

# Andrew G Clark

## List of Publications by Year in descending order

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Version: 2024-02-01

333  
papers

66,109  
citations

2093

100  
h-index

930

240  
g-index

369  
all docs

369  
docs citations

369  
times ranked

63115  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	6.0	12,623
2	Finding the missing heritability of complex diseases. <i>Nature</i> , 2009, 461, 747-753.	13.7	7,490
3	Human Genetics Shape the Gut Microbiome. <i>Cell</i> , 2014, 159, 789-799.	13.5	2,523
4	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
5	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 129-149.	6.0	1,859
6	RepeatModeler2 for automated genomic discovery of transposable element families. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9451-9457.	3.3	1,480
7	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	6.0	1,283
8	Genomic scans for selective sweeps using SNP data. <i>Genome Research</i> , 2005, 15, 1566-1575.	2.4	891
9	Natural selection shaped regional mtDNA variation in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 171-176.	3.3	889
10	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees. <i>PLoS Biology</i> , 2005, 3, e170.	2.6	870
11	Genetic Determinants of the Gut Microbiome in UK Twins. <i>Cell Host and Microbe</i> , 2016, 19, 731-743.	5.1	831
12	Evolutionary changes in cis and trans gene regulation. <i>Nature</i> , 2004, 430, 85-88.	13.7	771
13	Natural selection on protein-coding genes in the human genome. <i>Nature</i> , 2005, 437, 1153-1157.	13.7	718
14	Inferring Nonneutral Evolution from Human-Chimp-Mouse Orthologous Gene Trios. <i>Science</i> , 2003, 302, 1960-1963.	6.0	626
15	Host genetic variation impacts microbiome composition across human body sites. <i>Genome Biology</i> , 2015, 16, 191.	3.8	612
16	Haplotype Diversity and Linkage Disequilibrium at Human G6PD: Recent Origin of Alleles That Confer Malarial Resistance. <i>Science</i> , 2001, 293, 455-462.	6.0	590
17	Demographic history and rare allele sharing among human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11983-11988.	3.3	589
18	Assessing the Evolutionary Impact of Amino Acid Mutations in the Human Genome. <i>PLoS Genetics</i> , 2008, 4, e1000083.	1.5	586

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19	Recent Explosive Human Population Growth Has Resulted in an Excess of Rare Genetic Variants. <i>Science</i> , 2012, 336, 740-743.	6.0	489
20	DNA sequence diversity in a 9.7-kb region of the human lipoprotein lipase gene. <i>Nature Genetics</i> , 1998, 19, 233-240.	9.4	483
21	Genome-Wide Associations of Gene Expression Variation in Humans. <i>PLoS Genetics</i> , 2005, 1, e78.	1.5	467
22	Sequence variation in the human angiotensin converting enzyme. <i>Nature Genetics</i> , 1999, 22, 59-62.	9.4	452
23	Recent and ongoing selection in the human genome. <i>Nature Reviews Genetics</i> , 2007, 8, 857-868.	7.7	446
24	Haplotype Structure and Population Genetic Inferences from Nucleotide-Sequence Variation in Human Lipoprotein Lipase. <i>American Journal of Human Genetics</i> , 1998, 63, 595-612.	2.6	439
25	Localizing Recent Adaptive Evolution in the Human Genome. <i>PLoS Genetics</i> , 2007, 3, e90.	1.5	421
26	Evolution of Transcription Factor Binding Sites in Mammalian Gene Regulatory Regions: Conservation and Turnover. <i>Molecular Biology and Evolution</i> , 2002, 19, 1114-1121.	3.5	411
27	Ascertainment bias in studies of human genome-wide polymorphism. <i>Genome Research</i> , 2005, 15, 1496-1502.	2.4	410
28	Dynamic evolution of the innate immune system in <i>Drosophila</i> . <i>Nature Genetics</i> , 2007, 39, 1461-1468.	9.4	400
29	Apolipoprotein E Variation at the Sequence Haplotype Level: Implications for the Origin and Maintenance of a Major Human Polymorphism. <i>American Journal of Human Genetics</i> , 2000, 67, 881-900.	2.6	377
30	Linkage disequilibrium and the mapping of complex human traits. <i>Trends in Genetics</i> , 2002, 18, 19-24.	2.9	369
31	Proportionally more deleterious genetic variation in European than in African populations. <i>Nature</i> , 2008, 451, 994-997.	13.7	365
32	Sequence diversity and haplotype structure in the human ABCB1 (MDR1, multidrug resistance) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	9.7	361
33	Regulatory changes underlying expression differences within and between <i>Drosophila</i> species. <i>Nature Genetics</i> , 2008, 40, 346-350.	9.4	355
34	The role of haplotypes in candidate gene studies. <i>Genetic Epidemiology</i> , 2004, 27, 321-333.	0.6	349
35	Thrice Out of Africa: Ancient and Recent Expansions of the Honey Bee, <i>Apis mellifera</i> . <i>Science</i> , 2006, 314, 642-645.	6.0	333
36	Characterization of Greater Middle Eastern genetic variation for enhanced disease gene discovery. <i>Nature Genetics</i> , 2016, 48, 1071-1076.	9.4	314

