

Stephen N White

List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

4,096
citations

230014

27
h-index

134545

62
g-index

88
all docs

88
docs citations

88
times ranked

5280
citing authors

#	ARTICLE	IF	CITATIONS
1	A high-density genome-wide association with absolute blood monocyte count in domestic sheep identifies novel loci. PLoS ONE, 2022, 17, e0266748.	1.1	0
2	OvHV-2 Glycoprotein B Delivered by a Recombinant BoHV-4 Is Immunogenic and Induces Partial Protection against Sheep-Associated Malignant Catarrhal Fever in a Rabbit Model. Vaccines, 2021, 9, 90.	2.1	7
3	Natural genetic variation in <i>Drosophila melanogaster</i> reveals genes associated with <i>Coxiella burnetii</i> infection. Genetics, 2021, 217, .	1.2	7
4	Functional Variants Surrounding Endothelin 2 Are Associated With Mycobacterium avium Subspecies paratuberculosis Infection. Frontiers in Veterinary Science, 2021, 8, 625323.	0.9	6
5	Characterizing Genetic Regulatory Elements in Ovine Tissues. Frontiers in Genetics, 2021, 12, 628849.	1.1	8
6	A DNA Regulatory Element Haplotype at Zinc Finger Genes Is Associated with Host Resilience to Small Ruminant Lentivirus in Two Sheep Populations. Animals, 2021, 11, 1907.	1.0	1
7	Genes involved in immune, gene translation and chromatin organization pathways associated with Mycoplasma ovipneumoniae presence in nasal secretions of domestic sheep. PLoS ONE, 2021, 16, e0247209.	1.1	8
8	The EDN2 rs110287192 gene polymorphism is associated with paratuberculosis susceptibility in multibreed cattle population. PLoS ONE, 2020, 15, e0238631.	1.1	2
9	Association of TMEM8B and SPAG8 with Mature Weight in Sheep. Animals, 2020, 10, 2391.	1.0	3
10	Assay to compare cell- and antibody-mediated immune responses in domestic sheep and goats. Veterinary Immunology and Immunopathology, 2020, 230, 110125.	0.5	1
11	Genome-Wide Histone Modifications and CTCF Enrichment Predict Gene Expression in Sheep Macrophages. Frontiers in Genetics, 2020, 11, 612031.	1.1	9
12	Title is missing!. , 2020, 15, e0238631.		0
13	Title is missing!. , 2020, 15, e0238631.		0
14	Title is missing!. , 2020, 15, e0238631.		0
15	Title is missing!. , 2020, 15, e0238631.		0
16	Title is missing!. , 2020, 15, e0238631.		0
17	Title is missing!. , 2020, 15, e0238631.		0
18	A Vision for Development and Utilization of High-Throughput Phenotyping and Big Data Analytics in Livestock. Frontiers in Genetics, 2019, 10, 1197.	1.1	64

