Paul Flicek

List of Publications by Year in Descending Order

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	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
266	Standards recommendations for the Earth BioGenome Project.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	4
265	Sequence locally, think globally: The Darwin Tree of Life Project.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	9
264	Scripting Analyses of Genomes in Ensembl Plants.. *Methods in Molecular Biology*, **2022**, 2443, 27-55	1.4	0
263	The Human Pangenome Project: a global resource to map genomic diversity.. *Nature*, **2022**, 604, 437-446	50.4	7
262	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. *Nucleic Acids Research*, **2021**,	20.1	12
261	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. *Cell Genomics*, **2021**, 1, 100029-100029		20
260	The European Bioinformatics Institute (EMBL-EBI) in 2021. *Nucleic Acids Research*, **2021**,	20.1	2
259	The European Variation Archive: a FAIR resource of genomic variation for all species. *Nucleic Acids Research*, **2021**,	20.1	10
258	VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. *Nucleic Acids Research*, **2021**,	20.1	22
257	The European Genome-phenome Archive in 2021. *Nucleic Acids Research*, **2021**,	20.1	5
256	Ensembl 2022. *Nucleic Acids Research*, **2021**,	20.1	72
255	The European Bioinformatics Institute: empowering cooperation in response to a global health crisis. *Nucleic Acids Research*, **2021**, 49, D29-D37	20.1	12
254	Cell type-specific novel long non-coding RNA and circular RNA in the BLUEPRINT hematopoietic transcriptomes atlas. *Haematologica*, **2021**, 106, 2613-2623	6.6	5
253	Functional annotations of three domestic animal genomes provide vital resources for comparative and agricultural research. *Nature Communications*, **2021**, 12, 1821	17.4	12
252	Accessing Livestock Resources in Ensembl. *Frontiers in Genetics*, **2021**, 12, 650228	4.5	2
251	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. *Science* , **2021**, 372,	33.3	100

250	Towards complete and error-free genome assemblies of all vertebrate species. *Nature*, **2021**, 592, 737-746	56.4	161
249	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. *Nature Communications*, **2021**, 12, 2298	17.4	7
248	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. *Cell*, **2021**, 184, 2633-2648.e19	56.2	20
247	The FAANG Data Portal: Global, Open-Access, "FAIR", and Richly Validated Genotype to Phenotype Data for High-Quality Functional Annotation of Animal Genomes. *Frontiers in Genetics*, **2021**, 12, 639238	4.5	0
246	Ensembl 2021. *Nucleic Acids Research*, **2021**, 49, D884-D891	20.1	324
245	Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. *Nucleic Acids Research*, **2021**, 49, D1452-D1463	20.1	29
244	GENCODE 2021. *Nucleic Acids Research*, **2021**, 49, D916-D923	20.1	82
243	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. *Nucleic Acids Research*, **2021**,	20.1	3
242	A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. *Nature Communications*, **2021**, 12, 463	17.4	27
241	A Minimally Morphologically Destructive Approach for DNA Retrieval and Whole-Genome Shotgun Sequencing of Pinned Historic Dipteran Vector Species. *Genome Biology and Evolution*, **2021**, 13,	3.9	1
240	LINE retrotransposons characterize mammalian tissue-specific and evolutionarily dynamic regulatory regions. *Genome Biology*, **2021**, 22, 62	18.3	9
239	The value of primary transcripts to the clinical and non-clinical genomics community: Survey results and roadmap for improvements. *Molecular Genetics & Genomic Medicine*, **2021**, e1786	2.3	2
238	K-mer counting and curated libraries drive efficient annotation of repeats in plant genomes. *Plant Genome*, **2021**, 14, e20143	4.4	2
237	Progress, Challenges, and Surprises in Annotating the Human Genome. *Annual Review of Genomics and Human Genetics*, **2020**, 21, 55-79	9.7	6
236	Pervasive lesion segregation shapes cancer genome evolution. *Nature*, **2020**, 583, 265-270	50.4	20
235	An improved pig reference genome sequence to enable pig genetics and genomics research. *GigaScience*, **2020**, 9,	7.6	60
234	Identification of male heterogametic sex-determining regions on the Atlantic herring Clupea harengus genome. *Journal of Fish Biology*, **2020**, 97, 190-201	1.9	3
233	IPD-IMGT/HLA Database. *Nucleic Acids Research*, **2020**, 48, D948-D955	20.1	612