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37	Signatures of early frailty in the gut microbiota. <i>Genome Medicine</i> , 2016, 8, 8.	3.6	297
38	Genes Regulated by Mating, Sperm, or Seminal Proteins in Mated Female <i>Drosophila melanogaster</i> . <i>Current Biology</i> , 2004, 14, 1509-1514.	1.8	287
39	Genome-wide association study provides evidence for a breast cancer risk locus at 6q22.33. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4340-4345.	3.3	274
40	Evolution of protein-coding genes in <i>Drosophila</i> . <i>Trends in Genetics</i> , 2008, 24, 114-123.	2.9	262
41	Genome of the house fly, <i>Musca domestica</i> L., a global vector of diseases with adaptations to a septic environment. <i>Genome Biology</i> , 2014, 15, 466.	3.8	252
42	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	13.7	251
43	Evolution of Resistance Against CRISPR/Cas9 Gene Drive. <i>Genetics</i> , 2017, 205, 827-841.	1.2	250
44	Novel CRISPR/Cas9 gene drive constructs reveal insights into mechanisms of resistance allele formation and drive efficiency in genetically diverse populations. <i>PLoS Genetics</i> , 2017, 13, e1006796.	1.5	246
45	Targets of Balancing Selection in the Human Genome. <i>Molecular Biology and Evolution</i> , 2009, 26, 2755-2764.	3.5	245
46	The human microbiome in evolution. <i>BMC Biology</i> , 2017, 15, 127.	1.7	243
47	Cancer-associated fibroblasts lead tumor invasion through integrin- $\beta$ 3-dependent fibronectin assembly. <i>Journal of Cell Biology</i> , 2017, 216, 3509-3520.	2.3	241
48	Impact of microRNA regulation on variation in human gene expression. <i>Genome Research</i> , 2012, 22, 1243-1254.	2.4	237
49	The Relationship Between the Human Genome and Microbiome Comes into View. <i>Annual Review of Genetics</i> , 2017, 51, 413-433.	3.2	237
50	Estimating the mutation load in human genomes. <i>Nature Reviews Genetics</i> , 2015, 16, 333-343.	7.7	233
51	Cross-species comparisons of host genetic associations with the microbiome. <i>Science</i> , 2016, 352, 532-535.	6.0	233
52	Reducing resistance allele formation in CRISPR gene drive. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5522-5527.	3.3	233
53	Genetic Basis of Natural Variation in <i>D. melanogaster</i> Antibacterial Immunity. <i>Science</i> , 2004, 303, 1873-1876.	6.0	230
54	Natural variation in human membrane transporter genes reveals evolutionary and functional constraints. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5896-5901.	3.3	224

