

Andrew G Clark

List of Publications by Citations

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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.

336
papers

51,474
citations

93
h-index

224
g-index

369
ext. papers

60,229
ext. citations

10.5
avg, IF

7.33
L-index

#	Paper	IF	Citations
336	The sequence of the human genome. <i>Science</i> , 2001 , 291, 1304-51	33.3	10609
335	Finding the missing heritability of complex diseases. <i>Nature</i> , 2009 , 461, 747-53	50.4	6084
334	Human genetics shape the gut microbiome. <i>Cell</i> , 2014 , 159, 789-99	56.2	1750
333	The genome sequence of the malaria mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002 , 298, 129-49	33.3	1622
332	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
331	Evolutionary and biomedical insights from the rhesus macaque genome. <i>Science</i> , 2007 , 316, 222-34	33.3	1072
330	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, 171-6	11.5	783
329	A scan for positively selected genes in the genomes of humans and chimpanzees. <i>PLoS Biology</i> , 2005 , 3, e170	9.7	705
328	Genomic scans for selective sweeps using SNP data. <i>Genome Research</i> , 2005 , 15, 1566-75	9.7	668
327	Natural selection on protein-coding genes in the human genome. <i>Nature</i> , 2005 , 437, 1153-7	50.4	615
326	Evolutionary changes in cis and trans gene regulation. <i>Nature</i> , 2004 , 430, 85-8	50.4	577
325	Genetic Determinants of the Gut Microbiome in UK Twins. <i>Cell Host and Microbe</i> , 2016 , 19, 731-43	23.4	547
324	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios. <i>Science</i> , 2003 , 302, 1960-3	33.3	517
323	Haplotype diversity and linkage disequilibrium at human G6PD: recent origin of alleles that confer malarial resistance. <i>Science</i> , 2001 , 293, 455-62	33.3	475
322	Assessing the evolutionary impact of amino acid mutations in the human genome. <i>PLoS Genetics</i> , 2008 , 4, e1000083	6	473
321	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, 11983-8	11.5	455
320	DNA sequence diversity in a 9.7-kb region of the human lipoprotein lipase gene. <i>Nature Genetics</i> , 1998 , 19, 233-40	36.3	436

319	Genome-wide associations of gene expression variation in humans. <i>PLoS Genetics</i> , 2005 , 1, e78	6	431
318	Host genetic variation impacts microbiome composition across human body sites. <i>Genome Biology</i> , 2015 , 16, 191	18.3	428
317	Sequence variation in the human angiotensin converting enzyme. <i>Nature Genetics</i> , 1999 , 22, 59-62	36.3	408
316	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	11	397
315	Recent explosive human population growth has resulted in an excess of rare genetic variants. <i>Science</i> , 2012 , 336, 740-3	33.3	387
314	Recent and ongoing selection in the human genome. <i>Nature Reviews Genetics</i> , 2007 , 8, 857-68	30.1	365
313	Evolution of transcription factor binding sites in Mammalian gene regulatory regions: conservation and turnover. <i>Molecular Biology and Evolution</i> , 2002 , 19, 1114-21	8.3	354
312	Ascertainment bias in studies of human genome-wide polymorphism. <i>Genome Research</i> , 2005 , 15, 1496-502	50.2	351
311	Localizing recent adaptive evolution in the human genome. <i>PLoS Genetics</i> , 2007 , 3, e90	6	342
310	Sequence diversity and haplotype structure in the human ABCB1 (MDR1, multidrug resistance transporter) gene. <i>Pharmacogenetics and Genomics</i> , 2003 , 13, 481-94		335
309	Linkage disequilibrium and the mapping of complex human traits. <i>Trends in Genetics</i> , 2002 , 18, 19-24	8.5	327
308	Dynamic evolution of the innate immune system in <i>Drosophila</i> . <i>Nature Genetics</i> , 2007 , 39, 1461-8	36.3	318
307	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	11	314
306	The role of haplotypes in candidate gene studies. <i>Genetic Epidemiology</i> , 2004 , 27, 321-33	2.6	307
305	Proportionally more deleterious genetic variation in European than in African populations. <i>Nature</i> , 2008 , 451, 994-7	50.4	299
304	Regulatory changes underlying expression differences within and between <i>Drosophila</i> species. <i>Nature Genetics</i> , 2008 , 40, 346-50	36.3	280
303	Thrice out of Africa: ancient and recent expansions of the honey bee, <i>Apis mellifera</i> . <i>Science</i> , 2006 , 314, 642-5	33.3	271
302	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	11.5	268

