

Anthony D Long

List of Publications by Year in Descending Order

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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.

80
papers

7,265
citations

37
h-index

85
g-index

119
ext. papers

8,367
ext. citations

8.2
avg, IF

5.95
L-index

#	Paper	IF	Citations
80	HapSolo: an optimization approach for removing secondary haplotigs during diploid genome assembly and scaffolding. <i>BMC Bioinformatics</i> , 2021 , 22, 9	3.6	0
79	Genomic Signatures of Local Adaptation in Clam Shrimp (<i>Eulimnadia texana</i>) from Natural Vernal Pools. <i>Genome Biology and Evolution</i> , 2020 , 12, 1194-1206	3.9	0
78	Increased time sampling in an evolve-and-resequence experiment with outcrossing <i>Saccharomyces cerevisiae</i> reveals multiple paths of adaptive change. <i>Molecular Ecology</i> , 2020 , 29, 4898-4912	5.7	3
77	The genome of <i>Ixodes ricinus</i> , natural host for Lyme disease and other emerging infections. <i>Science Advances</i> , 2019 , 5, eaaw6441	14.3	12
76	The gene structure and hypervariability of the complete <i>Penaeus monodon</i> Dscam gene. <i>Scientific Reports</i> , 2019 , 9, 16595	4.9	7
75	Genomes, expression profiles, and diversity of mitochondria of the White-footed Deermouse <i>Peromyscus leucopus</i> , reservoir of Lyme disease and other zoonoses. <i>Scientific Reports</i> , 2019 , 9, 17618	4.9	2
74	Structural variants exhibit widespread allelic heterogeneity and shape variation in complex traits. <i>Nature Communications</i> , 2019 , 10, 4872	17.4	46
73	A New Standard for Crustacean Genomes: The Highly Contiguous, Annotated Genome Assembly of the Clam Shrimp <i>Eulimnadia texana</i> Reveals HOX Gene Order and Identifies the Sex Chromosome. <i>Genome Biology and Evolution</i> , 2018 , 10, 143-156	3.9	23
72	The Beavis Effect in Next-Generation Mapping Panels in. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 1643-1652	2	29
71	Genotype by random environmental interactions gives an advantage to non-favored minor alleles. <i>Scientific Reports</i> , 2017 , 7, 5193	4.9	9
70	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	6	24
69	Contiguous and accurate de novo assembly of metazoan genomes with modest long read coverage. <i>Nucleic Acids Research</i> , 2016 , 44, e147	20.1	183
68	Efficient Software for Multi-marker, Region-Based Analysis of GWAS Data. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 1023-30	3.2	6
67	Genome-wide analysis of long-term evolutionary domestication in <i>Drosophila melanogaster</i> . <i>Scientific Reports</i> , 2016 , 6, 39281	4.9	13
66	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	4	35
65	Identifying Loci Contributing to Natural Variation in Xenobiotic Resistance in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2015 , 11, e1005663	6	26
64	Genome-wide association study of extreme longevity in <i>Drosophila melanogaster</i> . <i>Genome Biology and Evolution</i> , 2014 , 6, 1-11	3.9	27

