Louis Bernatchez

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

536 papers	29,191 citations	90 h-index	142 g-index
585 ext. papers	33,751 ext. citations	4.7 avg, IF	7.54 L-index

#	Paper	IF	Citations
536	Cage transplant experiment shows weak transport effect on relative abundance of fish community composition as revealed by eDNA metabarcoding. *Ecological Indicators*, **2022**, 137, 108785	5.8	1
535	Thermal regime during parental sexual maturation, but not during offspring rearing, modulates DNA methylation in brook charr ().. *Proceedings of the Royal Society B: Biological Sciences*, **2022**, 289, 20220670	4.4	0
534	Environment-driven reprogramming of gamete DNA methylation occurs during maturation and is transmitted intergenerationally in Atlantic Salmon. *G3: Genes, Genomes, Genetics*, **2021**, 11,	3.2	2
533	Thermal adaptation rather than demographic history drives genetic structure inferred by copy number variants in a marine fish. *Molecular Ecology*, **2021**, 30, 1624-1641	5.7	4
532	Associative Overdominance and Negative Epistasis Shape Genome-Wide Ancestry Landscape in Supplemented Fish Populations. *Genes*, **2021**, 12,	4.2	1
531	Low effective population size in the genetically bottlenecked Australian sea lion is insufficient to maintain genetic variation. *Animal Conservation*, **2021**, 24, 847	3.2	1
530	Genomic data support management of anadromous Arctic Char fisheries in Nunavik by highlighting neutral and putatively adaptive genetic variation. *Evolutionary Applications*, **2021**, 14, 1880-1897	4.8	3
529	Epigenomic modifications induced by hatchery rearing persist in germ line cells of adult salmon after their oceanic migration. *Evolutionary Applications*, **2021**, 14, 2402-2413	4.8	6
528	Locally Adaptive Inversions Modulate Genetic Variation at Different Geographic Scales in a Seaweed Fly. *Molecular Biology and Evolution*, **2021**, 38, 3953-3971	8.3	5
527	Benchmarking bioinformatic tools for fast and accurate eDNA metabarcoding species identification. *Molecular Ecology Resources*, **2021**, 21, 2565-2579	8.4	7
526	Proper environmental DNA metabarcoding data transformation reveals temporal stability of fish communities in a dendritic river system. *Environmental DNA*, **2021**, 3, 1007-1022	7.6	5
525	Incorporating putatively neutral and adaptive genomic data into marine conservation planning. *Conservation Biology*, **2021**, 35, 909-920	6	8
524	Comparing environmental metabarcoding and trawling survey of demersal fish communities in the Gulf of St. Lawrence, Canada. *Environmental DNA*, **2021**, 3, 22-42	7.6	19
523	Contrasting Gene Decay in Subterranean Vertebrates: Insights from Cavefishes and Fossorial Mammals. *Molecular Biology and Evolution*, **2021**, 38, 589-605	8.3	13
522	Using environmental DNA for biomonitoring of freshwater fish communities: Comparison with established gillnet surveys in a boreal hydroelectric impoundment. *Environmental DNA*, **2021**, 3, 105-120	7.6	12
521	Detecting community change in Arctic marine ecosystems using the temporal dynamics of environmental DNA. *Environmental DNA*, **2021**, 3, 573-590	7.6	1
520	Comparing CRISPR-Cas and qPCR eDNA assays for the detection of Atlantic salmon (Salmo salar L.). *Environmental DNA*, **2021**, 3, 297-304	7.6	4

519	Population genomics and history of speciation reveal fishery management gaps in two related redfish species (and). *Evolutionary Applications*, **2021**, 14, 588-606	4.8	7
518	Population genomics of the southern Caspian Sea Vobla Rutilus lacustris. *Hydrobiologia*, **2021**, 848, 345-361	2.4	0
517	Genetic Diversity **2021**, 119-165		1
516	The rise and fall of the ancient northern pike master sex-determining gene. *ELife*, **2021**, 10,	8.9	7
515	Assessing the effects of genotype-by-environment interaction on epigenetic, transcriptomic, and phenotypic response in a Pacific salmon. *G3: Genes, Genomes, Genetics*, **2021**, 11,	3.2	3
