

Casey M Bergman

List of Publications by Year in descending order

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73
papers

10,981
citations

81900

39
h-index

79698

73
g-index

87
all docs

87
docs citations

87
times ranked

12686
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
2	The <i>Drosophila melanogaster</i> Genetic Reference Panel. <i>Nature</i> , 2012, 482, 173-178.	27.8	1,756
3	Population genomics of domestic and wild yeasts. <i>Nature</i> , 2009, 458, 337-341.	27.8	1,391
4	Evidence for stabilizing selection in a eukaryotic enhancer element. <i>Nature</i> , 2000, 403, 564-567.	27.8	553
5	The transposable elements of the <i>Drosophila melanogaster</i> euchromatin: a genomics perspective. <i>Genome Biology</i> , 2002, 3, RESEARCH0084.	9.6	467
6	Gene expression divergence recapitulates the developmental hourglass model. <i>Nature</i> , 2010, 468, 811-814.	27.8	364
7	Combined Evidence Annotation of Transposable Elements in Genome Sequences. <i>PLoS Computational Biology</i> , 2005, 1, e22.	3.2	347
8	LINNAEUS: A species name identification system for biomedical literature. <i>BMC Bioinformatics</i> , 2010, 11, 85.	2.6	232
9	ORegAnno: an open-access community-driven resource for regulatory annotation. <i>Nucleic Acids Research</i> , 2007, 36, D107-D113.	14.5	227
10	Discovering and detecting transposable elements in genome sequences. <i>Briefings in Bioinformatics</i> , 2007, 8, 382-392.	6.5	189
11	Recurrent insertion and duplication generate networks of transposable element sequences in the <i>Drosophila melanogaster</i> genome. <i>Genome Biology</i> , 2006, 7, R112.	9.6	188
12	Functional Evolution of a cis-Regulatory Module. <i>PLoS Biology</i> , 2005, 3, e93.	5.6	184
13	Population Genomics of the <i>Wolbachia</i> Endosymbiont in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2012, 8, e1003129.	3.5	178
14	Principles of Genome Evolution in the <i>Drosophila melanogaster</i> Species Group. <i>PLoS Biology</i> , 2007, 5, e152.	5.6	164
15	<i>Drosophila</i> DNase I footprint database: a systematic genome annotation of transcription factor binding sites in the fruitfly, <i>Drosophila melanogaster</i> . <i>Bioinformatics</i> , 2005, 21, 1747-1749.	4.1	155
16	REDfly v3.0: toward a comprehensive database of transcriptional regulatory elements in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2011, 39, D118-D123.	14.5	152
17	Analysis of Conserved Noncoding DNA in <i>Drosophila</i> Reveals Similar Constraints in Intergenic and Intronic Sequences. <i>Genome Research</i> , 2001, 11, 1335-1345.	5.5	146
18	<i>Drosophila</i> innate immunity: regional and functional specialization of prophenoloxidasases. <i>BMC Biology</i> , 2015, 13, 81.	3.8	146

