

Harnessing the power of RADseq for ecological and evolutionary genetics

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Citation Report

#	ARTICLE	IF	CITATIONS
1	High-density linkage map construction and QTL analysis for earliness-related traits in <i>Gossypium hirsutum</i> L. <i>BMC Genomics</i> , 2016, 17, 909.	1.2	51
2	Navigating the currents of seascape genomics: how spatial analyses can augment population genomic studies. <i>Environmental Epigenetics</i> , 2016, 62, 581-601.	0.9	108
3	Genetic load in marine animals: a review. <i>Environmental Epigenetics</i> , 2016, 62, 567-579.	0.9	78
4	A Linkage Map and QTL Analysis for Pyrethroid Resistance in the Bed Bug <i>Cimex lectularius</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 4059-4066.	0.8	9
5	Vive la résistance: genome-wide selection against introduced alleles in invasive hybrid zones. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161380.	1.2	40
6	Clonal Expansion and Migration of a Highly Virulent, Defoliating Lineage of <i>Verticillium dahliae</i> . <i>Phytopathology</i> , 2016, 106, 1038-1046.	1.1	34
7	Development of a universal and simplified ddRAD library preparation approach for SNP discovery and genotyping in angiosperm plants. <i>Plant Methods</i> , 2016, 12, 39.	1.9	86
8	The history of Old World camelids in the light of molecular genetics. <i>Tropical Animal Health and Production</i> , 2016, 48, 905-913.	0.5	56
9	What are we missing about marine invasions? Filling in the gaps with evolutionary genomics. <i>Marine Biology</i> , 2016, 163, 1.	0.7	39
10	Genome-wide nucleotide diversity of hatchery-reared Atlantic and Mediterranean strains of brown trout <i>Salmo trutta</i> compared to wild Mediterranean populations. <i>Journal of Fish Biology</i> , 2016, 89, 2717-2734.	0.7	29
11	Population structure and gene flow in the global pest, <i>Helicoverpa armigera</i> . <i>Molecular Ecology</i> , 2016, 25, 5296-5311.	2.0	71
12	Causes and consequences of large clonal assemblies in a poplar hybrid zone. <i>Molecular Ecology</i> , 2016, 25, 5330-5344.	2.0	7
13	Dealing with paralogy in RAD-seq data: in silico detection and single nucleotide polymorphism validation in <i>Robinia pseudoacacia</i> L. <i>Ecology and Evolution</i> , 2016, 6, 7323-7333.	0.8	32
14	On the maintenance of genetic variation and adaptation to environmental change: considerations from population genomics in fishes. <i>Journal of Fish Biology</i> , 2016, 89, 2519-2556.	0.7	187
15	Advances in genomics for adapting crops to climate change. <i>Current Plant Biology</i> , 2016, 6, 2-10.	2.3	82
16	Serial sequencing of isologous RAD tags for cost-efficient genome-wide profiling of genetic and epigenetic variations. <i>Nature Protocols</i> , 2016, 11, 2189-2200.	5.5	73
17	Angelfishes, Paper Tigers, and the Devilish Taxonomy of the <i>Centropyge flavissima</i> Complex. <i>Journal of Heredity</i> , 2016, 107, 647-653.	1.0	17
18	Is there a future for genome-editing technologies in conservation?. <i>Animal Conservation</i> , 2016, 19, 97-101.	1.5	45

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19	Finding the Genomic Basis of Local Adaptation: Pitfalls, Practical Solutions, and Future Directions. <i>American Naturalist</i> , 2016, 188, 379-397.	1.0	663
20	Genomics advances the study of inbreeding depression in the wild. <i>Evolutionary Applications</i> , 2016, 9, 1205-1218.	1.5	200
21	Genomic Methods Take the Plunge: Recent Advances in High-Throughput Sequencing of Marine Mammals. <i>Journal of Heredity</i> , 2016, 107, 481-495.	1.0	50
22	Building strong relationships between conservation genetics and primary industry leads to mutually beneficial genomic advances. <i>Molecular Ecology</i> , 2016, 25, 5267-5281.	2.0	16
