Daniel Lawson

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1324554/publications.pdf

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43 papers

14,710 citations

34 h-index 243625 44 g-index

47 all docs

47 docs citations

47 times ranked

20121 citing authors

#	Article	IF	CITATIONS
1	Genome Sequence of the Nematode <i>C. elegans</i> : A Platform for Investigating Biology. Science, 1998, 282, 2012-2018.	12.6	3,681
2	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. Nature, 2012, 487, 94-98.	27.8	1,086
3	Genome Sequence of Aedes aegypti, a Major Arbovirus Vector. Science, 2007, 316, 1718-1723.	12.6	1,025
4	The BioMart community portal: an innovative alternative to large, centralized data repositories. Nucleic Acids Research, 2015, 43, W589-W598.	14.5	682
5	WormBase: a multi-species resource for nematode biology and genomics. Nucleic Acids Research, 2004, 32, 411D-417.	14.5	610
6	VectorBase: an updated bioinformatics resource for invertebrate vectors and other organisms related with human diseases. Nucleic Acids Research, 2015, 43, D707-D713.	14.5	556
7	Ensembl Genomes 2016: more genomes, more complexity. Nucleic Acids Research, 2016, 44, D574-D580.	14.5	530
8	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. Science, 2015, 347, 1258522.	12.6	492
9	Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12168-12173.	7.1	482
10	Genomic insights into the Ixodes scapularis tick vector of Lyme disease. Nature Communications, 2016, 7, 10507.	12.8	450
11	Sequencing of <i>Culex quinquefasciatus</i> Establishes a Platform for Mosquito Comparative Genomics. Science, 2010, 330, 86-88.	12.6	424
12	The i5K Initiative: Advancing Arthropod Genomics for Knowledge, Human Health, Agriculture, and the Environment. Journal of Heredity, 2013, 104, 595-600.	2.4	358
13	A global analysis of Caenorhabditis elegans operons. Nature, 2002, 417, 851-854.	27.8	329
14	Genome of <i>Rhodnius prolixus</i> , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14936-14941.	7.1	329
15	The complete nucleotide sequence of chromosome 3 of Plasmodium falciparum. Nature, 1999, 400, 532-538.	27.8	312
16	VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. Nucleic Acids Research, 2022, 50, D898-D911.	14.5	277
17	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. Science, 2014, 344, 380-386.	12.6	254
18	Ensembl's 10th year. Nucleic Acids Research, 2010, 38, D557-D562.	14.5	251

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19	Widespread Divergence Between Incipient <i>Anopheles gambiae</i> Species Revealed by Whole Genome Sequences. Science, 2010, 330, 512-514.	12.6	250
20	VectorBase: a data resource for invertebrate vector genomics. Nucleic Acids Research, 2009, 37, D583-D587.	14.5	234
21	Ensembl Genomes 2013: scaling up access to genome-wide data. Nucleic Acids Research, 2014, 42, D546-D552.	14.5	205
22	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. Nature Communications, 2014, 5, 4737.	12.8	196
23	Creating a Buzz About Insect Genomes. Science, 2011, 331, 1386-1386.	12.6	185
24	Ensembl Genomes: an integrative resource for genome-scale data from non-vertebrate species. Nucleic Acids Research, 2012, 40, D91-D97.	14.5	179
25	Evolutionary superscaffolding and chromosome anchoring to improve Anopheles genome assemblies. BMC Biology, 2020, 18, 1.	3.8	177
26	Sequence of Plasmodium falciparum chromosomes 1, 3–9 and 13. Nature, 2002, 419, 527-531.	27.8	156
27	WormBase: a comprehensive data resource for Caenorhabditis biology and genomics. Nucleic Acids Research, 2004, 33, D383-D389.	14.5	155
28	BioMart Central Portal: an open database network for the biological community. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar041-bar041.	3.0	145
29	VectorBase: improvements to a bioinformatics resource for invertebrate vector genomics. Nucleic Acids Research, 2012, 40, D729-D734.	14.5	143
30	WormBase: a cross-species database for comparative genomics. Nucleic Acids Research, 2003, 31, 133-137.	14.5	107
31	VectorBase: a home for invertebrate vectors of human pathogens. Nucleic Acids Research, 2007, 35, D503-D505.	14.5	107
32	Comparative genomic analysis of six Glossina genomes, vectors of African trypanosomes. Genome Biology, 2019, 20, 187.	8.8	71
33	The Evolution of the <i>Anopheles</i> 16 Genomes Project. G3: Genes, Genomes, Genetics, 2013, 3, 1191-1194.	1.8	49
34	Studying Culicoides vectors of BTV in the post-genomic era: Resources, bottlenecks to progress and future directions. Virus Research, 2014, 182, 43-49.	2.2	49
35	A draft genome sequence of an invasive mosquito: an Italian <i>Aedes albopictus</i> . Pathogens and Global Health, 2015, 109, 207-220.	2.3	35
36	Gene discovery in Plasmodium chabaudi by genome survey sequencing. Molecular and Biochemical Parasitology, 2001, 113, 251-260.	1.1	25

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37	MIReAD, a minimum information standard for reporting arthropod abundance data. Scientific Data, 2019, 6, 40.	5.3	20
38	WormBase as an Integrated Platform for the C. elegans ORFeome. Genome Research, 2004, 14, 2155-2161.	5 . 5	19
39	The genome of the stable fly, Stomoxys calcitrans, reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. BMC Biology, 2021, 19, 41.	3.8	19
40	Genomic resources for invertebrate vectors of human pathogens, and the role of VectorBase. Infection, Genetics and Evolution, 2009, 9, 308-313.	2.3	14
41	RNA-Rocket: an RNA-Seq analysis resource for infectious disease research. Bioinformatics, 2015, 31, 1496-1498.	4.1	11
42	How can ontologies help vector biology?. Trends in Parasitology, 2008, 24, 249-252.	3.3	9
43	Transcriptional variation of sensory-related genes in natural populations of Aedes albopictus. BMC Genomics, 2020, 21, 547.	2.8	6