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19	Long-read, whole-genome shotgun sequence data for five model organisms. <i>Scientific Data</i> , 2014, 1, 140045.	5.3	138
20	Assessing the impact of comparative genomic sequence data on the functional annotation of the <i>Drosophila</i> genome. <i>Genome Biology</i> , 2002, 3, research0086.1.	9.6	120
21	Unique transposon landscapes are pervasive across <i>Drosophila melanogaster</i> genomes. <i>Nucleic Acids Research</i> , 2015, 43, 10655-10672.	14.5	114
22	Whole Genome Resequencing Reveals Natural Target Site Preferences of Transposable Elements in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2012, 7, e30008.	2.5	114
23	Benchmarking tools for the alignment of functional noncoding DNA. <i>BMC Bioinformatics</i> , 2004, 5, 6.	2.6	99
24	Recent LTR retrotransposon insertion contrasts with waves of non-LTR insertion since speciation in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11340-11345.	7.1	93
25	Evolutionary Genomics of Transposable Elements in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2012, 7, e50978.	2.5	91
26	REDfly 2.0: an integrated database of cis-regulatory modules and transcription factor binding sites in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2007, 36, D594-D598.	14.5	86
27	McClintock: An Integrated Pipeline for Detecting Transposable Element Insertions in Whole-Genome Shotgun Sequencing Data. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2763-2778.	1.8	81
28	Tracing the Evolutionary History of <i>Drosophila</i> Regulatory Regions with Models that Identify Transcription Factor Binding Sites. <i>Molecular Biology and Evolution</i> , 2003, 20, 703-714.	8.9	75
29	Text mining for biology - the way forward: opinions from leading scientists. <i>Genome Biology</i> , 2008, 9, S7.	9.6	74
30	<i>Drosophila melanogaster</i> : A case study of a model genomic sequence and its consequences. <i>Genome Research</i> , 2005, 15, 1661-1667.	5.5	69
31	Large-Scale Discovery of Promoter Motifs in <i>Drosophila melanogaster</i> . <i>PLoS Computational Biology</i> , 2007, 3, e7.	3.2	64
32	Purifying Selection Maintains Highly Conserved Noncoding Sequences in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2007, 24, 2222-2234.	8.9	63
33	The GNAT library for local and remote gene mention normalization. <i>Bioinformatics</i> , 2011, 27, 2769-2771.	4.1	63
34	An Age-of-Allele Test of Neutrality for Transposable Element Insertions. <i>Genetics</i> , 2014, 196, 523-538.	2.9	63
35	Population Genomic Inferences from Sparse High-Throughput Sequencing of Two Populations of <i>Drosophila melanogaster</i> . <i>Genome Biology and Evolution</i> , 2009, 1, 449-465.	2.5	60
36	Evolutionary Systems Biology of Amino Acid Biosynthetic Cost in Yeast. <i>PLoS ONE</i> , 2010, 5, e11935.	2.5	57

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37	Dynamics of <i>Wolbachia pipientis</i> Gene Expression Across the <i>Drosophila melanogaster</i> Life Cycle. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2843-2856.	1.8	55
38	Paucity of chimeric gene-transposable element transcripts in the <i>Drosophila melanogaster</i> genome. <i>BMC Biology</i> , 2005, 3, 24.	3.8	54
39	BioContext: an integrated text mining system for large-scale extraction and contextualization of biomolecular events. <i>Bioinformatics</i> , 2012, 28, 2154-2161.	4.1	45
40	Whole genome screen reveals a novel relationship between <i>Wolbachia</i> levels and <i>Drosophila</i> host translation. <i>PLoS Pathogens</i> , 2018, 14, e1007445.	4.7	42
41	The Evolution of tRNA Genes in <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2010, 2, 467-477.	2.5	40
42	Trapping a somatic endogenous retrovirus into a germline piRNA cluster immunizes the germline against further invasion. <i>Genome Biology</i> , 2019, 20, 127.	8.8	40
43	Testing the palindromic target site model for DNA transposon insertion using the <i>Drosophila melanogaster</i> P-element. <i>Nucleic Acids Research</i> , 2008, 36, 6199-6208.	14.5	36
44	Text-mining assisted regulatory annotation. <i>Genome Biology</i> , 2008, 9, R31.	9.6	34
45	Identifying cis-regulatory modules by combining comparative and compositional analysis of DNA. <i>Bioinformatics</i> , 2006, 22, 2858-2864.	4.1	33
46	pubmed2ensembl: A Resource for Mining the Biological Literature on Genes. <i>PLoS ONE</i> , 2011, 6, e24716.	2.5	33
47	Rare recombination events generate sequence diversity among balancer chromosomes in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1352-61.	7.1	30
48	Evolution of Ty1 copy number control in yeast by horizontal transfer and recombination. <i>PLoS Genetics</i> , 2020, 16, e1008632.	3.5	30
49	Annotating genes and genomes with DNA sequences extracted from biomedical articles. <i>Bioinformatics</i> , 2011, 27, 980-986.	4.1	23
50	Haplotype-resolved genome assembly enables gene discovery in the red palm weevil <i>Rhynchophorus ferrugineus</i> . <i>Scientific Reports</i> , 2021, 11, 9987.	3.3	20
51	A Large Palindrome With Interchromosomal Gene Duplications in the Pericentromeric Region of the <i>D. melanogaster</i> Y Chromosome. <i>Molecular Biology and Evolution</i> , 2011, 28, 1967-1971.	8.9	19
52	Horizontal transfer and proliferation of Tsu4 in <i>Saccharomyces paradoxus</i> . <i>Mobile DNA</i> , 2018, 9, 18.	3.6	18
53	Genomic analysis of P elements in natural populations of <i>Drosophila melanogaster</i> . <i>PeerJ</i> , 2017, 5, e3824.	2.0	18
54	Embryonic enhancers in the dpp disk region regulate a second round of Dpp signaling from the dorsal ectoderm to the mesoderm that represses Zfh-1 expression in a subset of pericardial cells. <i>Developmental Biology</i> , 2003, 262, 137-151.	2.0	16

