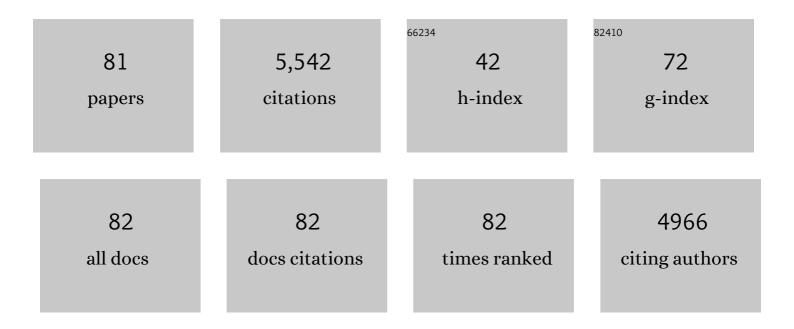
## John B Taggart

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Fitness reduction and potential extinction of wild populations of Atlantic salmon, Salmo salar , as a result of interactions with escaped farm salmon. Proceedings of the Royal Society B: Biological Sciences, 2003, 270, 2443-2450.	1.2	615
2	Considering adaptive genetic variation in climate change vulnerability assessment reduces species range loss projections. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10418-10423.	3.3	308
3	Major Quantitative Trait Loci Affect Resistance to Infectious Pancreatic Necrosis in Atlantic Salmon ( <i>Salmo salar</i> ). Genetics, 2008, 178, 1109-1115.	1.2	262
4	Comparative Genome Analysis of the Primary Sex-Determining Locus in Salmonid Fishes. Genome Research, 2003, 13, 272-280.	2.4	228
5	Development and validation of a high density SNP genotyping array for Atlantic salmon (Salmo salar). BMC Genomics, 2014, 15, 90.	1.2	219
6	Genomic prediction of host resistance to sea lice in farmed Atlantic salmon populations. Genetics Selection Evolution, 2016, 48, 47.	1.2	203
7	Functional genomics reveals increases in cholesterol biosynthetic genes and highly unsaturated fatty acid biosynthesis after dietary substitution of fish oil with vegetable oils in Atlantic salmon (Salmo) Tj ETQq1 1 (	).78442914 r	gBT9®verloc
8	A Linkage Map for Brown Trout (Salmo trutta): Chromosome Homeologies and Comparative Genome Organization With Other Salmonid Fish. Genetics, 2006, 172, 2405-2419.	1.2	147
9	Mapping and Validation of the Major Sex-Determining Region in Nile Tilapia (Oreochromis niloticus L.) Using RAD Sequencing. PLoS ONE, 2013, 8, e68389.	1.1	144
10	Genotype-specific responses in Atlantic salmon (Salmo salar) subject to dietary fish oil replacement by vegetable oil: a liver transcriptomic analysis. BMC Genomics, 2011, 12, 255.	1.2	142
11	Mapping the sex determination locus in the Atlantic halibut (Hippoglossus hippoglossus) using RAD sequencing. BMC Genomics, 2013, 14, 566.	1.2	133
12	A comparative analysis of the rainbow trout genome with 2 other species of fish (Arctic charr and) Tj ETQq0 0 0 2005, 48, 1037-1051.	rgBT /Ove 0.9	rlock 10 Tf 50 122
13	Characterisation of QTL-linked and genome-wide restriction site-associated DNA (RAD) markers in farmed Atlantic salmon. BMC Genomics, 2012, 13, 244.	1.2	120
14	Multiple genes for functional â^†6 fatty acyl desaturases (Fad) in Atlantic salmon (Salmo salar L.): Gene and cDNA characterization, functional expression, tissue distribution and nutritional regulation. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2010, 1801, 1072-1081.	1.2	119
15	A new SNP-based vision of the genetics of sex determination in European sea bass (Dicentrarchus) Tj ETQq1 1 0	.784314 r 1.2	gBT_/Qverloc
16	Genetic differentiation among the sympatric brown trout (Salmo trutta) populations of Lough Melvin, Ireland. Biological Journal of the Linnean Society, 1991, 43, 221-237.	0.7	102
17	A novel sex-determining QTL in Nile tilapia (Oreochromis niloticus). BMC Genomics, 2015, 16, 171.	1.2	102
18	Genotype Imputation To Improve the Cost-Efficiency of Genomic Selection in Farmed Atlantic Salmon. G3: Genes, Genomes, Genetics, 2017, 7, 1377-1383.	0.8	93

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19	Effects of genotype and dietary fish oil replacement with vegetable oil on the intestinal transcriptome and proteome of Atlantic salmon (Salmo salar). BMC Genomics, 2012, 13, 448.	1.2	89