232	Ensembl 2020. *Nucleic Acids Research*, **2020**, 48, D682-D688	20.1	645
231	Mouse mutant phenotyping at scale reveals novel genes controlling bone mineral density. *PLoS Genetics*, **2020**, 16, e1009190	6	8
230	Clustered CTCF binding is an evolutionary mechanism to maintain topologically associating domains. *Genome Biology*, **2020**, 21, 5	18.3	42
229	Ensembl Genomes 2020-enabling non-vertebrate genomic research. *Nucleic Acids Research*, **2020**, 48, D689-D695	20.1	214
228	Functional signatures of evolutionarily young CTCF binding sites. *BMC Biology*, **2020**, 18, 132	7.3	1
227	Transcriptional activity and strain-specific history of mouse pseudogenes. *Nature Communications*, **2020**, 11, 3695	17.4	8
226	Perspectives on ENCODE. *Nature*, **2020**, 583, 693-698	50.4	61
225	The tuatara genome reveals ancient features of amniote evolution. *Nature*, **2020**, 584, 403-409	50.4	49
224	Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma. *Genome Research*, **2020**, 30, 1217-1227	9.7	11
223	The International Genome Sample Resource (IGSR) collection of open human genomic variation resources. *Nucleic Acids Research*, **2020**, 48, D941-D947	20.1	48
222	Soft windowing application to improve analysis of high-throughput phenotyping data. *Bioinformatics*, **2020**, 36, 1492-1500	7.2	5
221	Leveraging European infrastructures to access 1 million human genomes by 2022. *Nature Reviews Genetics*, **2019**, 20, 693-701	30.1	36
220	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
219	Multi-platform discovery of haplotype-resolved structural variation in human genomes. *Nature Communications*, **2019**, 10, 1784	17.4	346
218	Federated discovery and sharing of genomic data using Beacons. *Nature Biotechnology*, **2019**, 37, 220-224	44.5	42
217	Getting the Entire Message: Progress in Isoform Sequencing. *Frontiers in Genetics*, **2019**, 10, 709	4.5	16
216	An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. *Molecular Ecology Resources*, **2019**, 19, 1497-1515	8.4	17
215	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

214	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
213	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
212	Using long and linked reads to improve an Atlantic herring (Clupea harengus) genome assembly. *Scientific Reports*, **2019**, 9, 17716	4.9	3
211	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmasks de novo variants in. *Npj Genomic Medicine*, **2019**, 4, 31	6.2	12
210	Adaptation of Proteins to the Cold in Antarctic Fish: A Role for Methionine?. *Genome Biology and Evolution*, **2019**, 11, 220-231	3.9	8
209	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
208	GENCODE reference annotation for the human and mouse genomes. *Nucleic Acids Research*, **2019**, 47, D766-D773	20.1	1140
207	Ensembl 2019. *Nucleic Acids Research*, **2019**, 47, D745-D751	20.1	554
206	Convergent genomic signatures of domestication in sheep and goats. *Nature Communications*, **2018** , 9, 813	17.4	112
205	Ensembl 2018. *Nucleic Acids Research*, **2018**, 46, D754-D761	20.1	1822
204	Identification of genetic elements in metabolism by high-throughput mouse phenotyping. *Nature Communications*, **2018**, 9, 288	17.4	48
203	Repeat associated mechanisms of genome evolution and function revealed by the and genomes. *Genome Research*, **2018**, 28, 448-459	9.7	57
202	Registered access: authorizing data access. *European Journal of Human Genetics*, **2018**, 26, 1721-1731	5.3	17
201	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
200	CTCF maintains regulatory homeostasis of cancer pathways. *Genome Biology*, **2018**, 19, 106	18.3	22
199	Combined HAT/EZH2 modulation leads to cancer-selective cell death. *Oncotarget*, **2018**, 9, 25630-25646	3.3	5
198	Complexity and conservation of regulatory landscapes underlie evolutionary resilience of mammalian gene expression. *Nature Ecology and Evolution*, **2018**, 2, 152-163	12.3	55
197	Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. *Oncotarget*, **2018**, 9, 25647-25660	3.3	11

