

Christine Elsik

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/4430123/christine-elsik-publications-by-year.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

73
papers

10,537
citations

37
h-index

78
g-index

78
ext. papers

12,571
ext. citations

10.6
avg, IF

6.14
L-index

#	Paper	IF	Citations
73	Nuclear translocation of vitellogenin in the honey bee (<i>Apis mellifera</i>). <i>Apidologie</i> , 2022 , 53, 13	2.3	0
72	Hymenoptera Genome Database: new genomes and annotation datasets for improved go enrichment and orthologue analyses. <i>Nucleic Acids Research</i> , 2021 ,	20.1	3
71	Multi-tiered analyses of honey bees that resist or succumb to parasitic mites and viruses. <i>BMC Genomics</i> , 2021 , 22, 720	4.5	2
70	The genomic basis of evolutionary differentiation among honey bees. <i>Genome Research</i> , 2021 ,	9.7	1
69	Detection of alternative splicing in western corn rootworm (<i>Diabrotica virgifera virgifera</i> LeConte) in association with eCry3.1Ab resistance using RNA-seq and PacBio Iso-Seq. <i>Insect Molecular Biology</i> , 2021 , 30, 436-445	3.4	1
68	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	2.3	2
67	Using online tools at the Bovine Genome Database to manually annotate genes in the new reference genome. <i>Animal Genetics</i> , 2020 , 51, 675-682	2.5	1
66	A chromosome-level assembly of the cat flea genome uncovers rampant gene duplication and genome size plasticity. <i>BMC Biology</i> , 2020 , 18, 70	7.3	16
65	Bovine Genome Database: new annotation tools for a new reference genome. <i>Nucleic Acids Research</i> , 2020 , 48, D676-D681	20.1	12
64	MaizeMine: A Data Mining Warehouse for the Maize Genetics and Genomics Database. <i>Frontiers in Plant Science</i> , 2020 , 11, 592730	6.2	3
63	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020 , 9,	7.6	140
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	4.9	7
61	Apollo: Democratizing genome annotation. <i>PLoS Computational Biology</i> , 2019 , 15, e1006790	5	90
60	MaizeGDB 2018: the maize multi-genome genetics and genomics database. <i>Nucleic Acids Research</i> , 2019 , 47, D1146-D1154	20.1	121
59	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	28
58	Bovine Genome Database: Tools for Mining the <i>Bos taurus</i> Genome. <i>Methods in Molecular Biology</i> , 2018 , 1757, 211-249	1.4	4
57	Hymenoptera Genome Database: Using HymenopteraMine to Enhance Genomic Studies of Hymenopteran Insects. <i>Methods in Molecular Biology</i> , 2018 , 1757, 513-556	1.4	6

56	Global misregulation of genes largely uncoupled to DNA methylome epimutations characterizes a congenital overgrowth syndrome. <i>Scientific Reports</i> , 2017 , 7, 12667	4.9	15
55	Global assessment of imprinted gene expression in the bovine conceptus by next generation sequencing. <i>Epigenetics</i> , 2016 , 11, 501-16	5.7	36
54	Hymenoptera Genome Database: integrating genome annotations in HymenopteraMine. <i>Nucleic Acids Research</i> , 2016 , 44, D793-800	20.1	80
53	Bovine Genome Database: new tools for gleaning function from the <i>Bos taurus</i> genome. <i>Nucleic Acids Research</i> , 2016 , 44, D834-9	20.1	69
52	JBrowse: a dynamic web platform for genome visualization and analysis. <i>Genome Biology</i> , 2016 , 17, 66	18.3	393
51	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015 , 16, 76	18.3	229
50	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015 , 16, 57	18.3	196
49	Identification of REST targets in the <i>Xenopus tropicalis</i> genome. <i>BMC Genomics</i> , 2015 , 16, 380	4.5	4
48	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, 4618-23	11.5	71
47	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014 , 15, 86	4.5	284
46	Molecular traces of alternative social organization in a termite genome. <i>Nature Communications</i> , 2014 , 5, 3636	17.4	250
45	Web Apollo: a web-based genomic annotation editing platform. <i>Genome Biology</i> , 2013 , 14, R93	18.3	237
44	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. <i>Genome Research</i> , 2013 , 23, 1235-47	9.7	166
43	The i5K Initiative: advancing arthropod genomics for knowledge, human health, agriculture, and the environment. <i>Journal of Heredity</i> , 2013 , 104, 595-600	2.4	253
42	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	4.4	102
41	Transcriptome sequencing as a platform to elucidate molecular components of the diapause response in the Asian tiger mosquito, <i>Physiological Entomology</i> , 2013 , 38, 173-181	1.9	21
40	RNA interference knockdown of DNA methyl-transferase 3 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, 12750-5	11.5	178
39	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	3	55

