## Susan E Johnston

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Sex-dependent dominance at a single locus maintains variation in age at maturity in salmon. Nature, 2015, 528, 405-408.	27.8	527
2	Variation in recombination frequency and distribution across eukaryotes: patterns and processes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160455.	4.0	306
3	Life history trade-offs at a single locus maintain sexually selected genetic variation. Nature, 2013, 502, 93-95.	27.8	296
4	Genomeâ€wide association mapping identifies the genetic basis of discrete and quantitative variation in sexual weaponry in a wild sheep population. Molecular Ecology, 2011, 20, 2555-2566.	3.9	217
5	Conserved Genetic Architecture Underlying Individual Recombination Rate Variation in a Wild Population of Soay Sheep ( <i>Ovis aries</i> ). Genetics, 2016, 203, 583-598.	2.9	144
6	Evolutionary mysteries in meiosis. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20160001.	4.0	110
7	Genomeâ€wide <scp>SNP</scp> analysis reveals a genetic basis for seaâ€age variation in a wild population of <scp>A</scp> tlantic salmon ( <i><scp>S</scp>almo salar</i> ). Molecular Ecology, 2014, 23, 3452-3468.	3.9	96
8	Genome mapping in intensively studied wild vertebrate populations. Trends in Genetics, 2010, 26, 275-284.	6.7	85
9	Molecular evolutionary and population genomic analysis of the nineâ€spined stickleback using a modified restrictionâ€siteâ€associated <scp>DNA</scp> tag approach. Molecular Ecology, 2013, 22, 565-582.	3.9	85
10	Genetic architecture and lifetime dynamics of inbreeding depression in a wild mammal. Nature Communications, 2021, 12, 2972.	12.8	58
11	A High-Density Linkage Map Reveals Sexual Dimorphism in Recombination Landscapes in Red Deer ( <i>Cervus elaphus</i> ). G3: Genes, Genomes, Genetics, 2017, 7, 2859-2870.	1.8	57
12	Horn type and horn length genes map to the same chromosomal region in Soay sheep. Heredity, 2010, 104, 196-205.	2.6	49
13	Butterfly speciation and the distribution of gene effect sizes fixed during adaptation. Heredity, 2009, 102, 57-65.	2.6	46
14	Low but significant genetic differentiation underlies biologically meaningful phenotypic divergence in a large Atlantic salmon population. Molecular Ecology, 2015, 24, 5158-5174.	3.9	45
15	Recombination: the good, the bad and the variable. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20170279.	4.0	39
16	Home ground advantage: Local Atlantic salmon have higher reproductive fitness than dispersers in the wild. Science Advances, 2019, 5, eaav1112.	10.3	37
17	A Genomic Region Containing <i>REC8</i> and <i>RNF212B</i> Is Associated with Individual Recombination Rate Variation in a Wild Population of Red Deer ( <i>Cervus elaphus</i> ). G3: Genes, Genomes, Genetics, 2018, 8, 2265-2276.	1.8	36
18	Effect of manipulating recombination rates on response to selection in livestock breeding programs. Genetics Selection Evolution, 2016, 48, 44.	3.0	33

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19	Fish scales and SNP chips: SNP genotyping and allele frequency estimation in individual and pooled DNA from historical samples of Atlantic salmon (Salmo salar). BMC Genomics, 2013, 14, 439.	2.8	32
20	Captive-bred Atlantic salmon released into the wild have fewer offspring than wild-bred fish and decrease population productivity. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20201671.	2.6	30
21	Mutation load decreases with haplotype age in wild Soay sheep. Evolution Letters, 2021, 5, 187-195.	3.3	29
22	The genetic architecture of helminth-specific immune responses in a wild population of Soay sheep (Ovis aries). PLoS Genetics, 2019, 15, e1008461.	3.5	26
23	Natural Selection on Antihelminth Antibodies in a Wild Mammal Population. American Naturalist, 2018, 192, 745-760.	2.1	25
24	Molecular pedigree reconstruction and estimation of evolutionary parameters in a wild Atlantic salmon river system with incomplete sampling: a power analysis. BMC Evolutionary Biology, 2014, 14, 68.	3.2	19
25	The potential of shifting recombination hotspots to increase genetic gain in livestock breeding. Genetics Selection Evolution, 2017, 49, 55.	3.0	18
26	Evolutionary stasis of a heritable morphological trait in a wild fish population despite apparent directional selection. Ecology and Evolution, 2019, 9, 7096-7111.	1.9	14
27	Genomic prediction in the wild: A case study in Soay sheep. Molecular Ecology, 2022, 31, 6541-6555.	3.9	14
28	Genomic analysis reveals a polygenic architecture of antler morphology in wild red deer ( <i>Cervus) Tj ETQq0 0 (</i>	) rgBT /Ov	erlock 10 Tf 5
29	Maternally derived anti-helminth antibodies predict offspring survival in a wild mammal. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20201931.	2.6	9
30	Using genomic prediction to detect microevolutionary change of a quantitative trait. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, 20220330.	2.6	8
31	The genome sequence of the red deer, Cervus elaphus Linnaeus 1758. Wellcome Open Research, 0, 6, 336.	1.8	7
32	Contemporary selection on MHC genes in a freeâ€living ruminant population. Ecology Letters, 2022, 25, 828-838.	6.4	6
33	Recombination rates in pigs differ between breeds, sexes and individuals, and are associated with the RNF212, SYCP2, PRDM7, MEI1 and MSH4 loci. Genetics Selection Evolution, 2022, 54, .	3.0	6
34	MHC class IIa haplotypes derived by high-throughput SNP screening in an isolated sheep population. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	3
35	Vitamin D status is heritable and under environmentâ€dependent selection in the wild. Molecular Ecology, 2022, 31, 4607-4621.	3.9	3
36	Associations between MHC class II variation and phenotypic traits in a freeâ€living sheep population. Molecular Ecology, 2022, 31, 902-915.	3.9	2