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55	Genome sequencing reveals complex speciation in the <i>Drosophila simulans</i> clade. <i>Genome Research</i> , 2012, 22, 1499-1511.	2.4	220
56	Inferring Genetic Ancestry: Opportunities, Challenges, and Implications. <i>American Journal of Human Genetics</i> , 2010, 86, 661-673.	2.6	214
57	The structure of human mitochondrial DNA variation. <i>Journal of Molecular Evolution</i> , 1991, 33, 543-555.	0.8	213
58	Deep resequencing reveals excess rare recent variants consistent with explosive population growth. <i>Nature Communications</i> , 2010, 1, 131.	5.8	213
59	Balancing Selection Maintains a Form of ERAP2 that Undergoes Nonsense-Mediated Decay and Affects Antigen Presentation. <i>PLoS Genetics</i> , 2010, 6, e1001157.	1.5	210
60	Compensatory cis-trans Evolution and the Dysregulation of Gene Expression in Interspecific Hybrids of <i>Drosophila</i> . <i>Genetics</i> , 2005, 171, 1813-1822.	1.2	209
61	Genetic incompatibilities are widespread within species. <i>Nature</i> , 2013, 504, 135-137.	13.7	200
62	Genes involved in convergent evolution of eusociality in bees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7472-7477.	3.3	199
63	Monitoring Actin Cortex Thickness in Live Cells. <i>Biophysical Journal</i> , 2013, 105, 570-580.	0.2	198
64	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.	1.1	187
65	Recombinational and Mutational Hotspots within the Human Lipoprotein Lipase Gene. <i>American Journal of Human Genetics</i> , 2000, 66, 69-83.	2.6	185
66	Polymorphisms in a human kidney xenobiotic transporter, OCT2, exhibit altered function. <i>Pharmacogenetics and Genomics</i> , 2002, 12, 395-405.	5.7	183
67	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016, 17, 189.	3.8	183
68	The evolutionary costs of immunological maintenance and deployment. <i>BMC Evolutionary Biology</i> , 2008, 8, 76.	3.2	181
69	Genomic Analyses of Transcription Factor Binding, Histone Acetylation, and Gene Expression Reveal Mechanistically Distinct Classes of Estrogen-Regulated Promoters. <i>Molecular and Cellular Biology</i> , 2007, 27, 5090-5104.	1.1	178
70	The functional spectrum of low-frequency coding variation. <i>Genome Biology</i> , 2011, 12, R84.	13.9	173
71	Full-Exon Resequencing Reveals Toll-Like Receptor Variants Contribute to Human Susceptibility to Tuberculosis Disease. <i>PLoS ONE</i> , 2007, 2, e1318.	1.1	171
72	Transcriptome-Wide Identification of Novel Imprinted Genes in Neonatal Mouse Brain. <i>PLoS ONE</i> , 2008, 3, e3839.	1.1	170

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73	Sexually Antagonistic Cytonuclear Fitness Interactions in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2001, 159, 173-187.	1.2	167
74	Microsatellite variation in North American populations of <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 1995, 23, 3882-3886.	6.5	166
75	Molecular Population Genetics of Male Accessory Gland Proteins in <i>Drosophila</i> . <i>Genetics</i> , 2000, 156, 1879-1888.	1.2	165
76	Whole-genome shotgun assembly and comparison of human genome assemblies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1916-1921.	3.3	164
77	Sperm Competitive Ability in <i>Drosophila melanogaster</i> Associated With Variation in Male Reproductive Proteins. <i>Genetics</i> , 2005, 169, 243-257.	1.2	163
78	Invasion and maintenance of a gene duplication.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 2950-2954.	3.3	159
79	Behavioral idiosyncrasy reveals genetic control of phenotypic variability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6706-6711.	3.3	159
80	Sequence Diversity and Large-Scale Typing of SNPs in the Human Apolipoprotein E Gene. <i>Genome Research</i> , 2000, 10, 1532-1545.	2.4	156
81	Selection for starvation resistance in <i>Drosophila melanogaster</i> : physiological correlates, enzyme activities and multiple stress responses. <i>Journal of Evolutionary Biology</i> , 1999, 12, 370-379.	0.8	150
82	Low conservation of gene content in the <i>Drosophila</i> Y chromosome. <i>Nature</i> , 2008, 456, 949-951.	13.7	150
83	Avian W and mammalian Y chromosomes convergently retained dosage-sensitive regulators. <i>Nature Genetics</i> , 2017, 49, 387-394.	9.4	147
84	Female Genotypes Affect Sperm Displacement in <i>Drosophila</i> . <i>Genetics</i> , 1998, 149, 1487-1493.	1.2	143
85	Satellite DNA evolution: old ideas, new approaches. <i>Current Opinion in Genetics and Development</i> , 2018, 49, 70-78.	1.5	142
86	Darwinian and demographic forces affecting human protein coding genes. <i>Genome Research</i> , 2009, 19, 838-849.	2.4	139
87	Post-mating Gene Expression Profiles of Female <i>Drosophila melanogaster</i> in Response to Time and to Four Male Accessory Gland Proteins. <i>Genetics</i> , 2008, 179, 1395-1408.	1.2	137
88	Paternally expressed genes predominate in the placenta. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10705-10710.	3.3	137
89	Gut-Microbiota-Metabolite Axis in Early Renal Function Decline. <i>PLoS ONE</i> , 2015, 10, e0134311.	1.1	134
90	Disentangling the relationship between sex-biased gene expression and X-linkage. <i>Genome Research</i> , 2012, 22, 1255-1265.	2.4	133