301	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, 4340-5	11.5	256
300	Genes regulated by mating, sperm, or seminal proteins in mated female <i>Drosophila melanogaster</i> . <i>Current Biology</i> , 2004 , 14, 1509-14	6.3	248
299	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, 5896-901	11.5	208
298	Evolution of protein-coding genes in <i>Drosophila</i> . <i>Trends in Genetics</i> , 2008 , 24, 114-23	8.5	206
297	Signatures of early frailty in the gut microbiota. <i>Genome Medicine</i> , 2016 , 8, 8	14.4	200
296	Targets of balancing selection in the human genome. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2755-648.3	3	199
295	Characterization of Greater Middle Eastern genetic variation for enhanced disease gene discovery. <i>Nature Genetics</i> , 2016 , 48, 1071-6	36.3	192
294	Evolution of Resistance Against CRISPR/Cas9 Gene Drive. <i>Genetics</i> , 2017 , 205, 827-841	4	189
293	Genetic basis of natural variation in <i>D. melanogaster</i> antibacterial immunity. <i>Science</i> , 2004 , 303, 1873-6	33.3	189
292	Deep resequencing reveals excess rare recent variants consistent with explosive population growth. <i>Nature Communications</i> , 2010 , 1, 131	17.4	183
291	The structure of human mitochondrial DNA variation. <i>Journal of Molecular Evolution</i> , 1991 , 33, 543-55	3.1	183
290	Impact of microRNA regulation on variation in human gene expression. <i>Genome Research</i> , 2012 , 22, 1243-54	3.54	182
289	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	6	176
288	Balancing selection maintains a form of ERAP2 that undergoes nonsense-mediated decay and affects antigen presentation. <i>PLoS Genetics</i> , 2010 , 6, e1001157	6	175
287	Estimating the mutation load in human genomes. <i>Nature Reviews Genetics</i> , 2015 , 16, 333-43	30.1	174
286	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	18.3	172
285	Polymorphisms in a human kidney xenobiotic transporter, OCT2, exhibit altered function. <i>Pharmacogenetics and Genomics</i> , 2002 , 12, 395-405		169
284	Cross-species comparisons of host genetic associations with the microbiome. <i>Science</i> , 2016 , 352, 532-5	33.3	168

283	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, 5090-104	4.8	166
282	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	3.8	166
281	Recombinational and mutational hotspots within the human lipoprotein lipase gene. <i>American Journal of Human Genetics</i> , 2000 , 66, 69-83	11	162
280	The functional spectrum of low-frequency coding variation. <i>Genome Biology</i> , 2011 , 12, R84	18.3	161
279	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, 7472-7	11.5	159
278	The Relationship Between the Human Genome and Microbiome Comes into View. <i>Annual Review of Genetics</i> , 2017 , 51, 413-433	14.5	158
277	Genome sequencing reveals complex speciation in the Drosophila simulans clade. <i>Genome Research</i> , 2012 , 22, 1499-511	9.7	158
276	Inferring genetic ancestry: opportunities, challenges, and implications. <i>American Journal of Human Genetics</i> , 2010 , 86, 661-73	11	158
275	Monitoring actin cortex thickness in live cells. <i>Biophysical Journal</i> , 2013 , 105, 570-80	2.9	156
274	Cancer-associated fibroblasts lead tumor invasion through integrin- β -dependent fibronectin assembly. <i>Journal of Cell Biology</i> , 2017 , 216, 3509-3520	7.3	152
273	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	11.5	151
272	Compensatory cis-trans evolution and the dysregulation of gene expression in interspecific hybrids of Drosophila. <i>Genetics</i> , 2005 , 171, 1813-22	4	151
271	Full-exon resequencing reveals toll-like receptor variants contribute to human susceptibility to tuberculosis disease. <i>PLoS ONE</i> , 2007 , 2, e1318	3.7	148
270	Sexually antagonistic cytonuclear fitness interactions in Drosophila melanogaster. <i>Genetics</i> , 2001 , 159, 173-87	4	147
269	Transcriptome-wide identification of novel imprinted genes in neonatal mouse brain. <i>PLoS ONE</i> , 2008 , 3, e3839	3.7	145
268	Microsatellite variation in North American populations of Drosophila melanogaster. <i>Nucleic Acids Research</i> , 1995 , 23, 3882-6	20.1	145
267	Invasion and maintenance of a gene duplication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994 , 91, 2950-4	11.5	145
266	The evolutionary costs of immunological maintenance and deployment. <i>BMC Evolutionary Biology</i> , 2008 , 8, 76	3	142

