

Susan J Brown

List of Publications by Year in descending order

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120
papers

9,521
citations

50276

46
h-index

40979

93
g-index

137
all docs

137
docs citations

137
times ranked

8412
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular detection of SARS-CoV-2 strains and differentiation of Delta variant strains. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 2879-2889.	3.0	25
2	Molecular detection of SARS-CoV-2 and differentiation of Omicron and Delta variant strains. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	3.0	14
3	Undergraduate Virtual Engagement in Community Genome Annotation Provides Flexibility to Overcome Course Disruptions. <i>Journal of Microbiology and Biology Education</i> , 2021, 22, .	1.0	2
4	High contiguity de novo genome assembly and DNA modification analyses for the fungus fly, <i>Sciara coprophila</i> , using single-molecule sequencing. <i>BMC Genomics</i> , 2021, 22, 643.	2.8	17
5	Genome-wide oscillations in G + C density and sequence conservation. <i>Genome Research</i> , 2021, 31, 2050-2057.	5.5	1
6	Reinterpretation of sperm pump or sperm syringe function with notes on other male internal reproductive organs in the Asian citrus psyllid, <i>Diaphorina citri</i> (Hemiptera: Liviidae). <i>Arthropod Structure and Development</i> , 2020, 54, 100915.	1.4	0
7	A quick guide for student-driven community genome annotation. <i>PLoS Computational Biology</i> , 2019, 15, e1006682.	3.2	33
8	Degenerative Expansion of a Young Supergene. <i>Molecular Biology and Evolution</i> , 2019, 36, 553-561.	8.9	42
9	Expression of teneurin-m/odd Oz during segmentation in the beetle <i>Tribolium castaneum</i> . <i>Gene Expression Patterns</i> , 2019, 31, 26-31.	0.8	2
10	Isolation of High Molecular Weight DNA from Insects. <i>Methods in Molecular Biology</i> , 2019, 1858, 27-32.	0.9	2
11	Asian citrus psyllid stylet morphology and applicability to the model for inter-instar stylet replacement in the potato psyllid. <i>Arthropod Structure and Development</i> , 2018, 47, 542-551.	1.4	5
12	Gender Bias in Human Systemic Lupus Erythematosus: A Problem of Steroid Receptor Action?. <i>Frontiers in Immunology</i> , 2018, 9, 611.	4.8	28
13	The transcriptome of the lone star tick, <i>Amblyomma americanum</i> , reveals molecular changes in response to infection with the pathogen, <i>Ehrlichia chaffeensis</i> . <i>Journal of Asia-Pacific Entomology</i> , 2018, 21, 852-863.	0.9	5
14	Speed regulation of genetic cascades allows for evolvability in the body plan specification of insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8646-E8655.	7.1	44
15	Membrane topology and identification of key residues of <i>Ea</i> DACT, a plant MBOAT with unusual substrate specificity. <i>Plant Journal</i> , 2017, 92, 82-94.	5.7	20
16	Regulation and function of odd-paired in <i>Tribolium</i> segmentation. <i>Development Genes and Evolution</i> , 2017, 227, 309-317.	0.9	13
17	Improved annotation of the insect vector of citrus greening disease: biocuration by a diverse genomics community. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	62
18	Hybrid de novo genome assembly and centromere characterization of the gray mouse lemur (<i>Microcebus murinus</i>). <i>BMC Biology</i> , 2017, 15, 110.	3.8	53

