

Anti VasemÃƒgi

List of Publications by Year in descending order

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Version: 2024-02-01

73
papers

2,523
citations

159525

30
h-index

223716

46
g-index

75
all docs

75
docs citations

75
times ranked

3385
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome sequencing illuminates multifaceted targets of selection to humic substances in Eurasian perch. <i>Molecular Ecology</i> , 2022, 31, 2367-2383.	2.0	6
2	Strong positive relationships between eDNA concentrations and biomass in juvenile and adult pike (<i>Esox lucius</i>) under controlled conditions: Implications for monitoring. <i>Environmental DNA</i> , 2022, 4, 881-893.	3.1	11
3	Are you ready for the heat? Phenotypic plasticity versus adaptation of heat tolerance in three-spined stickleback. <i>Ecosphere</i> , 2022, 13, .	1.0	5
4	Temporally stable small-scale genetic structure of Northern pike (<i>Esox lucius</i>) in the coastal Baltic Sea. <i>Fisheries Research</i> , 2022, 254, 106402.	0.9	6
5	The strength and form of natural selection on transcript abundance in the wild. <i>Molecular Ecology</i> , 2021, 30, 2724-2737.	2.0	11
6	Life in a drop: Sampling environmental DNA for marine fishery management and ecosystem monitoring. <i>Marine Policy</i> , 2021, 124, 104331.	1.5	52
7	Know your enemy – transcriptome of myxozoan <i>Tetracapsuloides bryosalmonae</i> reveals potential drug targets against proliferative kidney disease in salmonids. <i>Parasitology</i> , 2021, 148, 726-739.	0.7	9
8	Climate change-driven disease in sympatric hosts: Temporal dynamics of parasite burden and proliferative kidney disease in wild brown trout and Atlantic salmon. <i>Journal of Fish Diseases</i> , 2021, 44, 689-699.	0.9	6
9	A century of genetic homogenization in Baltic salmon – evidence from archival DNA. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20203147.	1.2	13
10	Draft Genome Assembly of the Freshwater Apex Predator Wels Catfish (<i>Silurus glanis</i>) Using Linked-Read Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3897-3906.	0.8	9
11	Humic-acid-driven escape from eye parasites revealed by RNA-seq and target-specific metabarcoding. <i>Parasites and Vectors</i> , 2020, 13, 433.	1.0	7
12	Population Connectivity Predicts Vulnerability to White-Nose Syndrome in the Chilean Myotis (<i>Myotis chiloensis</i>) - A Genomics Approach. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2117-2126.	0.8	9
13	Comparing RADseq and microsatellites for estimating genetic diversity and relatedness – Implications for brown trout conservation. <i>Ecology and Evolution</i> , 2019, 9, 2106-2120.	0.8	125
14	Association Mapping Based on a Common-Garden Migration Experiment Reveals Candidate Genes for Migration Tendency in Brown Trout. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2887-2896.	0.8	18
15	Mapping of quantitative trait loci for life history traits segregating within common frog populations. <i>Heredity</i> , 2019, 122, 800-808.	1.2	5
16	The complete mitochondrial DNA sequence of <i>Pectenocypris</i> sp. (Actinopterygii: Cyprinidae) from Serkap River, Sumatra, Indonesia. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 122-124.	0.2	0
17	Association mapping reveals candidate loci for resistance and anaemic response to an emerging temperature-driven parasitic disease in a wild salmonid fish. <i>Molecular Ecology</i> , 2018, 27, 1385-1401.	2.0	11
18	Genome-wide divergence patterns support fine-scaled genetic structuring associated with migration tendency in brown trout. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2018, 75, 1680-1692.	0.7	13