514	Uncovering endemism in a lake of invasive species introgression. *Molecular Ecology*, **2021**, 30, 880-883	5.7	2
513	A chromosome-anchored genome assembly for Lake Trout (Salvelinus namaycush). *Molecular Ecology Resources*, **2021**,	8.4	2
512	A genomic perspective on an old question: Salmo trouts or Salmo trutta (Teleostei: Salmonidae)?. *Molecular Phylogenetics and Evolution*, **2021**, 162, 107204	4.1	9
511	Epigenetic inheritance and reproductive mode in plants and animals. *Trends in Ecology and Evolution*, **2021**, 36, 1124-1140	10.9	17
510	The future of biodiversity monitoring and conservation utilizing environmental DNA. *Environmental DNA*, **2021**, 3, 3-7	7.6	9
509	60 specific eDNA qPCR assays to detect invasive, threatened, and exploited freshwater vertebrates and invertebrates in Eastern Canada. *Environmental DNA*, **2020**, 2, 373-386	7.6	12
508	Detecting fine-scale population structure in the age of genomics: a case study of lake sturgeon in the Great Lakes. *Fisheries Research*, **2020**, 230, 105646	2.3	4
507	Shared ancestral polymorphisms and chromosomal rearrangements as potential drivers of local adaptation in a marine fish. *Molecular Ecology*, **2020**, 29, 2379-2398	5.7	20
506	Effects of genetic origin on phenotypic divergence in Brook Trout populations stocked with domestic fish. *Ecosphere*, **2020**, 11, e03119	3.1	1
505	Deciphering lifelong thermal niche using otolith δ18O thermometry within supplemented lake trout (Salvelinus namaycush) populations. *Freshwater Biology*, **2020**, 65, 1114-1127	3.1	2
504	Adaptation of plasticity to projected maximum temperatures and across climatically defined bioregions. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 17112-17121	11.5	16
503	Fine-scale population genetic structure of Endangered Caspian Sea trout, Salmo caspius: implications for conservation. *Hydrobiologia*, **2020**, 847, 3339-3353	2.4	2
502	Space invaders: Searching for invasive Smallmouth Bass () in a renowned Atlantic Salmon () river. *Ecology and Evolution*, **2020**, 10, 2588-2596	2.8	6

501	Groundtruthing of pelagic forage fish detected by hydroacoustics in a whale feeding area using environmental DNA. *Environmental DNA*, **2020**, 2, 477-492	7.6	5
500	Balancing selection via life-history trade-offs maintains an inversion polymorphism in a seaweed fly. *Nature Communications*, **2020**, 11, 670	17.4	28
499	Accurate estimation of conservation unit contribution to coho salmon mixed-stock fisheries in British Columbia, Canada, using direct DNA sequencing for single nucleotide polymorphisms. *Canadian Journal of Fisheries and Aquatic Sciences*, **2020**, 77, 1302-1315	2.4	13
498	Genetic population structure and variation at phenology-related loci in anadromous Arctic char (Salvelinus alpinus). *Ecology of Freshwater Fish*, **2020**, 29, 170-183	2.1	3
497	Sexing a Monomorphic Plumage Seabird Using Morphometrics and Assortative Mating. *Waterbirds*, **2020**, 42, 380	0.5	4
496	The analysis of the relationship between Lorestan cave barbs (Garra typhlops and Garra lorestanensis) and Garra gymnothorax populations in Dez and Karkheh River drainages. *Yaftah*, **2020**, 7, 1-8	0.1	1
495	Resolving the genetic paradox of invasions: Preadapted genomes and postintroduction hybridization of bigheaded carps in the Mississippi River Basin. *Evolutionary Applications*, **2020**, 13, 263-277	4.8	9
494	Using Haplotype Information for Conservation Genomics. *Trends in Ecology and Evolution*, **2020**, 35, 245-258	15.9	35
493	Absence of founder effect and evidence for adaptive divergence in a recently introduced insular population of white-tailed deer (Odocoileus virginianus). *Molecular Ecology*, **2020**, 29, 86-104	5.7	7
492	Speciation history of European (Anguilla anguilla) and American eel (A. ´rostrata), analysed using genomic data. *Molecular Ecology*, **2020**, 29, 565-577	5.7	7
