Paul Flicek

List of Publications by Citations

267 papers	95,336 citations	103 h-index	307 g-index
307 ext. papers	121,561 ext. citations	20 avg, IF	8.45 L-index

#	Paper	IF	Citations
267	An integrated encyclopedia of DNA elements in the human genome. *Nature*, **2012**, 489, 57-74	50.4	11449
266	A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74	50.4	8599
265	A map of human genome variation from population-scale sequencing. *Nature*, **2010**, 467, 1061-73	50.4	6142
264	An integrated map of genetic variation from 1,092 human genomes. *Nature*, **2012**, 491, 56-65	50.4	6049
263	Initial sequencing and comparative analysis of the mouse genome. *Nature*, **2002**, 420, 520-62	50.4	5376
262	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, **2007**, 447, 799-816	50.4	4121
261	The Ensembl Variant Effect Predictor. *Genome Biology*, **2016**, 17, 122	18.3	2595
260	The NHGRI GWAS Catalog, a curated resource of SNP-trait associations. *Nucleic Acids Research*, **2014**, 42, D1001-6	20.1	2124
259	Ensembl 2018. *Nucleic Acids Research*, **2018**, 46, D754-D761	20.1	1822
258	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613
257	The IPD and IMGT/HLA database: allele variant databases. *Nucleic Acids Research*, **2015**, 43, D423-31	20.1	1449
256	The NHGRI-EBI GWAS Catalog of published genome-wide association studies, targeted arrays and summary statistics 2019. *Nucleic Acids Research*, **2019**, 47, D1005-D1012	20.1	1422
255	An integrated map of structural variation in 2,504 human genomes. *Nature*, **2015**, 526, 75-81	50.4	1368
254	Transcriptome and genome sequencing uncovers functional variation in humans. *Nature*, **2013**, 501, 506-11	50.4	1323
253	The new NHGRI-EBI Catalog of published genome-wide association studies (GWAS Catalog). *Nucleic Acids Research*, **2017**, 45, D896-D901	20.1	1321
252	Deriving the consequences of genomic variants with the Ensembl API and SNP Effect Predictor. *Bioinformatics*, **2010**, 26, 2069-70	7.2	1240
251	GENCODE reference annotation for the human and mouse genomes. *Nucleic Acids Research*, **2019**, 47, D766-D773	20.1	1140

250	Ensembl 2016. *Nucleic Acids Research*, **2016**, 44, D710-6	20.1	1094
249	Ensembl 2014. *Nucleic Acids Research*, **2014**, 42, D749-55	20.1	1087
248	A comparative encyclopedia of DNA elements in the mouse genome. *Nature*, **2014**, 515, 355-64	50.4	1026
247	Ensembl 2015. *Nucleic Acids Research*, **2015**, 43, D662-9	20.1	1013
246	Population genomics of human gene expression. *Nature Genetics*, **2007**, 39, 1217-24	36.3	936
245	A high-resolution map of human evolutionary constraint using 29 mammals. *Nature*, **2011**, 478, 476-82	50.4	802
244	Ensembl 2012. *Nucleic Acids Research*, **2012**, 40, D84-90	20.1	798
243	Ensembl 2013. *Nucleic Acids Research*, **2013**, 41, D48-55	20.1	797
242	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776
241	Ensembl BioMarts: a hub for data retrieval across taxonomic space. *Database: the Journal of Biological Databases and Curation*, **2011**, 2011, bar030	5	751
240	Molecular maps of the reorganization of genome-nuclear lamina interactions during differentiation. *Molecular Cell*, **2010**, 38, 603-13	17.6	746
239	The genome of a songbird. *Nature*, **2010**, 464, 757-62	50.4	655
238	Ensembl 2020. *Nucleic Acids Research*, **2020**, 48, D682-D688	20.1	645
237	IPD-IMGT/HLA Database. *Nucleic Acids Research*, **2020**, 48, D948-D955	20.1	612
236	High-throughput discovery of novel developmental phenotypes. *Nature*, **2016**, 537, 508-514	50.4	608
235	Ensembl 2011. *Nucleic Acids Research*, **2011**, 39, D800-6	20.1	590
234	Five-vertebrate ChIP-seq reveals the evolutionary dynamics of transcription factor binding. *Science*, **2010**, 328, 1036-40	33.3	559
233	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. *Cell*, **2016**, 167, 1369-1384.e19	56.2	556

