

Shona H Wood

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

1,476
citations

394421

19
h-index

454955

30
g-index

41
all docs

41
docs citations

41
times ranked

2148
citing authors

#	ARTICLE	IF	CITATIONS
1	A refined method to monitor arousal from hibernation in the European hamster. BMC Veterinary Research, 2021, 17, 14.	1.9	1
2	Immunologic Profiling of the Atlantic Salmon Gill by Single Nuclei Transcriptomics. Frontiers in Immunology, 2021, 12, 669889.	4.8	18
3	Diversified regulation of circadian clock gene expression following whole genome duplication. PLoS Genetics, 2020, 16, e1009097.	3.5	11
4	Circadian clock mechanism driving mammalian photoperiodism. Nature Communications, 2020, 11, 4291.	12.8	42
5	The Pars Tuberalis and Seasonal Timing. Masterclass in Neuroendocrinology, 2020, , 33-54.	0.1	0
6	Diversified regulation of circadian clock gene expression following whole genome duplication. , 2020, 16, e1009097.		0
7	Diversified regulation of circadian clock gene expression following whole genome duplication. , 2020, 16, e1009097.		0
8	Diversified regulation of circadian clock gene expression following whole genome duplication. , 2020, 16, e1009097.		0
9	Diversified regulation of circadian clock gene expression following whole genome duplication. , 2020, 16, e1009097.		0
10	Diversified regulation of circadian clock gene expression following whole genome duplication. , 2020, 16, e1009097.		0
11	Diversified regulation of circadian clock gene expression following whole genome duplication. , 2020, 16, e1009097.		0
12	An integrative view of mammalian seasonal neuroendocrinology. Journal of Neuroendocrinology, 2019, 31, e12729.	2.6	78
13	Maternal Photoperiodic Programming: Melatonin and Seasonal Synchronization Before Birth. Frontiers in Endocrinology, 2019, 10, 901.	3.5	14
14	Seasonal physiology: making the future a thing of the past. Current Opinion in Physiology, 2018, 5, 1-8.	1.8	16
15	The pars tuberalis: The site of the circannual clock in mammals?. General and Comparative Endocrinology, 2018, 258, 222-235.	1.8	51
16	Anti-angiogenic VEGFAxxxb transcripts are not expressed in the medio-basal hypothalamus of the seasonal sheep. PLoS ONE, 2018, 13, e0197123.	2.5	9
17	How can a binary switch within the pars tuberalis control seasonal timing of reproduction?. Journal of Endocrinology, 2018, 239, R13-R25.	2.6	8
18	Transcriptome analysis in calorie-restricted rats implicates epigenetic and post-translational mechanisms in neuroprotection and aging. Genome Biology, 2015, 16, 285.	8.8	49

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19	The Digital Ageing Atlas: integrating the diversity of age-related changes into a unified resource. <i>Nucleic Acids Research</i> , 2015, 43, D873-D878.	14.5	83
20	Binary Switching of Calendar Cells in the Pituitary Defines the Phase of the Circannual Cycle in Mammals. <i>Current Biology</i> , 2015, 25, 2651-2662.	3.9	97
21	Clocks for all seasons: unwinding the roles and mechanisms of circadian and interval timers in the hypothalamus and pituitary. <i>Journal of Endocrinology</i> , 2014, 222, R39-R59.	2.6	151
22	Whole transcriptome sequencing of the aging rat brain reveals dynamic RNA changes in the dark matter of the genome. <i>Age</i> , 2013, 35, 763-776.	3.0	94
23	A-to-I RNA editing does not change with age in the healthy male rat brain. <i>Biogerontology</i> , 2013, 14, 395-400.	3.9	15
24	Serotonin: from top to bottom. <i>Biogerontology</i> , 2013, 14, 21-45.	3.9	97
25	An analysis and validation pipeline for large-scale RNAi-based screens. <i>Scientific Reports</i> , 2013, 3, 1076.	3.3	5
26	Dissecting the Gene Network of Dietary Restriction to Identify Evolutionarily Conserved Pathways and New Functional Genes. <i>PLoS Genetics</i> , 2012, 8, e1002834.	3.5	58
27	GeneFriends: An online co-expression analysis tool to identify novel gene targets for aging and complex diseases. <i>BMC Genomics</i> , 2012, 13, 535.	2.8	67
28	Genome-Environment Interactions That Modulate Aging: Powerful Targets for Drug Discovery. <i>Pharmacological Reviews</i> , 2012, 64, 88-101.	16.0	118
29	Assessment of the functionality of genome-wide canine SNP arrays and implications for canine disease association studies. <i>Animal Genetics</i> , 2011, 42, 181-190.	1.7	11
30	Gathering insights on disease etiology from gene expression profiles of healthy tissues. <i>Bioinformatics</i> , 2011, 27, 3300-3305.	4.1	18
31	Despite identifying some shared gene associations with human atopic dermatitis the use of multiple dog breeds from various locations limits detection of gene associations in canine atopic dermatitis. <i>Veterinary Immunology and Immunopathology</i> , 2010, 138, 193-197.	1.2	51
32	Genome-wide association analysis of canine atopic dermatitis and identification of disease related SNPs. <i>Immunogenetics</i> , 2009, 61, 765-772.	2.4	49
33	Gene expression in canine atopic dermatitis and correlation with clinical severity scores. <i>Journal of Dermatological Science</i> , 2009, 55, 27-33.	1.9	55
34	Gene (mRNA) expression in canine atopic dermatitis: microarray analysis. <i>Veterinary Dermatology</i> , 2008, 19, 59-66.	1.2	47
35	Assessment of the quality and quantity of genomic DNA recovered from canine blood samples by three different extraction methods. <i>Research in Veterinary Science</i> , 2008, 85, 74-79.	1.9	27
36	Reference genes for canine skin when using quantitative real-time PCR. <i>Veterinary Immunology and Immunopathology</i> , 2008, 126, 392-395.	1.2	35

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37	Treatment of premenstrual syndrome with fluoxetine: a double-blind, placebo-controlled, crossover study. <i>Obstetrics and Gynecology</i> , 1992, 80, 339-44.	2.4	97