

# Christine Elsik

## List of Publications by Year in descending order

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74  
papers

13,700  
citations

76294

40  
h-index

76872

74  
g-index

78  
all docs

78  
docs citations

78  
times ranked

16308  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 2008, 452, 949-955.	13.7	1,255
3	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	6.0	1,038
4	The Genome of the Sea Urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 2006, 314, 941-952.	6.0	1,018
5	Functional and Evolutionary Insights from the Genomes of Three Parasitoid <i>Nasonia</i> Species. <i>Science</i> , 2010, 327, 343-348.	6.0	808
6	JBrowse: a dynamic web platform for genome visualization and analysis. <i>Genome Biology</i> , 2016, 17, 66.	3.8	690
7	Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12168-12173.	3.3	482
8	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	3.3	380
9	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014, 15, 86.	1.2	375
10	Molecular traces of alternative social organization in a termite genome. <i>Nature Communications</i> , 2014, 5, 3636.	5.8	371
11	The i5K Initiative: Advancing Arthropod Genomics for Knowledge, Human Health, Agriculture, and the Environment. <i>Journal of Heredity</i> , 2013, 104, 595-600.	1.0	358
12	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
13	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	3.8	330
14	Web Apollo: a web-based genomic annotation editing platform. <i>Genome Biology</i> , 2013, 14, R93.	13.9	329
15	Comparative Genomics of Plant Chromosomes. <i>Plant Cell</i> , 2000, 12, 1523-1539.	3.1	301
16	Creating a honey bee consensus gene set. <i>Genome Biology</i> , 2007, 8, R13.	13.9	300
17	Draft genome of the globally widespread and invasive Argentine ant ( <i>Linepithema humile</i> ). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5673-5678.	3.3	257
18	RNA interference knockdown of <i>DNA methyl-transferase 3</i> affects gene alternative splicing in the honey bee. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12750-12755.	3.3	237

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19	MaizeGDB 2018: the maize multi-genome genetics and genomics database. <i>Nucleic Acids Research</i> , 2019, 47, D1146-D1154.	6.5	235
20	The Genome Sequence of the Leaf-Cutter Ant <i>Atta cephalotes</i> Reveals Insights into Its Obligate Symbiotic Lifestyle. <i>PLoS Genetics</i> , 2011, 7, e1002007.	1.5	231
21	Draft genome of the red harvester ant <i>Pogonomyrmex barbatus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5667-5672.	3.3	222
22	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. <i>Genome Research</i> , 2013, 23, 1235-1247.	2.4	205
23	Apollo: Democratizing genome annotation. <i>PLoS Computational Biology</i> , 2019, 15, e1006790.	1.5	179
24	Hymenoptera Genome Database: integrated community resources for insect species of the order Hymenoptera. <i>Nucleic Acids Research</i> , 2011, 39, D658-D662.	6.5	142
25	Patterns of conservation and change in honey bee developmental genes. <i>Genome Research</i> , 2006, 16, 1376-1384.	2.4	139
26	Deep sequencing reveals complex mechanisms of diapause preparation in the invasive mosquito, <i>Aedes albopictus</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20130143.	1.2	134
27	Genomic survey of the ectoparasitic mite <i>Varroa destructor</i> , a major pest of the honey bee <i>Apis mellifera</i> . <i>BMC Genomics</i> , 2010, 11, 602.	1.2	118
28	A de novo transcriptome of the Asian tiger mosquito, <i>Aedes albopictus</i> , to identify candidate transcripts for diapause preparation. <i>BMC Genomics</i> , 2011, 12, 619.	1.2	118
29	Characterization of global loss of imprinting in fetal overgrowth syndrome induced by assisted reproduction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4618-4623.	3.3	114
30	Hymenoptera Genome Database: integrating genome annotations in HymenopteraMine. <i>Nucleic Acids Research</i> , 2016, 44, D793-D800.	6.5	105
31	Bovine Genome Database: new tools for gleaning function from the <i>Bos taurus</i> genome. <i>Nucleic Acids Research</i> , 2016, 44, D834-D839.	6.5	87
32	Low-copy microsatellite markers for <i>Pinus taeda</i> L.. <i>Genome</i> , 2000, 43, 550-555.	0.9	86
33	Computational and transcriptional evidence for microRNAs in the honey bee genome. <i>Genome Biology</i> , 2007, 8, R97.	13.9	82
34	Discovery of candidate genes and pathways in the endometrium regulating ovine blastocyst growth and conceptus elongation. <i>Physiological Genomics</i> , 2009, 39, 85-99.	1.0	76
35	RNA-Seq reveals early distinctions and late convergence of gene expression between diapause and quiescence in the Asian tiger mosquito, <i>Aedes albopictus</i> . <i>Journal of Experimental Biology</i> , 2013, 216, 4082-90.	0.8	68
36	Global assessment of imprinted gene expression in the bovine conceptus by next generation sequencing. <i>Epigenetics</i> , 2016, 11, 501-516.	1.3	65

