Paul Flicek

List of Publications by Year
in descending order

251 papers	136,822 citations	1172 114 h-index	748 256 g-index
307 all docs	307 docs citations	307 times ranked	152049 citing authors

#	Article	IF	Citations
1	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. Nucleic Acids Research, 2022, 50, D765-D770.	6.5	10
2	The European Variation Archive: a FAIR resource of genomic variation for all species. Nucleic Acids Research, 2022, 50, D1216-D1220.	6.5	50
3	VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. Nucleic Acids Research, 2022, 50, D898-D911.	6.5	277
4	The European Genome-phenome Archive in 2021. Nucleic Acids Research, 2022, 50, D980-D987.	6.5	55
5	Ensembl 2022. Nucleic Acids Research, 2022, 50, D988-D995.	6.5	1,103
6	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. Nucleic Acids Research, 2022, 50, D996-D1003.	6.5	141
7	The European Bioinformatics Institute (EMBL-EBI) in 2021. Nucleic Acids Research, 2022, 50, D11-D19.	6.5	34
8	The Earth BioGenome Project 2020: Starting the clock. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	124
9	Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	33
10	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, .	3.3	120
11	Scripting Analyses of Genomes in Ensembl Plants. Methods in Molecular Biology, 2022, 2443, 27-55.	0.4	6
12	A joint NCBI and EMBL-EBI transcript set for clinical genomics and research. Nature, 2022, 604, 310-315.	13.7	162
13	Annotating and prioritizing genomic variants using the Ensembl Variant Effect Predictorâ€"A tutorial. Human Mutation, 2022, 43, 986-997.	1.1	30
14	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	13.7	192
15	Standardized annotation of translated open reading frames. Nature Biotechnology, 2022, 40, 994-999.	9.4	86
16	Cell type-specific novel long non-coding RNA and circular RNA in the BLUEPRINT hematopoietic transcriptomes atlas. Haematologica, 2021, 106, 2613-2623.	1.7	12
17	Ensembl 2021. Nucleic Acids Research, 2021, 49, D884-D891.	6.5	1,231
18	Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. Nucleic Acids Research, 2021, 49, D1452-D1463.	6.5	83

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19	GENCODE 2021. Nucleic Acids Research, 2021, 49, D916-D923.	6.5	633
20	A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. Nature Communications, 2021, 12, 463.	5.8	109
21	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, .	1.1	12
22	LINE retrotransposons characterize mammalian tissue-specific and evolutionarily dynamic regulatory regions. Genome Biology, 2021, 22, 62.	3.8	38
23	Functional annotations of three domestic animal genomes provide vital resources for comparative and agricultural research. Nature Communications, 2021, 12, 1821.	5.8	105
24	Accessing Livestock Resources in Ensembl. Frontiers in Genetics, 2021, 12, 650228.	1.1	3
25	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	6.0	358
26	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	13.7	1,139
27	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. Nature Communications, 2021, 12, 2298.	5.8	32
28	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	13.5	94
29	The FAANG Data Portal: Global, Open-Access, â€œFAIRâ€, and Richly Validated Genotype to Phenotype Data for High-Quality Functional Annotation of Animal Genomes. Frontiers in Genetics, 2021, 12, 639238.	1.1	8
30	The value of primary transcripts to the clinical and nonâ€clinical genomics community: Survey results and roadmap for improvements. Molecular Genetics & Genomic Medicine, 2021, 9, e1786.	0.6	5
31	Kâ€mer counting and curated libraries drive efficient annotation of repeats in plant genomes. Plant Genome, 2021, 14, e20143.	1.6	5
32	The European Bioinformatics Institute: empowering cooperation in response to a global health crisis. Nucleic Acids Research, 2021, 49, D29-D37.	6.5	22
33	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	3.0	94
34	IPD-IMGT/HLA Database. Nucleic Acids Research, 2020, 48, D948-D955.	6.5	977
35	Ensembl 2020. Nucleic Acids Research, 2020, 48, D682-D688.	6.5	1,076
36	The International Genome Sample Resource (IGSR) collection of open human genomic variation resources. Nucleic Acids Research, 2020, 48, D941-D947.	6.5	221

