

Megan J Wilson

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

4,843
citations

257101

24
h-index

197535

49
g-index

56
all docs

56
docs citations

56
times ranked

6001
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of a novel Lbx1 mouse loss of function strain. <i>Differentiation</i> , 2022, 123, 30-41.	1.0	5
2	Using RNA-Seq for Transcriptome Profiling of <i>Botrylloides</i> sp. Regeneration. <i>Methods in Molecular Biology</i> , 2022, 2450, 599-615.	0.4	3
3	Genetic association and characterization of <i>FSTL5</i> in isolated clubfoot. <i>Human Molecular Genetics</i> , 2021, 29, 3717-3728.	1.4	5
4	The molecular pathways underlying early gonadal development. <i>Journal of Molecular Endocrinology</i> , 2019, 62, R47-R64.	1.1	25
5	Age and Sex-Related Changes to Gene Expression in the Mouse Spinal Cord. <i>Journal of Molecular Neuroscience</i> , 2019, 69, 419-432.	1.1	7
6	Histone deacetylase activity is required for <i>Botrylloides leachi</i> whole body regeneration. <i>Journal of Experimental Biology</i> , 2019, 222, .	0.8	13
7	Genome-wide analysis of H3K4me3 and H3K27me3 modifications throughout the mouse urogenital ridge at E11.5. <i>Gene Reports</i> , 2019, 16, 100412.	0.4	3
8	De novo draft assembly of the <i>Botrylloides leachi</i> genome provides further insight into tunicate evolution. <i>Scientific Reports</i> , 2018, 8, 5518.	1.6	36
9	Whole-Body Regeneration in the Colonial Tunicate <i>Botrylloides leachi</i> . <i>Results and Problems in Cell Differentiation</i> , 2018, 65, 337-355.	0.2	26
10	Hematological Analysis of the Ascidian <i>Botrylloides leachi</i> (Savigny, 1816) During Whole-Body Regeneration. <i>Biological Bulletin</i> , 2017, 232, 143-157.	0.7	27
11	Selection and evaluation of reference genes for analysis of mouse (<i>Mus musculus</i>) sex-dimorphic brain development. <i>PeerJ</i> , 2017, 5, e2909.	0.9	22
12	Uncovering the pathways underlying whole body regeneration in a chordate model, <i>Botrylloides leachi</i> using de novo transcriptome analysis. <i>BMC Genomics</i> , 2016, 17, 114.	1.2	34
13	Novel keratin preparation supports growth and differentiation of odontoblast-like cells. <i>International Endodontic Journal</i> , 2016, 49, 471-482.	2.3	23
14	Evolution of the Sox gene family within the chordate phylum. <i>Gene</i> , 2016, 575, 385-392.	1.0	35
15	Mutations Preventing Regulated Exon Skipping in MET Cause Osteofibrous Dysplasia. <i>American Journal of Human Genetics</i> , 2015, 97, 837-847.	2.6	22
16	Lhx9 gene expression during early limb development in mice requires the FGF signalling pathway. <i>Gene Expression Patterns</i> , 2015, 19, 45-51.	0.3	27
17	Components of the dorsal-ventral pathway also contribute to anterior-posterior patterning in honeybee embryos (<i>Apis mellifera</i>). <i>EvoDevo</i> , 2014, 5, 11.	1.3	33
18	RNA localization in the honeybee (<i>Apis mellifera</i>) oocyte reveals insights about the evolution of RNA localization mechanisms. <i>Developmental Biology</i> , 2013, 375, 193-201.	0.9	5