20	Multiple tissue transcriptomic responses to <i>Piscirickettsia salmonis</i> in Atlantic salmon ( <i>Salmo salar</i> ). Physiological Genomics, 2011, 43, 1241-1254.	1.0	88
21	PROGRAM NOTE: FAP: an exclusion-based parental assignment program with enhanced predictive functions. Molecular Ecology Notes, 2006, 7, 412-415.	1.7	84
22	Towards a System Level Understanding of Non-Model Organisms Sampled from the Environment: A Network Biology Approach. PLoS Computational Biology, 2011, 7, e1002126.	1.5	83
23	Gene expression comparison of resistant and susceptible Atlantic salmon fry challenged with Infectious Pancreatic Necrosis virus reveals a marked contrast in immune response. BMC Genomics, 2016, 17, 279.	1.2	78
24	An integrated framework to identify wildlife populations under threat from climate change. Molecular Ecology Resources, 2018, 18, 18-31.	2.2	71
25	Nutrigenomic profiling of transcriptional processes affected in liver and distal intestine in response to a soybean meal-induced nutritional stress in Atlantic salmon (Salmo salar). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2015, 15, 1-11.	0.4	66
26	Analysis of the parental contribution to a group of fry from a single day of spawning from a commercial Atlantic cod (Gadus morhua) breeding tank. Aquaculture, 2008, 274, 218-224.	1.7	64
27	Identification of a Sex-Linked SNP Marker in the Salmon Louse (Lepeophtheirus salmonis) Using RAD Sequencing. PLoS ONE, 2013, 8, e77832.	1.1	63
28	Differential Gene Expression During Smoltification of Atlantic Salmon (Salmo salar L.): a First Large-Scale Microarray Study. Marine Biotechnology, 2010, 12, 126-140.	1.1	59
29	Detection of hybridization between Chinese carp species (Hypophthalmichthys molitrix and) Tj ETQq1 1 C Aquaculture, 2005, 247, 267-273.	.784314 rgBT 1.7	Overlock 10 T 54
30	Parallel evolution and adaptation to environmental factors in a marine flatfish: Implications for fisheries and aquaculture management of the turbot ( <i>Scophthalmus maximus</i> ). Evolutionary Applications, 2018, 11, 1322-1341.	1.5	54
31	Mapping the sex determination locus in the hÄpuku (Polyprion oxygeneios) using ddRAD sequencing. BMC Genomics, 2016, 17, 448.	1.2	51
32	A minisatellite DNA marker for discriminating between European and North American Atlantic salmon (Salmo salar). Canadian Journal of Fisheries and Aquatic Sciences, 1995, 52, 2305-2311.	0.7	49
33	DietÂ×Âgenotype interactions in hepatic cholesterol and lipoprotein metabolism in Atlantic salmon ( <i>Salmo salar</i> ) in response to replacement of dietary fish oil with vegetable oil. British Journal of Nutrition, 2011, 106, 1457-1469.	1.2	49
34	Salmon lice (Lepeophtheirus salmonis) showing varying emamectin benzoate susceptibilities differ in neuronal acetylcholine receptor and GABA-gated chloride channel mRNA expression. BMC Genomics, 2013, 14, 408.	1.2	49
35	A comparison of communal and separate rearing of families in selective breeding of common carp (Cyprinus carpio): Estimation of genetic parameters. Aquaculture, 2011, 322-323, 39-46.	1.7	48

 $_{36}$  A comparison of gene transcription profiles of domesticated and wild Atlantic salmon (Salmo salar) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50

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37	Heritability estimation of silver carp (Hypophthalmichthys molitrix) harvest traits using microsatellite based parentage assignment. Aquaculture, 2009, 294, 187-193.	1.7	46
38	Exploring a Nonmodel Teleost Genome Through RAD Sequencing—Linkage Mapping in Common Pandora, <i>Pagellus erythrinus</i> and Comparative Genomic Analysis. G3: Genes, Genomes, Genetics, 2016, 6, 509-519.	0.8	46