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19	Multifaceted biological insights from a draft genome sequence of the tobacco hornworm moth, <i>Manduca sexta</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2016, 76, 118-147.	2.7	154
20	Life habits, hox genes, and affinities of a 311 million-year-old holometabolan larva. <i>BMC Evolutionary Biology</i> , 2015, 15, 208.	3.2	36
21	Tools and pipelines for BioNano data: molecule assembly pipeline and FASTA super scaffolding tool. <i>BMC Genomics</i> , 2015, 16, 734.	2.8	103
22	Editorial overview: Insect genomics: How to sequence five thousand insect genomes?. <i>Current Opinion in Insect Science</i> , 2015, 7, iv-v.	4.4	3
23	A Massive Expansion of Effector Genes Underlies Gall-Formation in the Wheat Pest <i>Mayetiola destructor</i> . <i>Current Biology</i> , 2015, 25, 613-620.	3.9	171
24	The Genome and Methylome of a Beetle with Complex Social Behavior, <i>Nicrophorus vespilloides</i> (Coleoptera: Silphidae). <i>Genome Biology and Evolution</i> , 2015, 7, 3383-3396.	2.5	87
25	Essential role of eIF5-mimic protein in animal development is linked to control of ATF4 expression. <i>Nucleic Acids Research</i> , 2014, 42, 10321-10330.	14.5	24
26	Caudal Regulates the Spatiotemporal Dynamics of Pair-Rule Waves in <i>Tribolium</i> . <i>PLoS Genetics</i> , 2014, 10, e1004677.	3.5	48
27	Interaction between 25S rRNA A Loop and Eukaryotic Translation Initiation Factor 5B Promotes Subunit Joining and Ensures Stringent AUG Selection. <i>Molecular and Cellular Biology</i> , 2013, 33, 3540-3548.	2.3	10
28	Random mutagenesis of yeast 25S rRNA identify bases critical for 60S subunit structural integrity and function. <i>Translation</i> , 2013, 1, e26402.	2.9	3
29	Parallel Duplication and Partial Subfunctionalization of \hat{A} -Catenin/Armadillo during Insect Evolution. <i>Molecular Biology and Evolution</i> , 2012, 29, 647-662.	8.9	28
30	Asymmetrically expressed <i>axin</i> required for anterior development in <i>Tribolium</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7782-7786.	7.1	65
31	Genomic and proteomic studies on the effects of the insect growth regulator diflubenzuron in the model beetle species <i>Tribolium castaneum</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 264-276.	2.7	80
32	A segmentation clock operating in blastoderm and germband stages of <i>Tribolium</i> development. <i>Development (Cambridge)</i> , 2012, 139, 4341-4346.	2.5	100
33	Dissecting Systemic RNA Interference in the Red Flour Beetle <i>Tribolium castaneum</i> : Parameters Affecting the Efficiency of RNAi. <i>PLoS ONE</i> , 2012, 7, e47431.	2.5	174
34	Comparisons of the embryonic development of <i>Drosophila</i> , <i>Nasonia</i> , and <i>Tribolium</i> . <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , 2012, 1, 16-39.	5.9	81
35	Creating a Buzz About Insect Genomes. <i>Science</i> , 2011, 331, 1386-1386.	12.6	185
36	Conservation, loss, and redeployment of Wnt ligands in protostomes: implications for understanding the evolution of segment formation. <i>BMC Evolutionary Biology</i> , 2010, 10, 374.	3.2	153

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37	BeetleBase in 2010: revisions to provide comprehensive genomic information for <i>Tribolium castaneum</i> . <i>Nucleic Acids Research</i> , 2010, 38, D437-D442.	14.5	138
38	Yeast 18 S rRNA Is Directly Involved in the Ribosomal Response to Stringent AUG Selection during Translation Initiation. <i>Journal of Biological Chemistry</i> , 2010, 285, 32200-32212.	3.4	22
39	Prediction of alternatively spliced exons using Support Vector Machines. <i>International Journal of Data Mining and Bioinformatics</i> , 2010, 4, 411.	0.1	14
40	Highly Polymorphic Microsatellites in the North American Snakeweed Grasshopper, <i>Hesperotettix viridis</i> . <i>Journal of Orthoptera Research</i> , 2009, 18, 19-21.	1.0	3
41	Loss of Tc-arrow and canonical Wnt signaling alters posterior morphology and pair-rule gene expression in the short-germ insect, <i>Tribolium castaneum</i> . <i>Development Genes and Evolution</i> , 2009, 219, 369-375.	0.9	27
42	Large-scale insertional mutagenesis of a coleopteran stored grain pest, the red flour beetle <i>Tribolium castaneum</i> , identifies embryonic lethal mutations and enhancer traps. <i>BMC Biology</i> , 2009, 7, 73.	3.8	93
43	Genetic regulation of engrailed and wingless in <i>Tribolium</i> segmentation and the evolution of pair-rule segmentation. <i>Developmental Biology</i> , 2009, 325, 482-491.	2.0	44
44	The Red Flour Beetle, <i>Tribolium castaneum</i> (Coleoptera): A Model for Studies of Development and Pest Biology: Figure 1.. <i>Cold Spring Harbor Protocols</i> , 2009, 2009, pdb.emo126.	0.3	119
45	Concurrent In Situ Hybridization and Antibody Staining in Red Flour Beetle (<i>Tribolium</i>) Embryos. <i>Cold Spring Harbor Protocols</i> , 2009, 2009, pdb.prot5257.	0.3	18
46	<i>Tribolium</i> Wnts: evidence for a larger repertoire in insects with overlapping expression patterns that suggest multiple redundant functions in embryogenesis. <i>Development Genes and Evolution</i> , 2008, 218, 193-202.	0.9	89
47	Hedgehog signaling pathway function conserved in <i>Tribolium</i> segmentation. <i>Development Genes and Evolution</i> , 2008, 218, 181-192.	0.9	87
48	Do teashirt family genes specify trunk identity? Insights from the single tiptop/teashirt homolog of <i>Tribolium castaneum</i> . <i>Development Genes and Evolution</i> , 2008, 218, 141-152.	0.9	22
49	Analysis of the <i>Tribolium</i> homeotic complex: insights into mechanisms constraining insect Hox clusters. <i>Development Genes and Evolution</i> , 2008, 218, 127-139.	0.9	60
50	Larval RNAi in <i>Drosophila</i> ?. <i>Development Genes and Evolution</i> , 2008, 218, 505-510.	0.9	112
51	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 2008, 452, 949-955.	27.8	1,255
52	Multiple Wnt Genes Are Required for Segmentation in the Short-Germ Embryo of <i>Tribolium castaneum</i> . <i>Current Biology</i> , 2008, 18, 1624-1629.	3.9	129
53	Analysis of repetitive DNA distribution patterns in the <i>Tribolium castaneum</i> genome. <i>Genome Biology</i> , 2008, 9, R61.	9.6	50
54	Large diversity of the piggyBac-like elements in the genome of <i>Tribolium castaneum</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 490-498.	2.7	15