23	The report of my death was an exaggeration: A review for researchers using microsatellites in the 21st century. <i>Applications in Plant Sciences</i> , 2016, 4, 1600025.	0.8	155
24	Development of SNP markers for analysis of population structure in white perch (<i>Morone americana</i>) using double digest restriction site-associated DNA sequencing. <i>Conservation Genetics Resources</i> , 2016, 8, 403-406.	0.4	2
25	<sc>RAD</sc>cap: sequence capture of dualâ€digest <sc>RAD</sc>seq libraries with identifiable duplicates and reduced missing data. <i>Molecular Ecology Resources</i> , 2016, 16, 1264-1278.	2.2	117
26	<sc>SNP</sc>s across time and space: population genomic signatures of founder events and epizootics in the House Finch (<i>Haemorrhous mexicanus</i>). <i>Ecology and Evolution</i> , 2016, 6, 7475-7489.	0.8	40
27	Next Gen Pop Gen: implementing a high-throughput approach to population genetics in boarfish (<i>Capros aper</i>). <i>Royal Society Open Science</i> , 2016, 3, 160651.	1.1	23
28	Salmonid chromosome evolution as revealed by a novel method for comparing RADseq linkage maps. <i>Genome Biology and Evolution</i> , 2016, 8, evw262.	1.1	67
29	Divergence and isolation of cryptic sympatric taxa within the annual legume <i>Amphicarpaea bracteata</i> . <i>Ecology and Evolution</i> , 2016, 6, 3367-3379.	0.8	7
30	Sorting duplicated loci disentangles complexities of polyploid genomes masked by genotyping by sequencing. <i>Molecular Ecology</i> , 2016, 25, 2117-2129.	2.0	46
31	Male Reproductive Morphology Across Latitudinal Clines and Under Long-Term Female Sex-Ratio Bias. <i>Integrative and Comparative Biology</i> , 2016, 56, 715-727.	0.9	7
32	Population Genomics of Fungal and Oomycete Pathogens. <i>Annual Review of Phytopathology</i> , 2016, 54, 323-346.	3.5	96
33	A High-Density SNP Genetic Linkage Map and QTL Analysis of Growth-Related Traits in a Hybrid Family of Oysters (<i>Crassostrea gigas</i> × <i>Crassostrea angulata</i>) Using Genotyping-by-Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1417-1426.	0.8	70
34	Conservation genomics of natural and managed populations: building a conceptual and practical framework. <i>Molecular Ecology</i> , 2016, 25, 2967-2977.	2.0	141
35	Using <sc>RAD</sc>â€seq to recognize sexâ€specific markers and sex chromosome systems. <i>Molecular Ecology</i> , 2016, 25, 2114-2116.	2.0	62
36	How fisheries management can benefit from genomics?. <i>Briefings in Functional Genomics</i> , 2016, 15, 352-357.	1.3	41

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37	Revisiting the particular role of host shifts in initiating insect speciation. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1126-1137.	1.1	137
38	Island floras as model systems for studies of plant speciation: Prospects and challenges. <i>Journal of Systematics and Evolution</i> , 2017, 55, 1-15.	1.6	28
39	The colonization history of the Mediterranean dwarf palm (<i>Chamaerops humilis</i> L., Palmae). <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	27
40	PCR-based assays for validation of single nucleotide polymorphism markers in rice and mungbean. <i>Hereditas</i> , 2017, 154, 3.	0.5	5
41	Genome-wide selection components analysis in a fish with male pregnancy. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1096-1105.	1.1	32
42	Minimum sample sizes for population genomics: an empirical study from an Amazonian plant species. <i>Molecular Ecology Resources</i> , 2017, 17, 1136-1147.	2.2	212
43	Climate change and alpine stream biology: progress, challenges, and opportunities for the future. <i>Biological Reviews</i> , 2017, 92, 2024-2045.	4.7	118