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19	Comparison of Migratory and Resident Populations of Brown Trout Reveals Candidate Genes for Migration Tendency. <i>Genome Biology and Evolution</i> , 2018, 10, 1493-1503.	1.1	50
20	Highly Continuous Genome Assembly of Eurasian Perch (<i>Perca fluviatilis</i>) Using Linked-Read Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3737-3743.	0.8	42
21	Otolith elemental characteristics of whitefish (<i>Coregonus lavaretus</i>) from brackish waters of the Gulf of Bothnia, Baltic Sea. <i>Ecology of Freshwater Fish</i> , 2017, 26, 66-74.	0.7	6
22	Parasite infection and decreased thermal tolerance: impact of proliferative kidney disease on a wild salmonid fish in the context of climate change. <i>Functional Ecology</i> , 2017, 31, 216-226.	1.7	90
23	Comparative High-Density Linkage Mapping Reveals Conserved Genome Structure but Variation in Levels of Heterochiasmy and Location of Recombination Cold Spots in the Common Frog. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 637-645.	0.8	12
24	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
25	Telomere length and antioxidant defense associate with parasite-induced retarded growth in wild brown trout. <i>Oecologia</i> , 2017, 185, 365-374.	0.9	16
26	Interacting environmental and chemical stresses under global change in temperate aquatic ecosystems: stress responses, adaptation, and scaling. <i>Regional Environmental Change</i> , 2017, 17, 2061-2077.	1.4	26
27	Prediction of harmful variants on mitochondrial genes: Test of habitat-dependent and demographic effects in a euryhaline fish. <i>Ecology and Evolution</i> , 2017, 7, 3826-3835.	0.8	5
28	Environmental feedbacks in temperate aquatic ecosystems under global change: why do we need to consider chemical stressors?. <i>Regional Environmental Change</i> , 2017, 17, 2079-2096.	1.4	11
29	Quantitative Genetic Variation in, and Environmental Effects on, Pathogen Resistance and Temperature-Dependent Disease Severity in a Wild Trout. <i>American Naturalist</i> , 2017, 190, 244-265.	1.0	40
30	Comprehensive microsatellite baseline for genetic stock identification of Atlantic salmon (<i>Salmo</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	1.2	19
31	Effect of Environmental Factors and an Emerging Parasitic Disease on Gut Microbiome of Wild Salmonid Fish. <i>MSphere</i> , 2017, 2, .	1.3	56
32	First record of proliferative kidney disease agent <i>Tetracapsuloides bryosalmonae</i> in wild brown trout and European grayling in Finland. <i>Diseases of Aquatic Organisms</i> , 2017, 125, 73-78.	0.5	25
33	Genes that affect Atlantic salmon growth in hatchery do not have the same effect in the wild. <i>Functional Ecology</i> , 2016, 30, 1687-1695.	1.7	13
34	Is telomere length a molecular marker of past thermal stress in wild fish?. <i>Molecular Ecology</i> , 2016, 25, 5412-5424.	2.0	51
35	Combining genetic markers with an adaptive meristic trait improves performance of mixed-stock analysis in Baltic whitefish. <i>ICES Journal of Marine Science</i> , 2016, 73, 2529-2538.	1.2	5
36	Genetic discrimination of brackish and freshwater populations of Eurasian perch (<i>Perca fluviatilis</i> L.) in the Baltic Sea drainage: implications for fish forensics. <i>Fisheries Research</i> , 2016, 183, 155-164.	0.9	11

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37	Can environmental DNA (eDNA) be used for detection and monitoring of introduced crab species in the Baltic Sea?. <i>Marine Pollution Bulletin</i> , 2016, 109, 350-355.	2.3	49
38	Genomewide introgressive hybridization patterns in wild Atlantic salmon influenced by inadvertent gene flow from hatchery releases. <i>Molecular Ecology</i> , 2016, 25, 1275-1293.	2.0	42
39	Genetic variation and population structure of the garden escaper <i>Lupinus polyphyllus</i> in Finland. <i>Plant Systematics and Evolution</i> , 2016, 302, 399-407.	0.3	12
40	Heritability, Environmental Effects, and Genetic and Phenotypic Correlations of Oxidative Stress Resistance-Related Enzyme Activities During Early Life Stages in Atlantic Salmon. <i>Evolutionary Biology</i> , 2016, 43, 215-226.	0.5	8
41	Genetic variation facilitates seedling establishment but not population growth rate of a perennial invader. <i>Annals of Botany</i> , 2016, 117, 187-194.	1.4	10
42	Use of sibling relationship reconstruction to complement traditional monitoring in fisheries management and conservation of brown trout. <i>Conservation Biology</i> , 2015, 29, 1164-1175.	2.4	8
43	Generation of a neutral <i>F_{ST}</i> baseline for testing local adaptation on gill raker number within and between European whitefish ecotypes in the Baltic Sea basin. <i>Journal of Evolutionary Biology</i> , 2015, 28, 1170-1183.	0.8	18
44	First microsatellite loci of the myxozoan parasite <i>Tetracapsuloides bryosalmonae</i> , the causative agent of proliferative kidney disease (PKD). <i>Diseases of Aquatic Organisms</i> , 2015, 113, 85-88.	0.5	3
45	Less is more: extreme genome complexity reduction with <i>ddRAD</i> using Ion Torrent semiconductor technology. <i>Molecular Ecology Resources</i> , 2015, 15, 1145-1152.	2.2	22
46	Population genomic analyses of early phase Atlantic salmon (<i>Salmo salar</i>) domestication/captive breeding. <i>Evolutionary Applications</i> , 2015, 8, 93-107.	1.5	59
47	Characterisation of polymorphic microsatellite loci for the bryozoan <i>Fredericella sultana</i> , the primary host of the causative agent of salmonid proliferative kidney disease. <i>Conservation Genetics Resources</i> , 2014, 6, 481-482.	0.4	1
48	Double-restriction-site-associated DNA (dRAD) approach for fast microsatellite marker development in Eurasian perch (<i>Perca fluviatilis</i> L.). <i>Conservation Genetics Resources</i> , 2014, 6, 183-184.	0.4	10
49	Proteome variance differences within populations of European whitefish (<i>Coregonus lavaretus</i>) originating from contrasting salinity environments. <i>Journal of Proteomics</i> , 2014, 105, 144-150.	1.2	14
50	Differences in the metabolic response to temperature acclimation in nine-spined stickleback (<i>Pungitius pungitius</i>) populations from contrasting thermal environments. <i>Journal of Experimental Zoology</i> , 2014, 321, 550-565.	1.2	15
51	Proliferative kidney disease (PKD) agent <i>Tetracapsuloides bryosalmonae</i> in brown trout populations in Estonia. <i>Diseases of Aquatic Organisms</i> , 2014, 109, 139-148.	0.5	42
52	Status and monitoring of the buff-tailed bumblebee <i>Bombus terrestris</i> Linnaeus (Hymenoptera: Tj ETQq0 0 0 rgBT /Overlock 10 T	0.6	2
53	Fish scales and SNP chips: SNP genotyping and allele frequency estimation in individual and pooled DNA from historical samples of Atlantic salmon (<i>Salmo salar</i>). <i>BMC Genomics</i> , 2013, 14, 439.	1.2	32
54	Cost-effective genome-wide estimation of allele frequencies from pooled DNA in Atlantic salmon (<i>Salmo salar</i> L.). <i>BMC Genomics</i> , 2013, 14, 12.	1.2	28