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55	Analysis of transcriptome data in the red flour beetle, <i>Tribolium castaneum</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 380-386.	2.7	46
56	Tubulin superfamily genes in <i>Tribolium castaneum</i> and the use of a Tubulin promoter to drive transgene expression. <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 749-755.	2.7	37
57	Exploring Alternative Splicing Features Using Support Vector Machines. , 2008, , .		3
58	BeetleBase: the model organism database for <i>Tribolium castaneum</i> . <i>Nucleic Acids Research</i> , 2007, 35, D476-D479.	14.5	66
59	Evolutionary flexibility of pair-rule patterning revealed by functional analysis of secondary pair-rule genes, paired and sloppy-paired in the short-germ insect, <i>Tribolium castaneum</i> . <i>Developmental Biology</i> , 2007, 302, 281-294.	2.0	94
60	piggyBac-based insertional mutagenesis in <i>Tribolium castaneum</i> using donor/helper hybrids. <i>Insect Molecular Biology</i> , 2007, 16, 265-275.	2.0	75
61	MtDNA haplotypes, sequence divergence, and morphological variation in Gray-breasted Wood Wrens (<i>Henichorina leucophrys</i>) and their conservation implications. <i>Journal of Field Ornithology</i> , 2007, 78, 117-123.	0.5	5
62	BindN: a web-based tool for efficient prediction of DNA and RNA binding sites in amino acid sequences. <i>Nucleic Acids Research</i> , 2006, 34, W243-W248.	14.5	375
63	Prediction of RNA-Binding Residues in Protein Sequences Using Support Vector Machines. , 2006, 2006, 5830-3.		19
64	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006, 443, 931-949.	27.8	1,648
65	Patterns of conservation and change in honey bee developmental genes. <i>Genome Research</i> , 2006, 16, 1376-1384.	5.5	139
66	The <i>Tribolium castaneum</i> Ortholog of Sex combs reduced Controls Dorsal Ridge Development. <i>Genetics</i> , 2006, 174, 297-307.	2.9	13
67	A pair-rule gene circuit defines segments sequentially in the short-germ insect <i>Tribolium castaneum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6560-6564.	7.1	192
68	PREDICTION OF DNA-BINDING RESIDUES FROM SEQUENCE FEATURES. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 1141-1158.	0.8	30
69	Prediction of RNA-Binding Residues in Protein Sequences Using Support Vector Machines. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2006, , .	0.5	1
70	Determination of cluster number in clustering microarray data. <i>Applied Mathematics and Computation</i> , 2005, 169, 1172-1185.	2.2	78
71	Anterior localization of maternal mRNAs in a short germ insect lacking bicoid. <i>Evolution & Development</i> , 2005, 7, 142-149.	2.0	52
72	Closing the Gap: Comparative Approaches to Studying Insect Development in the Red Flour Beetle <i>Tribolium castaneum</i> and Other Short and Intermediate Germ Insects. <i>Current Genomics</i> , 2005, 6, 571-578.	1.6	5