38	Transcriptome analysis of the honey bee fungal pathogen, <i>Ascosphaera apis</i> : implications for host pathogenesis. <i>BMC Genomics</i> , 2012 , 13, 285	4.5	25
37	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	4.5	88
36	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, 5673-8	11.5	214
35	Bovine Genome Database: integrated tools for genome annotation and discovery. <i>Nucleic Acids Research</i> , 2011 , 39, D830-4	20.1	24
34	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, 5667-72	11.5	200
33	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	6	191
32	Hymenoptera Genome Database: integrated community resources for insect species of the order Hymenoptera. <i>Nucleic Acids Research</i> , 2011 , 39, D658-62	20.1	130
31	Development and application of bovine and porcine oligonucleotide arrays with protein-based annotation. <i>Journal of Biomedicine and Biotechnology</i> , 2010 , 2010, 453638		7
30	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, 12168-73	11.5	383
29	Functional and evolutionary insights from the genomes of three parasitoid <i>Nasonia</i> species. <i>Science</i> , 2010 , 327, 343-8	33.3	682
28	The pea aphid genome sequence brings theories of insect defense into question. <i>Genome Biology</i> , 2010 , 11, 106	18.3	26
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	4.5	99
26	Bovine Genome Database: supporting community annotation and analysis of the <i>Bos taurus</i> genome. <i>BMC Genomics</i> , 2010 , 11, 645	4.5	21
25	Discovery of candidate genes and pathways in the endometrium regulating ovine blastocyst growth and conceptus elongation. <i>Physiological Genomics</i> , 2009 , 39, 85-99	3.6	66
24	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , 2009 , 324, 522-8	33.3	863
23	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 2008 , 452, 949-55	50.4	1043
22	Analysis of <i>Sus scrofa</i> liver proteome and identification of proteins differentially expressed between genders, and conventional and genetically enhanced lines. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2008 , 3, 234-42	2	17
21	The emerging world of wikis. <i>Science</i> , 2008 , 320, 1289-90	33.3	21

20	Prediction of Protein Interdomain Linker Regions by a Nonstationary Hidden Markov Model. <i>Journal of the American Statistical Association</i> , 2008 , 103, 1085-1099	2.8	1
19	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, 401-10	3.4	10
18	Computational and transcriptional evidence for microRNAs in the honey bee genome. <i>Genome Biology</i> , 2007 , 8, R97	18.3	74
17	Creating a honey bee consensus gene set. <i>Genome Biology</i> , 2007 , 8, R13	18.3	266
16	Community annotation: procedures, protocols, and supporting tools. <i>Genome Research</i> , 2006 , 16, 1329-337	3.7	39
15	Patterns of conservation and change in honey bee developmental genes. <i>Genome Research</i> , 2006 , 16, 1376-84	9.7	108
14	The genome of the sea urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 2006 , 314, 941-52	33.3	886
13	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006 , 443, 931-49	50.4	1414
12	Conserved ortholog sets in forest trees. <i>Tree Genetics and Genomes</i> , 2006 , 3, 61-70	2.1	18
11	Prediction of protein interdomain linker regions by a hidden Markov model. <i>Bioinformatics</i> , 2005 , 21, 2264-70	7.2	15
10	Low-copy microsatellite recovery from a conifer genome. <i>Theoretical and Applied Genetics</i> , 2001 , 103, 1189-1195	6	30
9	Families of clustered microsatellites in a conifer genome. <i>Molecular Genetics and Genomics</i> , 2001 , 265, 535-42	3.1	22
8	Microsatellite analysis of <i>Pinus taeda</i> L. in Zimbabwe. <i>Heredity</i> , 2000 , 84 (Pt 2), 261-8	3.6	18
7	Retroelements contribute to the excess low-copy-number DNA in pine. <i>Molecular Genetics and Genomics</i> , 2000 , 264, 47-55		27
6	Comparative genomics of plant chromosomes. <i>Plant Cell</i> , 2000 , 12, 1523-40	11.6	269
5	Low-copy microsatellite markers for <i>Pinus taeda</i> L.. <i>Genome</i> , 2000 , 43, 550-555	2.4	74
4	Low-copy microsatellite markers for <i>Pinus taeda</i> L.. <i>Genome</i> , 2000 , 43, 550-555	2.4	25
3	Low-copy microsatellite markers for <i>Pinus taeda</i> L. <i>Genome</i> , 2000 , 43, 550-5	2.4	9

2	Leaf-level and whole-plant gas exchange characteristics of shortleaf pine exposed to ozone and simulated acid rain. <i>Tree Physiology</i> , 1994 , 14, 361-74	4.2	15
1	Detection of alternative splicing in <i>Diabrotica virgifera virgifera</i> LeConte, in association with Bt resistance using RNA-seq and PacBio Iso-Seq		1