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91	Reconstituting the Frequency Spectrum of Ascertained Single-Nucleotide Polymorphism Data. <i>Genetics</i> , 2004, 168, 2373-2382.	1.2	131
92	Intron size and natural selection. <i>Nature</i> , 1999, 401, 344-344.	13.7	128
93	Global Diversity Linesâ€“A Five-Continent Reference Panel of Sequenced <i>Drosophila melanogaster</i> Strains. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 593-603.	0.8	124
94	Evolutionary Processes Acting on Candidate cis-Regulatory Regions in Humans Inferred from Patterns of Polymorphism and Divergence. <i>PLoS Genetics</i> , 2009, 5, e1000592.	1.5	123
95	Genetic Variation in <i>Drosophila melanogaster</i> Resistance to Infection: A Comparison Across Bacteria. <i>Genetics</i> , 2006, 174, 1539-1554.	1.2	120
96	Population genetic tools for dissecting innate immunity in humans. <i>Nature Reviews Immunology</i> , 2013, 13, 280-293.	10.6	119
97	Stresses at the Cell Surface during Animal Cell Morphogenesis. <i>Current Biology</i> , 2014, 24, R484-R494.	1.8	117
98	NATURAL SELECTION WITH NUCLEAR AND CYTOPLASMIC TRANSMISSION. I. A DETERMINISTIC MODEL. <i>Genetics</i> , 1984, 107, 679-701.	1.2	115
99	Integration of Single and Multicellular Wound Responses. <i>Current Biology</i> , 2009, 19, 1389-1395.	1.8	114
100	Optimal Haplotype Block-Free Selection of Tagging SNPs for Genome-Wide Association Studies. <i>Genome Research</i> , 2004, 14, 1633-1640.	2.4	113
101	Red fox genome assembly identifies genomic regions associated with tame and aggressive behaviours. <i>Nature Ecology and Evolution</i> , 2018, 2, 1479-1491.	3.4	113
102	A 3.9-Centimorgan-Resolution Human Single-Nucleotide Polymorphism Linkage Map and Screening Set. <i>American Journal of Human Genetics</i> , 2003, 73, 271-284.	2.6	112
103	Mechanical compartmentalization of the intestinal organoid enables crypt folding and collective cell migration. <i>Nature Cell Biology</i> , 2021, 23, 745-757.	4.6	112
104	Modeling the Manipulation of Natural Populations by the Mutagenic Chain Reaction. <i>Genetics</i> , 2015, 201, 425-431.	1.2	111
105	Population Genetic Structure of the People of Qatar. <i>American Journal of Human Genetics</i> , 2010, 87, 17-25.	2.6	110
106	INFERENCE OF SPERM COMPETITION FROM BROODS OF FIELD-COUGHT <i>DROSOPHILA</i> . <i>Evolution; International Journal of Organic Evolution</i> , 1998, 52, 1334-1341.	1.1	109
107	The linkage disequilibrium maps of three human chromosomes across four populations reflect their demographic history and a common underlying recombination pattern. <i>Genome Research</i> , 2005, 15, 454-462.	2.4	107
108	Neutral genomic regions refine models of recent rapid human population growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 757-762.	3.3	106