44	Managing mixed-stock fisheries: genotyping multi-SNP haplotypes increases power for genetic stock identification. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2017, 74, 429-434.	0.7	51
45	Evolutionary genetics of host shifts in herbivorous insects: insights from the age of genomics. <i>Annals of the New York Academy of Sciences</i> , 2017, 1389, 186-212.	1.8	37
46	QTL analysis and genomic selection using RADseq derived markers in Sitka spruce: the potential utility of within family data. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	17
47	Using a butterflyfish genome as a general tool for RAD-seq studies in specialized reef fish. <i>Molecular Ecology Resources</i> , 2017, 17, 1330-1341.	2.2	6
48	quaddRAD: a new high-throughput multiplexing and PCR duplicate removal ddRAD protocol produces novel evolutionary insights in a nonradiating cichlid lineage. <i>Molecular Ecology</i> , 2017, 26, 2783-2795.	2.0	57
49	Evolutionary toxicology in an omics world. <i>Evolutionary Applications</i> , 2017, 10, 752-761.	1.5	26
50	Genotyping-by-sequencing. <i>Current Protocols in Plant Biology</i> , 2017, 2, 64-77.	2.8	26
51	Conservation implications of limited genetic diversity and population structure in Tasmanian devils (<i>Sarcophilus harrisii</i>). <i>Conservation Genetics</i> , 2017, 18, 977-982.	0.8	50
52	A reassessment of the phylogeny and circumscription of <i>Zaluzianskya</i> (Scrophulariaceae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 194-208.	1.2	1
53	A genome-wide SNP-based genetic map and QTL mapping for agronomic traits in Chinese cabbage. <i>Scientific Reports</i> , 2017, 7, 46305.	1.6	16
54	Lineage divergence, local adaptation across a biogeographic break, and artificial transport, shape the genetic structure in the ascidian <i>Pyura chilensis</i> . <i>Scientific Reports</i> , 2017, 7, 44559.	1.6	16

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55	Genetic assignment with isotopes and habitat suitability (<scp>gaiah</scp>), a migratory bird case study. <i>Methods in Ecology and Evolution</i> , 2017, 8, 1241-1252.	2.2	28
56	Whole-Genome Restriction Mapping by α -Subhaploid-Based RAD Sequencing: An Efficient and Flexible Approach for Physical Mapping and Genome Scaffolding. <i>Genetics</i> , 2017, 206, 1237-1250.	1.2	1
57	Comparison and confirmation of SNP-bud burst associations in European beech populations in Germany. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	12
58	The role of dispersal for genetic and phenotypic variation: insights from comparisons of sympatric pygmy grasshoppers. <i>Biological Journal of the Linnean Society</i> , 2017, 122, 84-97.	0.7	9
59	A High-Density Genetic Linkage Map and QTL Fine Mapping for Body Weight in Crucian Carp (<i>Carassius auratus</i>) Using 2b-RAD Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2473-2487.	0.8	35
60	Phased Genotyping-by-Sequencing Enhances Analysis of Genetic Diversity and Reveals Divergent Copy Number Variants in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2161-2170.	0.8	29
61	Sex Chromosome Evolution, Heterochiasmy, and Physiological QTL in the Salmonid Brook Charr (<i>Salvelinus fontinalis</i>). <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2749-2762.	0.8	38
62	Assessing the potential of RAD-sequencing to resolve phylogenetic relationships within species radiations: The fly genus <i>Chiastocheta</i> (Diptera: Anthomyiidae) as a case study. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 189-198.	1.2	18
63	Phylogenomics. , 2017, , .		47
64	Screening of duplicated loci reveals hidden divergence patterns in a complex salmonid genome. <i>Molecular Ecology</i> , 2017, 26, 4509-4522.	2.0	18
