

# Elizabeth J Duncan

## List of Publications by Year in descending order

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Version: 2024-02-01

50  
papers

2,421  
citations

331259

21  
h-index

223531

46  
g-index

57  
all docs

57  
docs citations

57  
times ranked

3632  
citing authors

#	ARTICLE	IF	CITATIONS
1	Immunity and other defenses in pea aphids, <i>Acyrtosiphon pisum</i> . <i>Genome Biology</i> , 2010, 11, R21.	13.9	389
2	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	3.8	330
3	The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede <i>Strigamia maritima</i> . <i>PLoS Biology</i> , 2014, 12, e1002005.	2.6	221
4	Epigenetics, plasticity, and evolution: How do we link epigenetic change to phenotype?. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2014, 322, 208-220.	0.6	217
5	Unique features of a global human ectoparasite identified through sequencing of the bed bug genome. <i>Nature Communications</i> , 2016, 7, 10165.	5.8	184
6	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. <i>Genome Biology</i> , 2019, 20, 64.	3.8	114
7	Comprehensive survey of developmental genes in the pea aphid, <i>Acyrtosiphon pisum</i> : frequent lineage-specific duplications and losses of developmental genes. <i>Insect Molecular Biology</i> , 2010, 19, 47-62.	1.0	81
8	Biased gene expression in early honeybee larval development. <i>BMC Genomics</i> , 2013, 14, 903.	1.2	80
9	Notch signalling mediates reproductive constraint in the adult worker honeybee. <i>Nature Communications</i> , 2016, 7, 12427.	5.8	67
10	Genome-wide DNA methylation map of human neutrophils reveals widespread inter-individual epigenetic variation. <i>Scientific Reports</i> , 2015, 5, 17328.	1.6	59
11	In-Depth Characterization of Sheep ( <i>Ovis aries</i> ) Milk Whey Proteome and Comparison with Cow ( <i>Bos Tj</i> ETQq1 1 0,784314 rgBT /Overl	1.1	51
12	Canonical terminal patterning is an evolutionary novelty. <i>Developmental Biology</i> , 2013, 377, 245-261.	0.9	48
13	The genome of the water strider <i>Gerris buenoi</i> reveals expansions of gene repertoires associated with adaptations to life on the water. <i>BMC Genomics</i> , 2018, 19, 832.	1.2	47
14	Functional development of the adult ovine mammary gland—insights from gene expression profiling. <i>BMC Genomics</i> , 2015, 16, 748.	1.2	44
15	Clinical Reasoning in Musculoskeletal Practice: Students' Conceptualizations. <i>Physical Therapy</i> , 2009, 89, 430-442.	1.1	38
16	Sex differences in DNA methylation and expression in zebrafish brain: a test of an extended "male sex drive" hypothesis. <i>Gene</i> , 2016, 590, 307-316.	1.0	30
17	Genome Architecture Facilitates Phenotypic Plasticity in the Honeybee ( <i>Apis mellifera</i> ). <i>Molecular Biology and Evolution</i> , 2020, 37, 1964-1978.	3.5	30
18	Analysis of the genome of the New Zealand giant collembolan ( <i>Holacanthella duospinosa</i> ) sheds light on hexapod evolution. <i>BMC Genomics</i> , 2017, 18, 795.	1.2	28