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55	Transposable element profiles reveal cell line identity and loss of heterozygosity in <i>Drosophila</i> cell culture. <i>Genetics</i> , 2021, 219, .	2.9	15
56	Strain-specific and pooled genome sequences for populations of <i>Drosophila melanogaster</i> from three continents. <i>F1000Research</i> , 2015, 4, 31.	1.6	15
57	Conserved Noncoding Elements Influence the Transposable Element Landscape in <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 1533-1545.	2.5	14
58	Hybrid dysgenesis in <i>Drosophila virilis</i> results in clusters of mitotic recombination and loss-of-heterozygosity but leaves meiotic recombination unaltered. <i>Mobile DNA</i> , 2020, 11, 10.	3.6	14
59	Bringing PLOS Genetics Editors to Preprint Servers. <i>PLoS Genetics</i> , 2016, 12, e1006448.	3.5	12
60	A proposal for the reference-based annotation of de novo transposable element insertions. <i>Mobile Genetic Elements</i> , 2012, 2, 51-54.	1.8	11
61	A novel transposable element-based authentication protocol for <i>Drosophila</i> cell lines. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	8
62	Phased Diploid Genome Assemblies for Three Strains of <i>Candida albicans</i> from Oak Trees. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3547-3554.	1.8	6
63	Assigning roles to protein mentions: The case of transcription factors. <i>Journal of Biomedical Informatics</i> , 2009, 42, 887-894.	4.3	5
64	Complete Genome Assemblies for Three Variants of the <i>Wolbachia</i> Endosymbiont of <i>Drosophila melanogaster</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	5
65	Genome Assembly of the Ty1-Less <i>Saccharomyces paradoxus</i> Strain DG1768. <i>Microbiology Resource Announcements</i> , 2022, 11, e0086821.	0.6	5
66	Long-Read Genome Assembly of <i>Saccharomyces uvarum</i> Strain CBS 7001. <i>Microbiology Resource Announcements</i> , 2022, 11, e0097221.	0.6	4
67	Ongoing transposition in cell culture reveals the phylogeny of diverse <i>Drosophila</i> S2 sublines. <i>Genetics</i> , 2022, 221, .	2.9	4
68	<i>Drosophila</i> Polymorphism Database (DPDB) A Portal for Nucleotide Polymorphism in <i>Drosophila</i> . <i>Fly</i> , 2007, 1, 205-211.	1.7	3
69	Systems biology of energetic and atomic costs in the yeast transcriptome, proteome, and metabolome. <i>Nature Precedings</i> , 2008, , .	0.1	3
70	A Meta-Analysis of <i>Wolbachia</i> Transcriptomics Reveals a Stage-Specific <i>Wolbachia</i> Transcriptional Response Shared Across Different Hosts. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3243-3260.	1.8	3
71	Systems biology of energetic and atomic costs in the yeast transcriptome, proteome, and metabolome. <i>Nature Precedings</i> , 2008, , .	0.1	2
72	Complete mitochondrial genome of the longhorn date palm stem borer <i>Jebusaea hamerschmidtii</i> (Reiche, 1878). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3214-3216.	0.4	2

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73	Population genomics of domestic and wild yeasts. Nature Precedings, 2008, , .	0.1	1