491	Caged fish experiment and hydrodynamic bidimensional modeling highlight the importance to consider 2D dispersion in fluvial environmental DNA studies. *Environmental DNA*, **2020**, 2, 362-372	7.6	23
490	Mapping of Adaptive Traits Enabled by a High-Density Linkage Map for Lake Trout. *G3: Genes, Genomes, Genetics*, **2020**, 10, 1929-1947	3.2	1
489	Estimating the contribution of Greenland Halibut () stocks to nurseries by means of genotyping-by-sequencing: Sex and time matter. *Evolutionary Applications*, **2020**, 13, 2155-2167	4.8	4
488	Pathway to Increase Standards and Competency of eDNA Surveys (PISCeS)Advancing collaboration and standardization efforts in the field of eDNA. *Environmental DNA*, **2020**, 2, 255-260	7.6	17
487	Adaptive and maladaptive genetic diversity in small populations: Insights from the Brook Charr (Salvelinus fontinalis) case study. *Molecular Ecology*, **2020**, 29, 3429-3445	5.7	3
486	The structural variation landscape in 492 Atlantic salmon genomes. *Nature Communications*, **2020**, 11, 5176	17.4	24
485	Latitudinal variation in climate-associated genes imperils range edge populations. *Molecular Ecology*, **2020**, 29, 4337-4349	5.7	2
484	Fine-scale environmental heterogeneity shapes fluvial fish communities as revealed by eDNA metabarcoding. *Environmental DNA*, **2020**, 2, 647-666	7.6	10

483	Demographic history shaped geographical patterns of deleterious mutation load in a broadly distributed Pacific Salmon. *PLoS Genetics*, **2020**, 16, e1008348	6	14
482	Copy number variants outperform SNPs to reveal genotype-temperature association in a marine species. *Molecular Ecology*, **2020**, 29, 4765-4782	5.7	25
481	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. *Evolutionary Applications*, **2019**, 12, 230-254	4.8	28
480	Sex-Specific Co-expression Networks and Sex-Biased Gene Expression in the Salmonid Brook Charr. *G3: Genes, Genomes, Genetics*, **2019**, 9, 955-968	3.2	7
479	The role of ecotype-environment interactions in intraspecific trophic niche partitioning subsequent to stocking. *Ecological Applications*, **2019**, 29, e01857	4.9	9
478	Marine Conservation and Marine Protected Areas. *Population Genomics*, **2019**, 423-446	1.4	11
477	Model-based demographic inference of introgression history in European whitefish species pairsO *Journal of Evolutionary Biology*, **2019**, 32, 806-817	2.3	18
476	Going beyond SNPs: The role of structural genomic variants in adaptive evolution and species diversification. *Molecular Ecology*, **2019**, 28, 1203-1209	5.7	79
475	Impacts of stocking and its intensity on effective population size in Brook Charr (Salvelinus fontinalis) populations. *Conservation Genetics*, **2019**, 20, 729-742	2.6	13
474	Aquatic Landscape Genomics and Environmental Effects on Genetic Variation. *Trends in Ecology and Evolution*, **2019**, 34, 641-654	10.9	49
473	The genomic pool of standing structural variation outnumbers single nucleotide polymorphism by threefold in the marine teleost Chrysophrys auratus. *Molecular Ecology*, **2019**, 28, 1210-1223	5.7	24
472	Seascape genomics of eastern oyster () along the Atlantic coast of Canada. *Evolutionary Applications*, **2019**, 12, 587-609	4.8	26
471	Comparing Pool-seq, Rapture, and GBS genotyping for inferring weak population structure: The American lobster () as a case study. *Ecology and Evolution*, **2019**, 9, 6606-6623	2.8	18
470	DNA methylation reprogramming, TE derepression, and postzygotic isolation of nascent animal species. *Science Advances*, **2019**, 5, eaaw1644	14.3	22
469	Evidence for host effect on the intestinal microbiota of whitefish (sp.) species pairs and their hybrids. *Ecology and Evolution*, **2019**, 9, 11762-11774	2.8	12
468	Polygenic selection drives the evolution of convergent transcriptomic landscapes across continents within a Nearctic sister species complex. *Molecular Ecology*, **2019**, 28, 4388-4403	5.7	24