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37	Soft windowing application to improve analysis of high-throughput phenotyping data. Bioinformatics, 2020, 36, 1492-1500.	1.8	9
38	Clustered CTCF binding is an evolutionary mechanism to maintain topologically associating domains. Genome Biology, 2020, 21, 5.	3.8	89
39	Ensembl Genomes 2020â€"enabling non-vertebrate genomic research. Nucleic Acids Research, 2020, 48, D689-D695.	6.5	416
40	Functional signatures of evolutionarily young CTCF binding sites. BMC Biology, 2020, 18, 132.	1.7	9
41	Transcriptional activity and strain-specific history of mouse pseudogenes. Nature Communications, 2020, 11, 3695.	5.8	17
42	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
43	The tuatara genome reveals ancient features of amniote evolution. Nature, 2020, 584, 403-409.	13.7	105
44	Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma. Genome Research, 2020, 30, 1217-1227.	2.4	35
45	Progress, Challenges, and Surprises in Annotating the Human Genome. Annual Review of Genomics and Human Genetics, 2020, 21, 55-79.	2.5	20
46	Pervasive lesion segregation shapes cancer genome evolution. Nature, 2020, 583, 265-270.	13.7	36
47	An improved pig reference genome sequence to enable pig genetics and genomics research. GigaScience, 2020, 9, .	3.3	187
48	The Deep Genome Project. Genome Biology, 2020, 21, 18.	3.8	30
49	Identification of male heterogametic sexâ€determining regions on the Atlantic herringClupea harengusgenome. Journal of Fish Biology, 2020, 97, 190-201.	0.7	7
50	Mouse mutant phenotyping at scale reveals novel genes controlling bone mineral density. PLoS Genetics, 2020, 16, e1009190.	1.5	19
51	Getting the Entire Message: Progress in Isoform Sequencing. Frontiers in Genetics, 2019, 10, 709.	1.1	39
52	An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. Molecular Ecology Resources, 2019, 19, 1497-1515.	2.2	31
53	A chromosome-level assembly of the Atlantic herring genomeâ€"detection of a supergene and other signals of selection. Genome Research, 2019, 29, 1919-1928.	2.4	84
54	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	7.7	69

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55	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. Cell Reports, 2019, 26, 1059-1069.e6.	2.9	33
56	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	5.8	636
57	Federated discovery and sharing of genomic data using Beacons. Nature Biotechnology, 2019, 37, 220-224.	9.4	75
58	Using long and linked reads to improve an Atlantic herring (Clupea harengus) genome assembly. Scientific Reports, 2019, 9, 17716.	1.6	11
59	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmasks de novo variants in SCN1A. Npj Genomic Medicine, 2019, 4, 31.	1.7	27
60	Adaptation of Proteins to the Cold in Antarctic Fish: A Role for Methionine?. Genome Biology and Evolution, 2019, 11, 220-231.	1.1	25
61	The NHGRI-EBI GWAS Catalog of published genome-wide association studies, targeted arrays and summary statistics 2019. Nucleic Acids Research, 2019, 47, D1005-D1012.	6.5	3,179
62	GENCODE reference annotation for the human and mouse genomes. Nucleic Acids Research, 2019, 47, D766-D773.	6.5	2,350
63	Ensembl 2019. Nucleic Acids Research, 2019, 47, D745-D751.	6.5	879
64	Variant calling on the GRCh38 assembly with the data from phase three of the 1000 Genomes Project. Wellcome Open Research, 2019, 4, 50.	0.9	26
65	Variant calling on the GRCh38 assembly with the data from phase three of the 1000 Genomes Project. Wellcome Open Research, 2019, 4, 50.	0.9	73
66	Convergent genomic signatures of domestication in sheep and goats. Nature Communications, 2018, 9, 813.	5.8	220
67	Ensembl 2018. Nucleic Acids Research, 2018, 46, D754-D761.	6.5	2,710
68	Identification of genetic elements in metabolism by high-throughput mouse phenotyping. Nature Communications, 2018, 9, 288.	5.8	59
69	Repeat associated mechanisms of genome evolution and function revealed by the Mus caroli and Mus pahari genomes. Genome Research, 2018, 28, 448-459.	2.4	99
70	Complexity and conservation of regulatory landscapes underlie evolutionary resilience of mammalian gene expression. Nature Ecology and Evolution, 2018, 2, 152-163.	3.4	131
71	Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. Oncotarget, 2018, 9, 25647-25660.	0.8	13
72	Ensembl variation resources. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	377

