

Louis Bernatchez

List of Publications by Year in descending order

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536
papers

37,301
citations

2696

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7836

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docs citations

585
times ranked

25433
citing authors

#	ARTICLE	IF	CITATIONS
1	Long-distance migration is a major factor driving local adaptation at continental scale in Coho salmon. <i>Molecular Ecology</i> , 2023, 32, 542-559.	2.0	14
2	Genome assembly, structural variants, and genetic differentiation between lake whitefish young species pairs (<i>Coregonus</i> sp.) with long and short reads. <i>Molecular Ecology</i> , 2023, 32, 1458-1477.	2.0	18
3	Fish community shifts along a strong fluvial environmental gradient revealed by eDNA metabarcoding. <i>Environmental DNA</i> , 2022, 4, 117-134.	3.1	26
4	A chromosome-anchored genome assembly for Lake Trout (<i>Salvelinus namaycush</i>). <i>Molecular Ecology Resources</i> , 2022, 22, 679-694.	2.2	16
5	A melting pot in the Arctic: Analysis of mitogenome variation in Arctic char (<i>Salvelinus alpinus</i>) reveals a 1000-km contact zone between highly divergent lineages. <i>Ecology of Freshwater Fish</i> , 2022, 31, 330-346.	0.7	8
6	Effect of biotic and abiotic factors on the production and degradation of fish environmental DNA: An experimental evaluation. <i>Environmental DNA</i> , 2022, 4, 453-468.	3.1	19
7	eDNA metabarcoding as a means to assess distribution of subterranean fish communities: Iranian blind cave fishes as a case study. <i>Environmental DNA</i> , 2022, 4, 402-416.	3.1	10
8	Strong parallel differential gene expression induced by hatchery rearing weakly associated with methylation signals in adult Coho Salmon (<i>O. kisutch</i>). <i>Genome Biology and Evolution</i> , 2022, , .	1.1	4
9	Cage transplant experiment shows weak transport effect on relative abundance of fish community composition as revealed by eDNA metabarcoding. <i>Ecological Indicators</i> , 2022, 137, 108785.	2.6	15
10	Fish out of water: Genomic insights into persistence of rainbowfish populations in the desert. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 171-183.	1.1	10
11	Fuwen Wei – Recipient of the 2021 Molecular Ecology Prize. <i>Molecular Ecology</i> , 2022, 31, 31-36.	2.0	0
12	Thermal regime during parental sexual maturation, but not during offspring rearing, modulates DNA methylation in brook charr (<i>Salvelinus fontinalis</i>). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20220670.	1.2	13
13	Thirteen novel ideas and underutilised resources to support progress towards a range-wide American eel stock assessment. <i>Fisheries Management and Ecology</i> , 2022, 29, 516-541.	1.0	8
14	Genome-wide methylation in the panmictic European eel (<i>Anguilla anguilla</i>). <i>Molecular Ecology</i> , 2022, 31, 4286-4306.	2.0	5
15	Incorporating putatively neutral and adaptive genomic data into marine conservation planning. <i>Conservation Biology</i> , 2021, 35, 909-920.	2.4	35
16	Comparing environmental metabarcoding and trawling survey of demersal fish communities in the Gulf of St. Lawrence, Canada. <i>Environmental DNA</i> , 2021, 3, 22-42.	3.1	58
17	Contrasting Gene Decay in Subterranean Vertebrates: Insights from Cavefishes and Fossorial Mammals. <i>Molecular Biology and Evolution</i> , 2021, 38, 589-605.	3.5	43
18	Using environmental DNA for biomonitoring of freshwater fish communities: Comparison with established gillnet surveys in a boreal hydroelectric impoundment. <i>Environmental DNA</i> , 2021, 3, 105-120.	3.1	50

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19	Detecting community change in Arctic marine ecosystems using the temporal dynamics of environmental DNA. <i>Environmental DNA</i> , 2021, 3, 573-590.	3.1	11
20	Comparing CRISPR-Cas and qPCR eDNA assays for the detection of Atlantic salmon (<i>Salmo salar</i>) Tj ETQq0,0 0 rgBT /Overlock 1	3.1	23
21	Population genomics and history of speciation reveal fishery management gaps in two related redfish species (<i>Sebastes mentella</i> and <i>Sebastes fasciatus</i>). <i>Evolutionary Applications</i> , 2021, 14, 588-606.	1.5	24
22	Population genomics of the southern Caspian Sea Vobla <i>Rutilus lacustris</i> . <i>Hydrobiologia</i> , 2021, 848, 345-361.	1.0	2
23	Genetic Diversity. , 2021, , 119-165.		2
24	The rise and fall of the ancient northern pike master sex-determining gene. <i>ELife</i> , 2021, 10, .	2.8	24
25	Assessing the effects of genotype-by-environment interaction on epigenetic, transcriptomic, and phenotypic response in a Pacific salmon. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	15
26	Uncovering endemism in a lake of invasive species introgression. <i>Molecular Ecology</i> , 2021, 30, 880-883.	2.0	4
27	Thermal adaptation rather than demographic history drives genetic structure inferred by copy number variants in a marine fish. <i>Molecular Ecology</i> , 2021, 30, 1624-1641.	2.0	19
28	Associative Overdominance and Negative Epistasis Shape Genome-Wide Ancestry Landscape in Supplemented Fish Populations. <i>Genes</i> , 2021, 12, 524.	1.0	2
29	Low effective population size in the genetically bottlenecked Australian sea lion is insufficient to maintain genetic variation. <i>Animal Conservation</i> , 2021, 24, 847.	1.5	2
30	Genomic data support management of anadromous Arctic Char fisheries in Nunavik by highlighting neutral and putatively adaptive genetic variation. <i>Evolutionary Applications</i> , 2021, 14, 1880-1897.	1.5	17
31	Epigenomic modifications induced by hatchery rearing persist in germ line cells of adult salmon after their oceanic migration. <i>Evolutionary Applications</i> , 2021, 14, 2402-2413.	1.5	31
32	Locally Adaptive Inversions Modulate Genetic Variation at Different Geographic Scales in a Seaweed Fly. <i>Molecular Biology and Evolution</i> , 2021, 38, 3953-3971.	3.5	48
33	Benchmarking bioinformatic tools for fast and accurate eDNA metabarcoding species identification. <i>Molecular Ecology Resources</i> , 2021, 21, 2565-2579.	2.2	35
34	Proper environmental DNA metabarcoding data transformation reveals temporal stability of fish communities in a dendritic river system. <i>Environmental DNA</i> , 2021, 3, 1007-1022.	3.1	27
35	Environmental DNA as a detection and quantitative tool for stream-dwelling salamanders: A comparison with the traditional active search method. <i>Environmental DNA</i> , 2021, 3, 1128-1141.	3.1	8
36	A genomic perspective on an old question: <i>Salmo</i> trouts or <i>Salmo trutta</i> (Teleostei: Salmonidae)?. <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107204.	1.2	33