467	The role of recombination on genome-wide patterns of local ancestry exemplified by supplemented brook charr populations. *Molecular Ecology*, **2019**, 28, 4755-4769	5.7	11
466	Comparing eDNA metabarcoding and species collection for documenting Arctic metazoan biodiversity. *Environmental DNA*, **2019**, 1, 342-358	7.6	31

465	Comparing genomic signatures of domestication in two Atlantic salmon (L.) populations with different geographical origins. *Evolutionary Applications*, **2019**, 12, 137-156	4.8	22
464	Combining population genomics and forward simulations to investigate stocking impacts: A case study of Muskellunge () from the St. Lawrence River basin. *Evolutionary Applications*, **2019**, 12, 902-922	4.8	10
463	Domestication and Temperature Modulate Gene Expression Signatures and Growth in the Australasian Snapper. *G3: Genes, Genomes, Genetics*, **2019**, 9, 105-116	3.2	9
462	Chromosomal fusion and life history-associated genomic variation contribute to within-river local adaptation of Atlantic salmon. *Molecular Ecology*, **2019**, 28, 1439-1459	5.7	24
461	River-Specific Gene Expression Patterns Associated with Habitat Selection for Key Hormone-Coding Genes in Glass Eel-Stage American Eels. *Transactions of the American Fisheries Society*, **2018**, 147, 855-868	1.7	
460	Asymmetric oceanographic processes mediate connectivity and population genetic structure, as revealed by RADseq, in a highly dispersive marine invertebrate (Parastichopus californicus). *Molecular Ecology*, **2018**, 27, 2347-2364	5.7	51
459	The demographic history of Atlantic salmon (Salmo salar) across its distribution range reconstructed from approximate Bayesian computations. *Evolution; International Journal of Organic Evolution*, **2018**, 72, 1261-1277	3.8	35
458	Genetic and morphological support for possible sympatric origin of fish from subterranean habitats. *Scientific Reports*, **2018**, 8, 2909	4.9	7
457	Synergistic Integration of Genomics and Ecoevolutionary Dynamics for Sustainable Fisheries: A Reply to Kuparinen and Uusi-Heikkil *Trends in Ecology and Evolution*, **2018**, 33, 308-310	10.9	1
456	Eco-Evolutionary Genomics of Chromosomal Inversions. *Trends in Ecology and Evolution*, **2018**, 33, 427-440	10.9	190
455	A climate-associated multispecies cryptic cline in the northwest Atlantic. *Science Advances*, **2018**, 4, eaaq0929	10.3	49
454	Inferring phylogenetic structure, hybridization and divergence times within Salmoninae (Teleostei: Salmonidae) using RAD-sequencing. *Molecular Phylogenetics and Evolution*, **2018**, 124, 82-99	4.1	39
453	Linking genetic and ecological differentiation in an ungulate with a circumpolar distribution. *Ecography*, **2018**, 41, 922-937	6.5	10
452	The Lobster Node of the CFRN: co-constructed and collaborative research on productivity, stock structure, and connectivity in the American lobster (Homarus americanus). *Canadian Journal of Fisheries and Aquatic Sciences*, **2018**, 75, 813-824	2.4	7
451	Temporal variations in kidney metal concentrations and their implications for retinoid metabolism and oxidative stress response in wild yellow perch (Perca flavescens). *Aquatic Toxicology*, **2018**, 202, 26-35	5.1	4
450	On the roles of landscape heterogeneity and environmental variation in determining population genomic structure in a dendritic system. *Molecular Ecology*, **2018**, 27, 3484-3497	5.7	28
449	Impact of supplementation on deleterious mutation distribution in an exploited salmonid. *Evolutionary Applications*, **2018**, 11, 1053-1065	4.8	22
448	Supplementation stocking of Lake Trout (Salvelinus namaycush) in small boreal lakes: Ecotypes influence on growth and condition. *PLoS ONE*, **2018**, 13, e0200599	3.7	11

447	eDNA metabarcoding as a new surveillance approach for coastal Arctic biodiversity. *Ecology and Evolution*, **2018**, 8, 7763-7777	2.8	84