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73	Haplosaurus computes protein haplotypes for use in precision drug design. Nature Communications, 2018, 9, 4128.	5.8	21
74	Identification of genes required for eye development by high-throughput screening of mouse knockouts. Communications Biology, 2018, 1, 236.	2.0	37
75	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. Nature Genetics, 2018, 50, 1574-1583.	9.4	169
76	Chromosome assembly of large and complex genomes using multiple references. Genome Research, 2018, 28, 1720-1732.	2.4	94
77	The International Mouse Phenotyping Consortium (IMPC): a functional catalogue of the mammalian genome that informs conservation. Conservation Genetics, 2018, 19, 995-1005.	0.8	82
78	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. Cell Reports, 2018, 24, 2784-2794.	2.9	104
79	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	15.2	157
80	Registered access: authorizing data access. European Journal of Human Genetics, 2018, 26, 1721-1731.	1.4	33
81	A standardized framework for representation of ancestry data in genomics studies, with application to the NHGRI-EBI GWAS Catalog. Genome Biology, 2018, 19, 21.	3.8	159
82	CTCF maintains regulatory homeostasis of cancer pathways. Genome Biology, 2018, 19, 106.	3.8	38
83	Combined HAT/EZH2 modulation leads to cancer-selective cell death. Oncotarget, 2018, 9, 25630-25646.	0.8	5
84	Applications of the 1000 Genomes Project resources. Briefings in Functional Genomics, 2017, 16, elw027.	1.3	30
85	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. Genome Biology, 2017, 18, 50.	3.8	71
86	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. Genome Research, 2017, 27, 849-864.	2.4	728
87	Ensembl 2017. Nucleic Acids Research, 2017, 45, D635-D642.	6.5	535
88	Addressing Beacon re-identification attacks: quantification and mitigation of privacy risks. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 799-805.	2.2	62
89	Alignment of 1000 Genomes Project reads to reference assembly GRCh38. GigaScience, 2017, 6, 1-8.	3.3	49
90	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. Nature Genetics, 2017, 49, 1714-1721.	9.4	57

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91	A large scale hearing loss screen reveals an extensive unexplored genetic landscape for auditory dysfunction. Nature Communications, 2017, 8, 886.	5.8	116
92	Interplay of cis and trans mechanisms driving transcription factor binding and gene expression evolution. Nature Communications, 2017, 8, 1092.	5.8	60
93	Ensembl core software resources: storage and programmatic access for DNA sequence and genome annotation. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	56
94	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. Nature Genetics, 2017, 49, 1231-1238.	9.4	216
95	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. Nature Communications, 2017, 8, 16058.	5.8	50
96	The human-induced pluripotent stem cell initiativeâ€"data resources for cellular genetics. Nucleic Acids Research, 2017, 45, D691-D697.	6.5	81
97	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.	6.5	215
98	Genome variation and conserved regulation identify genomic regions responsible for strain specific phenotypes in rat. BMC Genomics, 2017, 18, 986.	1.2	3
99	The new NHGRI-EBI Catalog of published genome-wide association studies (GWAS Catalog). Nucleic Acids Research, 2017, 45, D896-D901.	6.5	1,932
100	IPD-MHC 2.0: an improved inter-species database for the study of the major histocompatibility complex. Nucleic Acids Research, 2017, 45, D860-D864.	6.5	168
101	Ensembl regulation resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav119.	1.4	45
102	Ensembl comparative genomics resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav096.	1.4	344
103	The Ensembl gene annotation system. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw093.	1.4	912
104	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. Nature Communications, 2016, 7, 13555.	5.8	142
105	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. Nature Genetics, 2016, 48, 593-599.	9.4	273
106	Mitochondrial heteroplasmy in vertebrates using ChIP-sequencing data. Genome Biology, 2016, 17, 139.	3.8	17
107	The Ensembl Variant Effect Predictor. Genome Biology, 2016, 17, 122.	3.8	5,181
108	The BLUEPRINT Data Analysis Portal. Cell Systems, 2016, 3, 491-495.e5.	2.9	123

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109	The Evolutionary Fates of a Large Segmental Duplication in Mouse. Genetics, 2016, 204, 267-285.	1.2	21
110	High-throughput discovery of novel developmental phenotypes. Nature, 2016, 537, 508-514.	13.7	1,001
111	Decoding the DNA Methylome of Mantle Cell Lymphoma in the Light of the Entire B Cell Lineage. Cancer Cell, 2016, 30, 806-821.	7.7	103
112	Î²-Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. Cell, 2016, 167, 1354-1368.e14.	13.5	467
113	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. Cell, 2016, 167, 1369-1384.e19.	13.5	863
114	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
115	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. Cell Reports, 2016, 17, 2101-2111.	2.9	54
116	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	13.5	573
117	Divergence in gene expression within and between two closely related flycatcher species. Molecular Ecology, 2016, 25, 2015-2028.	2.0	57
118	Making sense of big data in health research: Towards an EU action plan. Genome Medicine, 2016, 8, 71.	3.6	190
119	ncRNA orthologies in the vertebrate lineage. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav127.	1.4	19
120	LaGomiCsâ€"Lagomorph Genomics Consortium: An International Collaborative Effort for Sequencing the Genomes of an Entire Mammalian Order. Journal of Heredity, 2016, 107, 295-308.	1.0	19
121	Ensembl 2016. Nucleic Acids Research, 2016, 44, D710-D716.	6.5	1,372
122	Quantitative analysis of chromatin interaction changes upon a 4.3 Mb deletion at mouse 4E2. BMC Genomics, 2015, 16, 982.	1.2	2
123	Characterizing neutral genomic diversity and selection signatures in indigenous populations of Moroccan goats (Capra hircus) using WGS data. Frontiers in Genetics, 2015, 6, 107.	1.1	108
124	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. Nature Genetics, 2015, 47, 746-756.	9.4	278
125	Ascl1 Coordinately Regulates Gene Expression and the Chromatin Landscape during Neurogenesis. Cell Reports, 2015, 10, 1544-1556.	2.9	169
126	Spatial enhancer clustering and regulation of enhancer-proximal genes by cohesin. Genome Research, 2015, 25, 504-513.	2.4	149