232	Ensembl 2019. *Nucleic Acids Research*, **2019**, 47, D745-D751	20.1	554
231	Genome analysis of the platypus reveals unique signatures of evolution. *Nature*, **2008**, 453, 175-83	50.4	545
230	The Ensembl gene annotation system. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	537
229	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. *Nature Biotechnology*, **2008**, 26, 779-85	44.5	533
228	Insights into hominid evolution from the gorilla genome sequence. *Nature*, **2012**, 483, 169-75	50.4	517
227	Sequencing of the sea lamprey (Petromyzon marinus) genome provides insights into vertebrate evolution. *Nature Genetics*, **2013**, 45, 415-21, 421e1-2	36.3	465
226	De novo assembly and genotyping of variants using colored de Bruijn graphs. *Nature Genetics*, **2012** , 44, 226-32	36.3	433
225	Comparative and demographic analysis of orang-utan genomes. *Nature*, **2011**, 469, 529-33	50.4	431
224	Enhancer evolution across 20 mammalian species. *Cell*, **2015**, 160, 554-66	56.2	422
223	Ensembl 2008. *Nucleic Acids Research*, **2008**, 36, D707-14	20.1	408
222	Ensembl 2017. *Nucleic Acids Research*, **2017**, 45, D635-D642	20.1	404
221	Waves of retrotransposon expansion remodel genome organization and CTCF binding in multiple mammalian lineages. *Cell*, **2012**, 148, 335-48	56.2	390
220	Functional annotation of noncoding sequence variants. *Nature Methods*, **2014**, 11, 294-6	21.6	368
219	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. *Genome Research*, **2017**, 27, 849-864	9.7	365
218	Multi-platform discovery of haplotype-resolved structural variation in human genomes. *Nature Communications*, **2019**, 10, 1784	17.4	346
217	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. *Cell*, **2016**, 167, 1398-1414.e24	50.2	339
216	Ensembl 2021. *Nucleic Acids Research*, **2021**, 49, D884-D891	20.1	324
215	The landscape of histone modifications across 1% of the human genome in five human cell lines. *Genome Research*, **2007**, 17, 691-707	9.7	315

214	Multi-platform next-generation sequencing of the domestic turkey (Meleagris gallopavo): genome assembly and analysis. *PLoS Biology*, **2010**, 8, e1000475	9.7	311
213	An integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs). *Genome Research*, **2008**, 18, 1518-29	9.7	304
212	The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. *Nature Genetics*, **2013**, 45, 701-706	36.3	299
211	The sheep genome illuminates biology of the rumen and lipid metabolism. *Science*, **2014**, 344, 1168-1173	33.3	294
210	Modernizing reference genome assemblies. *PLoS Biology*, **2011**, 9, e1001091	9.7	294
209	A CTCF-independent role for cohesin in tissue-specific transcription. *Genome Research*, **2010**, 20, 578-88	9.7	286
208	Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. *Cell*, **2016**, 167, 1354-1368.e14	56.2	283
207	Integrative annotation of variants from 1092 humans: application to cancer genomics. *Science*, **2013**, 342, 1235587	33.3	281
206	BLUEPRINT to decode the epigenetic signature written in blood. *Nature Biotechnology*, **2012**, 30, 224-6	44.5	261
205	Sense from sequence reads: methods for alignment and assembly. *Nature Methods*, **2009**, 6, S6-S12	21.6	261
204	Gibbon genome and the fast karyotype evolution of small apes. *Nature*, **2014**, 513, 195-201	50.4	241
203	Ensembl 10th year. *Nucleic Acids Research*, **2010**, 38, D557-62	20.1	240
202	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. *Cell*, **2016**, 167, 1145-1149	56.2	232
201	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. *Genome Research*, **2013**, 23, 2066-77	9.7	232
200	Ensembl variation resources. *Database: the Journal of Biological Databases and Curation*, **2018**, 2018,	5	230
199	The European Genome-phenome Archive of human data consented for biomedical research. *Nature Genetics*, **2015**, 47, 692-5	36.3	224
198	Ensembl Genomes 2020-enabling non-vertebrate genomic research. *Nucleic Acids Research*, **2020**, 48, D689-D695	20.1	214
197	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. *Nature Genetics*, **2015**, 47, 746-56	36.3	209