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19	Evolution and diversity of the EMA families of the divergent equid parasites, <i>Theileria equi</i> and <i>T. haneyi</i> . <i>Infection, Genetics and Evolution</i> , 2019, 68, 153-160.	1.0	10
20	Goats singly heterozygous for PRNP S146 or K222 orally inoculated with classical scrapie at birth show no disease at ages well beyond 6 years. <i>Veterinary Journal</i> , 2018, 233, 19-24.	0.6	13
21	Verification of post-chemotherapeutic clearance of <i>Theileria equi</i> through concordance of nested PCR and immunoblot. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 135-140.	1.1	14
22	Tenascin-XB (TNXB) amino acid substitution E2004G is associated with mature weight and milk score in American Rambouillet, Targhee, Polypay, and Suffolk sheep. <i>Small Ruminant Research</i> , 2018, 166, 129-133.	0.6	4
23	Discovery of a novel species, <i>Theileria haneyi</i> n. sp., infective to equids, highlights exceptional genomic diversity within the genus <i>Theileria</i> : implications for apicomplexan parasite surveillance. <i>International Journal for Parasitology</i> , 2018, 48, 679-690.	1.3	61
24	Identification of genes associated with susceptibility to <i>Mycobacterium avium</i> ssp. <i>paratuberculosis</i> (Map) tissue infection in Holstein cattle using gene set enrichment analysisâ€”SNP. <i>Mammalian Genome</i> , 2018, 29, 539-549.	1.0	12
25	Immunization of bighorn sheep against <i>Mannheimia haemolytica</i> with a bovine herpesvirus 1-vectored vaccine. <i>Vaccine</i> , 2017, 35, 1630-1636.	1.7	8
26	Validation of an improved <i>Anaplasma</i> antibody competitive ELISA for detection of <i>Anaplasma ovis</i> antibody in domestic sheep. <i>Journal of Veterinary Diagnostic Investigation</i> , 2017, 29, 763-766.	0.5	15
27	Underdominant <i>KCC3b R31I</i> association with blood sodium concentration in domestic sheep suggests role in oligomer function. <i>Animal Genetics</i> , 2017, 48, 626-627.	0.6	3
28	Domestic sheep show average <i>Coxiella burnetii</i> seropositivity generations after a sheep-associated human Q fever outbreak and lack detectable shedding by placental, vaginal, and fecal routes. <i>PLoS ONE</i> , 2017, 12, e0188054.	1.1	10
29	Identification of loci associated with susceptibility to <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> (Map) tissue infection in cattle. <i>Journal of Animal Science</i> , 2017, 95, 1080-1091.	0.2	22
30	P5059 Ovine MYADM-like repeat gene association with lifetime cumulative ewe production and wool traits. <i>Journal of Animal Science</i> , 2016, 94, 144-144.	0.2	0
31	Ovar-DRB1 haplotypes *2001 and *0301 are associated with sheep growth and ewe lifetime prolificacy. <i>Gene</i> , 2016, 595, 187-192.	1.0	6
32	Ovine leukocyte profiles do not associate with variation in the prion gene, but are breed dependent. <i>Animal Genetics</i> , 2016, 47, 136-137.	0.6	1
33	GOFAANG meeting: a Gathering On Functional Annotation of Animal Genomes. <i>Animal Genetics</i> , 2016, 47, 528-533.	0.6	65
34	Differences in leukocyte differentiation molecule abundances on domestic sheep (<i>Ovis aries</i>) and bighorn sheep (<i>Ovis canadensis</i>) neutrophils identified by flow cytometry. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2016, 46, 40-46.	0.7	8
35	Role of the PRNP S127 allele in experimental infection of goats with classical caprine scrapie. <i>Animal Genetics</i> , 2015, 46, 341-341.	0.6	16
36	Genome-Wide Association Identifies SLC2A9 and NLN Gene Regions as Associated with Entropion in Domestic Sheep. <i>PLoS ONE</i> , 2015, 10, e0128909.	1.1	12

