

Kevin R Thornton

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7536625/publications.pdf>

Version: 2024-02-01

51
papers

8,102
citations

109321

35
h-index

182427

51
g-index

62
all docs

62
docs citations

62
times ranked

8974
citing authors

#	ARTICLE	IF	CITATIONS
1	Efficient ancestry and mutation simulation with msprime 1.0. <i>Genetics</i> , 2022, 220, .	2.9	133
2	Efficiently Summarizing Relationships in Large Samples: A General Duality Between Statistics of Genealogies and Genomes. <i>Genetics</i> , 2020, 215, 779-797.	2.9	51
3	Polygenic Adaptation to an Environmental Shift: Temporal Dynamics of Variation Under Gaussian Stabilizing Selection and Additive Effects on a Single Trait. <i>Genetics</i> , 2019, 213, 1513-1530.	2.9	49
4	Evidence of directional and stabilizing selection in contemporary humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 151-156.	7.1	90
5	Efficient pedigree recording for fast population genetics simulation. <i>PLoS Computational Biology</i> , 2018, 14, e1006581.	3.2	130
6	Genetic architecture and selective sweeps after polygenic adaptation to distant trait optima. <i>PLoS Genetics</i> , 2018, 14, e1007794.	3.5	48
7	Tandem duplications lead to novel expression patterns through exon shuffling in <i>Drosophila yakuba</i> . <i>PLoS Genetics</i> , 2017, 13, e1006795.	3.5	53
8	A Model of Compound Heterozygous, Loss-of-Function Alleles Is Broadly Consistent with Observations from Complex-Disease GWAS Datasets. <i>PLoS Genetics</i> , 2017, 13, e1006573.	3.5	31
9	Efficient Software for Multi-marker, Region-Based Analysis of GWAS Data. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1023-1030.	1.8	6
10	Tandem Duplications and the Limits of Natural Selection in <i>Drosophila yakuba</i> and <i>Drosophila simulans</i> . <i>PLoS ONE</i> , 2015, 10, e0132184.	2.5	25
11	Gene Expression Variation in <i>Drosophila melanogaster</i> Due to Rare Transposable Element Insertion Alleles of Large Effect. <i>Genetics</i> , 2015, 199, 85-93.	2.9	45
12	The Power to Detect Quantitative Trait Loci Using Resequenced, Experimentally Evolved Populations of Diploid, Sexual Organisms. <i>Molecular Biology and Evolution</i> , 2014, 31, 1040-1055.	8.9	88
13	A C++ Template Library for Efficient Forward-Time Population Genetic Simulation of Large Populations. <i>Genetics</i> , 2014, 198, 157-166.	2.9	78
14	Revised Annotations, Sex-Biased Expression, and Lineage-Specific Genes in the <i>Drosophila melanogaster</i> Group. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2345-2351.	1.8	17
15	Landscape of Standing Variation for Tandem Duplications in <i>Drosophila yakuba</i> and <i>Drosophila simulans</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 1750-1766.	8.9	89
16	A second-generation assembly of the <i>Drosophila simulans</i> genome provides new insights into patterns of lineage-specific divergence. <i>Genome Research</i> , 2013, 23, 89-98.	5.5	157
17	Properties and Modeling of GWAS when Complex Disease Risk Is Due to Non-Complementing, Deleterious Mutations in Genes of Large Effect. <i>PLoS Genetics</i> , 2013, 9, e1003258.	3.5	72
18	Abundance and Distribution of Transposable Elements in Two <i>Drosophila</i> QTL Mapping Resources. <i>Molecular Biology and Evolution</i> , 2013, 30, 2311-2327.	8.9	118