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73	Genetic Linkage Maps of the Red Flour Beetle, <i>Tribolium castaneum</i> , Based on Bacterial Artificial Chromosomes and Expressed Sequence Tags. <i>Genetics</i> , 2005, 170, 741-747.	2.9	53
74	Computational identification of novel chitinase-like proteins in the <i>Drosophila melanogaster</i> genome. <i>Bioinformatics</i> , 2004, 20, 161-169.	4.1	90
75	Incremental genetic K-means algorithm and its application in gene expression data analysis. <i>BMC Bioinformatics</i> , 2004, 5, 172.	2.6	87
76	Entomological contributions to genetics: Studies on insect germ cells linked genes to chromosomes and chromosomes to mendelian inheritance. <i>Archives of Insect Biochemistry and Physiology</i> , 2003, 53, 115-118.	1.5	2
77	piggyBac-mediated germline transformation in the beetle <i>Tribolium castaneum</i> . <i>Insect Molecular Biology</i> , 2003, 12, 433-440.	2.0	132
78	Beetling around the genome. <i>Genetical Research</i> , 2003, 82, 155-161.	0.9	46
79	The expression and function of the achaete-scute genes in <i>Tribolium castaneum</i> reveals conservation and variation in neural pattern formation and cell fate specification. <i>Development (Cambridge)</i> , 2003, 130, 4373-4381.	2.5	65
80	<i>Tribolium</i> Hox genes repress antennal development in the gnathos and trunk. <i>Molecular Phylogenetics and Evolution</i> , 2002, 24, 384-387.	2.7	23
81	Transgene expression from the <i>Tribolium castaneum</i> Polyubiquitin promoter. <i>Insect Molecular Biology</i> , 2002, 11, 399-407.	2.0	38
82	Cloning and Characterization of the <i>Tribolium castaneum</i> Eye-Color Genes Encoding Tryptophan Oxygenase and Kynurenine 3-Monooxygenase. <i>Genetics</i> , 2002, 160, 225-234.	2.9	116
83	Sequence of the <i>Tribolium castaneum</i> Homeotic Complex: The Region Corresponding to the <i>Drosophila melanogaster</i> Antennapedia Complex. <i>Genetics</i> , 2002, 160, 1067-1074.	2.9	47
84	The repressor activity of Even-skipped is highly conserved, and is sufficient to activate engrailed and to regulate both the spacing and stability of parasegment boundaries. <i>Development (Cambridge)</i> , 2002, 129, 4411-4421.	2.5	33
85	The repressor activity of Even-skipped is highly conserved, and is sufficient to activate engrailed and to regulate both the spacing and stability of parasegment boundaries. <i>Development (Cambridge)</i> , 2002, 129, 4411-21.	2.5	20
86	Pondering the procephalon: the segmental origin of the labrum. <i>Development Genes and Evolution</i> , 2001, 211, 89-95.	0.9	60
87	Homeotic evidence for the appendicular origin of the labrum in <i>Tribolium castaneum</i> . <i>Development Genes and Evolution</i> , 2001, 211, 96-102.	0.9	39
88	Molecular characterization of Tlabial and the 3' end of the <i>Tribolium</i> homeotic complex. <i>Development Genes and Evolution</i> , 2001, 211, 244-251.	0.9	22
89	Molecular characterization of Cephalothorax, the <i>Tribolium</i> ortholog of Sex combs reduced. <i>Genesis</i> , 2001, 30, 12-20.	1.6	40
90	Interactions of the <i>Tribolium</i> Sex combs reduced and proboscipedia Orthologs in Embryonic Labial Development. <i>Genetics</i> , 2001, 159, 1643-1648.	2.9	27