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127	Enhancer Evolution across 20 Mammalian Species. Cell, 2015, 160, 554-566.	13.5	671
128	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. Genome Research, 2015, 25, 478-487.	2.4	118
129	Avianbase: a community resource for bird genomics. Genome Biology, 2015, 16, 21.	3.8	28
130	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	0.6	97
131	The European Genome-phenome Archive of human data consented for biomedical research. Nature Genetics, 2015, 47, 692-695.	9.4	338
132	Extending reference assembly models. Genome Biology, 2015, 16, 13.	3.8	139
133	The IPD and IMGT/HLA database: allele variant databases. Nucleic Acids Research, 2015, 43, D423-D431.	6.5	1,712
134	The Ensembl REST API: Ensembl Data for Any Language. Bioinformatics, 2015, 31, 143-145.	1.8	161
135	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
136	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
137	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
138	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.	9.4	119
139	Epigenome data release: a participant-centered approach to privacy protection. Genome Biology, 2015, 16, 142.	3.8	34
140	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
141	Decoupling of evolutionary changes in transcription factor binding and gene expression in mammals. Genome Research, 2015, 25, 167-178.	2.4	54
142	Ensembl 2015. Nucleic Acids Research, 2015, 43, D662-D669.	6.5	1,145
143	Characterization of the neural stem cell gene regulatory network identifies OLIG2 as a multifunctional regulator of self-renewal. Genome Research, 2015, 25, 41-56.	2.4	60
144	Functional Annotation of Rare Genetic Variants. , 2015, , 57-70.		2

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145	Regulatory Divergence of Transcript Isoforms in a Mammalian Model System. PLoS ONE, 2015, 10, e0137367.	1.1	1
146	Multi-species, multi-transcription factor binding highlights conserved control of tissue-specific biological pathways. ELife, 2014, 3, e02626.	2.8	84
147	The NHGRI GWAS Catalog, a curated resource of SNP-trait associations. Nucleic Acids Research, 2014, 42, D1001-D1006.	6.5	2,608
148	Ensembl 2014. Nucleic Acids Research, 2014, 42, D749-D755.	6.5	1,211
149	WiggleTools: parallel processing of large collections of genome-wide datasets for visualization and statistical analysis. Bioinformatics, 2014, 30, 1008-1009.	1.8	134
150	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-D809.	6.5	252
151	Locus Reference Genomic: reference sequences for the reporting of clinically relevant sequence variants. Nucleic Acids Research, 2014, 42, D873-D878.	6.5	73
152	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.	1.7	41
153	Computational approaches to interpreting genomic sequence variation. Genome Medicine, 2014, 6, 87.	3.6	33
154	Evolution of transcription factor binding in metazoans â€" mechanisms and functional implications. Nature Reviews Genetics, 2014, 15, 221-233.	7.7	207
155	Random Monoallelic Gene Expression Increases upon Embryonic Stem Cell Differentiation. Developmental Cell, 2014, 28, 351-365.	3.1	143
156	Functional annotation of noncoding sequence variants. Nature Methods, 2014, 11, 294-296.	9.0	493
157	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	13.7	1,444
158	Characterizing genetic variants for clinical action. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2014, 166, 93-104.	0.7	50
159	Gibbon genome and the fast karyotype evolution of small apes. Nature, 2014, 513, 195-201.	13.7	320
160	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	6.0	253
161	The sheep genome illuminates biology of the rumen and lipid metabolism. Science, 2014, 344, 1168-1173.	6.0	436
162	Characterization of the DNA Methylome during Human B-Cell Differentiation. Blood, 2014, 124, 4346-4346.	0.6	0