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37	Epigenetic inheritance and reproductive mode in plants and animals. <i>Trends in Ecology and Evolution</i> , 2021, 36, 1124-1140.	4.2	70
38	Artificial Rearing of Atlantic Salmon Juveniles for Supportive Breeding Programs Induces Long-Term Effects on Gut Microbiota after Stocking. <i>Microorganisms</i> , 2021, 9, 1932.	1.6	9
39	The future of biodiversity monitoring and conservation utilizing environmental DNA. <i>Environmental DNA</i> , 2021, 3, 3-7.	3.1	49
40	DNA Transposon Expansion is Associated with Genome Size Increase in Mudminnows. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
41	Environment-driven reprogramming of gamete DNA methylation occurs during maturation and is transmitted intergenerationally in Atlantic Salmon. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	19
42	Chromosome-level assembly reveals a putative Y-autosomal fusion in the sex determination system of the Greenland Halibut (<i>Reinhardtius hippoglossoides</i>). <i>G3: Genes, Genomes, Genetics</i> , 2021, , .	0.8	13
43	Resolving the genetic paradox of invasions: Preadapted genomes and postintroduction hybridization of bigheaded carps in the Mississippi River Basin. <i>Evolutionary Applications</i> , 2020, 13, 263-277.	1.5	20
44	Using Haplotype Information for Conservation Genomics. <i>Trends in Ecology and Evolution</i> , 2020, 35, 245-258.	4.2	69
45	Absence of founder effect and evidence for adaptive divergence in a recently introduced insular population of white-tailed deer (<i>Odocoileus virginianus</i>). <i>Molecular Ecology</i> , 2020, 29, 86-104.	2.0	14
46	Speciation history of European (<i>Anguilla anguilla</i>) and American eel (<i>A. rostrata</i>), analysed using genomic data. <i>Molecular Ecology</i> , 2020, 29, 565-577.	2.0	13
47	Caged fish experiment and hydrodynamic bidimensional modeling highlight the importance to consider 2D dispersion in fluvial environmental DNA studies. <i>Environmental DNA</i> , 2020, 2, 362-372.	3.1	47
48	Mapping of Adaptive Traits Enabled by a High-Density Linkage Map for Lake Trout. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, g3.401184.2020.	0.8	9
49	Estimating the contribution of Greenland Halibut (<i>Reinhardtius hippoglossoides</i>) stocks to nurseries by means of genotyping-by-sequencing: Sex and time matter. <i>Evolutionary Applications</i> , 2020, 13, 2155-2167.	1.5	19
50	Pathway to Increase Standards and Competency of eDNA Surveys (PISCeS) – Advancing collaboration and standardization efforts in the field of eDNA. <i>Environmental DNA</i> , 2020, 2, 255-260.	3.1	32
51	Adaptive and maladaptive genetic diversity in small populations: Insights from the Brook Charr (<i>Salvelinus fontinalis</i>) case study. <i>Molecular Ecology</i> , 2020, 29, 3429-3445.	2.0	8
52	The structural variation landscape in 492 Atlantic salmon genomes. <i>Nature Communications</i> , 2020, 11, 5176.	5.8	60
53	Latitudinal variation in climate-associated genes imperils range edge populations. <i>Molecular Ecology</i> , 2020, 29, 4337-4349.	2.0	12
54	Fine-scale environmental heterogeneity shapes fluvial fish communities as revealed by eDNA metabarcoding. <i>Environmental DNA</i> , 2020, 2, 647-666.	3.1	26

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55	Demographic history shaped geographical patterns of deleterious mutation load in a broadly distributed Pacific Salmon. <i>PLoS Genetics</i> , 2020, 16, e1008348.	1.5	38
56	Copy number variants outperform SNPs to reveal genotype-temperature association in a marine species. <i>Molecular Ecology</i> , 2020, 29, 4765-4782.	2.0	67
57	60 specific eDNA qPCR assays to detect invasive, threatened, and exploited freshwater vertebrates and invertebrates in Eastern Canada. <i>Environmental DNA</i> , 2020, 2, 373-386.	3.1	37
58	Detecting fine-scale population structure in the age of genomics: a case study of lake sturgeon in the Great Lakes. <i>Fisheries Research</i> , 2020, 230, 105646.	0.9	13
59	Shared ancestral polymorphisms and chromosomal rearrangements as potential drivers of local adaptation in a marine fish. <i>Molecular Ecology</i> , 2020, 29, 2379-2398.	2.0	48
60	Effects of genetic origin on phenotypic divergence in Brook Trout populations stocked with domestic fish. <i>Ecosphere</i> , 2020, 11, e03119.	1.0	4
61	Deciphering lifelong thermal niche using otolith $\delta^{18}O$ thermometry within supplemented lake trout (<i>Salvelinus namaycush</i>) populations. <i>Freshwater Biology</i> , 2020, 65, 1114-1127.	1.2	5
62	Adaptation of plasticity to projected maximum temperatures and across climatically defined bioregions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17112-17121.	3.3	44
63	Fine-scale population genetic structure of Endangered Caspian Sea trout, <i>Salmo caspius</i> : implications for conservation. <i>Hydrobiologia</i> , 2020, 847, 3339-3353.	1.0	6
64	Space invaders: Searching for invasive Smallmouth Bass (<i>Micropterus dolomieu</i>) in a renowned Atlantic Salmon (<i>Salmo salar</i>) river. <i>Ecology and Evolution</i> , 2020, 10, 2588-2596.	0.8	9
65	Groundtruthing of pelagic forage fish detected by hydroacoustics in a whale feeding area using environmental DNA. <i>Environmental DNA</i> , 2020, 2, 477-492.	3.1	10
66	Balancing selection via life-history trade-offs maintains an inversion polymorphism in a seaweed fly. <i>Nature Communications</i> , 2020, 11, 670.	5.8	69
67	Accurate estimation of conservation unit contribution to coho salmon mixed-stock fisheries in British Columbia, Canada, using direct DNA sequencing for single nucleotide polymorphisms. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2020, 77, 1302-1315.	0.7	28
68	Genetic population structure and variation at phenology-related loci in anadromous Arctic char (<i>Salvelinus alpinus</i>). <i>Ecology of Freshwater Fish</i> , 2020, 29, 170-183.	0.7	9
69	Sexing a Monomorphic Plumage Seabird Using Morphometrics and Assortative Mating. <i>Waterbirds</i> , 2020, 42, 380.	0.2	11
70	The analysis of the relationship between Lorestan cave barb (Garra typhlops and Garra lorestanensis) and Garra gymnothorax populations in Dez and Karkheh River drainages. <i>Yaftah</i> , 2020, 7, 1-8.	0.1	1
71	Welcome to Environmental DNA!. <i>Environmental DNA</i> , 2019, 1, 3-4.	3.1	2
72	Comparing Pool-seq, Rapture, and GBS genotyping for inferring weak population structure: The American lobster (<i>Homarus americanus</i>) as a case study. <i>Ecology and Evolution</i> , 2019, 9, 6606-6623.	0.8	37