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37	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015, 16, 57.	3.8	331
38	Knockdown of the <i>Rhipicephalus microplus</i> Cytochrome c Oxidase Subunit III Gene Is Associated with a Failure of <i>Anaplasma marginale</i> Transmission. <i>PLoS ONE</i> , 2014, 9, e98614.	1.1	18
39	Deletion variant near <i>ZNF389</i> is associated with control of ovine lentivirus in multiple sheep flocks. <i>Animal Genetics</i> , 2014, 45, 297-300.	0.6	18
40	Mutations in <i>Ovis aries</i> <i>TMEM154</i> are associated with lower small ruminant lentivirus proviral concentration in one sheep flock. <i>Animal Genetics</i> , 2014, 45, 565-571.	0.6	15
41	Association analysis of variant near <i>ZNF389</i> with ewe cumulative production in three sheep breeds. <i>Animal Genetics</i> , 2014, 45, 613-614.	0.6	1
42	A single codon insertion in <i>PICALM</i> is associated with development of familial subvalvular aortic stenosis in Newfoundland dogs. <i>Human Genetics</i> , 2014, 133, 1139-1148.	1.8	17
43	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	6.0	436
44	Extent of linkage disequilibrium in large-breed dogs: chromosomal and breed variation. <i>Mammalian Genome</i> , 2013, 24, 409-415.	1.0	13
45	Expanding Possibilities for Intervention against Small Ruminant Lentiviruses through Genetic Marker-Assisted Selective Breeding. <i>Viruses</i> , 2013, 5, 1466-1499.	1.5	31
46	A Divergent Artiodactyl MYADM-like Repeat Is Associated with Erythrocyte Traits and Weight of Lamb Weaned in Domestic Sheep. <i>PLoS ONE</i> , 2013, 8, e74700.	1.1	15
47	Reduced Lentivirus Susceptibility in Sheep with <i>TMEM154</i> Mutations. <i>PLoS Genetics</i> , 2012, 8, e1002467.	1.5	78
48	Ovine herpesvirus 2 infection in American bison: virus and host dynamics in the development of sheep-associated malignant catarrhal fever. <i>Veterinary Microbiology</i> , 2012, 159, 307-319.	0.8	30
49	Extended scrapie incubation time in goats singly heterozygous for <i>PRNP</i> S146 or K222. <i>Gene</i> , 2012, 501, 49-51.	1.0	42
50	MHC class II DR allelic diversity in bighorn sheep. <i>Gene</i> , 2012, 506, 217-222.	1.0	4
51	A splice site mutation in a gene encoding for <i>PDK4</i> , a mitochondrial protein, is associated with the development of dilated cardiomyopathy in the Doberman pinscher. <i>Human Genetics</i> , 2012, 131, 1319-1325.	1.8	90
52	In vitro activity of ponazuril against <i>Theileria equi</i> . <i>Veterinary Parasitology</i> , 2012, 185, 282-285.	0.7	12
53	Re-Emergence of the Apicomplexan <i>Theileria equi</i> in the United States: Elimination of Persistent Infection and Transmission Risk. <i>PLoS ONE</i> , 2012, 7, e44713.	1.1	54
54	Genome-Wide Association Identifies Multiple Genomic Regions Associated with Susceptibility to and Control of Ovine Lentivirus. <i>PLoS ONE</i> , 2012, 7, e47829.	1.1	48

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55	Ovine Progressive Pneumonia Virus Is Transmitted More Effectively via Aerosol Nebulization than Oral Administration. <i>Open Journal of Veterinary Medicine</i> , 2012, 02, 113-119.	0.4	2
56	Characterization of ovine herpesvirus 2-induced malignant catarrhal fever in rabbits. <i>Veterinary Microbiology</i> , 2011, 150, 270-277.	0.8	14
57	Genome-wide association identifies a deletion in the 3' untranslated region of Striatin in a canine model of arrhythmogenic right ventricular cardiomyopathy. <i>Human Genetics</i> , 2010, 128, 315-324.	1.8	112
58	Association analysis of PRNP gene region with chronic wasting disease in Rocky Mountain elk. <i>BMC Research Notes</i> , 2010, 3, 314.	0.6	20
59	Non-maternal transmission is the major mode of ovine lentivirus transmission in a ewe flock: A molecular epidemiology study. <i>Infection, Genetics and Evolution</i> , 2010, 10, 998-1007.	1.0	27
60	An insertion mutation in ABCB4 is associated with gallbladder mucocele formation in dogs. <i>Comparative Hepatology</i> , 2010, 9, 6.	0.9	30
61	Association analysis of a CCR5 variant with ewe lifetime production in three breeds of sheep. <i>Animal Genetics</i> , 2010, 41, 222-223.	0.6	5
62	Ovine Progressive Pneumonia Virus Capsid Antigen as Found in CD163- and CD172a-Positive Alveolar Macrophages of Persistently Infected Sheep. <i>Veterinary Pathology</i> , 2010, 47, 518-528.	0.8	13
63	Evaluation of a Caprine Arthritis-Encephalitis Virus/Maedi-Visna Virus Indirect Enzyme-Linked Immunosorbent Assay in the Serological Diagnosis of Ovine Progressive Pneumonia Virus in U.S. Sheep. <i>Vaccine Journal</i> , 2010, 17, 307-310.	3.2	17
64	Increased risk of chronic wasting disease in Rocky Mountain elk associated with decreased magnesium and increased manganese in brain tissue. <i>Canadian Journal of Veterinary Research</i> , 2010, 74, 50-3.	0.2	6
65	Peripheral Ovine Progressive Pneumonia Provirus Levels Correlate with and Predict Histological Tissue Lesion Severity in Naturally Infected Sheep. <i>Vaccine Journal</i> , 2009, 16, 551-557.	3.2	31
66	Ovine progressive pneumonia provirus levels are unaffected by the prion 171R allele in an Idaho sheep flock. <i>Genetics Selection Evolution</i> , 2009, 41, 17.	1.2	2
67	<i>Babesia bovis</i> : Transcriptional analysis of rRNA gene unit expression. <i>Experimental Parasitology</i> , 2009, 123, 45-50.	0.5	9
68	Common promoter deletion is associated with 3.9-fold differential transcription of ovine CCR5 and reduced proviral level of ovine progressive pneumonia virus. <i>Animal Genetics</i> , 2009, 40, 583-589.	0.6	34
69	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	6.0	1,038
70	Genomic analysis of <i>Ovis aries</i> (Ovar) MHC class IIa loci. <i>Immunogenetics</i> , 2008, 60, 167-176.	1.2	16
71	Ovine progressive pneumonia provirus levels associate with breed and Ovar-DRB1. <i>Immunogenetics</i> , 2008, 60, 749-758.	1.2	50
72	Myenteric neurons of the ileum that express somatostatin are a target of prion neuroinvasion in an alimentary model of sheep scrapie. <i>Acta Neuropathologica</i> , 2008, 115, 651-661.	3.9	10