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109	Mapping Determinants of Variation in Energy Metabolism, Respiration and Flight in <i>Drosophila</i> . <i>Genetics</i> , 2003, 165, 623-635.	1.2	106
110	SEX LINKAGE, SEX-SPECIFIC SELECTION, AND THE ROLE OF RECOMBINATION IN THE EVOLUTION OF SEXUALLY DIMORPHIC GENE EXPRESSION. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 3417-3442.	1.1	102
111	A General Population Genetic Framework for Antagonistic Selection That Accounts for Demography and Recurrent Mutation. <i>Genetics</i> , 2012, 190, 1477-1489.	1.2	101
112	Associations Between Sperm Competition and Natural Variation in Male Reproductive Genes on the Third Chromosome of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2007, 176, 1245-1260.	1.2	100
113	Population Genetic Inference from Personal Genome Data: Impact of Ancestry and Admixture on Human Genomic Variation. <i>American Journal of Human Genetics</i> , 2012, 91, 660-671.	2.6	100
114	Host genetic determinants of microbiota-dependent nutrition revealed by genome-wide analysis of <i>Drosophila melanogaster</i> . <i>Nature Communications</i> , 2015, 6, 6312.	5.8	100
115	A toxin-antidote CRISPR gene drive system for regional population modification. <i>Nature Communications</i> , 2020, 11, 1082.	5.8	100
116	Molecular safeguarding of CRISPR gene drive experiments. <i>ELife</i> , 2019, 8, .	2.8	100
117	Efficient identification of Y chromosome sequences in the human and <i>Drosophila</i> genomes. <i>Genome Research</i> , 2013, 23, 1894-1907.	2.4	98
118	Balancing Selection in Species with Separate Sexes: Insights from Fisher's Geometric Model. <i>Genetics</i> , 2014, 197, 991-1006.	1.2	96
119	A CRISPR homing gene drive targeting a haplolethal gene removes resistance alleles and successfully spreads through a cage population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24377-24383.	3.3	91
120	Deconstructing isolation-by-distance: The genomic consequences of limited dispersal. <i>PLoS Genetics</i> , 2017, 13, e1006911.	1.5	91
121	Population dynamics of PIWI-interacting RNAs (piRNAs) and their targets in <i>Drosophila</i> . <i>Genome Research</i> , 2010, 20, 212-227.	2.4	89
122	A Survey for Novel Imprinted Genes in the Mouse Placenta by mRNA-seq. <i>Genetics</i> , 2011, 189, 109-122.	1.2	89
123	Gene-Based Testing of Interactions in Association Studies of Quantitative Traits. <i>PLoS Genetics</i> , 2013, 9, e1003321.	1.5	89
124	Indigenous Arabs are descendants of the earliest split from ancient Eurasian populations. <i>Genome Research</i> , 2016, 26, 151-162.	2.4	89
125	Genomewide Distribution of High-Frequency, Completely Mismatching SNP Haplotype Pairs Observed To Be Common across Human Populations. <i>American Journal of Human Genetics</i> , 2003, 73, 1073-1081.	2.6	88
126	Correlated variation and population differentiation in satellite DNA abundance among lines of <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18793-18798.	3.3	88



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127	Genus-wide sequencing supports a two-locus model for sex-determination in Phoenix. Nature Communications, 2018, 9, 3969.	5.8	86
128	Population genetic analysis of shotgun assemblies of genomic sequences from multiple individuals. Genome Research, 2008, 18, 1020-1029.	2.4	85
129	Natural Selection and <i>Y</i> -Linked Polymorphism. Genetics, 1987, 115, 569-577.	1.2	85
130	Molecular Population Genetics of Inducible Antibacterial Peptide Genes in <i>Drosophila melanogaster</i> . Molecular Biology and Evolution, 2003, 20, 914-923.	3.5	83
131	Faster-X Evolution of Gene Expression in <i>Drosophila</i> . PLoS Genetics, 2012, 8, e1003013.	1.5	83
132	Senescence and the Genetic-Correlation Hang-Up. American Naturalist, 1987, 129, 932-940.	1.0	83
133	Contributions of 18 Additional DNA Sequence Variations in the Gene Encoding Apolipoprotein E to Explaining Variation in Quantitative Measures of Lipid Metabolism. American Journal of Human Genetics, 2002, 71, 501-517.	2.6	81
134	Candidate genetic modifiers of retinitis pigmentosa identified by exploiting natural variation in <i>Drosophila</i> . Human Molecular Genetics, 2016, 25, 651-659.	1.4	81
135	NONTRANSITIVITY OF SPERM PRECEDENCE IN DROSOPHILA. Evolution; International Journal of Organic Evolution, 2000, 54, 1030-1035.	1.1	79
136	Genomic Consequences of Population Decline in the Endangered Florida Scrub-Jay. Current Biology, 2016, 26, 2974-2979.	1.8	79
137	Computational and experimental performance of CRISPR homing gene drive strategies with multiplexed gRNAs. Science Advances, 2020, 6, eaaz0525.	4.7	79
138	Linkage Disequilibrium and Inference of Ancestral Recombination in 538 Single-Nucleotide Polymorphism Clusters across the Human Genome. American Journal of Human Genetics, 2003, 73, 285-300.	2.6	76
139	The <i>Drosophila</i> seminal proteome and its role in postcopulatory sexual selection. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20200072.	1.8	76
140	Tracing the Evolutionary History of <i>Drosophila</i> Regulatory Regions with Models that Identify Transcription Factor Binding Sites. Molecular Biology and Evolution, 2003, 20, 703-714.	3.5	75
141	Determinants of the success of whole-genome association testing. Genome Research, 2005, 15, 1463-1467.	2.4	75
142	Population Growth Inflates the Per-Individual Number of Deleterious Mutations and Reduces Their Mean Effect. Genetics, 2013, 195, 969-978.	1.2	71
143	Non-Mendelian Segregation of Sex Chromosomes in Heterospecific <i>Drosophila</i> Males. Genetics, 2000, 154, 687-694.	1.2	71
144	A genome-wide approach to identifying novel-imprinted genes. Human Genetics, 2008, 122, 625-634.	1.8	70