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73	DNA methylation reprogramming, TE derepression, and postzygotic isolation of nascent animal species. <i>Science Advances</i> , 2019, 5, eaaw1644.	4.7	47
74	Evidence for host effect on the intestinal microbiota of whitefish (<i>Coregonus</i> sp.) species pairs and their hybrids. <i>Ecology and Evolution</i> , 2019, 9, 11762-11774.	0.8	29
75	Polygenic selection drives the evolution of convergent transcriptomic landscapes across continents within a Nearctic sister species complex. <i>Molecular Ecology</i> , 2019, 28, 4388-4403.	2.0	38
76	The role of recombination on genome-wide patterns of local ancestry exemplified by supplemented brook charr populations. <i>Molecular Ecology</i> , 2019, 28, 4755-4769.	2.0	14
77	Comparison of coded-wire tagging with parentage-based tagging and genetic stock identification in a large-scale coho salmon fisheries application in British Columbia, Canada. <i>Evolutionary Applications</i> , 2019, 12, 230-254.	1.5	40
78	Sex-Specific Co-expression Networks and Sex-Biased Gene Expression in the Salmonid Brook Charr <i>Salvelinus fontinalis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 955-968.	0.8	19
79	The role of ecotype-environment interactions in intraspecific trophic niche partitioning subsequent to stocking. <i>Ecological Applications</i> , 2019, 29, e01857.	1.8	10
80	Marine Conservation and Marine Protected Areas. <i>Population Genomics</i> , 2019, , 423-446.	0.2	15
81	Model-based demographic inference of introgression history in European whitefish species pairs'. <i>Journal of Evolutionary Biology</i> , 2019, 32, 806-817.	0.8	27
82	Going beyond SNPs: The role of structural genomic variants in adaptive evolution and species diversification. <i>Molecular Ecology</i> , 2019, 28, 1203-1209.	2.0	178
83	Impacts of stocking and its intensity on effective population size in Brook Charr (<i>Salvelinus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFS	0.8	18
84	Aquatic Landscape Genomics and Environmental Effects on Genetic Variation. <i>Trends in Ecology and Evolution</i> , 2019, 34, 641-654.	4.2	97
85	The genomic pool of standing structural variation outnumbers single nucleotide polymorphism by threefold in the marine teleost <i>Chrysophrys auratus</i> . <i>Molecular Ecology</i> , 2019, 28, 1210-1223.	2.0	67
86	Seascape genomics of eastern oyster (<i>Crassostrea virginica</i>) along the Atlantic coast of Canada. <i>Evolutionary Applications</i> , 2019, 12, 587-609.	1.5	43
87	Comparing eDNA metabarcoding and species collection for documenting Arctic metazoan biodiversity. <i>Environmental DNA</i> , 2019, 1, 342-358.	3.1	51
88	Comparing genomic signatures of domestication in two Atlantic salmon (<i>Salmo salar</i> L.) populations with different geographical origins. <i>Evolutionary Applications</i> , 2019, 12, 137-156.	1.5	58
89	Combining population genomics and forward simulations to investigate stocking impacts: A case study of Muskellunge (<i>Esox masquinongy</i>) from the St. Lawrence River basin. <i>Evolutionary Applications</i> , 2019, 12, 902-922.	1.5	13
90	Domestication and Temperature Modulate Gene Expression Signatures and Growth in the Australasian Snapper <i>Chrysophrys auratus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 105-116.	0.8	22

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91	Chromosomal fusion and life history-associated genomic variation contribute to within-river local adaptation of Atlantic salmon. <i>Molecular Ecology</i> , 2019, 28, 1439-1459.	2.0	56
92	River-specific Gene Expression Patterns Associated with Habitat Selection for Key Hormone-Coding Genes in Glass Eel-Stage American Eels. <i>Transactions of the American Fisheries Society</i> , 2018, 147, 855-868.	0.6	0
93	Asymmetric oceanographic processes mediate connectivity and population genetic structure, as revealed by <i>scnRAD</i> seq, in a highly dispersive marine invertebrate (<i>Parastichopus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 227 7	1.2	70
94	The demographic history of Atlantic salmon (<i>Salmo salar</i>) across its distribution range reconstructed from approximate Bayesian computations*. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 1261-1277.	1.1	75
95	Genetic and morphological support for possible sympatric origin of fish from subterranean habitats. <i>Scientific Reports</i> , 2018, 8, 2909.	1.6	16
96	Synergistic Integration of Genomics and Ecoevolutionary Dynamics for Sustainable Fisheries: A Reply to Kuparinen and Uusi-Heikkilä. <i>Trends in Ecology and Evolution</i> , 2018, 33, 308-310.	4.2	1
97	Eco-Evolutionary Genomics of Chromosomal Inversions. <i>Trends in Ecology and Evolution</i> , 2018, 33, 427-440.	4.2	399
98	A climate-associated multispecies cryptic cline in the northwest Atlantic. <i>Science Advances</i> , 2018, 4, eaq0929.	4.7	91
99	Inferring phylogenetic structure, hybridization and divergence times within Salmoninae (Teleostei) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 227 7	1.2	70
100	Linking genetic and ecological differentiation in an ungulate with a circumpolar distribution. <i>Ecography</i> , 2018, 41, 922-937.	2.1	15
101	The Lobster Node of the CFRN: co-constructed and collaborative research on productivity, stock structure, and connectivity in the American lobster (<i>Homarus americanus</i>). <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2018, 75, 813-824.	0.7	10
102	Predicting the genetic impact of stocking in Brook Charr (<i>Salvelinus fontinalis</i>) by combining <i>scnRAD</i> sequencing and modeling of explanatory variables. <i>Evolutionary Applications</i> , 2018, 11, 577-592.	1.5	36
103	Do differences in the activities of carbohydrate metabolism enzymes between Lake Whitefish ecotypes match predictions from transcriptomic studies?. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2018, 224, 138-149.	0.7	9
104	Putatively adaptive genetic variation in the giant California sea cucumber (<i>Parastichopus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 7 sequencing data. <i>Molecular Ecology</i> , 2018, 27, 5035-5048.	2.0	43
105	Range-wide regional assignment of Atlantic salmon (<i>Salmo salar</i>) using genome wide single-nucleotide polymorphisms. <i>Fisheries Research</i> , 2018, 206, 163-175.	0.9	27
106	Temporal variations in kidney metal concentrations and their implications for retinoid metabolism and oxidative stress response in wild yellow perch (<i>Perca flavescens</i>). <i>Aquatic Toxicology</i> , 2018, 202, 26-35.	1.9	5
107	On the roles of landscape heterogeneity and environmental variation in determining population genomic structure in a dendritic system. <i>Molecular Ecology</i> , 2018, 27, 3484-3497.	2.0	52
108	Impact of supplementation on deleterious mutation distribution in an exploited salmonid. <i>Evolutionary Applications</i> , 2018, 11, 1053-1065.	1.5	25