446	Introgressive hybridization between wild and domestic individuals and its relationship with parasitism in brook charr Salvelinus fontinalis. *Journal of Fish Biology*, **2018**, 93, 664-673	1.9	5
445	Genetic differentiation in the mountainous star coral Orbicella faveolata around Cuba. *Coral Reefs*, **2018**, 37, 1217-1227	4.2	2
444	Holobionts and ecological speciation: the intestinal microbiota of lake whitefish species pairs. *Microbiome*, **2018**, 6, 47	16.6	31
443	Ongoing niche differentiation under high gene flow in a polymorphic brackish water threespine stickleback (Gasterosteus aculeatus) population. *BMC Evolutionary Biology*, **2018**, 18, 14	3	5
442	Demographic and genetic approaches to study dispersal in wild animal populations: A methodological review. *Molecular Ecology*, **2018**, 27, 3976-4010	5.7	62
441	Effects of sampling effort on biodiversity patterns estimated from environmental DNA metabarcoding surveys. *Scientific Reports*, **2018**, 8, 8843	4.9	63
440	Next-generation conservation genetics and biodiversity monitoring. *Evolutionary Applications*, **2018** , 11, 1029-1034	4.8	29
439	Intercontinental karyotype-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,	4.4	19
438	Predicting the genetic impact of stocking in Brook Charr () by combining RAD sequencing and modeling of explanatory variables. *Evolutionary Applications*, **2018**, 11, 577-592	4.8	26
437	Do differences in the activities of carbohydrate metabolism enzymes between Lake Whitefish ecotypes match predictions from transcriptomic studies?. *Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology*, **2018**, 224, 138-149	2.3	9
436	Putatively adaptive genetic variation in the giant California sea cucumber (Parastichopus californicus) as revealed by environmental association analysis of restriction-site associated DNA sequencing data. *Molecular Ecology*, **2018**, 27, 5035-5048	5.7	23
435	Range-wide regional assignment of Atlantic salmon (Salmo salar) using genome wide single-nucleotide polymorphisms. *Fisheries Research*, **2018**, 206, 163-175	2.3	16
434	Investigating the extent of parallelism in morphological and genomic divergence among lake trout ecotypes in Lake Superior. *Molecular Ecology*, **2017**, 26, 1477-1497	5.7	37
433	Predicting Responses to Contemporary Environmental Change Using Evolutionary Response Architectures. *American Naturalist*, **2017**, 189, 463-473	3.7	72
432	Sex Chromosome Evolution, Heterochiasmy, and Physiological QTL in the Salmonid Brook Charr. *G3: Genes, Genomes, Genetics*, **2017**, 7, 2749-2762	3.2	22
431	De novo transcriptome assembly and annotation for the desert rainbowfish (Melanotaenia splendida tatei) with comparison with candidate genes for future climates. *Marine Genomics*, **2017**, 35, 63-68	1.9	3
430	Genomic patterns of diversity and divergence of two introduced salmonid species in Patagonia, South America. *Evolutionary Applications*, **2017**, 10, 402-416	4.8	15

429	Divergence in physiological factors affecting swimming performance between anadromous and resident populations of brook charr Salvelinus fontinalis. *Journal of Fish Biology*, **2017**, 90, 2170-2193	1.9	10
428	Unbroken: RADseq remains a powerful tool for understanding the genetics of adaptation in natural populations. *Molecular Ecology Resources*, **2017**, 17, 362-365	8.4	114
427	Genome Compositional Organization in Gars Shows More Similarities to Mammals than to Other Ray-Finned Fish. *Journal of Experimental Zoology Part B: Molecular and Developmental Evolution*, **2017**, 328, 607-619	1.8	19
426	Genomics and telemetry suggest a role for migration harshness in determining overwintering habitat choice, but not gene flow, in anadromous Arctic Char. *Molecular Ecology*, **2017**, 26, 6784-6800	5.7	37