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91	maxillopedia is the Tribolium ortholog of proboscipedia. <i>Evolution & Development</i> , 2000, 2, 145-151.	2.0	23
92	Analysis of <i>maxillopedia</i> Expression Pattern and Larval Cuticular Phenotype in Wild-Type and Mutant Tribolium. <i>Genetics</i> , 2000, 155, 721-731.	2.9	40
93	Using RNAi to investigate orthologous homeotic gene function during development of distantly related insects. <i>Evolution & Development</i> , 1999, 1, 11-15.	2.0	146
94	Molecular and genetic analysis of the Tribolium Ultrabithorax ortholog, Ultrathorax. <i>Development Genes and Evolution</i> , 1999, 209, 608-619.	0.9	36
95	RAPD-Based Genetic Linkage Maps of Tribolium castaneum. <i>Genetics</i> , 1999, 153, 333-338.	2.9	47
96	Molecular characterization of the Tribolium abdominal-A ortholog and implications for the products of the Drosophila gene. <i>Development Genes and Evolution</i> , 1998, 207, 446-452.	0.9	33
97	Molecular characterization and embryonic expression of the even-skipped ortholog of Tribolium castaneum. <i>Mechanisms of Development</i> , 1997, 61, 165-173.	1.7	67
98	The nuclear receptor homologue Ftz-F1 and the homeodomain protein Ftz are mutually dependent cofactors. <i>Nature</i> , 1997, 385, 548-552.	27.8	180
99	Useful DNA polymorphisms are identified by snapback, a midrepetitive element in Tribolium castaneum. <i>Genome</i> , 1996, 39, 568-578.	2.0	3
100	Two orthodenticle-related genes in the short-germ beetle Tribolium castaneum. <i>Development Genes and Evolution</i> , 1996, 206, 35-45.	0.9	59
101	The Tribolium decapentaplegic gene is similar in sequence, structure, and expression to the Drosophila dpp gene. <i>Development Genes and Evolution</i> , 1996, 206, 237-246.	0.9	64
102	<i>Woot</i> , an Active Gypsy-Class Retrotransposon in the Flour Beetle, <i>Tribolium castaneum</i> , is Associated With a Recent Mutation. <i>Genetics</i> , 1996, 143, 417-426.	2.9	28
103	Genetic Control of Early Embryogenesis in the Red Flour Beetle, <i>Tribolium castaneum</i> . <i>American Zoologist</i> , 1994, 34, 343-352.	0.7	23
104	Embryonic expression of the single Tribolium engrailed homolog. <i>Genesis</i> , 1994, 15, 7-18.	2.1	126
105	Structure and function of the homeotic gene complex (HOM-C) in the beetle, <i>Tribolium castaneum</i> . <i>BioEssays</i> , 1993, 15, 439-444.	2.5	93
106	A deficiency of the homeotic complex of the beetle Tribolium. <i>Nature</i> , 1991, 350, 72-74.	27.8	166
107	Molecular genetic manipulation of the red flour beetle: Genome organization and cloning of a ribosomal protein gene. <i>Insect Biochemistry</i> , 1990, 20, 185-193.	1.8	60
108	Sensory control of dauer larva formation in <i>Caenorhabditis elegans</i> . <i>Journal of Comparative Neurology</i> , 1981, 198, 435-451.	1.6	193

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109	Divergent host plant adaptation drives the evolution of sexual isolation in the grasshopper <i>Hesperotettix viridis</i> (Orthoptera: Acrididae) in the absence of reinforcement. <i>Biological Journal of the Linnean Society</i> , 0, 100, 866-878.	1.6	17
110	Utilizing a chromosomal-length genome assembly to annotate the Wnt signaling pathway in the Asian citrus psyllid, <i>Diaphorina citri</i> . <i>GigaByte</i> , 0, 2021, 1-15.	0.0	7
111	Annotation of yellow genes in <i>Diaphorina citri</i> , the vector for Huanglongbing disease. <i>GigaByte</i> , 0, 2021, 1-15.	0.0	5
112	Annotation of chitin biosynthesis genes in <i>Diaphorina citri</i> , the Asian citrus psyllid. <i>GigaByte</i> , 0, 2021, 1-12.	0.0	8
113	In silico characterization of chitin deacetylase genes in the <i>Diaphorina citri</i> genome. <i>GigaByte</i> , 0, 2021, 1-11.	0.0	4
114	Annotation of segmentation pathway genes in the Asian citrus psyllid, <i>Diaphorina citri</i> . <i>GigaByte</i> , 0, 2021, 1-13.	0.0	3
115	Genomic identification, annotation, and comparative analysis of Vacuolar-type ATP synthase subunits in <i>Diaphorina citri</i> . <i>GigaByte</i> , 0, 2022, 1-18.	0.0	1
116	Annotation of glycolysis, gluconeogenesis, and trehaloneogenesis pathways provide insight into carbohydrate metabolism in the Asian citrus psyllid. <i>GigaByte</i> , 0, 2022, 1-19.	0.0	2
117	Ubiquitin-proteasome pathway annotation in <i>Diaphorina citri</i> can reveal potential targets for RNAi-based pest management. <i>GigaByte</i> , 0, 2022, 1-10.	0.0	0
118	Manual curation and phylogenetic analysis of chitinase family genes in the Asian citrus psyllid, <i>Diaphorina citri</i> . <i>GigaByte</i> , 0, 2022, 1-17.	0.0	1
119	Annotation of putative circadian rhythm-associated genes in <i>Diaphorina citri</i> (Hemiptera: Liviidae). <i>GigaByte</i> , 0, 2022, 1-15.	0.0	0
120	Annotation of Hox cluster and Hox cofactor genes in the Asian citrus psyllid, <i>Diaphorina citri</i> , reveals novel features. <i>GigaByte</i> , 0, 2022, 1-18.	0.0	1