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19	The pea aphid ( <i>Acyrtosiphon pisum</i> ) genome encodes two divergent early developmental programs. <i>Developmental Biology</i> , 2013, 377, 262-274.	0.9	27
20	Phenotypic Plasticity: What Has DNA Methylation Got to Do with It?. <i>Insects</i> , 2022, 13, 110.	1.0	27
21	Stable reference genes for the measurement of transcript abundance during larval caste development in the honeybee. <i>Apidologie</i> , 2013, 44, 357-366.	0.9	25
22	Evolution of a genomic regulatory domain: The role of gene co-option and gene duplication in the Enhancer of split complex. <i>Genome Research</i> , 2010, 20, 917-928.	2.4	22
23	What Do Studies of Insect Polyphenisms Tell Us about Nutritionally-Triggered Epigenomic Changes and Their Consequences?. <i>Nutrients</i> , 2015, 7, 1787-1797.	1.7	21
24	The diversity and distribution of D1 proteins in cyanobacteria. <i>Photosynthesis Research</i> , 2020, 145, 111-128.	1.6	21
25	Evolutionary origin and genomic organisation of runt-domain containing genes in arthropods. <i>BMC Genomics</i> , 2008, 9, 558.	1.2	19
26	High-Quality Assemblies for Three Invasive Social Wasps from the <i>Vespula</i> Genus. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3479-3488.	0.8	19
27	Cloning, mapping and association studies of the ovine ABCG2 gene with facial eczema disease in sheep. <i>Animal Genetics</i> , 2007, 38, 126-131.	0.6	18
28	Sawfly Genomes Reveal Evolutionary Acquisitions That Fostered the Mega-Radiation of Parasitoid and Eusocial Hymenoptera. <i>Genome Biology and Evolution</i> , 2020, 12, 1099-1188.	1.1	17
29	Identification of reference genes for RT-qPCR in ovine mammary tissue during late pregnancy and lactation and in response to maternal nutritional programming. <i>Physiological Genomics</i> , 2014, 46, 560-570.	1.0	12
30	Evolution of the Torso activation cassette, a pathway required for terminal patterning and moulting. <i>Insect Molecular Biology</i> , 2019, 28, 392-408.	1.0	12
31	The Honeybee <i>Apis mellifera</i> . <i>Cold Spring Harbor Protocols</i> , 2009, 2009, pdb.emo123.	0.2	11
32	Gene expression indicates a zone of heterocyst differentiation within the thallus of the cyanolichen <i>Pseudocyphellaria crocata</i> . <i>New Phytologist</i> , 2012, 196, 862-872.	3.5	11
33	Zinc protection of HepG2 cells from sporidesmin toxicity does not require de novo gene transcription. <i>Toxicology Letters</i> , 2005, 159, 164-172.	0.4	10
34	Striatal mRNA expression patterns underlying peak dose l-DOPA-induced dyskinesia in the 6-OHDA hemiparkinsonian rat. <i>Neuroscience</i> , 2016, 324, 238-251.	1.1	10
35	Capturing embryonic development from metamorphosis: how did the terminal patterning signalling pathway of <i>Drosophila</i> evolve?. <i>Current Opinion in Insect Science</i> , 2014, 1, 45-51.	2.2	9
36	Genomic Signatures of Recent Adaptation in a Wild Bumblebee. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9

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37	RNA Interference (RNAi) in Honeybee <i>(Apis mellifera)</i> Embryos: Figure 1.. Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5228.	0.2	8
38	Fixation and Storage of Honeybee ( <i>Apis mellifera</i> ) Tissues. Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5224-pdb.prot5224.	0.2	6
39	Whole-Mount In Situ Hybridization of Honeybee ( <i>Apis mellifera</i> ) Tissues. Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5225-pdb.prot5225.	0.2	6
40	Ancestral hymenopteran queen pheromones do not share the broad phylogenetic repressive effects of honeybee queen mandibular pheromone. <i>Journal of Insect Physiology</i> , 2019, 119, 103968.	0.9	6
41	Mating status and the evolution of eusociality: Oogenesis is independent of mating status in the solitary bee <i>Osmia bicornis</i> . <i>Journal of Insect Physiology</i> , 2020, 121, 104003.	0.9	5
42	Social competition stimulates cognitive performance in a sex-specific manner. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201424.	1.2	4
43	Immunohistochemistry on Honeybee <i>(Apis mellifera)</i> Embryos. Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5227.	0.2	3
44	Simulation of the Radar Cross Section of a Noctuid Moth. <i>Remote Sensing</i> , 2022, 14, 1494.	1.8	3
45	Epigenetics and the Maternal Germline. , 2014, , 27-41.		2
46	In Situ Hybridization of Sectioned Honeybee <i>(Apis mellifera)</i> Tissues: Figure 1.. Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5226.	0.2	1
47	Development of a multiplex microsatellite marker set for the study of the solitary red mason bee, <i>Osmia bicornis</i> (Megachilidae). <i>Molecular Biology Reports</i> , 2021, , 1.	1.0	1
48	Noggin proteins are multifunctional extracellular regulators of cell signalling. <i>Genetics</i> , 2022, , .	1.2	1
49	Evolution and genomic organization of the insect sHSP gene cluster and coordinate regulation in phenotypic plasticity. <i>Bmc Ecology and Evolution</i> , 2021, 21, 154.	0.7	0
50	The development of an unsupervised hierarchical clustering analysis of dual-polarization weather surveillance radar observations to assess nocturnal insect abundance and diversity. <i>Remote Sensing in Ecology and Conservation</i> , 2022, 8, 698-716.	2.2	0