversity Records</i> , 2019, 12, .	1.2	1
97	Population genomics of rapidly invading lionfish in the Caribbean reveals signals of range expansion in the absence of spatial population structure. <i>Ecology and Evolution</i> , 2019, 9, 3306-3320.	0.8	24
98	Maximising genetic diversity during coral transplantation from a highly impacted source reef. <i>Conservation Genetics</i> , 2019, 20, 629-637.	0.8	9
99	Hitchhiking the high seas: Global genomics of rafting crabs. <i>Ecology and Evolution</i> , 2019, 9, 957-974.	0.8	11
100	Identification of male-specific SNP markers and development of PCR-based genetic sex identification technique in crucifix crab (<i>Charybdis feriatus</i>) with implication of an XX/XY sex determination system. <i>Genomics</i> , 2020, 112, 404-411.	1.3	30
101	Population genomic structure of the gelatinous zooplankton species <i>Mnemiopsis leidyi</i> in its nonindigenous range in the North Sea. <i>Ecology and Evolution</i> , 2020, 10, 11-25.	0.8	4
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103	Genomic Phylogeography of <i>Gymnocarpus przewalskii</i> (Caryophyllaceae): Insights into Habitat Fragmentation in Arid Northwestern China. <i>Diversity</i> , 2020, 12, 335.	0.7	12
104	Migration dynamics of an important rice pest: The brown planthopper (<i>Nilaparvata lugens</i>) across Asia—Insights from population genomics. <i>Evolutionary Applications</i> , 2020, 13, 2449-2459.	1.5	20
105	Population Genomic Analyses of the Sea Urchin <i>Echinometra</i> sp. EZ across an Extreme Environmental Gradient. <i>Genome Biology and Evolution</i> , 2020, 12, 1819-1829.	1.1	8
106	Seascape genomics reveals population isolation in the reef-building honeycomb worm, <i>Sabellaria alveolata</i> (L.). <i>BMC Evolutionary Biology</i> , 2020, 20, 100.	3.2	1
107	Some like it hot: population-specific adaptations in venom production to abiotic stressors in a widely distributed cnidarian. <i>BMC Biology</i> , 2020, 18, 121.	1.7	18
108	Mediators of invasions in the sea: life history strategies and dispersal vectors facilitating global sea anemone introductions. <i>Biological Invasions</i> , 2020, 22, 3195-3222.	1.2	19
109	Phylogeography and the Description of Geographic Patterns in Invasion Genomics. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	14

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110	Reproduction in Urbanised Coastal Waters: Shallow-Water Sea Anemones (<i>Entacmaea quadricolor</i>)	0.7	10
111	Chaotic genetic structure and past demographic expansion of the invasive gastropod <i>Tritia neritea</i> in its native range, the Mediterranean Sea. <i>Scientific Reports</i> , 2020, 10, 21624.	1.6	2
112	Pathways of Pelagic Connectivity: <i>Eukrohnia hamata</i> (Chaetognatha) in the Arctic Ocean. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	8
113	Population structure of <i>Apodemus flavicollis</i> and comparison to <i>Apodemus sylvaticus</i> in northern Poland based on RAD-seq. <i>BMC Genomics</i> , 2020, 21, 241.	1.2	10
114	Detecting glacial refugia in the Southern Ocean. <i>Ecography</i> , 2020, 43, 1639-1656.	2.1	23
115	Unraveling hierarchical genetic structure in a marine metapopulation: A comparison of three high-throughput genotyping approaches. <i>Molecular Ecology</i> , 2020, 29, 2189-2203.	2.0	26
116	Comparative Population Genomics and Biophysical Modeling of Shrimp Migration in the Gulf of Mexico Reveals Current-Mediated Connectivity. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	18
117	Re-examination of population structure in Arctic ringed seals using DArTseq genotyping. <i>Endangered Species Research</i> , 2021, 44, 11-31.	1.2	3
118	The Dynasty of the Pharaoh: Phylogeography and Cryptic Biodiversity of <i>Sepia pharaonis</i> Cuttlefish in Northwest Indian Ocean Peripheral Seas. , 2021, , 427-442.		2
119	Phenotypic plasticity rather than genotype drives reproductive choices in <i>Hydra</i> populations. <i>Molecular Ecology</i> , 2021, 30, 1206-1222.	2.0	11
120	Application of phylogenomic tools to unravel anthozoan evolution. <i>Coral Reefs</i> , 2022, 41, 475-495.	0.9	11
121	Population genomic structure of the black coral <i>Antipathella subpinnata</i> in Mediterranean Vulnerable Marine Ecosystems. <i>Coral Reefs</i> , 2021, 40, 751-766.	0.9	6