196	Ensembl variation resources. *Database: the Journal of Biological Databases and Curation*, **2018**, 2018,	5	230
195	Haplosaurus computes protein haplotypes for use in precision drug design. *Nature Communications*, **2018**, 9, 4128	17.4	8
194	Identification of genes required for eye development by high-throughput screening of mouse knockouts. *Communications Biology*, **2018**, 1, 236	6.7	20
193	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. *Nature Genetics*, **2018**, 50, 1574-1583	36.3	91
192	Chromosome assembly of large and complex genomes using multiple references. *Genome Research*, **2018**, 28, 1720-1732	9.7	54
191	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
190	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. *Cell Reports*, **2018**, 24, 2784-2794	10.6	54
189	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. *Nature Medicine*, **2018**, 24, 868-880	50.5	103
188	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
187	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
186	Ensembl 2017. *Nucleic Acids Research*, **2017**, 45, D635-D642	20.1	404
185	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
184	Alignment of 1000 Genomes Project reads to reference assembly GRCh38. *GigaScience*, **2017**, 6, 1-8	7.6	31
183	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. *Nature Genetics*, **2017**, 49, 1714-1721	36.3	43
182	A large scale hearing loss screen reveals an extensive unexplored genetic landscape for auditory dysfunction. *Nature Communications*, **2017**, 8, 886	17.4	81
181	Interplay of cis and trans mechanisms driving transcription factor binding and gene expression evolution. *Nature Communications*, **2017**, 8, 1092	17.4	31
180	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
179	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

178	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. *Nature Genetics*, **2017**, 49, 1231-1238	36.3	145
177	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. *Nature Communications*, **2017**, 8, 16058	17.4	30
176	The human-induced pluripotent stem cell initiative-data resources for cellular genetics. *Nucleic Acids Research*, **2017**, 45, D691-D697	20.1	63
175	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
174	Genome variation and conserved regulation identify genomic regions responsible for strain specific phenotypes in rat. *BMC Genomics*, **2017**, 18, 986	4.5	1
173	The new NHGRI-EBI Catalog of published genome-wide association studies (GWAS Catalog). *Nucleic Acids Research*, **2017**, 45, D896-D901	20.1	1321
172	Applications of the 1000 Genomes Project resources. *Briefings in Functional Genomics*, **2017**, 16, 163-170	4.9	18
171	The BLUEPRINT Data Analysis Portal. *Cell Systems*, **2016**, 3, 491-495.e5	10.6	71
170	The Evolutionary Fates of a Large Segmental Duplication in Mouse. *Genetics*, **2016**, 204, 267-85	4	14
169	High-throughput discovery of novel developmental phenotypes. *Nature*, **2016**, 537, 508-514	50.4	608
168	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
167	Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. *Cell*, **2016**, 167, 1354-1368.e14	56.2	283
166	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. *Cell*, **2016**, 167, 1369-1384.e19	56.2	556
165	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. *Cell*, **2016**, 167, 1145-1149	56.2	232
164	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. *Cell Reports*, **2016**, 17, 2101-2111	10.6	42
163	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. *Cell*, **2016**, 167, 1398-1414.e24	56.2	339
162	Divergence in gene expression within and between two closely related flycatcher species. *Molecular Ecology*, **2016**, 25, 2015-28	5.7	37
161	Making sense of big data in health research: Towards an EU action plan. *Genome Medicine*, **2016**, 8, 71	14.4	146