65	Small- and large-scale heterogeneity in genetic variation across the collard flycatcher genome: implications for estimating genetic diversity in nonmodel organisms. <i>Molecular Ecology Resources</i> , 2017, 17, 583-585.	2.2	0
66	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
67	Molecular tools provide a range of powerful options for the conservationist's toolbox. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2017, 27, 296-302.	0.9	5
68	Molecular Population Genetics. <i>Genetics</i> , 2017, 205, 1003-1035.	1.2	100
69	Resequencing Helminth Genomes for Population and Genetic Studies. <i>Trends in Parasitology</i> , 2017, 33, 388-399.	1.5	31
70	Lost in parameter space: a road map for <scp>stacks</scp>. <i>Methods in Ecology and Evolution</i> , 2017, 8, 1360-1373.	2.2	466
71	A phylogenomic perspective on the biogeography of skinks in the <i>Plestiodon brevirostris</i> group inferred from target enrichment of ultraconserved elements. <i>Journal of Biogeography</i> , 2017, 44, 2033-2044.	1.4	24
72	Unbroken: RADseq remains a powerful tool for understanding the genetics of adaptation in natural populations. <i>Molecular Ecology Resources</i> , 2017, 17, 362-365.	2.2	156

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73	International workshop on advancing methods to overcome challenges associated with life history and stock assessments of data-poor deep-water snappers and groupers. <i>Marine Policy</i> , 2017, 79, 78-83.	1.5	18
74	Analysis of phylogenetic relationships and genome size evolution of the <i>Amaranthus</i> genus using GBS indicates the ancestors of an ancient crop. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 80-92.	1.2	95
75	History, geography and host use shape genomewide patterns of genetic variation in the redheaded pine sawfly (<i>Neodiprion lecontei</i>). <i>Molecular Ecology</i> , 2017, 26, 1022-1044.	2.0	46
76	Pleiotropy, constraint, and modularity in the evolution of life histories: insights from genomic analyses. <i>Annals of the New York Academy of Sciences</i> , 2017, 1389, 76-91.	1.8	38
77	Seascape genomics reveals fine-scale patterns of dispersal for a reef fish along the ecologically divergent coast of Northwestern Australia. <i>Molecular Ecology</i> , 2017, 26, 6206-6223.	2.0	44
78	Genomics and telemetry suggest a role for migration harshness in determining overwintering habitat choice, but not gene flow, in anadromous Arctic Char. <i>Molecular Ecology</i> , 2017, 26, 6784-6800.	2.0	58
79	Discovery of new QTLs underlying hybrid fertility and reproductive isolation in rice. <i>Plant Journal</i> , 2017, 92, 347-348.	2.8	0
80	DnaSP 6: DNA Sequence Polymorphism Analysis of Large Data Sets. <i>Molecular Biology and Evolution</i> , 2017, 34, 3299-3302.	3.5	4,056
81	Genomic differentiation and patterns of gene flow between two long-tailed tit species (<i>Aegithalos</i>). <i>Molecular Ecology</i> , 2017, 26, 6654-6665.	2.0	11
82	Invasion genomics: genotyping-by-sequencing approach reveals regional genetic structure and signatures of temporal selection in an introduced mud crab. <i>Marine Biology</i> , 2017, 164, 1.	0.7	13
83	Invertebrate population genetics across Earth's largest habitat: The deep-sea floor. <i>Molecular Ecology</i> , 2017, 26, 4872-4896.	2.0	87
84	The genetics of drought tolerance in conifers. <i>New Phytologist</i> , 2017, 216, 1034-1048.	3.5	133
85	Admixture on the northern front: population genomics of range expansion in the white-footed mouse (<i>Peromyscus leucopus</i>) and secondary contact with the deer mouse (<i>Peromyscus maniculatus</i>). <i>Heredity</i> , 2017, 119, 447-458.	1.2	27
86	Reference-based RADseq resolves robust relationships among closely related species of lichen-forming fungi using metagenomic DNA. <i>Scientific Reports</i> , 2017, 7, 9884.	1.6	33