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163	Whole-Genome Epigenomic Analysis in Multiple Myeloma Reveals DNA Hypermethylation of B-Cell Specific Enhancers. Blood, 2014, 124, 2032-2032.	0.6	0
164	Cooperativity and Rapid Evolution of Cobound Transcription Factors in Closely Related Mammals. Cell, 2013, 154, 530-540.	13.5	148
165	Computational approaches to identify functional genetic variants in cancer genomes. Nature Methods, 2013, 10, 723-729.	9.0	161
166	Latent Regulatory Potential of Human-Specific Repetitive Elements. Molecular Cell, 2013, 49, 262-272.	4.5	62
167	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, 460-467.	2.6	23
168	CAST-ChIP Maps Cell-Type-Specific Chromatin States in the Drosophila Central Nervous System. Cell Reports, 2013, 5, 271-282.	2.9	34
169	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
170	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. Genome Research, 2013, 23, 2066-2077.	2.4	282
171	The handiwork of tinkering. Nature, 2013, 500, 158-159.	13.7	1
172	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	13.7	1,857
173	Genome Sequencing Reveals Loci under Artificial Selection that Underlie Disease Phenotypes in the Laboratory Rat. Cell, 2013, 154, 691-703.	13.5	154
174	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.	9.4	409
175	Sequencing of the sea lamprey (Petromyzon marinus) genome provides insights into vertebrate evolution. Nature Genetics, 2013, 45, 415-421.	9.4	588
176	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. Nature Genetics, 2013, 45, 767-775.	9.4	176
177	Co-binding by YY1 identifies the transcriptionally active, highly conserved set of CTCF-bound regions in primate genomes. Genome Biology, 2013, 14, R148.	13.9	68
178	dbVar and DGVa: public archives for genomic structural variation. Nucleic Acids Research, 2012, 41, D936-D941.	6.5	222
179	Extensive compensatory cis-trans regulation in the evolution of mouse gene expression. Genome Research, 2012, 22, 2376-2384.	2.4	170
180	Accessing data from the International Mouse Phenotyping Consortium: state of the art and future plans. Mammalian Genome, 2012, 23, 641-652.	1.0	37

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181	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516
182	Ensembl 2012. Nucleic Acids Research, 2012, 40, D84-D90.	6.5	840
183	The 1000 Genomes Project: data management and community access. Nature Methods, 2012, 9, 459-462.	9.0	308
184	Ensembl 2013. Nucleic Acids Research, 2012, 41, D48-D55.	6.5	856
185	Waves of Retrotransposon Expansion Remodel Genome Organization and CTCF Binding in Multiple Mammalian Lineages. Cell, 2012, 148, 335-348.	13.5	528
186	An integrated functional genomics approach identifies the regulatory network directed by brachyury (T) in chordoma. Journal of Pathology, 2012, 228, 274-285.	2.1	83
187	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
188	BLUEPRINT to decode the epigenetic signature written in blood. Nature Biotechnology, 2012, 30, 224-226.	9.4	323
189	De novo assembly and genotyping of variants using colored de Bruijn graphs. Nature Genetics, 2012, 44, 226-232.	9.4	564
190	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	13.7	663
191	Cohesin regulates tissue-specific expression by stabilizing highly occupied cis-regulatory modules. Genome Research, 2012, 22, 2163-2175.	2.4	140
192	Genome sequence of an Australian kangaroo, Macropus eugenii, provides insight into the evolution of mammalian reproduction and development. Genome Biology, 2011, 12, R81.	13.9	167
193	Closure of the NCBI SRA and implications for the long-term future of genomics data storage. Genome Biology, 2011, 12, 402.	3.8	29
194	Considerations for the inclusion of 2x mammalian genomes in phylogenetic analyses. Genome Biology, 2011, 12, 401.	13.9	7
195	The functional spectrum of low-frequency coding variation. Genome Biology, 2011, 12, R84.	13.9	173
196	Ensembl BioMarts: a hub for data retrieval across taxonomic space. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar030-bar030.	1.4	1,186
197	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	13.7	541
198	A high-resolution map of human evolutionary constraint using 29 mammals. Nature, 2011, 478, 476-482.	13.7	1,016

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199	Ensembl 2011. Nucleic Acids Research, 2011, 39, D800-D806.	6.5	630
200	Modernizing Reference Genome Assemblies. PLoS Biology, 2011, 9, e1001091.	2.6	458
201	A database and API for variation, dense genotyping and resequencing data. BMC Bioinformatics, 2010, 11, 238.	1.2	33
202	eHive: An Artificial Intelligence workflow system for genomic analysis. BMC Bioinformatics, 2010, 11, 240.	1.2	37
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