

Andrew G Clark

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.

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	Migration restores hybrid incompatibility driven by mitochondrial-nuclear sexual conflict.. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022 , 289, 20212561	4.4	
335	Advancing discovery of risk-altering variants for complex diseases by functionally informed fine-mapping.. <i>Neuron</i> , 2022 , 110, 905-907	13.9	
334	Collective effects of human genomic variation on microbiome function.. <i>Scientific Reports</i> , 2022 , 12, 3839	1.9	0
333	A homing suppression gene drive with multiplexed gRNAs maintains high drive conversion efficiency and avoids functional resistance alleles.. <i>G3: Genes, Genomes, Genetics</i> , 2022 ,	3.2	6
332	Experimental demonstration of tethered gene drive systems for confined population modification or suppression. <i>BMC Biology</i> , 2022 , 20,	7.3	4
331	Extent of myosin penetration within the actin cortex regulates cell surface mechanics. <i>Nature Communications</i> , 2021 , 12, 6511	17.4	3
330	The genetic architecture of DNA replication timing in human pluripotent stem cells. <i>Nature Communications</i> , 2021 , 12, 6746	17.4	4
329	Thousands of Qatari genomes inform human migration history and improve imputation of Arab haplotypes. <i>Nature Communications</i> , 2021 , 12, 5929	17.4	4
328	Ethnic Differences in Iron Status. <i>Advances in Nutrition</i> , 2021 , 12, 1838-1853	10	5
327	Dense time-course gene expression profiling of the <i>Drosophila melanogaster</i> innate immune response. <i>BMC Genomics</i> , 2021 , 22, 304	4.5	8
326	Genetically predicted serum vitamin D and COVID-19: a Mendelian randomisation study. <i>BMJ Nutrition, Prevention and Health</i> , 2021 , 4, 213-225	6.7	9
325	Mechanical compartmentalization of the intestinal organoid enables crypt folding and collective cell migration. <i>Nature Cell Biology</i> , 2021 , 23, 745-757	23.4	26
324	Differences in Postmating Transcriptional Responses between Conspecific and Heterospecific Matings in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2021 , 38, 986-999	8.3	5
323	Mutation Rate Variability across Human Y-Chromosome Haplogroups. <i>Molecular Biology and Evolution</i> , 2021 , 38, 1000-1005	8.3	0
322	Leveraging phenotypic variability to identify genetic interactions in human phenotypes. <i>American Journal of Human Genetics</i> , 2021 , 108, 49-67	11	10
321	Design and analysis of CRISPR-based underdominance toxin-antidote gene drives. <i>Evolutionary Applications</i> , 2021 , 14, 1052-1069	4.8	14
320	A polygenic-score-based approach for identification of gene-drug interactions stratifying breast cancer risk. <i>American Journal of Human Genetics</i> , 2021 , 108, 1752-1764	11	1

319	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	5.7	21
318	Mitochondrial-Y chromosome epistasis in. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020 , 287, 20200469	4.4	1
317	Demographic and genetic factors influence the abundance of infiltrating immune cells in human tissues. <i>Nature Communications</i> , 2020 , 11, 2213	17.4	11
316	Genome Diversity and the Origin of the Arabian Horse. <i>Scientific Reports</i> , 2020 , 10, 9702	4.9	14
315	Computational and experimental performance of CRISPR homing gene drive strategies with multiplexed gRNAs. <i>Science Advances</i> , 2020 , 6, eaaz0525	14.3	41
314	Performance analysis of novel toxin-antidote CRISPR gene drive systems. <i>BMC Biology</i> , 2020 , 18, 27	7.3	31
313	A toxin-antidote CRISPR gene drive system for regional population modification. <i>Nature Communications</i> , 2020 , 11, 1082	17.4	56
312	The evolutionary arms race between transposable elements and piRNAs in <i>Drosophila melanogaster</i> . <i>BMC Evolutionary Biology</i> , 2020 , 20, 14	3	9
311	Evolutionary Dynamics of Abundant 7-bp Satellites in the Genome of <i>Drosophila virilis</i> . <i>Molecular Biology and Evolution</i> , 2020 , 37, 1362-1375	8.3	11
310	Dissecting Fertility Functions of a Chromosome Genes with CRISPR. <i>Genetics</i> , 2020 , 214, 977-990	4	2
309	Hypothalamic transcriptome of tame and aggressive silver foxes (<i>Vulpes vulpes</i>) identifies gene expression differences shared across brain regions. <i>Genes, Brain and Behavior</i> , 2020 , 19, e12614	3.6	9
308	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020 , 587, 252-257	50.4	89
307	Interactions between the microbiome and mating influence the female's transcriptional profile in <i>Drosophila melanogaster</i> . <i>Scientific Reports</i> , 2020 , 10, 18168	4.9	7
306	The seminal proteome and its role in postcopulatory sexual selection. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020 , 375, 20200072	5.8	19
305	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	11.5	37
304	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
303	Extensive disruption of protein interactions by genetic variants across the allele frequency spectrum in human populations. <i>Nature Communications</i> , 2019 , 10, 4141	17.4	23
302	Maximum Likelihood Estimation of Fitness Components in Experimental Evolution. <i>Genetics</i> , 2019 , 211, 1005-1017	4	22