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145	Evidence for the fixation of gene duplications by positive selection in <i>Drosophila</i> . <i>Genome Research</i> , 2016, 26, 787-798.	2.4	69
146	Evidence for Recurrent Paralogous Gene Conversion and Exceptional Allelic Divergence in the <i>Attacin</i> Genes of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2001, 159, 659-671.	1.2	69
147	Distortion of genealogical properties when the sample is very large. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2385-2390.	3.3	68
148	Allele frequency dynamics in a pedigreed natural population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2158-2164.	3.3	68
149	Suppression gene drive in continuous space can result in unstable persistence of both drive and wild-type alleles. <i>Molecular Ecology</i> , 2021, 30, 1086-1101.	2.0	68
150	Contrasting the Efficacy of Selection on the X and Autosomes in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 454-467.	3.5	67
151	Variable Rates of Simple Satellite Gains across the <i>Drosophila</i> Phylogeny. <i>Molecular Biology and Evolution</i> , 2018, 35, 925-941.	3.5	65
152	Understanding the accuracy of statistical haplotype inference with sequence data of known phase. <i>Genetic Epidemiology</i> , 2007, 31, 659-671.	0.6	64
153	Paternally biased X inactivation in mouse neonatal brain. <i>Genome Biology</i> , 2010, 11, R79.	13.9	64
154	Knowledge-Driven Analysis Identifies a Gene-Gene Interaction Affecting High-Density Lipoprotein Cholesterol Levels in Multi-Ethnic Populations. <i>PLoS Genetics</i> , 2012, 8, e1002714.	1.5	64
155	Genomic responses to selection for tame/aggressive behaviors in the silver fox ( <i>Vulpes vulpes</i> ) Tj ETQq1 1 0.784314 rgBT /Over 10398-10403.	3.3	64
156	Performance analysis of novel toxin-antidote CRISPR gene drive systems. <i>BMC Biology</i> , 2020, 18, 27.	1.7	63
157	Molecular Population Genetics of <i>Drosophila</i> Immune System Genes. <i>Genetics</i> , 1997, 147, 713-724.	1.2	63
158	Finding genes underlying risk of complex disease by linkage disequilibrium mapping. <i>Current Opinion in Genetics and Development</i> , 2003, 13, 296-302.	1.5	62
159	Selfish genetic elements. <i>PLoS Genetics</i> , 2018, 14, e1007700.	1.5	62
160	Epistasis in Measured Genotypes: <i>Drosophila</i> P-Element Insertions. <i>Genetics</i> , 1997, 147, 157-163.	1.2	62
161	Birth of a new gene on the Y chromosome of <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12450-12455.	3.3	61
162	ABO antigen and secretor statuses are not associated with gut microbiota composition in 1,500 twins. <i>BMC Genomics</i> , 2016, 17, 941.	1.2	61

#	ARTICLE	IF	CITATIONS
163	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.	1.1	60
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