425	Do genetic drift and accumulation of deleterious mutations preclude adaptation? Empirical investigation using RADseq in a northern lacustrine fish. *Molecular Ecology*, **2017**, 26, 6317-6335	5.7	33
424	RAD-Seq Reveals Patterns of Additive Polygenic Variation Caused by Spatially-Varying Selection in the American Eel (Anguilla rostrata). *Genome Biology and Evolution*, **2017**, 9, 2974-2986	3.9	21
423	Harnessing the Power of Genomics to Secure the Future of Seafood. *Trends in Ecology and Evolution* , **2017**, 32, 665-680	10.9	123
422	Modeling the Multiple Facets of Speciation-with-Gene-Flow toward Inferring the Divergence History of Lake Whitefish Species Pairs (Coregonus clupeaformis). *Genome Biology and Evolution*, **2017**, 9, 2057-2074	3.9	72
421	Environmental DNA metabarcoding: Transforming how we survey animal and plant communities. *Molecular Ecology*, **2017**, 26, 5872-5895	5.7	635
420	Characterization of natural variation in North American Atlantic Salmon populations (Salmonidae:) at a locus with a major effect on sea age. *Ecology and Evolution*, **2017**, 7, 5797-5807	2.8	19
419	The complete mitochondrial DNA of the Cuban gar (). *Mitochondrial DNA Part B: Resources*, **2017**, 2, 359-360	0.5	1
418	Parallel epigenetic modifications induced by hatchery rearing in a Pacific salmon. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 12964-12969	11.5	107
417	Range-wide parallel climate-associated genomic clines in Atlantic salmon. *Royal Society Open Science*, **2017**, 4, 171394	3.3	24
416	Sex matters in massive parallel sequencing: Evidence for biases in genetic parameter estimation and investigation of sex determination systems. *Molecular Ecology*, **2017**, 26, 6767-6783	5.7	27
415	Draft genome of the American Eel (Anguilla rostrata). *Molecular Ecology Resources*, **2017**, 17, 806-811	8.4	11
414	Dressing down: convergent reduction of the mental disc in Garra (Teleostei: Cyprinidae) in the Middle East. *Hydrobiologia*, **2017**, 785, 47-59	2.4	7
413	Standing chromosomal variation in Lake Whitefish species pairs: the role of historical contingency and relevance for speciation. *Molecular Ecology*, **2017**, 26, 178-192	5.7	27
412	Convergence in organ size but not energy metabolism enzyme activities among wild Lake Whitefish (Coregonus clupeaformis) species pairs. *Molecular Ecology*, **2017**, 26, 225-244	5.7	8

411	Null alleles are ubiquitous at microsatellite loci in the Wedge Clam (). *PeerJ*, **2017**, 5, e3188	3.1	24
410	Effective number of breeders in relation to census size as management tools for Atlantic salmon conservation in a context of stocked populations. *Conservation Genetics*, **2016**, 17, 31-44	2.6	13
409	Seascape genomics provides evidence for thermal adaptation and current-mediated population structure in American lobster (Homarus americanus). *Molecular Ecology*, **2016**, 25, 5073-5092	5.7	102
408	Making sense of the relationships between Ne, Nb and Nc towards defining conservation thresholds in Atlantic salmon (Salmo salar). *Heredity*, **2016**, 117, 268-78	3.6	28
407	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	2.7	18
406	Salmonid Chromosome Evolution as Revealed by a Novel Method for Comparing RADseq Linkage Maps. *Genome Biology and Evolution*, **2016**, 8, 3600-3617	3.9	51
405	Estimating fish abundance and biomass from eDNA concentrations: variability among capture methods and environmental conditions. *Molecular Ecology Resources*, **2016**, 16, 1401-1414	8.4	134
404	Detecting the exposure to Cd and PCBs by means of a non-invasive transcriptomic approach in laboratory and wild contaminated European eels (Anguilla anguilla). *Environmental Science and Pollution Research*, **2016**, 23, 5431-41	5.1	8
403	Combined effects of temperature changes and metal contamination at different levels of biological organization in yellow perch. *Aquatic Toxicology*, **2016**, 177, 324-32	5.1	16