123	Gaps in genetic knowledge affect conservation management of kiwi (<i>Apteryx</i>) species. <i>Ibis</i> , 2021, 163, 1155-1174.	1.0	4
124	Population structure and phylogeography of two North Atlantic <i>Littorina</i> species with contrasting larval development. <i>Marine Biology</i> , 2021, 168, 1.	0.7	10
125	Facilitating population genomics of non-model organisms through optimized experimental design for reduced representation sequencing. <i>BMC Genomics</i> , 2021, 22, 625.	1.2	6
126	Comparison of sequence-capture and ddRAD approaches in resolving species and populations in hexacorallian anthozoans. <i>Molecular Phylogenetics and Evolution</i> , 2021, 163, 107233.	1.2	9
127	Genetic Rescue and the Plight of Ponui Hybrids. <i>Frontiers in Conservation Science</i> , 2021, 1, .	0.9	5
133	Large-Scale Genotyping-by-Sequencing Indicates High Levels of Gene Flow in the Deep-Sea Octocoral <i>Swiftia simplex</i> (Nutting 1909) on the West Coast of the United States. <i>PLoS ONE</i> , 2016, 11, e0165279.	1.1	14

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136	Lack of genetic introgression between wild and selectively bred Sydney rock oysters <i>Saccostrea glomerata</i> . <i>Marine Ecology - Progress Series</i> , 2017, 570, 127-139.	0.9	16
137	Genome-wide survey of single-nucleotide polymorphisms reveals fine-scale population structure and signs of selection in the threatened Caribbean elkhorn coral, <i>Acropora palmata</i> . <i>PeerJ</i> , 2017, 5, e4077.	0.9	36
138	Similarity thresholds used in DNA sequence assembly from short reads can reduce the comparability of population histories across species. <i>PeerJ</i> , 2015, 3, e895.	0.9	59
139	A Revised Classification of Glossopetalon (Crossosomataceae) Based on Restriction Site-Associated DNA Sequencing. <i>Systematic Botany</i> , 2021, 46, 562-572.	0.2	0
145	Biyoteknolojinin Geliştirilmesi ve Uygulamaları Üzerine Su Ürünleri Genetik Alanında Kullanılması: Yeni Nesil Düzileme Teknolojileri. <i>Journal of Limnology and Freshwater Fisheries Research</i> , 2018, 4, 192-204.	0.4	0
148	Understanding heat stress response in dairy animals: an overview. , 2022, , 393-404.		0
149	Phylogeography of Paramuricea: The Role of Depth and Water Mass in the Evolution and Distribution of Deep-Sea Corals. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	9
150	Species identification in <i>Haliotis</i> genus from the northeastern Pacific Ocean using genome-wide RAD-SNPs. <i>Food Control</i> , 2022, 138, 108979.	2.8	1
151	Common Environmental Pollutants Negatively Affect Development and Regeneration in the Sea Anemone <i>Nematostella vectensis</i> Holobiont. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	5
152	Kilometer-Scale Larval Dispersal Processes Predict Metapopulation Connectivity Pathways for <i>Paramuricea biscaya</i> in the Northern Gulf of Mexico. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	6
153	Seascape Genomics Reveals Metapopulation Connectivity Network of <i>Paramuricea biscaya</i> in the Northern Gulf of Mexico. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	3
154	Population genomics for symbiotic anthozoans: can reduced representation approaches be used for taxa without reference genomes?. <i>Heredity</i> , 2022, , .	1.2	1
163	Population structure of lake whitefish (<i>Coregonus clupeaformis</i>) from the Mississippian lineage in North America. <i>Facets</i> , 2022, 7, 853-874.	1.1	1
166	Genetic impacts of physical disturbance processes in coastal marine ecosystems. <i>Journal of Biogeography</i> , 2022, 49, 1877-1890.	1.4	8
167	Islands in the desert: assessing fine scale population genomic variation of a group of imperiled desert fishes. <i>Conservation Genetics</i> , 2022, 23, 935-947.	0.8	2
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170	Micro and macroevolution of sea anemone venom phenotype. Nature Communications, 2023, 14, .	5.8	10
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172	Genotypeâ€environment interactions determine microbiota plasticity in the sea anemone Nematostella vectensis. PLoS Biology, 2023, 21, e3001726.	2.6	5
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