160	ncRNA orthologies in the vertebrate lineage. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	14
159	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
158	Ensembl 2016. *Nucleic Acids Research*, **2016**, 44, D710-6	20.1	1094
157	Ensembl regulation resources. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	33
156	Ensembl comparative genomics resources. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	186
155	The Ensembl gene annotation system. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	537
154	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. *Nature Communications*, **2016**, 7, 13555	17.4	95
153	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. *Nature Genetics*, **2016**, 48, 593-9	36.3	204
152	Mitochondrial heteroplasmy in vertebrates using ChIP-sequencing data. *Genome Biology*, **2016**, 17, 139	18.3	13
151	The Ensembl Variant Effect Predictor. *Genome Biology*, **2016**, 17, 122	18.3	2595
150	Avianbase: a community resource for bird genomics. *Genome Biology*, **2015**, 16, 21	18.3	22
149	Third Report on Chicken Genes and Chromosomes 2015. *Cytogenetic and Genome Research*, **2015**, 145, 78-179	1.9	57
148	The European Genome-phenome Archive of human data consented for biomedical research. *Nature Genetics*, **2015**, 47, 692-5	36.3	224
147	Extending reference assembly models. *Genome Biology*, **2015**, 16, 13	18.3	107
146	The IPD and IMGT/HLA database: allele variant databases. *Nucleic Acids Research*, **2015**, 43, D423-31	20.1	1449
145	The Ensembl REST API: Ensembl Data for Any Language. *Bioinformatics*, **2015**, 31, 143-5	7.2	108
144	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. *Science*, **2015**, 348, 666-9	33.3	170
143	A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74	50.4	8599

142	An integrated map of structural variation in 2,504 human genomes. *Nature*, **2015**, 526, 75-81	50.4	1368
141	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
140	Epigenome data release: a participant-centered approach to privacy protection. *Genome Biology*, **2015**, 16, 142	18.3	30
139	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776
138	Decoupling of evolutionary changes in transcription factor binding and gene expression in mammals. *Genome Research*, **2015**, 25, 167-78	9.7	37
137	Ensembl 2015. *Nucleic Acids Research*, **2015**, 43, D662-9	20.1	1013
136	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
135	Quantitative analysis of chromatin interaction changes upon a 4.3 Mb deletion at mouse 4E2. *BMC Genomics*, **2015**, 16, 982	4.5	2
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	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. *Nature Genetics*, **2015**, 47, 746-56	36.3	209
132	Ascl1 Coordinately Regulates Gene Expression and the Chromatin Landscape during Neurogenesis. *Cell Reports*, **2015**, 10, 1544-1556	10.6	113
131	Spatial enhancer clustering and regulation of enhancer-proximal genes by cohesin. *Genome Research*, **2015**, 25, 504-13	9.7	106
130	Enhancer evolution across 20 mammalian species. *Cell*, **2015**, 160, 554-66	56.2	422
129	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. *Genome Research*, **2015**, 25, 478-87	9.7	92
128	Functional Annotation of Rare Genetic Variants **2015**, 57-70		1
127	Regulatory Divergence of Transcript Isoforms in a Mammalian Model System. *PLoS ONE*, **2015**, 10, e0137367	3.7	0
126	Evolution of transcription factor binding in metazoans - mechanisms and functional implications. *Nature Reviews Genetics*, **2014**, 15, 221-33	30.1	143
125	Random monoallelic gene expression increases upon embryonic stem cell differentiation. *Developmental Cell*, **2014**, 28, 351-65	10.2	82