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109	Supplementation stocking of Lake Trout (<i>Salvelinus namaycush</i>) in small boreal lakes: Ecotypes influence on growth and condition. PLoS ONE, 2018, 13, e0200599.	1.1	15
110	<scp>eDNA</scp> metabarcoding as a new surveillance approach for coastal Arctic biodiversity. Ecology and Evolution, 2018, 8, 7763-7777.	0.8	154
111	Introgressive hybridization between wild and domestic individuals and its relationship with parasitism in brook charr <i>Salvelinus fontinalis</i>. Journal of Fish Biology, 2018, 93, 664-673.	0.7	6
112	Genetic differentiation in the mountainous star coral <i>Orbicella faveolata</i> around Cuba. Coral Reefs, 2018, 37, 1217-1227.	0.9	6
113	Holobionts and ecological speciation: the intestinal microbiota of lake whitefish species pairs. Microbiome, 2018, 6, 47.	4.9	67
114	Ongoing niche differentiation under high gene flow in a polymorphic brackish water threespine stickleback (<i>Gasterosteus aculeatus</i>) population. BMC Evolutionary Biology, 2018, 18, 14.	3.2	9
115	Demographic and genetic approaches to study dispersal in wild animal populations: A methodological review. Molecular Ecology, 2018, 27, 3976-4010.	2.0	113
116	Effects of sampling effort on biodiversity patterns estimated from environmental DNA metabarcoding surveys. Scientific Reports, 2018, 8, 8843.	1.6	113
117	Next-generation conservation genetics and biodiversity monitoring. Evolutionary Applications, 2018, 11, 1029-1034.	1.5	43
118	Intercontinental karyotypeâ€“environment parallelism supports a role for a chromosomal inversion in local adaptation in a seaweed fly. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20180519.	1.2	37
119	Investigating the extent of parallelism in morphological and genomic divergence among lake trout ecotypes in Lake Superior. Molecular Ecology, 2017, 26, 1477-1497.	2.0	46
120	Predicting Responses to Contemporary Environmental Change Using Evolutionary Response Architectures. American Naturalist, 2017, 189, 463-473.	1.0	136
121	Sex Chromosome Evolution, Heterochiasmy, and Physiological QTL in the Salmonid Brook Charr <i>Salvelinus fontinalis</i>. G3: Genes, Genomes, Genetics, 2017, 7, 2749-2762.	0.8	38
122	De novo transcriptome assembly and annotation for the desert rainbowfish (<i>Melanotaenia splendida</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.4	8
123	Genomic patterns of diversity and divergence of two introduced salmonid species in Patagonia, South America. Evolutionary Applications, 2017, 10, 402-416.	1.5	17
124	Divergence in physiological factors affecting swimming performance between anadromous and resident populations of brook charr <i>Salvelinus fontinalis</i>. Journal of Fish Biology, 2017, 90, 2170-2193.	0.7	14
125	Unbroken: RADseq remains a powerful tool for understanding the genetics of adaptation in natural populations. Molecular Ecology Resources, 2017, 17, 362-365.	2.2	156
126	Genome Compositional Organization in Gars Shows More Similarities to Mammals than to Other Rayâ€“Finned Fish. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2017, 328, 607-619.	0.6	27

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127	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
128	Do genetic drift and accumulation of deleterious mutations preclude adaptation? Empirical investigation using <i>RAD</i> -seq in a northern lacustrine fish. <i>Molecular Ecology</i> , 2017, 26, 6317-6335.	2.0	53
129	Harnessing the Power of Genomics to Secure the Future of Seafood. <i>Trends in Ecology and Evolution</i> , 2017, 32, 665-680.	4.2	202
130	Modeling the Multiple Facets of Speciation-with-Gene-Flow toward Inferring the Divergence History of Lake Whitefish Species Pairs (<i>Coregonus clupeaformis</i>). <i>Genome Biology and Evolution</i> , 2017, 9, 2057-2074.	1.1	120
131	Environmental <i>DNA</i> metabarcoding: Transforming how we survey animal and plant communities. <i>Molecular Ecology</i> , 2017, 26, 5872-5895.	2.0	1,210
132	Characterization of natural variation in North American Atlantic Salmon populations (Salmonidae:). <i>Trends in Ecology and Evolution</i> , 2017, 32, 1010-1018.	8.8	28
133	The complete mitochondrial DNA of the Cuban gar (<i>Atractosteus tristoechus</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 359-360.	0.2	2
134	Parallel epigenetic modifications induced by hatchery rearing in a Pacific salmon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12964-12969.	3.3	170
135	Range-wide parallel climate-associated genomic clines in Atlantic salmon. <i>Royal Society Open Science</i> , 2017, 4, 171394.	1.1	35
136	Functional Annotation of All Salmonid Genomes (FAASG): an international initiative supporting future salmonid research, conservation and aquaculture. <i>BMC Genomics</i> , 2017, 18, 484.	1.2	99
137	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
138	Draft genome of the American Eel (<i>Anguilla rostrata</i>). <i>Molecular Ecology Resources</i> , 2017, 17, 806-811.	2.2	21
139	Dressing down: convergent reduction of the mental disc in Garra (Teleostei: Cyprinidae) in the Middle East. <i>Hydrobiologia</i> , 2017, 785, 47-59.	1.0	12
140	Standing chromosomal variation in Lake Whitefish species pairs: the role of historical contingency and relevance for speciation. <i>Molecular Ecology</i> , 2017, 26, 178-192.	2.0	36
141	Convergence in organ size but not energy metabolism enzyme activities among wild Lake Whitefish (<i>Coregonus clupeaformis</i>) species pairs. <i>Molecular Ecology</i> , 2017, 26, 225-244.	2.0	13
142	RAD-Seq Reveals Patterns of Additive Polygenic Variation Caused by Spatially-Varying Selection in the American Eel (<i>Anguilla rostrata</i>). <i>Genome Biology and Evolution</i> , 2017, 9, 2974-2986.	1.1	35
143	Null alleles are ubiquitous at microsatellite loci in the Wedge Clam (<i>Donax trunculus</i>). <i>PeerJ</i> , 2017, 5, e3188.	0.9	35
144	Adaptation and acclimation of traits associated with swimming capacity in Lake Whitefish (<i>Coregonus</i>). <i>Trends in Ecology and Evolution</i> , 2017, 32, 1010-1018.	8.8	28

