

Susan E Johnston

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

2,570
citations

361413

20
h-index

361022

35
g-index

50
all docs

50
docs citations

50
times ranked

3078
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic prediction in the wild: A case study in Soay sheep. <i>Molecular Ecology</i> , 2022, 31, 6541-6555.	3.9	14
2	Associations between MHC class II variation and phenotypic traits in a free-living sheep population. <i>Molecular Ecology</i> , 2022, 31, 902-915.	3.9	2
3	Genomic analysis reveals a polygenic architecture of antler morphology in wild red deer (<i>Cervus</i>). <i>Evolution</i> , 2022, 76, 1000-1010.	3.9	10
4	Contemporary selection on MHC genes in a free-living ruminant population. <i>Ecology Letters</i> , 2022, 25, 828-838.	6.4	6
5	Vitamin D status is heritable and under environment-dependent selection in the wild. <i>Molecular Ecology</i> , 2022, 31, 4607-4621.	3.9	3
6	Using genomic prediction to detect microevolutionary change of a quantitative trait. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20220330.	2.6	8
7	Recombination rates in pigs differ between breeds, sexes and individuals, and are associated with the RNF212, SYCP2, PRDM7, MEI1 and MSH4 loci. <i>Genetics Selection Evolution</i> , 2022, 54, .	3.0	6
8	Genetic architecture and lifetime dynamics of inbreeding depression in a wild mammal. <i>Nature Communications</i> , 2021, 12, 2972.	12.8	58
9	Mutation load decreases with haplotype age in wild Soay sheep. <i>Evolution Letters</i> , 2021, 5, 187-195.	3.3	29
10	MHC class IIa haplotypes derived by high-throughput SNP screening in an isolated sheep population. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	3
11	Captive-bred Atlantic salmon released into the wild have fewer offspring than wild-bred fish and decrease population productivity. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201671.	2.6	30
12	Maternally derived anti-helminth antibodies predict offspring survival in a wild mammal. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201931.	2.6	9
13	The genetic architecture of helminth-specific immune responses in a wild population of Soay sheep (<i>Ovis aries</i>). <i>PLoS Genetics</i> , 2019, 15, e1008461.	3.5	26
14	Evolutionary stasis of a heritable morphological trait in a wild fish population despite apparent directional selection. <i>Ecology and Evolution</i> , 2019, 9, 7096-7111.	1.9	14
15	Home ground advantage: Local Atlantic salmon have higher reproductive fitness than dispersers in the wild. <i>Science Advances</i> , 2019, 5, eaav1112.	10.3	37
16	Natural Selection on Antihelminth Antibodies in a Wild Mammal Population. <i>American Naturalist</i> , 2018, 192, 745-760.	2.1	25
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>). <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2265-2276.	1.8	36
18	Recombination: the good, the bad and the variable. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20170279.	4.0	39

#	ARTICLE	IF	CITATIONS
19	Variation in recombination frequency and distribution across eukaryotes: patterns and processes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160455.	4.0	306
20	A High-Density Linkage Map Reveals Sexual Dimorphism in Recombination Landscapes in Red Deer (<i>Cervus elaphus</i>). <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2859-2870.	1.8	57
21	The potential of shifting recombination hotspots to increase genetic gain in livestock breeding. <i>Genetics Selection Evolution</i> , 2017, 49, 55.	3.0	18
22	Effect of manipulating recombination rates on response to selection in livestock breeding programs. <i>Genetics Selection Evolution</i> , 2016, 48, 44.	3.0	33
23	Conserved Genetic Architecture Underlying Individual Recombination Rate Variation in a Wild Population of Soay Sheep (<i>Ovis aries</i>). <i>Genetics</i> , 2016, 203, 583-598.	2.9	144
24	Evolutionary mysteries in meiosis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20160001.	4.0	110
25	Low but significant genetic differentiation underlies biologically meaningful phenotypic divergence in a large Atlantic salmon population. <i>Molecular Ecology</i> , 2015, 24, 5158-5174.	3.9	45
26	Sex-dependent dominance at a single locus maintains variation in age at maturity in salmon. <i>Nature</i> , 2015, 528, 405-408.	27.8	527
27	Genome-wide SNP analysis reveals a genetic basis for sea-age variation in a wild population of Atlantic salmon (<i>Salmo salar</i>). <i>Molecular Ecology</i> , 2014, 23, 3452-3468.	3.9	96
28	Molecular pedigree reconstruction and estimation of evolutionary parameters in a wild Atlantic salmon river system with incomplete sampling: a power analysis. <i>BMC Evolutionary Biology</i> , 2014, 14, 68.	3.2	19
29	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.	2.8	32
30	Life history trade-offs at a single locus maintain sexually selected genetic variation. <i>Nature</i> , 2013, 502, 93-95.	27.8	296
31	Molecular evolutionary and population genomic analysis of the nine-spined stickleback using a modified restriction-associated DNA tag approach. <i>Molecular Ecology</i> , 2013, 22, 565-582.	3.9	85
32	Genome-wide association mapping identifies the genetic basis of discrete and quantitative variation in sexual weaponry in a wild sheep population. <i>Molecular Ecology</i> , 2011, 20, 2555-2566.	3.9	217
33	Genome mapping in intensively studied wild vertebrate populations. <i>Trends in Genetics</i> , 2010, 26, 275-284.	6.7	85
34	Horn type and horn length genes map to the same chromosomal region in Soay sheep. <i>Heredity</i> , 2010, 104, 196-205.	2.6	49
35	Butterfly speciation and the distribution of gene effect sizes fixed during adaptation. <i>Heredity</i> , 2009, 102, 57-65.	2.6	46
36	The genome sequence of the red deer, <i>Cervus elaphus</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 0, 6, 336.	1.8	7