265	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, 1916-21	11.5	142
264	Sperm competitive ability in <i>Drosophila melanogaster</i> associated with variation in male reproductive proteins. <i>Genetics</i> , 2005 , 169, 243-57	4	141
263	Molecular population genetics of male accessory gland proteins in <i>Drosophila</i> . <i>Genetics</i> , 2000 , 156, 1879-88	5.8	138
262	The human microbiome in evolution. <i>BMC Biology</i> , 2017 , 15, 127	7.3	136
261	Genetic incompatibilities are widespread within species. <i>Nature</i> , 2013 , 504, 135-7	50.4	136
260	Sequence diversity and large-scale typing of SNPs in the human apolipoprotein E gene. <i>Genome Research</i> , 2000 , 10, 1532-45	9.7	131
259	Female genotypes affect sperm displacement in <i>Drosophila</i> . <i>Genetics</i> , 1998 , 149, 1487-93	4	128
258	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	2.3	124
257	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016 , 17, 189	18.3	124
256	Darwinian and demographic forces affecting human protein coding genes. <i>Genome Research</i> , 2009 , 19, 838-49	9.7	122
255	Reconstituting the frequency spectrum of ascertained single-nucleotide polymorphism data. <i>Genetics</i> , 2004 , 168, 2373-82	4	117
254	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, 6706-11	11.5	113
253	Low conservation of gene content in the <i>Drosophila</i> Y chromosome. <i>Nature</i> , 2008 , 456, 949-51	50.4	113
252	A 3.9-centimorgan-resolution human single-nucleotide polymorphism linkage map and screening set. <i>American Journal of Human Genetics</i> , 2003 , 73, 271-84	11	109
251	INFERENCE OF SPERM COMPETITION FROM BROODS OF FIELD-CAUGHT DROSOPHILA. <i>Evolution; International Journal of Organic Evolution</i> , 1998 , 52, 1334-1341	3.8	102
250	Evolutionary processes acting on candidate cis-regulatory regions in humans inferred from patterns of polymorphism and divergence. <i>PLoS Genetics</i> , 2009 , 5, e1000592	6	101
249	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, 1395-408	4	100
248	Intron size and natural selection. <i>Nature</i> , 1999 , 401, 344	50.4	100

247	Paternally expressed genes predominate in the placenta. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 10705-10	11.5	97
246	Integration of single and multicellular wound responses. <i>Current Biology</i> , 2009 , 19, 1389-95	6.3	95
245	Mapping determinants of variation in energy metabolism, respiration and flight in <i>Drosophila</i> . <i>Genetics</i> , 2003 , 165, 623-35	4	94
244	Genetic variation in <i>Drosophila melanogaster</i> resistance to infection: a comparison across bacteria. <i>Genetics</i> , 2006 , 174, 1539-54	4	93
243	Avian W and mammalian Y chromosomes convergently retained dosage-sensitive regulators. <i>Nature Genetics</i> , 2017 , 49, 387-394	36.3	92
242	Disentangling the relationship between sex-biased gene expression and X-linkage. <i>Genome Research</i> , 2012 , 22, 1255-65	9.7	91
241	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020 , 587, 252-257	50.4	89
240	Stresses at the cell surface during animal cell morphogenesis. <i>Current Biology</i> , 2014 , 24, R484-94	6.3	88
239	Population genetic tools for dissecting innate immunity in humans. <i>Nature Reviews Immunology</i> , 2013 , 13, 280-93	36.5	87
238	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, 454-62	9.7	87
237	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, 757-62	11.5	86
236	Population genetic structure of the people of Qatar. <i>American Journal of Human Genetics</i> , 2010 , 87, 17-25	11.5	86
235	Gut-Microbiota-Metabolite Axis in Early Renal Function Decline. <i>PLoS ONE</i> , 2015 , 10, e0134311	3.7	85
234	Optimal haplotype block-free selection of tagging SNPs for genome-wide association studies. <i>Genome Research</i> , 2004 , 14, 1633-40	9.7	84
233	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, 1245-60	4	83
232	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, 1073-81	11.5	83
231	Modeling the Manipulation of Natural Populations by the Mutagenic Chain Reaction. <i>Genetics</i> , 2015 , 201, 425-31	4	82
230	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, 3417-42	3.8	82