402	Regional variation of gene regulation associated with storage lipid metabolism in American glass eels (Anguilla rostrata). *Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology*, **2016**, 196, 30-37	2.6	6
401	RAD sequencing reveals within-generation polygenic selection in response to anthropogenic organic and metal contamination in North Atlantic Eels. *Molecular Ecology*, **2016**, 25, 219-37	5.7	104
400	The past, present and future of genomic scans for selection. *Molecular Ecology*, **2016**, 25, 1-4	5.7	64
399	Genetic structure and within-generation genome scan analysis of fisheries-induced evolution in a Lake Whitefish (Coregonus clupeaformis) population. *Conservation Genetics*, **2016**, 17, 473-483	2.6	8
398	Integrating ecological and genetic structure to define management units for caribou in Eastern Canada. *Conservation Genetics*, **2016**, 17, 437-453	2.6	21
397	Genomics in Conservation: Case Studies and Bridging the Gap between Data and Application. *Trends in Ecology and Evolution*, **2016**, 31, 81-83	10.9	115
396	Comparative analysis of complete mitochondrial genomes suggests that relaxed purifying selection is driving high nonsynonymous evolutionary rate of the NADH2 gene in whitefish (Coregonus ssp.). *Molecular Phylogenetics and Evolution*, **2016**, 95, 161-70	4.1	38
395	Genetic mixed stock analysis of an interceptory Atlantic salmon fishery in the Northwest Atlantic. *Fisheries Research*, **2016**, 174, 234-244	2.3	33
394	Adaptation and acclimation of traits associated with swimming capacity in Lake Whitefish (coregonus clupeaformis) ecotypes. *BMC Evolutionary Biology*, **2016**, 16, 160	3	18

393	Go West: A One Way Stepping-Stone Dispersion Model for the Cavefish Lucifuga dentata in Western Cuba. *PLoS ONE*, **2016**, 11, e0153545	3.7	5
392	Quantifying relative fish abundance with eDNA: a promising tool for fisheries management. *Journal of Applied Ecology*, **2016**, 53, 1148-1157	5.8	149
391	Genomewide single nucleotide polymorphism discovery in Atlantic salmon (Salmo salar): validation in wild and farmed American and European populations. *Molecular Ecology Resources*, **2016**, 16, 1002-11	8.4	79
390	Implications for management and conservation of the population genetic structure of the wedge clam Donax trunculus across two biogeographic boundaries. *Scientific Reports*, **2016**, 6, 39152	4.9	21
389	Preference for nearshore and estuarine habitats in anadromous Arctic char (Salvelinus alpinus) from the Canadian high Arctic (Victoria Island, Nunavut) revealed by acoustic telemetry. *Canadian Journal of Fisheries and Aquatic Sciences*, **2016**, 73, 1434-1445	2.4	29
388	Improving herpetological surveys in eastern North America using the environmental DNA method. *Genome*, **2016**, 59, 991-1007	2.4	46
387	Transcriptional response of yellow perch to changes in ambient metal concentrations-A reciprocal field transplantation experiment. *Aquatic Toxicology*, **2016**, 173, 132-142	5.1	10
386	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	1.9	121
385	Gene transcription profiling in wild and laboratory-exposed eels: Effect of captivity and in situ chronic exposure to pollution. *Science of the Total Environment*, **2016**, 571, 92-102	10.2	9
384	Investigating genomic and phenotypic parallelism between piscivorous and planktivorous lake trout (Salvelinus namaycush) ecotypes by means of RADseq and morphometrics analyses. *Molecular Ecology*, **2016**, 25, 4773-92	5.7	40
383	The adaptive potential of subtropical rainbowfish in the face of climate change: heritability and heritable plasticity for the expression of candidate genes. *Evolutionary Applications*, **2016**, 9, 531-45	4.8	33
382	Genetic and phenotypic changes in an Atlantic salmon population supplemented with non-local individuals: a longitudinal study over 21 years. *Proceedings of the Royal Society B: Biological Sciences* , **2015**, 282,	4.4	22