196	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. *Nature Genetics*, **2016**, 48, 593-9	36.3	204
195	The 1000 Genomes Project: data management and community access. *Nature Methods*, **2012**, 9, 459-62	21.6	202
194	The DNA sequence of human chromosome 7. *Nature*, **2003**, 424, 157-64	50.4	202
193	The International Mouse Phenotyping Consortium Web Portal, a unified point of access for knockout mice and related phenotyping data. *Nucleic Acids Research*, **2014**, 42, D802-9	20.1	189
192	CHD7 targets active gene enhancer elements to modulate ES cell-specific gene expression. *PLoS Genetics*, **2010**, 6, e1001023	6	188
191	Transcriptional diversity during lineage commitment of human blood progenitors. *Science*, **2014**, 345, 1251033	33.3	187
190	EGASP: the human ENCODE Genome Annotation Assessment Project. *Genome Biology*, **2006**, 7 Suppl 1, S2.1-31	18.3	187
189	Ensembl comparative genomics resources. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	186
188	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. *Science*, **2015**, 348, 666-9	33.3	170
187	DbVar and DGVa: public archives for genomic structural variation. *Nucleic Acids Research*, **2013**, 41, D936-41	20.1	162
186	The functional spectrum of low-frequency coding variation. *Genome Biology*, **2011**, 12, R84	18.3	161
185	Towards complete and error-free genome assemblies of all vertebrate species. *Nature*, **2021**, 592, 737-746	36.4	161
184	SNP and haplotype mapping for genetic analysis in the rat. *Nature Genetics*, **2008**, 40, 560-6	36.3	150
183	Making sense of big data in health research: Towards an EU action plan. *Genome Medicine*, **2016**, 8, 71	14.4	146
182	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. *Nature Genetics*, **2017**, 49, 1231-1238	36.3	145
181	Evolution of transcription factor binding in metazoans - mechanisms and functional implications. *Nature Reviews Genetics*, **2014**, 15, 221-33	30.1	143
180	Genome sequence of an Australian kangaroo, Macropus eugenii, provides insight into the evolution of mammalian reproduction and development. *Genome Biology*, **2011**, 12, R81	18.3	142
179	Genome-wide nucleotide-level mammalian ancestor reconstruction. *Genome Research*, **2008**, 18, 1829-43	9.7	136

178	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. *Nature Genetics*, **2013**, 45, 767-75	36.3	131
177	Computational approaches to identify functional genetic variants in cancer genomes. *Nature Methods*, **2013**, 10, 723-9	21.6	129
176	Genome sequencing reveals loci under artificial selection that underlie disease phenotypes in the laboratory rat. *Cell*, **2013**, 154, 691-703	56.2	127
175	Cohesin regulates tissue-specific expression by stabilizing highly occupied cis-regulatory modules. *Genome Research*, **2012**, 22, 2163-75	9.7	117
174	Ascl1 Coordinately Regulates Gene Expression and the Chromatin Landscape during Neurogenesis. *Cell Reports*, **2015**, 10, 1544-1556	10.6	113
173	Convergent genomic signatures of domestication in sheep and goats. *Nature Communications*, **2018**, 9, 813	17.4	112
172	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. *Genome Research*, **2008**, 18, 393-403	9.7	111
171	The Ensembl REST API: Ensembl Data for Any Language. *Bioinformatics*, **2015**, 31, 143-5	7.2	108
170	Extending reference assembly models. *Genome Biology*, **2015**, 16, 13	18.3	107
169	Cooperativity and rapid evolution of cobound transcription factors in closely related mammals. *Cell*, **2013**, 154, 530-40	56.2	107
168	Spatial enhancer clustering and regulation of enhancer-proximal genes by cohesin. *Genome Research*, **2015**, 25, 504-13	9.7	106
167	Extensive compensatory cis-trans regulation in the evolution of mouse gene expression. *Genome Research*, **2012**, 22, 2376-84	9.7	106
166	Ensembl variation resources. *BMC Genomics*, **2010**, 11, 293	4.5	104
165	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. *Nature Medicine*, **2018**, 24, 868-880	50.5	103
164	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. *Nature Genetics*, **2015**, 47, 1316-1325	36.3	101
163	The international Genome sample resource (IGSR): A worldwide collection of genome variation incorporating the 1000 Genomes Project data. *Nucleic Acids Research*, **2017**, 45, D854-D859	20.1	101
162	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. *Science*, **2021**, 372,	33.3	100
161	A gene regulatory network directed by zebrafish No tail accounts for its roles in mesoderm formation. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 3829-34	11.5	95