301	Sexual conflict through mother's curse and father's curse. <i>Theoretical Population Biology</i> , 2019 , 129, 9-17.	1.2	14
300	CRISPR Gene Drive Efficiency and Resistance Rate Is Highly Heritable with No Common Genetic Loci of Large Effect. <i>Genetics</i> , 2019 , 212, 333-341	4	31
299	Lack of spatial and temporal genetic structure of Japanese eel (<i>Anguilla japonica</i>) populations. <i>Conservation Genetics</i> , 2019 , 20, 467-475	2.6	4
298	Demographic History of the Human Commensal <i>Drosophila melanogaster</i> . <i>Genome Biology and Evolution</i> , 2019 , 11, 844-854	3.9	24
297	Cancer cells in the tumor core exhibit spatially coordinated migration patterns. <i>Journal of Cell Science</i> , 2019 , 132,	5.3	19
296	Overexpression of a glutathione S-transferase (Mdgst) and a galactosyltransferase-like gene (Mdg1) is responsible for imidacloprid resistance in house flies. <i>Pest Management Science</i> , 2019 , 75, 37-44	4.6	18
295	Molecular safeguarding of CRISPR gene drive experiments. <i>ELife</i> , 2019 , 8,	8.9	65
294	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
293	Female Genetic Contributions to Sperm Competition in. <i>Genetics</i> , 2019 , 212, 789-800	4	11
292	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	11.5	25
291	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
290	Satellite DNA evolution: old ideas, new approaches. <i>Current Opinion in Genetics and Development</i> , 2018 , 49, 70-78	4.9	74
289	Rates and Patterns of Mutation in Tandem Repetitive DNA in Six Independent Lineages of <i>Chlamydomonas reinhardtii</i> . <i>Genome Biology and Evolution</i> , 2018 , 10, 1673-1686	3.9	7
288	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
287	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
286	Allele-specific expression elucidates cis-regulatory logic. <i>PLoS Genetics</i> , 2018 , 14, e1007690	6	2
285	Selfish genetic elements. <i>PLoS Genetics</i> , 2018 , 14, e1007700	6	25
284	Genus-wide sequencing supports a two-locus model for sex-determination in Phoenix. <i>Nature Communications</i> , 2018 , 9, 3969	17.4	57

283	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
282	Avian W and mammalian Y chromosomes convergently retained dosage-sensitive regulators. <i>Nature Genetics</i> , 2017 , 49, 387-394	36.3	92
281	Rapid Expansion of Immune-Related Gene Families in the House Fly, <i>Musca domestica</i> . <i>Molecular Biology and Evolution</i> , 2017 , 34, 857-872	8.3	22
280	Estimating mating rates in wild <i>Drosophila melanogaster</i> females by decay rates of male reproductive proteins in their reproductive tracts. <i>Molecular Ecology Resources</i> , 2017 , 17, 1202-1209	8.4	9
279	Genomic signatures of local adaptation in the <i>Drosophila</i> immune response. <i>Fly</i> , 2017 , 11, 277-283	1.3	5
278	A Pooled Sequencing Approach Identifies a Candidate Meiotic Driver in. <i>Genetics</i> , 2017 , 206, 451-465	4	32
277	Survey of Global Genetic Diversity Within the <i>Drosophila</i> Immune System. <i>Genetics</i> , 2017 , 205, 353-366	4	23
276	Evolution of Resistance Against CRISPR/Cas9 Gene Drive. <i>Genetics</i> , 2017 , 205, 827-841	4	189
275	Variation in Position Effect Variegation Within a Natural Population. <i>Genetics</i> , 2017 , 207, 1157-1166	4	7
274	A tuneable microfluidic system for long duration chemotaxis experiments in a 3D collagen matrix. <i>Lab on A Chip</i> , 2017 , 17, 3851-3861	7.2	15
273	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
272	The human microbiome in evolution. <i>BMC Biology</i> , 2017 , 15, 127	7.3	136
271	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
270	The Relationship Between the Human Genome and Microbiome Comes into View. <i>Annual Review of Genetics</i> , 2017 , 51, 413-433	14.5	158
269	Selection Constrains High Rates of Tandem Repetitive DNA Mutation in. <i>Genetics</i> , 2017 , 207, 697-710	4	15
268	Evolutionary Dynamics of Male Reproductive Genes in the Subgroup. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 3145-3155	3.2	16
267	Roles of Female and Male Genotype in Post-Mating Responses in <i>Drosophila melanogaster</i> . <i>Journal of Heredity</i> , 2017 , 108, 740-753	2.4	24
266	Deconstructing isolation-by-distance: The genomic consequences of limited dispersal. <i>PLoS Genetics</i> , 2017 , 13, e1006911	6	52