39	Heritability and mechanisms of nâ^'3 long chain polyunsaturated fatty acid deposition in the flesh of Atlantic salmon. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2011, 6, 62-69.	0.4	45
40	Single locus inheritance and joint segregation analysis of minisatellite (VNTR) DNA loci in brown trout (Salmo trutta L.). Heredity, 1994, 73, 556-566.	1.2	44
41	An evolutionary perspective on Elovl5 fatty acid elongase: comparison of Northern pike and duplicated paralogs from Atlantic salmon. BMC Evolutionary Biology, 2013, 13, 85.	3.2	44
42	A comparative analysis of the response of the hepatic transcriptome to dietary docosahexaenoic acid in Atlantic salmon (Salmo salar) post-smolts. BMC Genomics, 2015, 16, 684.	1.2	44
43	Expanding the miRNA Repertoire in Atlantic Salmon; Discovery of IsomiRs and miRNAs Highly Expressed in Different Tissues and Developmental Stages. Cells, 2019, 8, 42.	1.8	44
44	Construction and Annotation of a High Density SNP Linkage Map of the Atlantic Salmon ( <i>Salmo) Tj ETQq0 0 C</i>	) rgBT /Ove	erlock 10 Tf
45	DNA fingerprint analysis. Hereditas, 2008, 117, 45-50.	0.5	38
46	A comparison of communal and separate rearing of families in selective breeding of common carp (Cyprinus carpio): Responses to selection. Aquaculture, 2013, 408-409, 152-159.	1.7	36
47	Whole genome duplication and transposable element proliferation drive genome expansion in Corydoradinae catfishes. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20172732.	1.2	32
48	Hepatic transcriptome analysis of inter-family variability in flesh n-3 long-chain polyunsaturated fatty acid content in Atlantic salmon. BMC Genomics, 2012, 13, 410.	1.2	31
49	Allozyme variation in the brown trout (Salmo trutta L.): Single locus and joint segregation inheritance studies. Heredity, 1984, 53, 339-359.	1.2	29
50	Sequencing and Characterisation of an Extensive Atlantic Salmon (Salmo salar L.) MicroRNA Repertoire. PLoS ONE, 2013, 8, e70136.	1.1	29
51	Sex determination in the GIFT strain of tilapia is controlled by a locus in linkage group 23. BMC Genetics, 2020, 21, 49.	2.7	28
52	Parentage allocation in a complex situation: A large commercial Atlantic cod (Gadus morhua) mass spawning tank. Aquaculture, 2007, 272, S195-S203.	1.7	27
53	Transcriptomic analysis of the host response to early stage salmonid alphavirus (SAV-1) infection in Atlantic salmon Salmo salar L Fish and Shellfish Immunology, 2012, 32, 796-807.	1.6	27

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55	Mycobacterium stomatepiae sp. nov., a slowly growing, non-chromogenic species isolated from fish. International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 2821-2827.	0.8	24
56	Parental contribution and spawning performance in captive common snook Centropomus undecimalis broodstock. Aquaculture, 2014, 432, 144-153.	1.7	24
57	Potential physiological effects of pharmaceutical compounds in Atlantic salmon (Salmo salar) implied by transcriptomic analysis. Environmental Science and Pollution Research, 2010, 17, 917-933.	2.7	23
58	Identification and validation of single nucleotide polymorphisms as tools to detect hybridization and population structure in freshwater stingrays. Molecular Ecology Resources, 2017, 17, 550-556.	2.2	23
59	Genetic analysis of goldsinny wrasse reveals evolutionary insights into population connectivity and potential evidence of inadvertent translocation via aquaculture. ICES Journal of Marine Science, 2017, 74, 2135-2147.	1.2	23