63	Standing genetic variation drives repeatable experimental evolution in outcrossing populations of <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology and Evolution</i> , 2014 , 31, 3228-39	8.3	85
62	Dissecting complex traits using the <i>Drosophila</i> Synthetic Population Resource. <i>Trends in Genetics</i> , 2014 , 30, 488-95	8.5	48
61	Using <i>Drosophila melanogaster</i> to identify chemotherapy toxicity genes. <i>Genetics</i> , 2014 , 198, 31-43	4	21
60	The power to detect quantitative trait loci using resequenced, experimentally evolved populations of diploid, sexual organisms. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1040-55	8.3	62
59	Genetic dissection of the <i>Drosophila melanogaster</i> female head transcriptome reveals widespread allelic heterogeneity. <i>PLoS Genetics</i> , 2014 , 10, e1004322	6	43
58	Fine-mapping nicotine resistance loci in <i>Drosophila</i> using a multiparent advanced generation inter-cross population. <i>Genetics</i> , 2014 , 198, 45-57	4	37
57	The genetic architecture of methotrexate toxicity is similar in <i>Drosophila melanogaster</i> and humans. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 1301-10	3.2	20
56	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	6	61
55	Abundance and distribution of transposable elements in two <i>Drosophila</i> QTL mapping resources. <i>Molecular Biology and Evolution</i> , 2013 , 30, 2311-27	8.3	84
54	Diversification of complex butterfly wing patterns by repeated regulatory evolution of a Wnt ligand. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 12632-7	11.5	187
53	The molecular diversity of adaptive convergence. <i>Science</i> , 2012 , 335, 457-61	33.3	511
52	Genetic dissection of a model complex trait using the <i>Drosophila</i> Synthetic Population Resource. <i>Genome Research</i> , 2012 , 22, 1558-66	9.7	134
51	What paths do advantageous alleles take during short-term evolutionary change?. <i>Molecular Ecology</i> , 2012 , 21, 4913-6	5.7	17
50	Properties and power of the <i>Drosophila</i> Synthetic Population Resource for the routine dissection of complex traits. <i>Genetics</i> , 2012 , 191, 935-49	4	117
49	Chemotherapy-induced toxicity is highly heritable in <i>Drosophila melanogaster</i> . <i>Pharmacogenetics and Genomics</i> , 2012 , 22, 285-9	1.9	9
48	Genomic sequence around butterfly wing development genes: annotation and comparative analysis. <i>PLoS ONE</i> , 2011 , 6, e23778	3.7	13
47	Genome-wide analysis of a long-term evolution experiment with <i>Drosophila</i> . <i>Nature</i> , 2010 , 467, 587-90	50.4	321
46	Evolutionary Nutrigenomics 2010 , 357-366		3

45	Cis-regulatory variation is typically polyallelic in <i>Drosophila</i> . <i>Genetics</i> , 2009 , 181, 661-70	4	14
44	A gene-based linkage map for <i>Bicyclus anynana</i> butterflies allows for a comprehensive analysis of synteny with the lepidopteran reference genome. <i>PLoS Genetics</i> , 2009 , 5, e1000366	6	81
43	Experimental evolution reveals natural selection on standing genetic variation. <i>Nature Genetics</i> , 2009 , 41, 251-7	36.3	114
42	Microsatellite markers associated with genes expressed in developing wings of <i>Bicyclus anynana</i> butterflies. <i>Molecular Ecology Resources</i> , 2009 , 9, 1487-92	8.4	2
41	Joint estimates of quantitative trait locus effect and frequency using synthetic recombinant populations of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2007 , 176, 1261-81	4	48
40	How repeatable are associations between polymorphisms in achaete-scute and bristle number variation in <i>Drosophila</i> ?. <i>Genetics</i> , 2007 , 175, 1987-97	4	23
39	Estimation of population heterozygosity and library construction-induced mutation rate from expressed sequence tag collections. <i>Genetics</i> , 2007 , 176, 711-4	4	12
38	A wing expressed sequence tag resource for <i>Bicyclus anynana</i> butterflies, an evo-devo model. <i>BMC Genomics</i> , 2006 , 7, 130	4.5	83
37	A cis-regulatory sequence within the yellow locus of <i>Drosophila melanogaster</i> required for normal male mating success. <i>Genetics</i> , 2006 , 172, 1009-30	4	51
36	Fine scale structural variants distinguish the genomes of <i>Drosophila melanogaster</i> and <i>D. pseudoobscura</i> . <i>Genome Biology</i> , 2006 , 7, R67	18.3	9
35	A low-cost open-source SNP genotyping platform for association mapping applications. <i>Genome Biology</i> , 2005 , 6, R105	18.3	21
34	Generating phenotypic variation: prospects from "evo-devo" research on <i>Bicyclus anynana</i> wing patterns. <i>Evolution & Development</i> , 2005 , 7, 101-7	2.6	44
33	Prospects for identifying functional variation across the genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102 Suppl 1, 6614-21	11.5	10
32	Changes in gene expression following high-temperature adaptation in experimentally evolved populations of <i>E. coli</i> . <i>Physiological and Biochemical Zoology</i> , 2005 , 78, 299-315	2	18
31	The effect of polymorphisms in the enhancer of split gene complex on bristle number variation in a large wild-caught cohort of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2005 , 171, 1741-56	4	35
30	Identifying signatures of selection at the enhancer of split neurogenic gene complex in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2005 , 22, 607-19	8.3	13
29	Differential Patterns of Gene Expression and Gene Complement in Laboratory-Evolved Lines of <i>E. coli</i> . <i>Integrative and Comparative Biology</i> , 2005 , 45, 532-8	2.8	5
28	No evidence for an association between common nonsynonymous polymorphisms in delta and bristle number variation in natural and laboratory populations of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2004 , 166, 291-306	4	31