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152	On the maintenance of genetic variation and adaptation to environmental change: considerations from population genomics in fishes. Journal of Fish Biology, 2016, 89, 2519-2556.	0.7	187
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156	Seascape genomics provides evidence for thermal adaptation and current-mediated population structure in American lobster (<i>Homarus americanus</i>). Molecular Ecology, 2016, 25, 5073-5092.	2.0	148
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158	Genetic mixed-stock analysis disentangles spatial and temporal variation in composition of the West Greenland Atlantic Salmon fishery. ICES Journal of Marine Science, 2016, 73, 2311-2321.	1.2	26
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177	RAD-QTL Mapping Reveals Both Genome-Level Parallelism and Different Genetic Architecture Underlying the Evolution of Body Shape in Lake Whitefish (<i>Coregonus clupeaformis</i>) Species Pairs. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1481-1491.	0.8	62
178	How does salinity influence habitat selection and growth in juvenile American eels <i>Anguilla rostrata</i>?. <i>Journal of Fish Biology</i> , 2015, 86, 765-784.	0.7	23
179	Dietary sodium protects fish against copper-induced olfactory impairment. <i>Aquatic Toxicology</i> , 2015, 161, 1-9.	1.9	12
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182	Reproductive isolation in a nascent species pair is associated with aneuploidy in hybrid offspring. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20142862.	1.2	27
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185	Growth, Female Size, and Sex Ratio Variability in American Eel of Different Origins in Both Controlled Conditions and the Wild: Implications for Stocking Programs. <i>Transactions of the American Fisheries Society</i> , 2015, 144, 246-257.	0.6	31
186	Gonadal transcriptome analysis of wild contaminated female European eels during artificial gonad maturation. <i>Chemosphere</i> , 2015, 139, 303-309.	4.2	11
187	Regional variation in energy storage strategies in American glass eels from Eastern Canada. <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2015, 188, 87-95.	0.8	6
188	Signatures of natural selection between life cycle stages separated by metamorphosis in European eel. <i>BMC Genomics</i> , 2015, 16, 600.	1.2	17
189	Evolutionary Relationships, Population Genetics, and Ecological and Genomic Adaptations of Perch (<i>Perca</i>). , 2015, , 7-46.		9
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191	Inter Individual Variations of the Fish Skin Microbiota: Host Genetics Basis of Mutualism?. <i>PLoS ONE</i> , 2014, 9, e102649.	1.1	119
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195	Temperature, oxygen, and diet modulate gene transcription and metabolic capacities in yellow perch. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2014, 71, 1635-1641.	0.7	13
196	Genome-wide single-generation signatures of local selection in the panmictic European eel. <i>Molecular Ecology</i> , 2014, 23, 2514-2528.	2.0	135
197	Landscape variability explains spatial pattern of population structure of northern pike (<i>Esox lucius</i>) in a large fluvial system. <i>Ecology and Evolution</i> , 2014, 4, 3723-3735.	0.8	11
198	Influence of Forest Road Culverts and Waterfalls on the Fine-scale Distribution of Brook Trout Genetic Diversity in a Boreal Watershed. <i>Transactions of the American Fisheries Society</i> , 2014, 143, 1577-1591.	0.6	57

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200	EST-based microsatellites for northern pike (<i>Esox lucius</i>) and cross-amplification across all <i>Esox</i> species. <i>Conservation Genetics Resources</i> , 2014, 6, 451-454.	0.4	4
201	Assessing patterns of hybridization between North Atlantic eels using diagnostic single-nucleotide polymorphisms. <i>Heredity</i> , 2014, 112, 627-637.	1.2	65
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203	PHENOTYPE-ENVIRONMENT ASSOCIATION OF THE OXYGEN TRANSPORT SYSTEM IN TRIMORPHIC EUROPEAN WHITEFISH (<i>Coregonus lavaretus</i>) POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, n/a-n/a.	1.1	9
204	Population size, habitat fragmentation, and the nature of adaptive variation in a stream fish. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140370.	1.2	51
205	Genetic diversity in caribou linked to past and future climate change. <i>Nature Climate Change</i> , 2014, 4, 132-137.	8.1	154
206	Conservation genomics of anadromous Atlantic salmon across its North American range: outlier loci identify the same patterns of population structure as neutral loci. <i>Molecular Ecology</i> , 2014, 23, 5680-5697.	2.0	115
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208	Detecting genotypic changes associated with selective mortality at sea in Atlantic salmon: polygenic multilocus analysis surpasses genome scan. <i>Molecular Ecology</i> , 2014, 23, 4444-4457.	2.0	60
209	Genomic footprints of speciation in Atlantic eels (<i>Anguilla anguilla</i> and <i>A. rostrata</i>). <i>Molecular Ecology</i> , 2014, 23, 4785-4798.	2.0	37
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211	Temporally dynamic habitat suitability predicts genetic relatedness among caribou. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140502.	1.2	13
212	Microbiome investigation in the ecological speciation context of lake whitefish (<i>Coregonus</i>). <i>PLoS ONE</i> , 2014, 9, 1029-1046.	0.8	35
213	Do North Atlantic eels show parallel patterns of spatially varying selection?. <i>BMC Evolutionary Biology</i> , 2014, 14, 138.	3.2	19
214	Speciation and demographic history of Atlantic eels (<i>Anguilla anguilla</i> and <i>A. rostrata</i>) revealed by mitogenome sequencing. <i>Heredity</i> , 2014, 113, 432-442.	1.2	38
215	RNA-seq Reveals Transcriptomic Shock Involving Transposable Elements Reactivation in Hybrids of Young Lake Whitefish Species. <i>Molecular Biology and Evolution</i> , 2014, 31, 1188-1199.	3.5	112
216	Waterborne cadmium and nickel impact oxidative stress responses and retinoid metabolism in yellow perch. <i>Aquatic Toxicology</i> , 2014, 154, 207-220.	1.9	30