87	Characterizing the allopolyploid species among the wild relatives of soybean: Utility of reduced representation genotyping methodologies. <i>Journal of Systematics and Evolution</i> , 2017, 55, 365-376.	1.6	21
88	Evaluating hybridization capture with <i>scRAD</i> probes as a tool for museum genomics with historical bird specimens. <i>Ecology and Evolution</i> , 2017, 7, 4755-4767.	0.8	34
89	Whole-genome sequencing approaches for conservation biology: Advantages, limitations and practical recommendations. <i>Molecular Ecology</i> , 2017, 26, 5369-5406.	2.0	249
90	A genomic glance through the fog of plasticity and diversification in <i>Pocillopora</i> . <i>Scientific Reports</i> , 2017, 7, 5991.	1.6	87

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91	Profiling the immunome of little brown myotis provides a yardstick for measuring the genetic response to white-nose syndrome. <i>Evolutionary Applications</i> , 2017, 10, 1076-1090.	1.5	28
92	Interpreting the genomic landscape of speciation: a road map for finding barriers to gene flow. <i>Journal of Evolutionary Biology</i> , 2017, 30, 1450-1477.	0.8	399
93	A Tree-Thinker's Guide to Genomics. <i>Trends in Ecology and Evolution</i> , 2017, 32, 715-716.	4.2	0
94	Identifying hybridization and admixture using SNPs: application of the DArTseq platform in phylogeographic research on vertebrates. <i>Royal Society Open Science</i> , 2017, 4, 161061.	1.1	80
95	Cross-platform compatibility of <i>de novo</i> -aligned <i>scn</i> SNPs in a nonmodel butterfly genus. <i>Molecular Ecology Resources</i> , 2017, 17, e84-e93.	2.2	14
96	Past, present, and future research in bipolar lichen-forming fungi and their photobionts. <i>American Journal of Botany</i> , 2017, 104, 1660-1674.	0.8	25
97	Cryptic genetic variation in an inbreeding and cosmopolitan pest, <i>Xylosandrus crassiusculus</i> , revealed using <i>scn</i> RADseq. <i>Ecology and Evolution</i> , 2017, 7, 10974-10986.	0.8	35
98	Estimating genomic diversity and population differentiation – an empirical comparison of microsatellite and SNP variation in <i>Arabidopsis halleri</i> . <i>BMC Genomics</i> , 2017, 18, 69.	1.2	216
99	Characterization of novel microsatellite markers of the Emei Shan <i>Liocichla</i> using restriction site-associated DNA sequencing. <i>Avian Research</i> , 2017, 8, .	0.5	5
100	New insights into global biogeography, population structure and natural selection from the genome of the epipelagic copepod <i>Oithona</i> . <i>Molecular Ecology</i> , 2017, 26, 4467-4482.	2.0	37
101	Genomic footprints of adaptation in a cooperatively breeding tropical bird across a vegetation gradient. <i>Molecular Ecology</i> , 2017, 26, 4483-4496.	2.0	16
102	Bioinformatic processing of RADseq data dramatically impacts downstream population genetic inference. <i>Methods in Ecology and Evolution</i> , 2017, 8, 907-917.	2.2	253
103	Variability in total project and per sample genotyping costs under varying study designs including with microsatellites or SNPs to answer conservation genetic questions. <i>Conservation Genetics Resources</i> , 2017, 9, 289-304.	0.4	51
104	Breaking RAD: an evaluation of the utility of restriction site-associated DNA sequencing for genome scans of adaptation. <i>Molecular Ecology Resources</i> , 2017, 17, 142-152.	2.2	322
105	Prediction and Prevention of Parasitic Diseases Using a Landscape Genomics Framework. <i>Trends in Parasitology</i> , 2017, 33, 264-275.	1.5	26
106	Genotyping-by-sequencing approaches to characterize crop genomes: choosing the right tool for the right application. <i>Plant Biotechnology Journal</i> , 2017, 15, 149-161.	4.1	240
107	Bee conservation in the age of genomics. <i>Conservation Genetics</i> , 2017, 18, 713-729.	0.8	50