229	Global diversity lines - a five-continent reference panel of sequenced <i>Drosophila melanogaster</i> strains. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 593-603	3.2	79
228	Natural selection with nuclear and cytoplasmic transmission. I. A deterministic model. <i>Genetics</i> , 1984 , 107, 679-701	4	79
227	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, 660-71	11	77
226	Population genetic analysis of shotgun assemblies of genomic sequences from multiple individuals. <i>Genome Research</i> , 2008 , 18, 1020-9	9.7	77
225	Nontransitivity of sperm precedence in <i>Drosophila</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2000 , 54, 1030-5	3.8	77
224	A general population genetic framework for antagonistic selection that accounts for demography and recurrent mutation. <i>Genetics</i> , 2012 , 190, 1477-89	4	76
223	A survey for novel imprinted genes in the mouse placenta by mRNA-seq. <i>Genetics</i> , 2011 , 189, 109-22	4	75
222	Satellite DNA evolution: old ideas, new approaches. <i>Current Opinion in Genetics and Development</i> , 2018 , 49, 70-78	4.9	74
221	Red fox genome assembly identifies genomic regions associated with tame and aggressive behaviours. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1479-1491	12.3	74
220	Population dynamics of PIWI-interacting RNAs (piRNAs) and their targets in <i>Drosophila</i> . <i>Genome Research</i> , 2010 , 20, 212-27	9.7	73
219	Linkage disequilibrium and inference of ancestral recombination in 538 single-nucleotide polymorphism clusters across the human genome. <i>American Journal of Human Genetics</i> , 2003 , 73, 285-300	11	72
218	Molecular population genetics of inducible antibacterial peptide genes in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2003 , 20, 914-23	8.3	72
217	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, 703-14	8.3	71
216	Efficient identification of Y chromosome sequences in the human and <i>Drosophila</i> genomes. <i>Genome Research</i> , 2013 , 23, 1894-907	9.7	68
215	Gene-based testing of interactions in association studies of quantitative traits. <i>PLoS Genetics</i> , 2013 , 9, e1003321	6	67
214	Contributions of 18 additional DNA sequence variations in the gene encoding apolipoprotein E to explaining variation in quantitative measures of lipid metabolism. <i>American Journal of Human Genetics</i> , 2002 , 71, 501-17	11	67
213	Balancing selection in species with separate sexes: insights from Fisher's geometric model. <i>Genetics</i> , 2014 , 197, 991-1006	4	66
212	Determinants of the success of whole-genome association testing. <i>Genome Research</i> , 2005 , 15, 1463-7	9.7	66

211	Molecular safeguarding of CRISPR gene drive experiments. <i>ELife</i> , 2019 , 8,	8.9	65
210	Host genetic determinants of microbiota-dependent nutrition revealed by genome-wide analysis of <i>Drosophila melanogaster</i> . <i>Nature Communications</i> , 2015 , 6, 6312	17.4	64
209	Faster-X evolution of gene expression in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2012 , 8, e1003013	6	63
208	Senescence and the Genetic-Correlation Hang-Up. <i>American Naturalist</i> , 1987 , 129, 932-940	3.7	63
207	Natural selection and Y-linked polymorphism. <i>Genetics</i> , 1987 , 115, 569-77	4	62
206	Contrasting the efficacy of selection on the X and autosomes in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2008 , 25, 454-67	8.3	61
205	Indigenous Arabs are descendants of the earliest split from ancient Eurasian populations. <i>Genome Research</i> , 2016 , 26, 151-62	9.7	60
204	Non-Mendelian segregation of sex chromosomes in heterospecific <i>Drosophila</i> males. <i>Genetics</i> , 2000 , 154, 687-94	4	58
203	Genus-wide sequencing supports a two-locus model for sex-determination in Phoenix. <i>Nature Communications</i> , 2018 , 9, 3969	17.4	57
202	A toxin-antidote CRISPR gene drive system for regional population modification. <i>Nature Communications</i> , 2020 , 11, 1082	17.4	56
201	A genome-wide approach to identifying novel-imprinted genes. <i>Human Genetics</i> , 2008 , 122, 625-34	6.3	56
200	Finding genes underlying risk of complex disease by linkage disequilibrium mapping. <i>Current Opinion in Genetics and Development</i> , 2003 , 13, 296-302	4.9	56
199	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, 18793-8	11.5	55
198	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	6	55
197	Understanding the accuracy of statistical haplotype inference with sequence data of known phase. <i>Genetic Epidemiology</i> , 2007 , 31, 659-71	2.6	54
196	Epistasis in measured genotypes: <i>Drosophila</i> P-element insertions. <i>Genetics</i> , 1997 , 147, 157-63	4	53
195	Deconstructing isolation-by-distance: The genomic consequences of limited dispersal. <i>PLoS Genetics</i> , 2017 , 13, e1006911	6	52
194	The genetic basis for male x female interactions underlying variation in reproductive phenotypes of <i>Drosophila</i> . <i>Genetics</i> , 2010 , 186, 1355-65	4	51