60	The nedd-8 activating enzyme gene underlies genetic resistance to infectious pancreatic necrosis virus in Atlantic salmon. Genomics, 2021, 113, 3842-3850.	1.3	22
61	Communal larval rearing of European lobster (Homarus gammarus): Family identification by microsatellite DNA profiling and offspring fitness comparisons. Aquaculture, 2005, 247, 275-285.	1.7	20
62	Singleâ€nucleotide polymorphism discovery and panel characterization in the African forest elephant. Ecology and Evolution, 2018, 8, 2207-2217.	0.8	20
63	Species-Specific Marker Discovery in Tilapia. Scientific Reports, 2019, 9, 13001.	1.6	20
64	Comparing the transcriptomes of embryos from domesticated and wild Atlantic salmon (Salmo salar) Tj ETQq0 0 Evolution, 2016, 48, 20.	0 rgBT /O 1.2	verlock 10 Tf 19
65	A Survey of the ATP-Binding Cassette (ABC) Gene Superfamily in the Salmon Louse (Lepeophtheirus) Tj ETQq1 1	0.784314 1.1	rgßT /Overlo
66	Molecular epidemiological study on Infectious Pancreatic Necrosis Virus isolates from aquafarms in Scotland over three decades. Journal of General Virology, 2018, 99, 1567-1581.	1.3	18
67	The Impact of Escaped Farmed Atlantic Salmon (Salmo salar L.) on Catch Statistics in Scotland. PLoS ONE, 2012, 7, e43560.	1.1	15
68	Genetic analysis redraws the management boundaries for the European sprat. Evolutionary Applications, 2020, 13, 1906-1922.	1.5	15
69	Genetically monomorphic brown trout (Salmo trutta L.) populations, as revealed by mitochondrial DNA, multilocus and single-locus minisatellite (VNTR) analyses. Heredity, 1997, 79, 208-213.	1.2	14
70	Impact of Salmonid alphavirus infection in diploid and triploid Atlantic salmon (Salmo salar L.) fry. PLoS ONE, 2017, 12, e0179192.	1.1	13
71	Copper induces Cu-ATPase ATP7A mRNA in a fish cell line, SAF1. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2011, 154, 93-99.	1.3	12
72	Forensic identification of severely degraded Atlantic salmon (Salmo salar) and rainbow trout (Oncorhynchus mykiss) tissues. Investigative Genetics, 2010, 1, 12.	3.3	10

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73	Gene-centromere mapping in meiotic gynogenetic European seabass. BMC Genomics, 2017, 18, 449.	1.2	10
74	Development and validation of a mixed-tissue oligonucleotide DNA microarray for Atlantic bluefin tuna, Thunnus thynnus (Linnaeus, 1758). BMC Genomics, 2015, 16, 1007.	1.2	8
75	Suitability of DNA sampled from Nile tilapia skin mucus swabs as a template for ddRAD-based studies. Conservation Genetics Resources, 2017, 9, 39-42.	0.4	8
76	A panel of minisatellite (VNTR) DNA locus specific probes for potential application to problems in salmonid aquaculture. Aquaculture, 1995, 137, 87-97.	1.7	5
77	Transcriptomic comparison of communally reared wild, domesticated and hybrid Atlantic salmon fry under stress and control conditions. BMC Genetics, 2020, 21, 57.	2.7	5
78	Differential Survival among Batches of Atlantic Cod (Gadus morhua L.) from Fertilisation through to Post-Metamorphosis. PLoS ONE, 2016, 11, e0158091.	1.1	3
79	Linking Scales of Life-History Variation With Population Structure in Atlantic Cod. Frontiers in Marine Science, 2021, 8, .	1.2	3
80	Genetically monomorphic brown trout (Salmo trutta L.) populations, as revealed by mitochondrial DNA, multilocus and single-locus minisatellite (VNTR) analyses. Heredity, 1997, 79, 208-213.	1.2	2
81	Community Parameters and Genome-Wide RAD-Seq Loci of Ceratothoa oestroides Imply Its Transfer between Farmed European Sea Bass and Wild Farm-Aggregating Fish. Pathogens, 2021, 10, 100.	1.2	1