108	Paralogs are revealed by proportion of heterozygotes and deviations in read ratios in genotyping-by-sequencing data from natural populations. <i>Molecular Ecology Resources</i> , 2017, 17, 656-669.	2.2	167

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109	Construction of a Framework Genetic Linkage Map in <i>Gleditsia triacanthos</i> L.. <i>Plant Molecular Biology Reporter</i> , 2017, 35, 177-187.	1.0	7
110	Application of PE-RADSeq to the study of genomic diversity and divergence of two Brazilian marmoset species (<i>Callithrix jacchus</i> and <i>C. penicillata</i>). <i>American Journal of Primatology</i> , 2017, 79, 1-12.	0.8	5
111	Comparative performance of double-digest RAD sequencing across divergent arachnid lineages. <i>Molecular Ecology Resources</i> , 2017, 17, 418-430.	2.2	24
112	A Bigger Toolbox: Biotechnology in Biodiversity Conservation. <i>Trends in Biotechnology</i> , 2017, 35, 55-65.	4.9	103
113	Discovery and preliminary multi-species evaluation of single nucleotide polymorphism resources for genus <i>Buteo</i> developed from restriction site-associated DNA paired-end data. <i>Conservation Genetics Resources</i> , 2017, 9, 151-156.	0.4	0
114	Marine genomics: News and views. <i>Marine Genomics</i> , 2017, 31, 1-8.	0.4	12
115	Using DNA Sequence Data to Enhance Understanding and Conservation of Plant Diversity at the Species Level. , 2017, , 23-48.		2
116	Adding loci improves phylogeographic resolution in red mangroves despite increased missing data: comparing microsatellites and RAD-Seq and investigating loci filtering. <i>Scientific Reports</i> , 2017, 7, 17598.	1.6	99
117	scRAD-seq dataset with 90% missing data fully resolves recent radiation of <i>Petalidium</i> (Acanthaceae) in the ultra-arid deserts of Namibia. <i>Ecology and Evolution</i> , 2017, 7, 7920-7936.	0.8	91
118	Landscape Genomics: Understanding Relationships Between Environmental Heterogeneity and Genomic Characteristics of Populations. <i>Population Genomics</i> , 2017, , 261-322.	0.2	46
119	Advances in the Application of Genetics in Marine Turtle Biology and Conservation. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	64
120	Optimized double-digest genotyping by sequencing (ddGBS) method with high-density SNP markers and high genotyping accuracy for chickens. <i>PLoS ONE</i> , 2017, 12, e0179073.	1.1	33
121	Global genotype flow in <i>Cercospora beticola</i> populations confirmed through genotyping-by-sequencing. <i>PLoS ONE</i> , 2017, 12, e0186488.	1.1	19
122	2b-RAD genotyping for population genomic studies of Chagas disease vectors: <i>Rhodnius ecuadoriensis</i> in Ecuador. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005710.	1.3	13
123	Genetic variation in populations of the earthworm, <i>Lumbricus rubellus</i> , across contaminated mine sites. <i>BMC Genetics</i> , 2017, 18, 97.	2.7	29
124	An Empirical Test of Reduced-Representation Genomics to Infer Species-Level Phylogenies for Two Ant Groups. <i>Insect Systematics and Diversity</i> , 2017, 1, .	0.7	5
126	An NGS-based approach for the identification of sex-specific markers in snakehead (<i>Channa</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 100	0.8	42
127	Convergent evolution of high elevation plant growth forms and geographically structured variation in Andean <i>Lupinus</i> (Fabaceae). <i>Botanical Journal of the Linnean Society</i> , 2018, 187, 118-136.	0.8	48

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128	RADpainter and fineRADstructure: Population Inference from RADseq Data. <i>Molecular Biology and Evolution</i> , 2018, 35, 1284-1290.	3.5	265