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218	Speciation Reversal in European Whitefish (<i>Coregonus lavaretus</i> (L.)) Caused by Competitor Invasion. PLoS ONE, 2014, 9, e91208.	1.1	46
219	Nonparallelism in <i>MHCII</i> diversity accompanies nonparallelism in pathogen infection of lake whitefish (<i>Coregonus clupeaformis</i>) species pairs as revealed by next-generation sequencing. Molecular Ecology, 2013, 22, 3833-3849.	2.0	38
220	RNA-seq analysis reveals extensive transcriptional plasticity to temperature stress in a freshwater fish species. BMC Genomics, 2013, 14, 375.	1.2	152
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222	Targeted sequence capture and resequencing implies a predominant role of regulatory regions in the divergence of a sympatric lake whitefish species pair (<i>Coregonus clupeaformis</i>). Molecular Ecology, 2013, 22, 4896-4914.	2.0	37
223	Parallel and nonparallel genome-wide divergence among replicate population pairs of freshwater and anadromous Atlantic salmon. Molecular Ecology, 2013, 22, 5577-5593.	2.0	71
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225	Reduced fitness of Atlantic salmon released in the wild after one generation of captive breeding. Evolutionary Applications, 2013, 6, 472-485.	1.5	99
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227	Population genetics of the American eel (<i>Anguilla rostrata</i>): <i>F_{ST}</i> and <i>N_{orth}</i> Atlantic <i>Oscillation</i> effects on demographic fluctuations of a panmictic species. Molecular Ecology, 2013, 22, 1763-1776.	2.0	101
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229	SNP array reveals genome-wide patterns of geographical and potential adaptive divergence across the natural range of Atlantic salmon (<i>Salmo salar</i>). Molecular Ecology, 2013, 22, 532-551.	2.0	212
230	How does exposure to nickel and cadmium affect the transcriptome of yellow perch (<i>Perca</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tj 50 222 Tj 33	1.9	33
231	THE GENETIC ARCHITECTURE OF REPRODUCTIVE ISOLATION DURING SPECIATION-WITH-GENE-FLOW IN LAKE WHITEFISH SPECIES PAIRS ASSESSED BY RAD SEQUENCING. Evolution; International Journal of Organic Evolution, 2013, 67, 2483-2497.	1.1	187
232	Does catch and release affect the mating system and individual reproductive success of wild Atlantic salmon (<i>Salmo salar</i> L.)?. Molecular Ecology, 2013, 22, 187-200.	2.0	68
233	A road map for molecular ecology. Molecular Ecology, 2013, 22, 2605-2626.	2.0	100
234	LANDSCAPE GENOMICS IN ATLANTIC SALMON (<i>SALMO SALAR</i>): SEARCHING FOR GENE-ENVIRONMENT INTERACTIONS DRIVING LOCAL ADAPTATION. Evolution; International Journal of Organic Evolution, 2013, 67, 3469-3487.	1.1	106

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236	Mapping phenotypic, expression and transmission ratio distortion QTL using RAD markers in the Lake Whitefish (<i>Coregonus clupeaformis</i>). <i>Molecular Ecology</i> , 2013, 22, 3036-3048.	2.0	96
237	Genetically based population divergence in overwintering energy mobilization in brook charr (<i>Salvelinus fontinalis</i>). <i>Genetica</i> , 2013, 141, 51-64.	0.5	19
238	Linking transcriptomic and genomic variation to growth in brook charr hybrids (<i>Salvelinus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 Td (fo	1.2	10
239	Strain Specific Genotype ² Environment Interactions and Evolutionary Potential for Body Mass in Brook Charr (<i>Salvelinus fontinalis</i>). <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 379-386.	0.8	19
240	Combining next-generation sequencing and online databases for microsatellite development in non-model organisms. <i>Scientific Reports</i> , 2013, 3, 3376.	1.6	22
241	New feature: themed sections. <i>Evolutionary Applications</i> , 2013, 6, 411-411.	1.5	0
242	Stocking impacts the expression of candidate genes and physiological condition in introgressed brook charr (<i>Salvelinus fontinalis</i>) populations. <i>Evolutionary Applications</i> , 2013, 6, 393-407.	1.5	27
243	Coding Gene Single Nucleotide Polymorphism Population Genetics of Nonnative Brook Trout: The Ghost of Introductions Past. <i>Transactions of the American Fisheries Society</i> , 2013, 142, 1215-1231.	0.6	8
244	Multidisciplinary population monitoring when demographic data are sparse: a case study of remote trout populations. <i>Ecology and Evolution</i> , 2013, 3, 4954-4969.	0.8	11
245	Gene Coexpression Networks Reveal Key Drivers of Phenotypic Divergence in Lake Whitefish. <i>Molecular Biology and Evolution</i> , 2013, 30, 1384-1396.	3.5	115
246	Variable extent of parallelism in respiratory, circulatory, and neurological traits across lake whitefish species pairs. <i>Ecology and Evolution</i> , 2013, 3, 546-557.	0.8	22
247	Metabolic Rate and Climatic Fluctuations Shape Continental Wide Pattern of Genetic Divergence and Biodiversity in Fishes. <i>PLoS ONE</i> , 2013, 8, e70296.	1.1	30
248	Network Analysis Highlights Complex Interactions between Pathogen, Host and Commensal Microbiota. <i>PLoS ONE</i> , 2013, 8, e84772.	1.1	205
249	Coding Gene Single Nucleotide Polymorphism Mapping and Quantitative Trait Loci Detection for Physiological Reproductive Traits in Brook Charr, <i>Salvelinus fontinalis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 379-392.	0.8	24
250	Coding Gene SNP Mapping Reveals QTL Linked to Growth and Stress Response in Brook Charr (<i>Salvelinus fontinalis</i>). <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 707-720.	0.8	18
251	Genome-wide patterns of divergence during speciation: the lake whitefish case study. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 354-363.	1.8	99
252	Environmental factors correlate with hybridization in stocked brook charr (<i>Salvelinus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62 Td (fo	0.7	41