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37	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	52
38	Unlocking the bovine genome. BMC Genomics, 2009, 10, 193.	1.2	46
39	The pea aphid genome sequence brings theories of insect defense into question. Genome Biology, 2010, 11, 106.	13.9	45
40	Low-copy microsatellite markers for <i>Pinus taeda</i> L. Genome, 2000, 43, 550-555.	0.9	43
41	Community annotation: Procedures, protocols, and supporting tools. Genome Research, 2006, 16, 1329-1333.	2.4	42
42	Low-copy microsatellite recovery from a conifer genome. Theoretical and Applied Genetics, 2001, 103, 1189-1195.	1.8	36
43	Transcriptome analysis of the honey bee fungal pathogen, <i>Ascosphaera apis</i> : implications for host pathogenesis. BMC Genomics, 2012, 13, 285.	1.2	36
44	Retroelements contribute to the excess low-copy-number DNA in pine. Molecular Genetics and Genomics, 2000, 264, 47-55.	2.4	34
45	Global misregulation of genes largely uncoupled to DNA methylome epimutations characterizes a congenital overgrowth syndrome. Scientific Reports, 2017, 7, 12667.	1.6	30
46	A chromosome-level assembly of the cat flea genome uncovers rampant gene duplication and genome size plasticity. BMC Biology, 2020, 18, 70.	1.7	29
47	Families of clustered microsatellites in a conifer genome. Molecular Genetics and Genomics, 2001, 265, 535-542.	1.0	28
48	Bovine Genome Database: integrated tools for genome annotation and discovery. Nucleic Acids Research, 2011, 39, D830-D834.	6.5	27
49	Transcriptome sequencing as a platform to elucidate molecular components of the diapause response in the Asian tiger mosquito <i>Aedes albopictus</i> . Physiological Entomology, 2013, 38, 173-181.	0.6	26
50	Bovine Genome Database: supporting community annotation and analysis of the <i>Bos taurus</i> genome. BMC Genomics, 2010, 11, 645.	1.2	24
51	The Emerging World of Wikis. Science, 2008, 320, 1289-1290.	6.0	23
52	Conserved ortholog sets in forest trees. Tree Genetics and Genomes, 2006, 3, 61-70.	0.6	22
53	Prediction of protein interdomain linker regions by a hidden Markov model. Bioinformatics, 2005, 21, 2264-2270.	1.8	19
54	Analysis of <i>Sus scrofa</i> liver proteome and identification of proteins differentially expressed between genders, and conventional and genetically enhanced lines. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2008, 3, 234-242.	0.4	19

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55	Hymenoptera Genome Database: new genomes and annotation datasets for improved go enrichment and orthologue analyses. <i>Nucleic Acids Research</i> , 2022, 50, D1032-D1039.	6.5	19
56	Microsatellite analysis of <i>Pinus taeda</i> L. in Zimbabwe. <i>Heredity</i> , 2000, 84, 261-268.	1.2	18
57	Bovine Genome Database: new annotation tools for a new reference genome. <i>Nucleic Acids Research</i> , 2019, 48, D676-D681.	6.5	18
58	The genomic basis of evolutionary differentiation among honey bees. <i>Genome Research</i> , 2021, 31, 1203-1215.	2.4	17
59	Leaf-level and whole-plant gas exchange characteristics of shortleaf pine exposed to ozone and simulated acid rain. <i>Tree Physiology</i> , 1994, 14, 361-374.	1.4	16
60	MaizeMine: A Data Mining Warehouse for the Maize Genetics and Genomics Database. <i>Frontiers in Plant Science</i> , 2020, 11, 592730.	1.7	13
61	Hymenoptera Genome Database: Using HymenopteraMine to Enhance Genomic Studies of Hymenopteran Insects. <i>Methods in Molecular Biology</i> , 2018, 1757, 513-556.	0.4	12
62	Differential gene expression in response to eCry3.1Ab ingestion in an unselected and eCry3.1Ab-selected western corn rootworm ( <i>Diabrotica virgifera virgifera</i> LeConte) population. <i>Scientific Reports</i> , 2019, 9, 4896.	1.6	12
63	Nuclear translocation of vitellogenin in the honey bee ( <i>Apis mellifera</i> ). <i>Apidologie</i> , 2022, 53, 13.	0.9	11
64	Manual superscaffolding of honey bee ( <i>Apis mellifera</i> ) chromosomes 12?16: implications for the draft genome assembly version 4, gene annotation, and chromosome structure. <i>Insect Molecular Biology</i> , 2007, 16, 401-410.	1.0	10
65	Low-copy microsatellite markers for <i>Pinus taeda</i> L. <i>Genome</i> , 2000, 43, 550-5.	0.9	10
66	Multi-tiered analyses of honey bees that resist or succumb to parasitic mites and viruses. <i>BMC Genomics</i> , 2021, 22, 720.	1.2	8
67	Development and Application of Bovine and Porcine Oligonucleotide Arrays with Protein-Based Annotation. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-11.	3.0	7
68	Detection of alternative splicing in western corn rootworm ( <i>Diabrotica virgifera</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td (<sc>RNA-seq and <sc>PacBio Iso-seq). <i>Insect Molecular Biology</i> , 2021, 30, 436-445.	1.0	6
69	Identification of large offspring syndrome during pregnancy through ultrasonography and maternal blood transcriptome analyses. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
70	Bovine Genome Database: Tools for Mining the <i>Bos taurus</i> Genome. <i>Methods in Molecular Biology</i> , 2018, 1757, 211-249.	0.4	5
71	Identification of REST targets in the <i>Xenopus tropicalis</i> genome. <i>BMC Genomics</i> , 2015, 16, 380.	1.2	4
72	A scientific note defining allelic nomenclature standards for the highly diverse complementary sex-determiner ( <i>csd</i> ) locus in honey bees. <i>Apidologie</i> , 2021, 52, 749-754.	0.9	4

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73	Prediction of Protein Interdomain Linker Regions by a Nonstationary Hidden Markov Model. Journal of the American Statistical Association, 2008, 103, 1085-1099.	1.8	3
74	Using online tools at the Bovine Genome Database to manually annotate genes in the new reference genome. Animal Genetics, 2020, 51, 675-682.	0.6	2