#	ARTICLE	IF	CITATIONS
19	The <i>Drosophila melanogaster</i> Genetic Reference Panel. <i>Nature</i> , 2012, 482, 173-178.	27.8	1,756
20	Genome sequencing reveals complex speciation in the <i>Drosophila simulans</i> clade. <i>Genome Research</i> , 2012, 22, 1499-1511.	5.5	220
21	Experiments with the Site Frequency Spectrum. <i>Bulletin of Mathematical Biology</i> , 2011, 73, 829-872.	1.9	11
22	Validation of Rearrangement Break Points Identified by Paired-End Sequencing in Natural Populations of <i>Drosophila melanogaster</i> . <i>Genome Biology and Evolution</i> , 2010, 2, 83-101.	2.5	46
23	Genome-wide analysis of a long-term evolution experiment with <i>Drosophila</i> . <i>Nature</i> , 2010, 467, 587-590.	27.8	410
24	Characterizing natural variation using next-generation sequencing technologies. <i>Trends in Genetics</i> , 2009, 25, 463-471.	6.7	116
25	Automating approximate Bayesian computation by local linear regression. <i>BMC Genetics</i> , 2009, 10, 35.	2.7	33
26	Inferring Selection in Partially Sequenced Regions. <i>Molecular Biology and Evolution</i> , 2008, 25, 438-446.	8.9	13
27	An Approximate Bayesian Estimator Suggests Strong, Recurrent Selective Sweeps in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2008, 4, e1000198.	3.5	94
28	Controlling the False-Positive Rate in Multilocus Genome Scans for Selection. <i>Genetics</i> , 2007, 175, 737-750.	2.9	163
29	The Neutral Coalescent Process for Recent Gene Duplications and Copy-Number Variants. <i>Genetics</i> , 2007, 177, 987-1000.	2.9	26
30	On the Utility of Linkage Disequilibrium as a Statistic for Identifying Targets of Positive Selection in Nonequilibrium Populations. <i>Genetics</i> , 2007, 176, 2371-2379.	2.9	84
31	A New Approach for Using Genome Scans to Detect Recent Positive Selection in the Human Genome. <i>PLoS Biology</i> , 2007, 5, e171.	5.6	413
32	Progress and prospects in mapping recent selection in the genome. <i>Heredity</i> , 2007, 98, 340-348.	2.6	121
33	Identification by full-coverage array CGH of human DNA copy number increases relative to chimpanzee and gorilla. <i>Genome Research</i> , 2006, 16, 173-181.	5.5	48
34	EXTENSIVE INTROGRESSION OF MITOCHONDRIAL DNA RELATIVE TO NUCLEAR GENES IN THE DROSOPHILA YAKUBA SPECIES GROUP. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 292.	2.3	4
35	EXTENSIVE INTROGRESSION OF MITOCHONDRIAL DNA RELATIVE TO NUCLEAR GENES IN THE DROSOPHILA YAKUBA SPECIES GROUP. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 292-302.	2.3	187
36	Approximate Bayesian Inference Reveals Evidence for a Recent, Severe Bottleneck in a Netherlands Population of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2006, 172, 1607-1619.	2.9	239

#	ARTICLE	IF	CITATIONS
37	X chromosomes and autosomes evolve at similar rates in <i>Drosophila</i> : No evidence for faster-X protein evolution. <i>Genome Research</i> , 2006, 16, 498-504.	5.5	67
38	Extensive introgression of mitochondrial DNA relative to nuclear genes in the <i>Drosophila yakuba</i> species group. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 292-302.	2.3	69
39	Recombination and the Properties of Tajima's D in the Context of Approximate-Likelihood Calculation. <i>Genetics</i> , 2005, 171, 2143-2148.	2.9	35
40	Comparative genome sequencing of <i>Drosophila pseudoobscura</i> : Chromosomal, gene, and cis-element evolution. <i>Genome Research</i> , 2005, 15, 1-18.	5.5	453
41	Multilocus patterns of nucleotide variability and the demographic and selection history of <i>Drosophila melanogaster</i> populations. <i>Genome Research</i> , 2005, 15, 790-799.	5.5	247
42	Excess of Amino Acid Substitutions Relative to Polymorphism Between X-Linked Duplications in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2004, 22, 273-284.	8.9	46
43	Nucleotide Variation and Recombination Along the Fourth Chromosome in <i>Drosophila simulans</i> . <i>Genetics</i> , 2004, 166, 1783-1794.	2.9	25
44	Nucleotide Variation and Recombination Along the Fourth Chromosome in <i>Drosophila simulans</i> . <i>Genetics</i> , 2004, 166, 1783-1794.	2.9	13
45	The origin of new genes: glimpses from the young and old. <i>Nature Reviews Genetics</i> , 2003, 4, 865-875.	16.3	775
46	libsequence: a C++ class library for evolutionary genetic analysis. <i>Bioinformatics</i> , 2003, 19, 2325-2327.	4.1	307
47	Nucleotide Variation Along the <i>Drosophila melanogaster</i> Fourth Chromosome. <i>Science</i> , 2002, 295, 134-137.	12.6	81
48	Rapid Divergence of Gene Duplicates on the <i>Drosophila melanogaster</i> X Chromosome. <i>Molecular Biology and Evolution</i> , 2002, 19, 918-925.	8.9	83
49	Retroposed New Genes Out of the X in <i>Drosophila</i> . <i>Genome Research</i> , 2002, 12, 1854-1859.	5.5	399
50	Retroposed New Genes Out of the X in <i>Drosophila</i> . <i>Genome Research</i> , 2002, 12, 1854-1859.	5.5	99
51	Gene Duplication and Evolution. <i>Science</i> , 2001, 293, 1551a-1551.	12.6	103