160	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. *Nature Communications*, **2016**, 7, 13555	17.4	95
159	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. *Genome Research*, **2015**, 25, 478-87	9.7	92
158	IPD-MHC 2.0: an improved inter-species database for the study of the major histocompatibility complex. *Nucleic Acids Research*, **2017**, 45, D860-D864	20.1	91
157	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. *Nature Genetics*, **2018**, 50, 1574-1583	36.3	91
156	A standardized framework for representation of ancestry data in genomics studies, with application to the NHGRI-EBI GWAS Catalog. *Genome Biology*, **2018**, 19, 21	18.3	87
155	Locus Reference Genomic sequences: an improved basis for describing human DNA variants. *Genome Medicine*, **2010**, 2, 24	14.4	86
154	Random monoallelic gene expression increases upon embryonic stem cell differentiation. *Developmental Cell*, **2014**, 28, 351-65	10.2	82
153	GENCODE 2021. *Nucleic Acids Research*, **2021**, 49, D916-D923	20.1	82
152	A large scale hearing loss screen reveals an extensive unexplored genetic landscape for auditory dysfunction. *Nature Communications*, **2017**, 8, 886	17.4	81
151	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. *Genome Research*, **2010**, 20, 791-803	9.7	77
150	Leveraging the mouse genome for gene prediction in human: from whole-genome shotgun reads to a global synteny map. *Genome Research*, **2003**, 13, 46-54	9.7	77
149	Decoding the DNA Methylome of Mantle Cell Lymphoma in the Light of the Entire B Cell Lineage. *Cancer Cell*, **2016**, 30, 806-821	24.3	73
148	Ensembl 2022. *Nucleic Acids Research*, **2021**,	20.1	72
147	The BLUEPRINT Data Analysis Portal. *Cell Systems*, **2016**, 3, 491-495.e5	10.6	71
146	A standard variation file format for human genome sequences. *Genome Biology*, **2010**, 11, R88	18.3	71
145	Functional diversity for REST (NRSF) is defined by in vivo binding affinity hierarchies at the DNA sequence level. *Genome Research*, **2009**, 19, 994-1005	9.7	68
144	Public data archives for genomic structural variation. *Nature Genetics*, **2010**, 42, 813-4	36.3	67
143	The human-induced pluripotent stem cell initiative-data resources for cellular genetics. *Nucleic Acids Research*, **2017**, 45, D691-D697	20.1	63

142	Multi-species, multi-transcription factor binding highlights conserved control of tissue-specific biological pathways. *ELife*, **2014**, 3, e02626	8.9	62
141	Perspectives on ENCODE. *Nature*, **2020**, 583, 693-698	50.4	61
140	An improved pig reference genome sequence to enable pig genetics and genomics research. *GigaScience*, **2020**, 9,	7.6	60
139	An integrated functional genomics approach identifies the regulatory network directed by brachyury (T) in chordoma. *Journal of Pathology*, **2012**, 228, 274-85	9.4	59
138	Locus Reference Genomic: reference sequences for the reporting of clinically relevant sequence variants. *Nucleic Acids Research*, **2014**, 42, D873-8	20.1	58
137	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. *Genome Biology*, **2017**, 18, 50	18.3	57
136	Third Report on Chicken Genes and Chromosomes 2015. *Cytogenetic and Genome Research*, **2015**, 145, 78-179	1.9	57
135	Repeat associated mechanisms of genome evolution and function revealed by the and genomes. *Genome Research*, **2018**, 28, 448-459	9.7	57
134	Characterizing neutral genomic diversity and selection signatures in indigenous populations of Moroccan goats (Capra hircus) using WGS data. *Frontiers in Genetics*, **2015**, 6, 107	4.5	55
133	Complexity and conservation of regulatory landscapes underlie evolutionary resilience of mammalian gene expression. *Nature Ecology and Evolution*, **2018**, 2, 152-163	12.3	55
132	Chromosome assembly of large and complex genomes using multiple references. *Genome Research*, **2018**, 28, 1720-1732	9.7	54
131	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. *Cell Reports*, **2018**, 24, 2784-2794	10.6	54
130	Latent regulatory potential of human-specific repetitive elements. *Molecular Cell*, **2013**, 49, 262-72	17.6	53
129	nGASP--the nematode genome annotation assessment project. *BMC Bioinformatics*, **2008**, 9, 549	3.6	51
128	Co-binding by YY1 identifies the transcriptionally active, highly conserved set of CTCF-bound regions in primate genomes. *Genome Biology*, **2013**, 14, R148	18.3	50
127	GENETICS. The Human Variome Project. *Science*, **2008**, 322, 861-2	33.3	50
126	A chromosome-level assembly of the Atlantic herring genome-detection of a supergene and other signals of selection. *Genome Research*, **2019**, 29, 1919-1928	9.7	49
125	The tuatara genome reveals ancient features of amniote evolution. *Nature*, **2020**, 584, 403-409	50.4	49