124	Functional annotation of noncoding sequence variants. *Nature Methods*, **2014**, 11, 294-6	21.6	368
123	A comparative encyclopedia of DNA elements in the mouse genome. *Nature*, **2014**, 515, 355-64	50.4	1026
122	Characterizing genetic variants for clinical action. *American Journal of Medical Genetics, Part C: Seminars in Medical Genetics*, **2014**, 166C, 93-104	3.1	41
121	Gibbon genome and the fast karyotype evolution of small apes. *Nature*, **2014**, 513, 195-201	50.4	241
120	Transcriptional diversity during lineage commitment of human blood progenitors. *Science*, **2014**, 345, 1251033	33.3	187
119	The sheep genome illuminates biology of the rumen and lipid metabolism. *Science*, **2014**, 344, 1168-1173	33.3	294
118	Multi-species, multi-transcription factor binding highlights conserved control of tissue-specific biological pathways. *ELife*, **2014**, 3, e02626	8.9	62
117	The NHGRI GWAS Catalog, a curated resource of SNP-trait associations. *Nucleic Acids Research*, **2014**, 42, D1001-6	20.1	2124
116	Ensembl 2014. *Nucleic Acids Research*, **2014**, 42, D749-55	20.1	1087
115	WiggleTools: parallel processing of large collections of genome-wide datasets for visualization and statistical analysis. *Bioinformatics*, **2014**, 30, 1008-9	7.2	44
114	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
113	Locus Reference Genomic: reference sequences for the reporting of clinically relevant sequence variants. *Nucleic Acids Research*, **2014**, 42, D873-8	20.1	58
112	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
111	Computational approaches to interpreting genomic sequence variation. *Genome Medicine*, **2014**, 6, 87	14.4	28
110	Characterization of the DNA Methylome during Human B-Cell Differentiation. *Blood*, **2014**, 124, 4346-4346	11.2	
109	Whole-Genome Epigenomic Analysis in Multiple Myeloma Reveals DNA Hypermethylation of B-Cell Specific Enhancers. *Blood*, **2014**, 124, 2032-2032	2.2	
108	Cooperativity and rapid evolution of cobound transcription factors in closely related mammals. *Cell*, **2013**, 154, 530-40	56.2	107
107	Computational approaches to identify functional genetic variants in cancer genomes. *Nature Methods*, **2013**, 10, 723-9	21.6	129

106	Latent regulatory potential of human-specific repetitive elements. *Molecular Cell*, **2013**, 49, 262-72	17.6	53
105	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
104	CAST-ChIP maps cell-type-specific chromatin states in the Drosophila central nervous system. *Cell Reports*, **2013**, 5, 271-82	10.6	26
103	Integrative annotation of variants from 1092 humans: application to cancer genomics. *Science*, **2013**, 342, 1235587	33.3	281
102	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. *Genome Research*, **2013**, 23, 2066-77	9.7	232
101	Transcriptome and genome sequencing uncovers functional variation in humans. *Nature*, **2013**, 501, 506-11	50.4	1323
100	Genome sequencing reveals loci under artificial selection that underlie disease phenotypes in the laboratory rat. *Cell*, **2013**, 154, 691-703	56.2	127
99	Ensembl 2013. *Nucleic Acids Research*, **2013**, 41, D48-55	20.1	797
98	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
97	Sequencing of the sea lamprey (Petromyzon marinus) genome provides insights into vertebrate evolution. *Nature Genetics*, **2013**, 45, 415-21, 421e1-2	36.3	465
96	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. *Nature Genetics*, **2013**, 45, 767-75	36.3	131
95	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
94	DbVar and DGVa: public archives for genomic structural variation. *Nucleic Acids Research*, **2013**, 41, D936-41	20.1	162
93	Accessing data from the International Mouse Phenotyping Consortium: state of the art and future plans. *Mammalian Genome*, **2012**, 23, 641-52	3.2	32
92	An integrated encyclopedia of DNA elements in the human genome. *Nature*, **2012**, 489, 57-74	50.4	11449
91	Ensembl 2012. *Nucleic Acids Research*, **2012**, 40, D84-90	20.1	798
90	The 1000 Genomes Project: data management and community access. *Nature Methods*, **2012**, 9, 459-62	21.6	202
89	Waves of retrotransposon expansion remodel genome organization and CTCF binding in multiple mammalian lineages. *Cell*, **2012**, 148, 335-48	56.2	390

