

Christine Elsik

List of Publications by Citations

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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	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006 , 443, 931-49	50.4	1414
72	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 2008 , 452, 949-55	50.4	1043
71	The genome of the sea urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 2006 , 314, 941-52	33.3	886
70	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , 2009 , 324, 522-8	33.3	863
69	Functional and evolutionary insights from the genomes of three parasitoid <i>Nasonia</i> species. <i>Science</i> , 2010 , 327, 343-8	33.3	682
68	JBrowse: a dynamic web platform for genome visualization and analysis. <i>Genome Biology</i> , 2016 , 17, 66	18.3	393
67	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
66	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014 , 15, 86	4.5	284
65	Comparative genomics of plant chromosomes. <i>Plant Cell</i> , 2000 , 12, 1523-40	11.6	269
64	Creating a honey bee consensus gene set. <i>Genome Biology</i> , 2007 , 8, R13	18.3	266
63	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
62	Molecular traces of alternative social organization in a termite genome. <i>Nature Communications</i> , 2014 , 5, 3636	17.4	250
61	Web Apollo: a web-based genomic annotation editing platform. <i>Genome Biology</i> , 2013 , 14, R93	18.3	237
60	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015 , 16, 76	18.3	229
59	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
58	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
57	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

56	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
55	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
54	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
53	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020 , 9,	7.6	140
52	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
51	MaizeGDB 2018: the maize multi-genome genetics and genomics database. <i>Nucleic Acids Research</i> , 2019 , 47, D1146-D1154	20.1	121
50	Patterns of conservation and change in honey bee developmental genes. <i>Genome Research</i> , 2006 , 16, 1376-84	9.7	108
49	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
48	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
47	Apollo: Democratizing genome annotation. <i>PLoS Computational Biology</i> , 2019 , 15, e1006790	5	90
46	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
45	Hymenoptera Genome Database: integrating genome annotations in HymenopteraMine. <i>Nucleic Acids Research</i> , 2016 , 44, D793-800	20.1	80
44	Computational and transcriptional evidence for microRNAs in the honey bee genome. <i>Genome Biology</i> , 2007 , 8, R97	18.3	74
43	Low-copy microsatellite markers for <i>Pinus taeda</i> L.. <i>Genome</i> , 2000 , 43, 550-555	2.4	74
42	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
41	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
40	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
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	Community annotation: procedures, protocols, and supporting tools. <i>Genome Research</i> , 2006 , 16, 1329-337	33.7	39
37	Global assessment of imprinted gene expression in the bovine conceptus by next generation sequencing. <i>Epigenetics</i> , 2016 , 11, 501-16	5.7	36
36	Low-copy microsatellite recovery from a conifer genome. <i>Theoretical and Applied Genetics</i> , 2001 , 103, 1189-1195	6	30
35	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
34	Retroelements contribute to the excess low-copy-number DNA in pine. <i>Molecular Genetics and Genomics</i> , 2000 , 264, 47-55		27
33	The pea aphid genome sequence brings theories of insect defense into question. <i>Genome Biology</i> , 2010 , 11, 106	18.3	26
32	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
31	Low-copy microsatellite markers for <i>Pinus taeda</i> L.. <i>Genome</i> , 2000 , 43, 550-555	2.4	25
30	Bovine Genome Database: integrated tools for genome annotation and discovery. <i>Nucleic Acids Research</i> , 2011 , 39, D830-4	20.1	24
29	Families of clustered microsatellites in a conifer genome. <i>Molecular Genetics and Genomics</i> , 2001 , 265, 535-42	3.1	22
28	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
27	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
26	The emerging world of wikis. <i>Science</i> , 2008 , 320, 1289-90	33.3	21
25	Conserved ortholog sets in forest trees. <i>Tree Genetics and Genomes</i> , 2006 , 3, 61-70	2.1	18
24	Microsatellite analysis of <i>Pinus taeda</i> L. in Zimbabwe. <i>Heredity</i> , 2000 , 84 (Pt 2), 261-8	3.6	18
23	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
22	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
21	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

20	Prediction of protein interdomain linker regions by a hidden Markov model. <i>Bioinformatics</i> , 2005 , 21, 2264-70	7.2	15
19	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
18	Bovine Genome Database: new annotation tools for a new reference genome. <i>Nucleic Acids Research</i> , 2020 , 48, D676-D681	20.1	12
17	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
16	Low-copy microsatellite markers for <i>Pinus taeda</i> L. <i>Genome</i> , 2000 , 43, 550-5	2.4	9
15	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
14	Development and application of bovine and porcine oligonucleotide arrays with protein-based annotation. <i>Journal of Biomedicine and Biotechnology</i> , 2010 , 2010, 453638		7
13	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
12	Identification of REST targets in the <i>Xenopus tropicalis</i> genome. <i>BMC Genomics</i> , 2015 , 16, 380	4.5	4
11	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
10	Hymenoptera Genome Database: new genomes and annotation datasets for improved go enrichment and orthologue analyses. <i>Nucleic Acids Research</i> , 2021 ,	20.1	3
9	MaizeMine: A Data Mining Warehouse for the Maize Genetics and Genomics Database. <i>Frontiers in Plant Science</i> , 2020 , 11, 592730	6.2	3
8	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
7	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
6	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
5	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
4	Detection of alternative splicing in <i>Diabrotica virgifera virgifera</i> LeConte, in association with Bt resistance using RNA-seq and PacBio Iso-Seq		1
3	The genomic basis of evolutionary differentiation among honey bees. <i>Genome Research</i> , 2021 ,	9.7	1

2	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
1	Nuclear translocation of vitellogenin in the honey bee (<i>Apis mellifera</i>).. <i>Apidologie</i> , 2022 , 53, 13	2,3	0