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73	Technical Note: Comparison of traditional needle vaccination with pneumatic, needle-free vaccination for sheep ^{1,2} . <i>Journal of Animal Science</i> , 2008, 86, 1468-1471.	0.2	20
74	Development and Validation of an Ovine Progressive Pneumonia Virus Quantitative PCR. <i>Vaccine Journal</i> , 2007, 14, 1274-1278.	3.2	31
75	Association of a single nucleotide polymorphism in SPP1 with growth traits and twinning in a cattle population selected for twinning rate ^{1,2} . <i>Journal of Animal Science</i> , 2007, 85, 341-347.	0.2	39
76	Assessing the association of single nucleotide polymorphisms at the thyroglobulin gene with carcass traits in beef cattle ^{1,2} . <i>Journal of Animal Science</i> , 2007, 85, 2807-2814.	0.2	32
77	Evaluation in beef cattle of six deoxyribonucleic acid markers developed for dairy traits reveals an osteopontin polymorphism associated with postweaning growth. <i>Journal of Animal Science</i> , 2007, 85, 1-10.	0.2	81
78	Localization of a TNF-activated transcription site and interactions with the gamma activated site within the CAEV U3 70 base pair repeat. <i>Virology</i> , 2007, 364, 196-207.	1.1	14
79	Effects of calpastatin and $\frac{1}{4}$ -calpain markers in beef cattle on tenderness traits ^{1,2} . <i>Journal of Animal Science</i> , 2006, 84, 520-525.	0.2	197
80	Identification of genetic variation and putative regulatory regions in bovine CARD15. <i>Mammalian Genome</i> , 2006, 17, 892-901.	1.0	25
81	Assessment of single nucleotide polymorphisms in genes residing on chromosomes 14 and 29 for association with carcass composition traits in <i>Bos indicus</i> cattle ^{1,2} . <i>Journal of Animal Science</i> , 2005, 83, 13-19.	0.2	148
82	TLR4 variation in Yellowstone bison. <i>Animal Genetics</i> , 2005, 36, 051020043343003-???	0.6	2
83	A new single nucleotide polymorphism in CAPN1 extends the current tenderness marker test to include cattle of <i>Bos indicus</i> , <i>Bos taurus</i> , and crossbred descent ¹ . <i>Journal of Animal Science</i> , 2005, 83, 2001-2008.	0.2	157
84	Association of markers in the bovine CAPN1 gene with meat tenderness in large crossbred populations that sample influential industry sires ^{1,2} . <i>Journal of Animal Science</i> , 2004, 82, 3474-3481.	0.2	125
85	Comparative fine maps of bovine toll-like receptor 4 and toll-like receptor 2 regions. <i>Mammalian Genome</i> , 2003, 14, 149-155.	1.0	23
86	The bovine 5' AMPK gene family: mapping and single nucleotide polymorphism detection. <i>Mammalian Genome</i> , 2003, 14, 853-858.	1.0	17
87	Haplotype variation in bovine Toll-like receptor 4 and computational prediction of a positively selected ligand-binding domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10364-10369.	3.3	98