124	Identification of genetic elements in metabolism by high-throughput mouse phenotyping. *Nature Communications*, **2018**, 9, 288	17.4	48
123	The International Genome Sample Resource (IGSR) collection of open human genomic variation resources. *Nucleic Acids Research*, **2020**, 48, D941-D947	20.1	48
122	Characterization of the neural stem cell gene regulatory network identifies OLIG2 as a multifunctional regulator of self-renewal. *Genome Research*, **2015**, 25, 41-56	9.7	47
121	Optimized design and assessment of whole genome tiling arrays. *Bioinformatics*, **2007**, 23, i195-204	7.2	46
120	WiggleTools: parallel processing of large collections of genome-wide datasets for visualization and statistical analysis. *Bioinformatics*, **2014**, 30, 1008-9	7.2	44
119	The International Mouse Phenotyping Consortium (IMPC): a functional catalogue of the mammalian genome that informs conservation. *Conservation Genetics*, **2018**, 19, 995-1005	2.6	44
118	Addressing Beacon re-identification attacks: quantification and mitigation of privacy risks. *Journal of the American Medical Informatics Association: JAMIA*, **2017**, 24, 799-805	8.6	43
117	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. *Nature Genetics*, **2017**, 49, 1714-1721	36.3	43
116	Federated discovery and sharing of genomic data using Beacons. *Nature Biotechnology*, **2019**, 37, 220-224	44.5	42
115	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. *Cell Reports*, **2016**, 17, 2101-2111	10.6	42
114	Clustered CTCF binding is an evolutionary mechanism to maintain topologically associating domains. *Genome Biology*, **2020**, 21, 5	18.3	42
113	Characterizing genetic variants for clinical action. *American Journal of Medical Genetics, Part C: Seminars in Medical Genetics*, **2014**, 166C, 93-104	3.1	41
112	Towards complete and error-free genome assemblies of all vertebrate species		38
111	Decoupling of evolutionary changes in transcription factor binding and gene expression in mammals. *Genome Research*, **2015**, 25, 167-78	9.7	37
110	Divergence in gene expression within and between two closely related flycatcher species. *Molecular Ecology*, **2016**, 25, 2015-28	5.7	37
109	Leveraging European infrastructures to access 1 million human genomes by 2022. *Nature Reviews Genetics*, **2019**, 20, 693-701	30.1	36
108	eHive: an artificial intelligence workflow system for genomic analysis. *BMC Bioinformatics*, **2010**, 11, 240	3.6	36
107	Ensembl core software resources: storage and programmatic access for DNA sequence and genome annotation. *Database: the Journal of Biological Databases and Curation*, **2017**, 2017,	5	35

106	Strand selective generation of endo-siRNAs from the Na/phosphate transporter gene Slc34a1 in murine tissues. *Nucleic Acids Research*, **2009**, 37, 2274-82	20.1	33
105	Ensembl regulation resources. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	33
104	Accessing data from the International Mouse Phenotyping Consortium: state of the art and future plans. *Mammalian Genome*, **2012**, 23, 641-52	3.2	32
103	Alignment of 1000 Genomes Project reads to reference assembly GRCh38. *GigaScience*, **2017**, 6, 1-8	7.6	31
102	Interplay of cis and trans mechanisms driving transcription factor binding and gene expression evolution. *Nature Communications*, **2017**, 8, 1092	17.4	31
101	High coverage whole genome sequencing of the expanded 1000 Genomes Project cohort including 602 trios		31
100	Epigenome data release: a participant-centered approach to privacy protection. *Genome Biology*, **2015**, 16, 142	18.3	30
99	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. *Nature Communications*, **2017**, 8, 16058	17.4	30
98	Global identification of Smad2 and Eomesodermin targets in zebrafish identifies a conserved transcriptional network in mesendoderm and a novel role for Eomesodermin in repression of ectodermal gene expression. *BMC Biology*, **2014**, 12, 81	7.3	30
97	Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. *Nucleic Acids Research*, **2021**, 49, D1452-D1463	20.1	29
96	Computational approaches to interpreting genomic sequence variation. *Genome Medicine*, **2014**, 6, 87	14.4	28
95	Uncovering information on expression of natural antisense transcripts in Affymetrix MOE430 datasets. *BMC Genomics*, **2007**, 8, 200	4.5	27
94	A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. *Nature Communications*, **2021**, 12, 463	17.4	27
93	CAST-ChIP maps cell-type-specific chromatin states in the Drosophila central nervous system. *Cell Reports*, **2013**, 5, 271-82	10.6	26
92	A database and API for variation, dense genotyping and resequencing data. *BMC Bioinformatics*, **2010**, 11, 238	3.6	26
91	Gene finding in the chicken genome. *BMC Bioinformatics*, **2005**, 6, 131	3.6	26
90	Multi-platform discovery of haplotype-resolved structural variation in human genomes		26
89	Variant calling on the GRCh38 assembly with the data from phase three of the 1000 Genomes Project. *Wellcome Open Research*, **2019**, 4, 50	4.8	24