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19	Deep sequencing and expression of microRNAs from early honeybee (<i>Apis mellifera</i>) embryos reveals a role in regulating early embryonic patterning. <i>BMC Evolutionary Biology</i> , 2012, 12, 211.	3.2	18
20	Pair-Rule Gene Orthologues Have Unexpected Maternal Roles in the Honeybee (<i>Apis mellifera</i>). <i>PLoS ONE</i> , 2012, 7, e46490.	1.1	29
21	The evolution of oocyte patterning in insects: multiple cell-signaling pathways are active during honeybee oogenesis and are likely to play a role in axis patterning. <i>Evolution & Development</i> , 2011, 13, 127-137.	1.1	28
22	Diversity in insect axis formation: two <i>orthodenticle</i> genes and <i>hunchback</i> act in anterior patterning and influence dorsoventral organization in the honeybee (<i>Apis mellifera</i>). <i>Development (Cambridge)</i> , 2011, 138, 3497-3507.	1.2	36
23	Notch signaling does not regulate segmentation in the honeybee, <i>Apis mellifera</i> . <i>Development Genes and Evolution</i> , 2010, 220, 179-190.	0.4	21
24	Giant, Kr ¹⁴ ppel, and caudal act as gap genes with extensive roles in patterning the honeybee embryo. <i>Developmental Biology</i> , 2010, 339, 200-211.	0.9	54
25	Immunohistochemistry on Honeybee (<i>Apis mellifera</i>) Embryos. <i>Cold Spring Harbor Protocols</i> , 2009, 2009, pdb.prot5227.	0.2	3
26	In Situ Hybridization of Sectioned Honeybee (<i>Apis mellifera</i>) Tissues: Figure 1.. <i>Cold Spring Harbor Protocols</i> , 2009, 2009, pdb.prot5226.	0.2	1
27	RNA Interference (RNAi) in Honeybee (<i>Apis mellifera</i>) Embryos: Figure 1.. <i>Cold Spring Harbor Protocols</i> , 2009, 2009, pdb.prot5228.	0.2	8
28	Fixation and Storage of Honeybee (<i>Apis mellifera</i>) Tissues. <i>Cold Spring Harbor Protocols</i> , 2009, 2009, pdb.prot5224-pdb.prot5224.	0.2	6
29	Whole-Mount In Situ Hybridization of Honeybee (<i>Apis mellifera</i>) Tissues. <i>Cold Spring Harbor Protocols</i> , 2009, 2009, pdb.prot5225-pdb.prot5225.	0.2	6
30	Tailless patterning functions are conserved in the honeybee even in the absence of Torso signaling. <i>Developmental Biology</i> , 2009, 335, 276-287.	0.9	46
31	The Honeybee <i>Apis mellifera</i> . <i>Cold Spring Harbor Protocols</i> , 2009, 2009, pdb.emo123.	0.2	11
32	Evolution of the insect Sox genes. <i>BMC Evolutionary Biology</i> , 2008, 8, 120.	3.2	53
33	Evolutionary origin and genomic organisation of runt-domain containing genes in arthropods. <i>BMC Genomics</i> , 2008, 9, 558.	1.2	19
34	Retinoid Signaling Determines Germ Cell Fate in Mice. <i>Science</i> , 2006, 312, 596-600.	6.0	888
35	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006, 443, 931-949.	13.7	1,648
36	The matricellular protein SPARC is internalized in Sertoli, Leydig, and germ cells during testis differentiation. <i>Molecular Reproduction and Development</i> , 2006, 73, 531-539.	1.0	17

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37	Patterns of conservation and change in honey bee developmental genes. <i>Genome Research</i> , 2006, 16, 1376-1384.	2.4	139
38	Mutational Analysis of an Extracytoplasmic-Function Sigma Factor To Investigate Its Interactions with RNA Polymerase and DNA. <i>Journal of Bacteriology</i> , 2006, 188, 1935-1942.	1.0	27
39	Osteopontin and related SIBLING glycoprotein genes are expressed by Sertoli cells during mouse testis development. <i>Developmental Dynamics</i> , 2005, 233, 1488-1495.	0.8	16
40	Evaluation of candidate markers for the peritubular myoid cell lineage in the developing mouse testis. <i>Reproduction</i> , 2005, 130, 509-516.	1.1	48
41	The Transcription Factors Steroidogenic Factor-1 and SOX9 Regulate Expression of Vanin-1 during Mouse Testis Development. <i>Journal of Biological Chemistry</i> , 2005, 280, 5917-5923.	1.6	72
42	Sertoli cell differentiation is induced both cell-autonomously and through prostaglandin signaling during mammalian sex determination. <i>Developmental Biology</i> , 2005, 287, 111-124.	0.9	251
43	Expression of the tudor-related gene <i>Tdrd5</i> during development of the male germline in mice. <i>Gene Expression Patterns</i> , 2004, 4, 701-705.	0.3	34
44	HMG box transcription factor <i>geneHbp1</i> is expressed in germ cells of the developing mouse testis. <i>Developmental Dynamics</i> , 2004, 230, 366-370.	0.8	15
45	SOX8 Is Expressed during Testis Differentiation in Mice and Synergizes with SF1 to Activate the <i>Amh</i> Promoter in Vitro. <i>Journal of Biological Chemistry</i> , 2003, 278, 28101-28108.	1.6	154
46	Matching SOX: partner proteins and co-factors of the SOX family of transcriptional regulators. <i>Current Opinion in Genetics and Development</i> , 2002, 12, 441-446.	1.5	279
47	Iron transport and regulation, cell signalling and genomics: lessons from <i>Escherichia coli</i> and <i>Pseudomonas</i> . <i>Molecular Microbiology</i> , 2002, 45, 1177-1190.	1.2	255
48	Analysis of Promoters Recognized by PvdS, an Extracytoplasmic-Function Sigma Factor Protein from <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2001, 183, 2151-2155.	1.0	83
49	Characterization of an Endoprotease (PrpL) Encoded by a PvdS-Regulated Gene in <i>Pseudomonas aeruginosa</i> . <i>Infection and Immunity</i> , 2001, 69, 5385-5394.	1.0	174
50	Characterization of an ECF Sigma Factor Protein from <i>Pseudomonas aeruginosa</i> . <i>Biochemical and Biophysical Research Communications</i> , 2000, 273, 578-583.	1.0	51