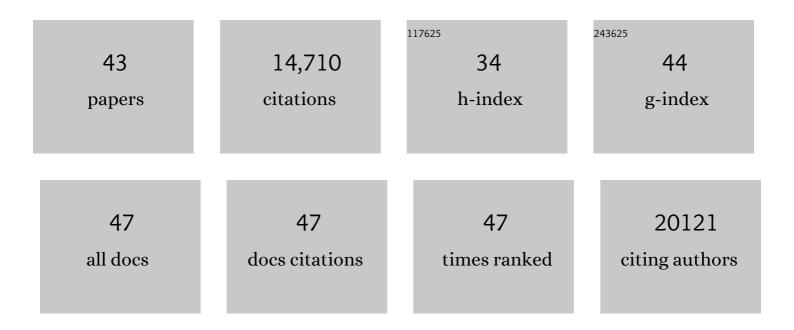
## Daniel Lawson

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1324554/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. Nucleic Acids Research, 2022, 50, D898-D911.	14.5	277
2	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
3	Evolutionary superscaffolding and chromosome anchoring to improve Anopheles genome assemblies. BMC Biology, 2020, 18, 1.	3.8	177
4	Transcriptional variation of sensory-related genes in natural populations of Aedes albopictus. BMC Genomics, 2020, 21, 547.	2.8	6
5	Comparative genomic analysis of six Glossina genomes, vectors of African trypanosomes. Genome Biology, 2019, 20, 187.	8.8	71
6	MIReAD, a minimum information standard for reporting arthropod abundance data. Scientific Data, 2019, 6, 40.	5.3	20
7	Ensembl Genomes 2016: more genomes, more complexity. Nucleic Acids Research, 2016, 44, D574-D580.	14.5	530
8	Genomic insights into the Ixodes scapularis tick vector of Lyme disease. Nature Communications, 2016, 7, 10507.	12.8	450
9	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
10	The BioMart community portal: an innovative alternative to large, centralized data repositories. Nucleic Acids Research, 2015, 43, W589-W598.	14.5	682
11	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
12	RNA-Rocket: an RNA-Seq analysis resource for infectious disease research. Bioinformatics, 2015, 31, 1496-1498.	4.1	11
13	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
14	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. Science, 2015, 347, 1258522.	12.6	492
15	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. Nature Communications, 2014, 5, 4737.	12.8	196
16	Genome Sequence of the Tsetse Fly ( <i>Glossina morsitans</i> ): Vector of African Trypanosomiasis. Science, 2014, 344, 380-386.	12.6	254
17	Ensembl Genomes 2013: scaling up access to genome-wide data. Nucleic Acids Research, 2014, 42, D546-D552.	14.5	205
18	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

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19	The i5K Initiative: Advancing Arthropod Genomics for Knowledge, Human Health, Agriculture, and the Environment. Journal of Heredity, 2013, 104, 595-600.	2.4	358
20	The Evolution of the <i>Anopheles</i> 16 Genomes Project. G3: Genes, Genomes, Genetics, 2013, 3, 1191-1194.	1.8	49
21	VectorBase: improvements to a bioinformatics resource for invertebrate vector genomics. Nucleic Acids Research, 2012, 40, D729-D734.	14.5	143
22	Ensembl Genomes: an integrative resource for genome-scale data from non-vertebrate species. Nucleic Acids Research, 2012, 40, D91-D97.	14.5	179
23	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. Nature, 2012, 487, 94-98.	27.8	1,086
24	Creating a Buzz About Insect Genomes. Science, 2011, 331, 1386-1386.	12.6	185
25	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
26	Sequencing of <i>Culex quinquefasciatus</i> Establishes a Platform for Mosquito Comparative Genomics. Science, 2010, 330, 86-88.	12.6	424
27	Ensembl's 10th year. Nucleic Acids Research, 2010, 38, D557-D562.	14.5	251
28	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
29	Widespread Divergence Between Incipient <i>Anopheles gambiae</i> Species Revealed by Whole Genome Sequences. Science, 2010, 330, 512-514.	12.6	250
30	VectorBase: a data resource for invertebrate vector genomics. Nucleic Acids Research, 2009, 37, D583-D587.	14.5	234
31	Genomic resources for invertebrate vectors of human pathogens, and the role of VectorBase. Infection, Genetics and Evolution, 2009, 9, 308-313.	2.3	14
32	How can ontologies help vector biology?. Trends in Parasitology, 2008, 24, 249-252.	3.3	9
33	VectorBase: a home for invertebrate vectors of human pathogens. Nucleic Acids Research, 2007, 35, D503-D505.	14.5	107
34	Genome Sequence of Aedes aegypti, a Major Arbovirus Vector. Science, 2007, 316, 1718-1723.	12.6	1,025
35	WormBase: a comprehensive data resource for Caenorhabditis biology and genomics. Nucleic Acids Research, 2004, 33, D383-D389.	14.5	155
36	WormBase as an Integrated Platform for the C. elegans ORFeome. Genome Research, 2004, 14, 2155-2161.	5.5	19

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37	WormBase: a multi-species resource for nematode biology and genomics. Nucleic Acids Research, 2004, 32, 411D-417.	14.5	610
38	WormBase: a cross-species database for comparative genomics. Nucleic Acids Research, 2003, 31, 133-137.	14.5	107
39	A global analysis of Caenorhabditis elegans operons. Nature, 2002, 417, 851-854.	27.8	329
40	Sequence of Plasmodium falciparum chromosomes 1, $3\hat{a}\in$ 9 and 13. Nature, 2002, 419, 527-531.	27.8	156
41	Gene discovery in Plasmodium chabaudi by genome survey sequencing. Molecular and Biochemical Parasitology, 2001, 113, 251-260.	1.1	25
42	The complete nucleotide sequence of chromosome 3 of Plasmodium falciparum. Nature, 1999, 400, 532-538.	27.8	312
43	Genome Sequence of the Nematode <i>C. elegans</i> : A Platform for Investigating Biology. Science, 1998, 282, 2012-2018.	12.6	3,681