193	Robustness of inference of haplotype block structure. <i>Journal of Computational Biology</i> , 2003 , 10, 13-9	1.7	51
192	Sequence variation and linkage disequilibrium in the human T-cell receptor beta (TCRB) locus. <i>American Journal of Human Genetics</i> , 2001 , 69, 381-95	11	51
191	Population growth inflates the per-individual number of deleterious mutations and reduces their mean effect. <i>Genetics</i> , 2013 , 195, 969-78	4	50
190	ABO antigen and secretor statuses are not associated with gut microbiota composition in 1,500 twins. <i>BMC Genomics</i> , 2016 , 17, 941	4.5	49
189	Association between sex-biased gene expression and mutations with sex-specific phenotypic consequences in <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2011 , 3, 151-5	3.9	49
188	Genotype and gene expression associations with immune function in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2010 , 6, e1000797	6	49
187	Population genomic inferences from sparse high-throughput sequencing of two populations of <i>Drosophila melanogaster</i> . <i>Genome Biology and Evolution</i> , 2009 , 1, 449-65	3.9	49
186	Molecular population genetics of <i>Drosophila</i> immune system genes. <i>Genetics</i> , 1997 , 147, 713-24	4	49
185	Evidence for recurrent paralogous gene conversion and exceptional allelic divergence in the Attacin genes of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2001 , 159, 659-71	4	49
184	Refinement of primate copy number variation hotspots identifies candidate genomic regions evolving under positive selection. <i>Genome Biology</i> , 2011 , 12, R52	18.3	48
183	Methods for human demographic inference using haplotype patterns from genomewide single-nucleotide polymorphism data. <i>Genetics</i> , 2009 , 182, 217-31	4	48
182	Candidate genetic modifiers of retinitis pigmentosa identified by exploiting natural variation in <i>Drosophila</i> . <i>Human Molecular Genetics</i> , 2016 , 25, 651-9	5.6	47
181	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, 12450-5	11.5	44
180	GENETIC COMPONENTS OF VARIATION IN ENERGY STORAGE IN DROSOPHILA MELANOGASTER. <i>Evolution; International Journal of Organic Evolution</i> , 1990 , 44, 637-650	3.8	44
179	Genetic conflicts, multiple paternity and the evolution of genomic imprinting. <i>Genetics</i> , 1998 , 148, 893-904	4	44
178	Genomic Consequences of Population Decline in the Endangered Florida Scrub-Jay. <i>Current Biology</i> , 2016 , 26, 2974-2979	6.3	43
177	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, 2385-90	11.5	43
176	Evolutionary constraint and adaptation in the metabolic network of <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2008 , 25, 2537-46	8.3	43

175	Mechanics and regulation of cell shape during the cell cycle. <i>Results and Problems in Cell Differentiation</i> , 2011 , 53, 31-73	1.4	43
174	Rehabilitation and the single cell. <i>Current Opinion in Cell Biology</i> , 2007 , 19, 95-100	9	42
173	Seminal fluid causes temporarily reduced egg hatch in previously mated females. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000 , 267, 201-3	4.4	42
172	Integrated analysis of population genomics, transcriptomics and virulence provides novel insights into <i>Streptococcus pyogenes</i> pathogenesis. <i>Nature Genetics</i> , 2019 , 51, 548-559	36.3	42
171	Computational and experimental performance of CRISPR homing gene drive strategies with multiplexed gRNAs. <i>Science Advances</i> , 2020 , 6, eaaz0525	14.3	41
170	Variable Rates of Simple Satellite Gains across the <i>Drosophila</i> Phylogeny. <i>Molecular Biology and Evolution</i> , 2018 , 35, 925-941	8.3	41
169	The effects of scale: variation in the APOA1/C3/A4/A5 gene cluster. <i>Human Genetics</i> , 2004 , 115, 36-56	6.3	40
168	Evidence for the fixation of gene duplications by positive selection in <i>Drosophila</i> . <i>Genome Research</i> , 2016 , 26, 787-98	9.7	40
167	Genomic responses to selection for tame/aggressive behaviors in the silver fox (). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 10398-10403	11.5	40
166	Independent effects of cis- and trans-regulatory variation on gene expression in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2008 , 178, 1831-5	4	39
165	Y chromosome and other heterochromatic sequences of the <i>Drosophila melanogaster</i> genome: how far can we go?. <i>Genetica</i> , 2003 , 117, 227-37	1.5	39
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163	Genetic and epigenetic architecture of sex-biased expression in the jewel wasps <i>Nasonia vitripennis</i> and <i>giraulti</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E3545-54	11.5	38
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