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254	Comparative transcriptomics of anadromous and resident brook charr <i>Salvelinus fontinalis</i> before their first salt water transition. <i>Environmental Epigenetics</i> , 2012, 58, 158-170.	0.9	17
255	Genetic differentiation between two sympatric morphs of the blind Iran cave barb <i>Iranocypris tymphlops</i> . <i>Journal of Fish Biology</i> , 2012, 81, 1747-1753.	0.7	12
256	Phylogenetic status of brown trout <i>Salmo trutta</i> populations in five rivers from the southern Caspian Sea and two inland lake basins, Iran: a morphogenetic approach. <i>Journal of Fish Biology</i> , 2012, 81, 1479-1500.	0.7	22
257	Mate choice for major histocompatibility complex genetic divergence as a bet-hedging strategy in the Atlantic salmon (<i>Salmo salar</i>). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 379-386.	1.2	34
258	Effects of Rearing Environment and Strain Combination on Heterosis in Brook Trout. <i>North American Journal of Aquaculture</i> , 2012, 74, 188-198.	0.7	9
259	Small-scale dispersal and population structure in stream-living brown trout (<i>Salmo trutta</i>) inferred by mark-recapture, pedigree reconstruction, and population genetics. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2012, 69, 1513-1524.	0.7	36
260	The Genetic Consequences of Spatially Varying Selection in the Panmictic American Eel (<i>Anguilla</i>)	1.2	109
261	Short-Term Genetic Changes: Evaluating Effective Population Size Estimates in a Comprehensively Described Brown Trout (<i>Salmo trutta</i>) Population. <i>Genetics</i> , 2012, 191, 579-592.	1.2	38
262	What is needed for next-generation ecological and evolutionary genomics?. <i>Trends in Ecology and Evolution</i> , 2012, 27, 673-678.	4.2	77
263	Evidence for metabolic imbalance of vitamin A2 in wild fish chronically exposed to metals. <i>Ecotoxicology and Environmental Safety</i> , 2012, 85, 88-95.	2.9	21
264	Framing the Salmonidae Family Phylogenetic Portrait: A More Complete Picture from Increased Taxon Sampling. <i>PLoS ONE</i> , 2012, 7, e46662.	1.1	201
265	Negative density-dependent dispersal in the American black bear (<i>Ursus americanus</i>) revealed by noninvasive sampling and genotyping. <i>Ecology and Evolution</i> , 2012, 2, 525-537.	0.8	28
266	RNA/DNA ratios in American glass eels (<i>Anguilla rostrata</i>): evidence for latitudinal variation in physiological status and constraints to oceanic migration?. <i>Ecology and Evolution</i> , 2012, 2, 875-884.	0.8	12
267	Regulatory versus coding signatures of natural selection in a candidate gene involved in the adaptive divergence of whitefish species pairs (<i>Coregonus</i> spp.). <i>Ecology and Evolution</i> , 2012, 2, 258-271.	0.8	12
268	Life history and demographic determinants of effective/census size ratios as exemplified by brown trout (<i>Salmo trutta</i>). <i>Evolutionary Applications</i> , 2012, 5, 607-618.	1.5	34
269	<i>Evolutionary Applications</i> open to all. <i>Evolutionary Applications</i> , 2012, 5, 1-1.	1.5	0
270	A fast, highly sensitive double-nested PCR-based method to screen fish immunobiomes. <i>Molecular Ecology Resources</i> , 2012, 12, 1027-1039.	2.2	11

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271	Antagonistic effect of indigenous skin bacteria of brook charr (<i>Salvelinus fontinalis</i>) against <i>Flavobacterium columnare</i> and <i>F. psychrophilum</i> . <i>Veterinary Microbiology</i> , 2012, 155, 355-361.	0.8	62
272	Mitogenome sequencing reveals shallow evolutionary histories and recent divergence time between morphologically and ecologically distinct European whitefish (<i>Coregonus</i> spp.). <i>Molecular Ecology</i> , 2012, 21, 2727-2742.	2.0	83
273	Differences in transcription levels among wild, domesticated, and hybrid Atlantic salmon (<i>Salmo</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5	2.0	45
274	Dynamics of introgressive hybridization assessed by SNP population genomics of coding genes in stocked brook charr (<i>Salvelinus fontinalis</i>). <i>Molecular Ecology</i> , 2012, 21, 2877-2895.	2.0	77
275	Parallelism in the oxygen transport system of the lake whitefish: the role of physiological divergence in ecological speciation. <i>Molecular Ecology</i> , 2012, 21, 4038-4050.	2.0	29
276	Plasticity and heritability of morphological variation within and between parapatric stickleback demes. <i>Journal of Evolutionary Biology</i> , 2012, 25, 1097-1112.	0.8	44
277	Oxidative phosphorylation gene transcription in whitefish species pairs reveals patterns of parallel and nonparallel physiological divergence. <i>Journal of Evolutionary Biology</i> , 2012, 25, 1823-1834.	0.8	30
278	Genetic calibration of species diversity among North America's freshwater fishes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10602-10607.	3.3	241
279	Heterosis and outbreeding depression between strains of young-of-the-year brook trout (<i>Salvelinus fontinalis</i>). <i>Canadian Journal of Zoology</i> , 2011, 89, 190-198.	0.4	30
280	Molecular phylogeny and phylogeography of the Cuban cave-fishes of the genus <i>Lucifuga</i> : Evidence for cryptic allopatric diversity. <i>Molecular Phylogenetics and Evolution</i> , 2011, 61, 470-483.	1.2	25
281	BAC library construction, screening and clone sequencing of lake whitefish (<i>Coregonus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5 <i>Ecology Resources</i> , 2011, 11, 541-549.	2.2	11
282	Alternative developmental pathways and the propensity to migrate: a case study in the Atlantic salmon. <i>Journal of Evolutionary Biology</i> , 2011, 24, 245-255.	0.8	38
283	Putative causes and consequences of MHC variation within and between locally adapted stickleback demes. <i>Molecular Ecology</i> , 2011, 20, 486-502.	2.0	23
284	SNP signatures of selection on standing genetic variation and their association with adaptive phenotypes along gradients of ecological speciation in lake whitefish species pairs (<i>Coregonus</i> spp.). <i>Molecular Ecology</i> , 2011, 20, 545-559.	2.0	88
285	All roads lead to home: panmixia of European eel in the Sargasso Sea. <i>Molecular Ecology</i> , 2011, 20, 1333-1346.	2.0	176
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311	Introgressive hybridization between two Iberian endemic cyprinid fish: a comparison between two independent hybrid zones. <i>Journal of Evolutionary Biology</i> , 2010, 23, 817-828.	0.8	71
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326	Transcriptional responses to environmental metal exposure in wild yellow perch (<i>Perca flavescens</i>) collected in lakes with differing environmental metal concentrations (Cd, Cu, Ni). <i>Ecotoxicology</i> , 2009, 18, 620-631.	1.1	68
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374	The disruption of dominance hierarchies by a non-native species: an individual-based analysis. <i>Oecologia</i> , 2007, 152, 569-581.	0.9	30
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383	Parallelism in gene transcription among sympatric lake whitefish (<i>Coregonus clupeaformis</i> Mitchell) ecotypes. <i>Molecular Ecology</i> , 2006, 15, 1239-1249.	2.0	144
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392	Local heterozygosity-fitness correlations with global positive effects on fitness in threespine stickleback. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 1658-68.	1.1	15
393	Isolation and cross-familial amplification of 41 microsatellites for the brook charr (<i>Salvelinus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 109	1.7	29
394	pasos (parental allocation of singles in open systems): a computer program for individual parental allocation with missing parents. <i>Molecular Ecology Notes</i> , 2005, 5, 701-704.	1.7	51
395	Morphological divergence and origin of sympatric populations of European whitefish (<i>Coregonus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 109	0.8	109
396	Maternal genetic effects on adaptive divergence between anadromous and resident brook charr during early life history. <i>Journal of Evolutionary Biology</i> , 2005, 18, 1348-1361.	0.8	51