88	Avianbase: a community resource for bird genomics. *Genome Biology*, **2015**, 16, 21	18.3	22
87	CTCF maintains regulatory homeostasis of cancer pathways. *Genome Biology*, **2018**, 19, 106	18.3	22
86	VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. *Nucleic Acids Research*, **2021**,	20.1	22
85	Consistent annotation of gene expression arrays. *BMC Genomics*, **2010**, 11, 294	4.5	21
84	Pervasive lesion segregation shapes cancer genome evolution. *Nature*, **2020**, 583, 265-270	50.4	20
83	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. *Cell Genomics*, **2021**, 1, 100029-100029		20
82	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. *Cell*, **2021**, 184, 2633-2648.e19	56.2	20
81	Identification of genes required for eye development by high-throughput screening of mouse knockouts. *Communications Biology*, **2018**, 1, 236	6.7	20
80	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. *Cell Reports*, **2019**, 26, 1059-1069.e6	10.6	19
79	A CpG mutational hotspot in a ONECUT binding site accounts for the prevalent variant of hemophilia B Leyden. *American Journal of Human Genetics*, **2013**, 92, 460-7	11	19
78	Variant calling on the GRCh38 assembly with the data from phase three of the 1000 Genomes Project. *Wellcome Open Research*, **2019**, 4, 50	4.8	19
77	Applications of the 1000 Genomes Project resources. *Briefings in Functional Genomics*, **2017**, 16, 163-170	4.9	18
76	Registered access: authorizing data access. *European Journal of Human Genetics*, **2018**, 26, 1721-1731	5.3	17
75	An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. *Molecular Ecology Resources*, **2019**, 19, 1497-1515	8.4	17
74	Getting the Entire Message: Progress in Isoform Sequencing. *Frontiers in Genetics*, **2019**, 10, 709	4.5	16
73	LaGomiCs-Lagomorph Genomics Consortium: An International Collaborative Effort for Sequencing the Genomes of an Entire Mammalian Order. *Journal of Heredity*, **2016**, 107, 295-308	2.4	15
72	The Earth BioGenome Project 2020: Starting the clock.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	15
71	An improved pig reference genome sequence to enable pig genetics and genomics research		15

70	The Evolutionary Fates of a Large Segmental Duplication in Mouse. *Genetics*, **2016**, 204, 267-85	4	14
69	ncRNA orthologies in the vertebrate lineage. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	14
68	TranscriptSNPView: a genome-wide catalog of mouse coding variation. *Nature Genetics*, **2006**, 38, 853	36.3	14
67	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly		13
66	Mitochondrial heteroplasmy in vertebrates using ChIP-sequencing data. *Genome Biology*, **2016**, 17, 139	18.3	13
65	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. *Nucleic Acids Research*, **2021**,	20.1	12
64	The European Bioinformatics Institute: empowering cooperation in response to a global health crisis. *Nucleic Acids Research*, **2021**, 49, D29-D37	20.1	12
63	Functional annotations of three domestic animal genomes provide vital resources for comparative and agricultural research. *Nature Communications*, **2021**, 12, 1821	17.4	12
62	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmasks de novo variants in. *Npj Genomic Medicine*, **2019**, 4, 31	6.2	12
61	The need for speed. *Genome Biology*, **2009**, 10, 212	18.3	11
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