265	Drosophila Genotype Influences Commensal Bacterial Levels. <i>PLoS ONE</i> , 2017 , 12, e0170332	3.7	24
264	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
263	Characterization of Greater Middle Eastern genetic variation for enhanced disease gene discovery. <i>Nature Genetics</i> , 2016 , 48, 1071-6	36.3	192
262	Genomic Consequences of Population Decline in the Endangered Florida Scrub-Jay. <i>Current Biology</i> , 2016 , 26, 2974-2979	6.3	43
261	Candidate genetic modifiers of retinitis pigmentosa identified by exploiting natural variation in Drosophila. <i>Human Molecular Genetics</i> , 2016 , 25, 651-9	5.6	47
260	Signatures of early frailty in the gut microbiota. <i>Genome Medicine</i> , 2016 , 8, 8	14.4	200
259	Indigenous Arabs are descendants of the earliest split from ancient Eurasian populations. <i>Genome Research</i> , 2016 , 26, 151-62	9.7	60
258	Strong Constraint on Human Genes Escaping X-Inactivation Is Modulated by their Expression Level and Breadth in Both Sexes. <i>Molecular Biology and Evolution</i> , 2016 , 33, 384-93	8.3	12
257	Allele-Specific Transcriptome and Methylome Analysis Reveals Stable Inheritance and Cis-Regulation of DNA Methylation in Nasonia. <i>PLoS Biology</i> , 2016 , 14, e1002500	9.7	33
256	Extensive local adaptation within the chemosensory system following Drosophila melanogaster's global expansion. <i>Nature Communications</i> , 2016 , 7, ncomms11855	17.4	31
255	Integrative modelling of tumour DNA methylation quantifies the contribution of metabolism. <i>Nature Communications</i> , 2016 , 7, 13666	17.4	29
254	Evidence for the fixation of gene duplications by positive selection in Drosophila. <i>Genome Research</i> , 2016 , 26, 787-98	9.7	40
253	Cross-species comparisons of host genetic associations with the microbiome. <i>Science</i> , 2016 , 352, 532-5	33.3	168
252	Genetic Determinants of the Gut Microbiome in UK Twins. <i>Cell Host and Microbe</i> , 2016 , 19, 731-43	23.4	547
251	Integrated network analysis reveals distinct regulatory roles of transcription factors and microRNAs. <i>Rna</i> , 2016 , 22, 1663-1672	5.8	17
250	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016 , 17, 189	18.3	124
249	Host genetic determinants of microbiota-dependent nutrition revealed by genome-wide analysis of Drosophila melanogaster. <i>Nature Communications</i> , 2015 , 6, 6312	17.4	64
248	Characterizing male-female interactions using natural genetic variation in Drosophila melanogaster. <i>Journal of Heredity</i> , 2015 , 106, 67-79	2.4	24