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55	Genetic biodiversity in the Baltic Sea: species-specific patterns challenge management. <i>Biodiversity and Conservation</i> , 2013, 22, 3045-3065.	1.2	50
56	Molecular evolutionary and population genomic analysis of the nine-spined stickleback using a modified restriction-associated <sc>DNA</sc> tag approach. <i>Molecular Ecology</i> , 2013, 22, 565-582.	2.0	85
57	SNP-array reveals genome-wide patterns of geographical and potential adaptive divergence across the natural range of <sc>A</sc>tlantic salmon (<i><sc>S</sc>almo salar</i>). <i>Molecular Ecology</i> , 2013, 22, 532-551.	2.0	212
58	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 February 2013â€“31 March 2013. <i>Molecular Ecology Resources</i> , 2013, 13, 760-762.	2.2	58
59	Genetic and life-history changes associated with fisheries-induced population collapse. <i>Evolutionary Applications</i> , 2013, 6, 749-760.	1.5	36
60	Finding Markers That Make a Difference: DNA Pooling and SNP-Arrays Identify Population Informative Markers for Genetic Stock Identification. <i>PLoS ONE</i> , 2013, 8, e82434.	1.1	45
61	High Lactose Tolerance in North Europeans: A Result of Migration, Not In Situ Milk Consumption. <i>Perspectives in Biology and Medicine</i> , 2012, 55, 163-174.	0.3	38
62	Screen for Footprints of Selection during Domestication/Captive Breeding of Atlantic Salmon. <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-14.	2.0	50
63	A proteomics approach reveals divergent molecular responses to salinity in populations of European whitefish (<i>Coregonus lavaretus</i>). <i>Molecular Ecology</i> , 2012, 21, 3516-3530.	2.0	54
64	Historical and recent genetic bottlenecks in European grayling, <i>Thymallus thymallus</i> . <i>Conservation Genetics</i> , 2010, 11, 279-292.	0.8	39
65	Discovery and application of insertion-deletion (INDEL) polymorphisms for QTL mapping of early life-history traits in Atlantic salmon. <i>BMC Genomics</i> , 2010, 11, 156.	1.2	44
66	Beyond MHC: signals of elevated selection pressure on Atlantic salmon (<i>Salmo salar</i>) immune-relevant loci. <i>Molecular Ecology</i> , 2010, 19, 1273-1282.	2.0	46
67	Unanticipated population structure of European grayling in its northern distribution: implications for conservation prioritization. <i>Frontiers in Zoology</i> , 2009, 6, 6.	0.9	19
68	A Comparison of Biallelic Markers and Microsatellites for the Estimation of Population and Conservation Genetic Parameters in Atlantic Salmon (<i>Salmo salar</i>). <i>Journal of Heredity</i> , 2007, 98, 692-704.	1.0	61
69	The Adaptive Hypothesis of Clinal Variation Revisited: Single-Locus Clines as a Result of Spatially Restricted Gene Flow. <i>Genetics</i> , 2006, 173, 2411-2414.	1.2	120
70	Seventy-five EST-linked Atlantic salmon (<i>Salmo salar</i> L.) microsatellite markers and their cross-amplification in five salmonid species. <i>Molecular Ecology Notes</i> , 2005, 5, 282-288.	1.7	34
71	Analysis of gene associated tandem repeat markers in Atlantic salmon (<i>Salmo salar</i> L.) populations: implications for restoration and conservation in the Baltic Sea. <i>Conservation Genetics</i> , 2005, 6, 385-397.	0.8	22
72	Expressed Sequence Tag-Linked Microsatellites as a Source of Gene-Associated Polymorphisms for Detecting Signatures of Divergent Selection in Atlantic Salmon (<i>Salmo salar</i> L.). <i>Molecular Biology and Evolution</i> , 2005, 22, 1067-1076.	3.5	252

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73	Population genetic structure and postglacial colonization of Atlantic salmon (<i>Salmo salar</i>) in the Baltic Sea area based on microsatellite DNA variation. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2005, 62, 1887-1904.	0.7	76