88	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
87	An integrated map of genetic variation from 1,092 human genomes. *Nature*, **2012**, 491, 56-65	50.4	6049
86	BLUEPRINT to decode the epigenetic signature written in blood. *Nature Biotechnology*, **2012**, 30, 224-6	44.5	261
85	De novo assembly and genotyping of variants using colored de Bruijn graphs. *Nature Genetics*, **2012**, 44, 226-32	36.3	433
84	Insights into hominid evolution from the gorilla genome sequence. *Nature*, **2012**, 483, 169-75	50.4	517
83	Cohesin regulates tissue-specific expression by stabilizing highly occupied cis-regulatory modules. *Genome Research*, **2012**, 22, 2163-75	9.7	117
82	Extensive compensatory cis-trans regulation in the evolution of mouse gene expression. *Genome Research*, **2012**, 22, 2376-84	9.7	106
81	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
80	Considerations for the inclusion of 2x mammalian genomes in phylogenetic analyses. *Genome Biology*, **2011**, 12, 401	18.3	7
79	The functional spectrum of low-frequency coding variation. *Genome Biology*, **2011**, 12, R84	18.3	161
78	Ensembl BioMarts: a hub for data retrieval across taxonomic space. *Database: the Journal of Biological Databases and Curation*, **2011**, 2011, bar030	5	751
77	Comparative and demographic analysis of orang-utan genomes. *Nature*, **2011**, 469, 529-33	50.4	431
76	A high-resolution map of human evolutionary constraint using 29 mammals. *Nature*, **2011**, 478, 476-82	50.4	802
75	Ensembl 2011. *Nucleic Acids Research*, **2011**, 39, D800-6	20.1	590
74	Modernizing reference genome assemblies. *PLoS Biology*, **2011**, 9, e1001091	9.7	294
73	The genome of a songbird. *Nature*, **2010**, 464, 757-62	50.4	655
72	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613
71	A map of human genome variation from population-scale sequencing. *Nature*, **2010**, 467, 1061-73	50.4	6142

70	Journal club. A computational geneticist looks at mechanisms of chromosomal evolution. *Nature*, **2010**, 463, 713	50.4	
69	Public data archives for genomic structural variation. *Nature Genetics*, **2010**, 42, 813-4	36.3	67
68	Ensembl@ 10th year. *Nucleic Acids Research*, **2010**, 38, D557-62	20.1	240
67	Deriving the consequences of genomic variants with the Ensembl API and SNP Effect Predictor. *Bioinformatics*, **2010**, 26, 2069-70	7.2	1240
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19	Chromosome assembly of large and complex genomes using multiple references		7
18	Complexity and conservation of regulatory landscapes underlie evolutionary resilience of mammalian gene expression		2
17	A standardized framework for representation of ancestry data in genomics studies, with application to the NHGRI-EBI GWAS Catalog		2

16	Multi-platform discovery of haplotype-resolved structural variation in human genomes	26
15	Towards complete and error-free genome assemblies of all vertebrate species	38
14	De novo assembly of 64 haplotype-resolved human genomes of diverse ancestry and integrated analysis of structural variation	3
13	Multiple laboratory mouse reference genomes define strain specific haplotypes and novel functional loci	7
12	Comparative analysis of neutrophil and monocyte epigenomes	2
11	Nearly all new protein-coding predictions in the CHESS database are not protein-coding	8
10	Pseudogenes in the mouse lineage: transcriptional activity and strain-specific history	1
9	A chromosome-level assembly of the Atlantic herring detection of a supergene and other signals of selection	2
8	Clustered CTCF binding is an evolutionary mechanism to maintain topologically associating domains	4
7	An improved pig reference genome sequence to enable pig genetics and genomics research	15
6	Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma	1
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