27	A potential regulatory polymorphism upstream of hairy is not associated with bristle number variation in wild-caught <i>Drosophila</i> . <i>Genetics</i> , 2004 , 167, 2127-31	4	28
26	Evolutionary changes in heat-inducible gene expression in lines of <i>Escherichia coli</i> adapted to high temperature. <i>Physiological Genomics</i> , 2003 , 14, 47-58	3.6	71
25	Inferences regarding the numbers and locations of QTLs under multiple-QTL models using interval mapping and composite interval mapping. <i>Genetical Research</i> , 2003 , 82, 139-49	1.1	16
24	A gene necessary for normal male courtship, yellow, acts downstream of fruitless in the <i>Drosophila melanogaster</i> larval brain. <i>Journal of Neurobiology</i> , 2003 , 55, 53-72		76
23	The lowdown on linkage disequilibrium. <i>Plant Cell</i> , 2003 , 15, 1502-6	11.6	179
22	Ageing: the many-headed monster. <i>Current Biology</i> , 2002 , 12, R311-2	6.3	13
21	Contribution of Distal-less to quantitative variation in butterfly eyespots. <i>Nature</i> , 2002 , 415, 315-8	50.4	118
20	Bioinformatics and cytogenetics of unusual <i>Drosophila melanogaster</i> X-chromosome morphology. <i>DNA Sequence</i> , 2002 , 13, 241-3		2
19	Pharmacology, genomics, and the evolutionary biology of ageing. <i>Free Radical Research</i> , 2002 , 36, 1293-7		10
18	Immunohistochemical colocalization of Yellow and male-specific Fruitless in <i>Drosophila melanogaster</i> neuroblasts. <i>Biochemical and Biophysical Research Communications</i> , 2002 , 293, 1262-4	3.4	16
17	hairy: A quantitative trait locus for <i>drosophila</i> sensory bristle number. <i>Genetics</i> , 2002 , 162, 155-64	4	49
16	Genetic architecture of thermal adaptation in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 525-530	11.5	193
15	Patterns of DNA sequence polymorphism along chromosome 1 of maize (<i>Zea mays</i> ssp. <i>mays</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 9161-6	11.5	567
14	Improved statistical inference from DNA microarray data using analysis of variance and a Bayesian statistical framework. Analysis of global gene expression in <i>Escherichia coli</i> K12. <i>Journal of Biological Chemistry</i> , 2001 , 276, 19937-44	5.4	282
13	A Bayesian framework for the analysis of microarray expression data: regularized t-test and statistical inferences of gene changes. <i>Bioinformatics</i> , 2001 , 17, 509-19	7.2	1360
12	Genetic architecture of thermal adaptation in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 525-30	11.5	130
11	Global gene expression profiling in <i>Escherichia coli</i> K12. The effects of integration host factor. <i>Journal of Biological Chemistry</i> , 2000 , 275, 29672-84	5.4	209
10	Both naturally occurring insertions of transposable elements and intermediate frequency polymorphisms at the achaete-scute complex are associated with variation in bristle number in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2000 , 154, 1255-69	4	83

9	The power of association studies to detect the contribution of candidate genetic loci to variation in complex traits. <i>Genome Research</i> , 1999 , 9, 720-31	9.7	268
8	The Power of Association Studies to Detect the Contribution of Candidate Genetic Loci to Variation in Complex Traits. <i>Genome Research</i> , 1999 , 9, 720-731	9.7	159
7	Two sites in the Delta gene region contribute to naturally occurring variation in bristle number in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 1998 , 149, 999-1017	4	152
6	Genetic interactions between naturally occurring alleles at quantitative trait loci and mutant alleles at candidate loci affecting bristle number in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 1996 , 144, 1497-510	4	117
5	High resolution mapping of genetic factors affecting abdominal bristle number in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 1995 , 139, 1273-91	4	179
4	Naturally occurring variation in bristle number and DNA polymorphisms at the scabrous locus of <i>Drosophila melanogaster</i> . <i>Science</i> , 1994 , 266, 1697-702	33.3	151
3	Structural variants exhibit allelic heterogeneity and shape variation in complex traits		2
2	A model of compound heterozygous, loss-of-function alleles is broadly consistent with observations from complex-disease GWAS datasets		2
1	Adaptation in outbred sexual yeast is repeatable, polygenic, and favors rare haplotypes		1