247	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
246	Aberrant Time to Most Recent Common Ancestor as a Signature of Natural Selection. <i>Molecular Biology and Evolution</i> , 2015 , 32, 2784-97	8.3	13
245	The genetic architecture of the genome-wide transcriptional response to ER stress in the mouse. <i>PLoS Genetics</i> , 2015 , 11, e1004924	6	20
244	Estimating the mutation load in human genomes. <i>Nature Reviews Genetics</i> , 2015 , 16, 333-43	30.1	174
243	Sex-ratio meiotic drive and Y-linked resistance in <i>Drosophila affinis</i> . <i>Genetics</i> , 2015 , 199, 831-40	4	17
242	Host genetic variation impacts microbiome composition across human body sites. <i>Genome Biology</i> , 2015 , 16, 191	18.3	428
241	Modeling the Manipulation of Natural Populations by the Mutagenic Chain Reaction. <i>Genetics</i> , 2015 , 201, 425-31	4	82
240	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
239	The distribution of fitness effects in an uncertain world. <i>Evolution; International Journal of Organic Evolution</i> , 2015 , 69, 1610-1618	3.8	14
238	Induction of excessive endoplasmic reticulum stress in the <i>Drosophila</i> male accessory gland results in infertility. <i>PLoS ONE</i> , 2015 , 10, e0119386	3.7	25
237	Gut-Microbiota-Metabolite Axis in Early Renal Function Decline. <i>PLoS ONE</i> , 2015 , 10, e0134311	3.7	85
236	Inference of Heterosis and Epistasis in Transposon Tagged <i>Drosophila</i> . <i>CSSA Special Publication - Crop Science Society of America</i> , 2015 , 89-97		
235	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
234	TRIM28 Controls Genomic Imprinting through Distinct Mechanisms during and after Early Genome-wide Reprogramming. <i>Cell Reports</i> , 2015 , 13, 1194-1205	10.6	26
233	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
232	Transcriptome Differences between Alternative Sex Determining Genotypes in the House Fly, <i>Musca domestica</i> . <i>Genome Biology and Evolution</i> , 2015 , 7, 2051-61	3.9	19
231	Evolutionary genomics. Conundrum of jumbled mosquito genomes. <i>Science</i> , 2015 , 347, 27-8	33.3	25
230	Population genomic analysis of 962 whole genome sequences of humans reveals natural selection in non-coding regions. <i>PLoS ONE</i> , 2015 , 10, e0121644	3.7	12

229	Biological knowledge-driven analysis of epistasis in human GWAS with application to lipid traits. <i>Methods in Molecular Biology</i> , 2015 , 1253, 35-45	1.4	9
228	Comparative metabolomics in primates reveals the effects of diet and gene regulatory variation on metabolic divergence. <i>Scientific Reports</i> , 2014 , 4, 5809	4.9	14
227	Genome-wide histone state profiling of fibroblasts from the opossum, <i>Monodelphis domestica</i> , identifies the first marsupial-specific imprinted gene. <i>BMC Genomics</i> , 2014 , 15, 89	4.5	1
226	Genetics: The vital Y chromosome. <i>Nature</i> , 2014 , 508, 463-5	50.4	11
225	Limited gene misregulation is exacerbated by allele-specific upregulation in lethal hybrids between <i>Drosophila melanogaster</i> and <i>Drosophila simulans</i> . <i>Molecular Biology and Evolution</i> , 2014 , 31, 1767-78	8.3	10
224	Chromosome-wide profiling of X-chromosome inactivation and epigenetic states in fetal brain and placenta of the opossum, <i>Monodelphis domestica</i> . <i>Genome Research</i> , 2014 , 24, 70-83	9.7	37
223	Human genetics shape the gut microbiome. <i>Cell</i> , 2014 , 159, 789-99	56.2	1750
222	Balancing selection in species with separate sexes: insights from Fisher's geometric model. <i>Genetics</i> , 2014 , 197, 991-1006	4	66
221	Positive and purifying selection on the <i>Drosophila</i> Y chromosome. <i>Molecular Biology and Evolution</i> , 2014 , 31, 2612-23	8.3	20
220	Stresses at the cell surface during animal cell morphogenesis. <i>Current Biology</i> , 2014 , 24, R484-94	6.3	88
219	Genomics of ecological adaptation in cactophilic <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2014 , 7, 349-56	38	
218	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
217	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
216	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
215	Using Mendelian inheritance to improve high-throughput SNP discovery. <i>Genetics</i> , 2014 , 198, 847-57	4	21
214	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
213	Monitoring actin cortex thickness in live cells. <i>Biophysical Journal</i> , 2013 , 105, 570-80	2.9	156
212	Genetic incompatibilities are widespread within species. <i>Nature</i> , 2013 , 504, 135-7	50.4	136