129	Double-digest RAD sequencing outperforms microsatellite loci at assigning paternity and estimating relatedness: A proof of concept in a highly promiscuous bird. <i>Molecular Ecology Resources</i> , 2018, 18, 953-965.	2.2	61
130	Phylogeographic analysis suggests two origins for the riparian azalea <i>Rhododendron indicum</i> (L.) Sweet. <i>Heredity</i> , 2018, 121, 594-604.	1.2	16
131	An optimized approach for local de novo assembly of overlapping paired-end RAD reads from multiple individuals. <i>Royal Society Open Science</i> , 2018, 5, 171589.	1.1	10
132	Genome-wide single nucleotide polymorphisms (SNPs) for a model invasive ascidian <i>Botryllus schlosseri</i> . <i>Genetica</i> , 2018, 146, 227-234.	0.5	5
133	Performance and precision of double digestion RAD (ddRAD) genotyping in large multiplexed datasets of marine fish species. <i>Marine Genomics</i> , 2018, 39, 64-72.	0.4	21
134	Genome-Wide SNPs Identify Limits to Connectivity in the Extreme Freshwater Disperser, Spangled Perch <i>Leiopotherapon unicolor</i> (Terapontidae). <i>Journal of Heredity</i> , 2018, 109, 320-325.	1.0	3
135	An integrated genetic map based on EST-SNPs and QTL analysis of shell color traits in Pacific oyster <i>Crassostrea gigas</i> . <i>Aquaculture</i> , 2018, 492, 226-236.	1.7	18
136	Roads to isolation: Similar genomic history patterns in two species of freshwater crabs with contrasting environmental tolerances and range sizes. <i>Ecology and Evolution</i> , 2018, 8, 4657-4668.	0.8	2
137	Information Dropout Patterns in Restriction Site Associated DNA Phylogenomics and a Comparison with Multilocus Sanger Data in a Species-Rich Moth Genus. <i>Systematic Biology</i> , 2018, 67, 925-939.	2.7	46
138	Let's talk about sex: A rigorous statistical framework to assign the sex of individuals from reduced-representation sequencing data. <i>Molecular Ecology Resources</i> , 2018, 18, 191-193.	2.2	2
139	Population Genomics Provides Key Insights in Ecology and Evolution. <i>Population Genomics</i> , 2018, , 483-510.	0.2	28
140	Genetic sex assignment in wild populations using genotyping-by-sequencing data: A statistical threshold approach. <i>Molecular Ecology Resources</i> , 2018, 18, 179-190.	2.2	17
141	Genetic and genomic monitoring with minimally invasive sampling methods. <i>Evolutionary Applications</i> , 2018, 11, 1094-1119.	1.5	126
142	Valuing and understanding fish populations in the Anthropocene: key questions to address. <i>Journal of Fish Biology</i> , 2018, 92, 828-845.	0.7	7
143	Genetic and morphological support for possible sympatric origin of fish from subterranean habitats. <i>Scientific Reports</i> , 2018, 8, 2909.	1.6	16
144	Migration-Selection Balance Drives Genetic Differentiation in Genes Associated with High-Altitude Function in the Speckled Teal (<i>Anas flavirostris</i>) in the Andes. <i>Genome Biology and Evolution</i> , 2018, 10, 14-32.	1.1	18
145	Combining allele frequency and tree-based approaches improves phylogeographic inference from natural history collections. <i>Molecular Ecology</i> , 2018, 27, 1012-1024.	2.0	9

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147	Recent lineage diversification in a venomous snake through dispersal across the Amazon River. <i>Biological Journal of the Linnean Society</i> , 2018, 123, 651-665.	0.7	16
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511	Knowledge status and sampling strategies to maximize cost-benefit ratio of studies in landscape genomics of wild plants. <i>Scientific Reports</i> , 2020, 10, 3706.	1.6	11
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555	Stock structure and effective population size of the commercially exploited gummy shark <i>Mustelus antarcticus</i> . <i>Marine Ecology - Progress Series</i> , 0, , .	0.9	4
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