381	Growth, Female Size, and Sex Ratio Variability in American Eel of Different Origins in Both Controlled Conditions and the Wild: Implications for Stocking Programs. *Transactions of the American Fisheries Society*, **2015**, 144, 246-257	1.7	23
380	Gonadal transcriptome analysis of wild contaminated female European eels during artificial gonad maturation. *Chemosphere*, **2015**, 139, 303-9	8.4	10
379	Regional variation in energy storage strategies in American glass eels from Eastern Canada. *Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology*, **2015**, 188, 87-95	2.6	5
378	Signatures of natural selection between life cycle stages separated by metamorphosis in European eel. *BMC Genomics*, **2015**, 16, 600	4.5	12
377	RAD genotyping reveals fine-scale genetic structuring and provides powerful population assignment in a widely distributed marine species, the American lobster (Homarus americanus). *Molecular Ecology*, **2015**, 24, 3299-315	5.7	173
376	Adaptation and acclimation of aerobic exercise physiology in Lake Whitefish ecotypes (Coregonus clupeaformis). *Evolution; International Journal of Organic Evolution*, **2015**, 69, 2167-86	3.8	24

375	Transatlantic secondary contact in Atlantic Salmon, comparing microsatellites, a single nucleotide polymorphism array and restriction-site associated DNA sequencing for the resolution of complex spatial structure. *Molecular Ecology*, **2015**, 24, 5130-44	5.7	65
374	RAD sequencing highlights polygenic discrimination of habitat ecotypes in the panmictic American eel. *Current Biology*, **2015**, 25, 1666-71	6.3	70
373	Transcriptional and biochemical markers in transplanted Perca flavescens to characterize cadmium- and copper-induced oxidative stress in the field. *Aquatic Toxicology*, **2015**, 162, 39-53	5.1	17
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19	Standing genetic variation and chromosomal rearrangements facilitate local adaptation in a marine fish		3
18	Copy number variants outperform SNPs to reveal genotype-temperature association in a marine species		3
17	The rise and fall of the ancient northern pike master sex determining gene		1
16	A study of fluctuating asymmetry in hybrids of dwarf and normal lake whitefish ecotypes (Coregonus clupeaformis) from different glacial races		2

15	Salmonid chromosome evolution as revealed by a novel method for comparing RADseq linkage maps		2
14	Modeling the Multiple Facets of Speciation-with-Gene-Flow Towards Inferring the Divergence History of Lake Whitefish Species Pairs (Coregonus Clupeaformis)		2
13	Functional Analysis of All Salmonid Genomes (FAASG): an international initiative supporting future salmonid research, conservation and aquaculture		7
12	Sex matters in Massive Parallel Sequencing: Evidence for biases in genetic parameter estimation and investigation of sex determination systems		2
11	Genomics and telemetry suggest a role for migration harshness in determining overwintering habitat choice, but not gene flow, in anadromous Arctic Char		2
10	Parallel epigenetic modifications induced by hatchery rearing in a Pacific Salmon		3
9	Contrasted gene decay in subterranean vertebrates: insights from cavefishes and fossorial mammals		2
8	Population structure and genomic evidence for local adaptation to freshwater and marine environments in anadromous Arctic Char (Salvelinus alpinus) throughout Nunavik, Québec, Canada		1
7	Environment-driven reprogramming of gamete DNA methylation occurs during maturation and is transmitted intergenerationally in salmon		1
6	Polygenic selection drives the evolution of convergent transcriptomic landscapes across continents within a Nearctic sister-species complex		2
5	Intestinal microbiota of whitefish (Coregonus sp.) species pairs and their hybrids in natural and controlled environment		2
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