211	Efficient identification of Y chromosome sequences in the human and Drosophila genomes. <i>Genome Research</i> , 2013 , 23, 1894-907	9.7	68
210	Population growth inflates the per-individual number of deleterious mutations and reduces their mean effect. <i>Genetics</i> , 2013 , 195, 969-78	4	50
209	Large neurological component to genetic differences underlying biased sperm use in Drosophila. <i>Genetics</i> , 2013 , 193, 177-85	4	31
208	Antagonistic versus nonantagonistic models of balancing selection: characterizing the relative timescales and hitchhiking effects of partial selective sweeps. <i>Evolution; International Journal of Organic Evolution</i> , 2013 , 67, 908-17	3.8	31
207	Population genetic tools for dissecting innate immunity in humans. <i>Nature Reviews Immunology</i> , 2013 , 13, 280-93	36.5	87
206	Gene-based testing of interactions in association studies of quantitative traits. <i>PLoS Genetics</i> , 2013 , 9, e1003321	6	67
205	Reproduction and immunity-driven natural selection in the human WFDC locus. <i>Molecular Biology and Evolution</i> , 2013 , 30, 938-50	8.3	16
204	Inferences of demography and selection in an African population of Drosophila melanogaster. <i>Genetics</i> , 2013 , 193, 215-28	4	20
203	Natural genetic variation in male reproductive genes contributes to nontransitivity of sperm competitive ability in Drosophila melanogaster. <i>Molecular Ecology</i> , 2013 , 22, 1400-15	5.7	35
202	Sequence diversity of Pan troglodytes subspecies and the impact of WFDC6 selective constraints in reproductive immunity. <i>Genome Biology and Evolution</i> , 2013 , 5, 2512-23	3.9	1
201	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
200	Characterizing the infection-induced transcriptome of Nasonia vitripennis reveals a preponderance of taxonomically-restricted immune genes. <i>PLoS ONE</i> , 2013 , 8, e83984	3.7	28
199	Identification of small molecule inhibitors of cytokinesis and single cell wound repair. <i>Cytoskeleton</i> , 2012 , 69, 1010-20	2.4	5
198	A general population genetic framework for antagonistic selection that accounts for demography and recurrent mutation. <i>Genetics</i> , 2012 , 190, 1477-89	4	76
197	Random X inactivation in the mule and horse placenta. <i>Genome Research</i> , 2012 , 22, 1855-63	9.7	29
196	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
195	Recent explosive human population growth has resulted in an excess of rare genetic variants. <i>Science</i> , 2012 , 336, 740-3	33.3	387
194	Disentangling the relationship between sex-biased gene expression and X-linkage. <i>Genome Research</i> , 2012 , 22, 1255-65	9.7	91

193	Genome sequencing reveals complex speciation in the <i>Drosophila simulans</i> clade. <i>Genome Research</i> , 2012 , 22, 1499-511	9.7	158
192	Impact of microRNA regulation on variation in human gene expression. <i>Genome Research</i> , 2012 , 22, 1243-54	9.7	182
191	Faster-X evolution of gene expression in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2012 , 8, e1003013	6	63
190	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
189	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
188	The functional spectrum of low-frequency coding variation. <i>Genome Biology</i> , 2011 , 12, R84	18.3	161
187	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
186	Female influence on pre- and post-copulatory sexual selection and its genetic basis in <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2011 , 20, 4098-108	5.7	13
185	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
184	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
183	Associations between Variation in X Chromosome Male Reproductive Genes and Sperm Competitive Ability in <i>Drosophila melanogaster</i> . <i>International Journal of Evolutionary Biology</i> , 2011 , 2011, 214280		13
182	Detecting directional selection in the presence of recent admixture in African-Americans. <i>Genetics</i> , 2011 , 187, 823-35	4	28
181	A survey for novel imprinted genes in the mouse placenta by mRNA-seq. <i>Genetics</i> , 2011 , 189, 109-22	4	75
180	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
179	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
178	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
177	The effect of recent admixture on inference of ancient human population history. <i>Genetics</i> , 2010 , 185, 611-22	4	23
176	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

175	A hierarchical Bayesian model for a novel sparse partial diallel crossing design. <i>Genetics</i> , 2010 , 185, 361-73		27
174	Genotype and gene expression associations with immune function in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2010 , 6, e1000797	6	49
173	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
172	Functional regulatory divergence of the innate immune system in interspecific <i>Drosophila</i> hybrids. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2596-605	8.3	3
171	Deep resequencing reveals excess rare recent variants consistent with explosive population growth. <i>Nature Communications</i> , 2010 , 1, 131	17.4	183
170	Contrasting methods of quantifying fine structure of human recombination. <i>Annual Review of Genomics and Human Genetics</i> , 2010 , 11, 45-64	9.7	23
169	Paternally biased X inactivation in mouse neonatal brain. <i>Genome Biology</i> , 2010 , 11, R79	18.3	35
168	Inferring genetic ancestry: opportunities, challenges, and implications. <i>American Journal of Human Genetics</i> , 2010 , 86, 661-73	11	158
167	Population genetic structure of the people of Qatar. <i>American Journal of Human Genetics</i> , 2010 , 87, 17-25	11	86
166	Strong evidence for lineage and sequence specificity of substitution rates and patterns in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2009 , 26, 1591-605	8.3	36
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