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401	Rapid parallel evolutionary changes of gene transcription profiles in farmed Atlantic salmon. <i>Molecular Ecology</i> , 2005, 15, 9-20.	2.0	120
402	ADAPTIVE MIGRATORY DIVERGENCE AMONG SYMPATRIC BROOK CHARR POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 611-624.	1.1	48
403	Offspring genetic diversity increases fitness of female Atlantic salmon (<i>Salmo salar</i>). <i>Behavioral Ecology and Sociobiology</i> , 2005, 57, 240-244.	0.6	50
404	ADAPTIVE MIGRATORY DIVERGENCE AMONG SYMPATRIC BROOK CHARR POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 611.	1.1	50
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406	Regional variation in the spatial scale of selection at MPI* and GPI* in the acorn barnacle <i>Semibalanus balanoides</i> (Crustacea). <i>Journal of Evolutionary Biology</i> , 2004, 17, 953-966.	0.8	43
407	Individual assignment test reveals differential restriction to dispersal between two salmonids despite no increase of genetic differences with distance. <i>Molecular Ecology</i> , 2004, 13, 1299-1312.	2.0	68
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409	Isolation and identification of 21 microsatellite loci in the Copper redhorse (<i>Moxostoma hubbsi</i>); Tj ETQq1 1 0.784314 rgBT /Overlock 1.7 13		
410	SHIFTING PATTERNS IN GENETIC CONTROL AT THE EMBRYO-ALEVIN BOUNDARY IN BROOK CHARR. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 2002-2012.	1.1	38
411	NONLINEAR EFFECTS OF FEMALE MATE CHOICE IN WILD THREESPINE STICKLEBACKS. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 2498-2510.	1.1	23
412	The Rainbow Smelt, <i>Osmerus mordax</i> , Complex of Lake Utopia: Threatened or Misunderstood?. <i>Environmental Biology of Fishes</i> , 2004, 69, 153-166.	0.4	13
413	Consequences of unequal population size, asymmetric gene flow and sex-biased dispersal on population structure in brook charr (<i>Salvelinus fontinalis</i>). <i>Molecular Ecology</i> , 2004, 13, 67-80.	2.0	145
414	Isolation, characterization and cross-salmonid amplification of 31 microsatellite loci in the lake whitefish (<i>Coregonus clupeaformis</i> , Mitchill). <i>Molecular Ecology Notes</i> , 2004, 4, 89-92.	1.7	60

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416	Generic Scan Using AFLP Markers as a Means to Assess the Role of Directional Selection in the Divergence of Sympatric Whitefish Ecotypes. <i>Molecular Biology and Evolution</i> , 2004, 21, 945-956.	3.5	248
417	The rainbow smelt, <i>Osmerus mordax</i> , complex of Lake Utopia: threatened or misunderstood?. <i>Developments in Environmental Biology of Fishes</i> , 2004, , 153-166.	0.2	0
418	Significance of caribou (<i>Rangifer tarandus</i>) ecotypes from a molecular genetics viewpoint. <i>Conservation Genetics</i> , 2003, 4, 393-404.	0.8	50
419	Title is missing!. <i>Conservation Genetics</i> , 2003, 4, 67-81.	0.8	74
420	Patterns of sexual cohabitation and female ejaculate storage in the American lobster (<i>Homarus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5	0.6	52
421	MHC studies in nonmodel vertebrates: what have we learned about natural selection in 15â€¢years?. <i>Journal of Evolutionary Biology</i> , 2003, 16, 363-377.	0.8	786
422	Divergent selection maintains adaptive differentiation despite high gene flow between sympatric rainbow smelt ecotypes (<i>Osmerus mordax</i> Mitchill). <i>Molecular Ecology</i> , 2003, 12, 315-330.	2.0	133
423	Genetic divergence between cave and surface populations of <i>Astyanax</i> in Mexico (Characidae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 5	2.0	132
424	AFLP utility for population assignment studies: analytical investigation and empirical comparison with microsatellites. <i>Molecular Ecology</i> , 2003, 12, 1979-1991.	2.0	163
425	Alternative male life-history tactics as potential vehicles for speeding introgression of farm salmon traits into wild populations. <i>Ecology Letters</i> , 2003, 6, 541-549.	3.0	77
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427	DIFFERENTIAL REPRODUCTIVE SUCCESS AND HERITABILITY OF ALTERNATIVE REPRODUCTIVE TACTICS IN WILD ATLANTIC SALMON (<i>SALMO SALAR</i> L.). <i>Evolution; International Journal of Organic Evolution</i> , 2003, 57, 1133.	1.1	95
428	Decline of North Atlantic eels: a fatal synergy?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003, 270, 681-688.	1.2	125
429	The Rise and Fall of Isolation by Distance in the Anadromous Brook Charr (<i>Salvelinus fontinalis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 5	1.2	132
430	A Comparative Mitogenomic Analysis of the Potential Adaptive Value of Arctic Charr mtDNA Introgression in Brook Charr Populations (<i>Salvelinus fontinalis</i> Mitchill). <i>Molecular Biology and Evolution</i> , 2002, 19, 1902-1909.	3.5	96
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448	Mitochondrial DNA phylogeography of lake cisco (<i>Coregonus artedii</i>): evidence supporting extensive secondary contacts between two glacial races. Molecular Ecology, 2001, 10, 987-1001.	2.0	60
449	Contrasting patterns of mitochondrial DNA and microsatellite introgressive hybridization between lineages of lake whitefish (<i>Coregonus clupeaformis</i>); relevance for speciation. Molecular Ecology, 2001, 10, 965-985.	2.0	130
450	Combining the analyses of introgressive hybridisation and linkage mapping to investigate the genetic architecture of population divergence in the lake whitefish (<i>Coregonus clupeaformis</i> , Mitchill). Genetica, 2001, 111, 25-41.	0.5	40

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467	Individual-based genotype analysis in studies of parentage and population assignment: how many loci, how many alleles?. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2000, 57, 1-12.	0.7	248
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481	Species Flock in the North American Great Lakes: Molecular Ecology of Lake Nipigon Ciscoes (Teleostei: <i>Coregonus</i>)	1.1	96
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496	A major sextet of mitochondrial DNA phylogenetic assemblages extant in eastern North American brook trout (<i>Salvelinus fontinalis</i>): distribution and postglacial dispersal patterns. <i>Canadian Journal of Zoology</i> , 1998, 76, 1300-1318.	0.4	52
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