Paul Flicek

List of Publications by Year
in descending order

251	136,822	993 114	640 256
papers	citations	h-index	g-index

307	307	307	138701
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516
2	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
3	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
4	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
5	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	13.7	6,319
6	The Ensembl Variant Effect Predictor. Genome Biology, 2016, 17, 122.	3.8	5,181
7	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
8	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
9	Ensembl 2018. Nucleic Acids Research, 2018, 46, D754-D761.	6.5	2,710
10	The NHGRI GWAS Catalog, a curated resource of SNP-trait associations. Nucleic Acids Research, 2014, 42, D1001-D1006.	6.5	2,608
11	GENCODE reference annotation for the human and mouse genomes. Nucleic Acids Research, 2019, 47, D766-D773.	6.5	2,350
12	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
13	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
14	The new NHGRI-EBI Catalog of published genome-wide association studies (GWAS Catalog). Nucleic Acids Research, 2017, 45, D896-D901.	6.5	1,932
15	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	13.7	1,857
16	The IPD and IMGT/HLA database: allele variant databases. Nucleic Acids Research, 2015, 43, D423-D431.	6.5	1,712
17	Deriving the consequences of genomic variants with the Ensembl API and SNP Effect Predictor. Bioinformatics, 2010, 26, 2069-2070.	1.8	1,461
18	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	13.7	1,444

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19	Ensembl 2016. Nucleic Acids Research, 2016, 44, D710-D716.	6.5	1,372
20	Ensembl 2021. Nucleic Acids Research, 2021, 49, D884-D891.	6.5	1,231
21	Ensembl 2014. Nucleic Acids Research, 2014, 42, D749-D755.	6.5	1,211
22	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
23	Ensembl 2015. Nucleic Acids Research, 2015, 43, D662-D669.	6.5	1,145
24	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	13.7	1,139
25	Ensembl 2022. Nucleic Acids Research, 2022, 50, D988-D995.	6.5	1,103
26	Ensembl 2020. Nucleic Acids Research, 2020, 48, D682-D688.	6.5	1,076
27	Population genomics of human gene expression. Nature Genetics, 2007, 39, 1217-1224.	9.4	1,072
28	A high-resolution map of human evolutionary constraint using 29 mammals. Nature, 2011, 478, 476-482.	13.7	1,016
29	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
30	High-throughput discovery of novel developmental phenotypes. Nature, 2016, 537, 508-514.	13.7	1,001
31	IPD-IMGT/HLA Database. Nucleic Acids Research, 2020, 48, D948-D955.	6.5	977
32	Molecular Maps of the Reorganization of Genome-Nuclear Lamina Interactions during Differentiation. Molecular Cell, 2010, 38, 603-613.	4.5	916
33	The Ensembl gene annotation system. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw093.	1.4	912
34	Ensembl 2019. Nucleic Acids Research, 2019, 47, D745-D751.	6.5	879
35	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. Cell, 2016, 167, 1369-1384.e19.	13.5	863
36	Ensembl 2013. Nucleic Acids Research, 2012, 41, D48-D55.	6.5	856

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37	Ensembl 2012. Nucleic Acids Research, 2012, 40, D84-D90.	6.5	840
38	The genome of a songbird. Nature, 2010, 464, 757-762.	13.7	770
39	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
40	Enhancer Evolution across 20 Mammalian Species. Cell, 2015, 160, 554-566.	13.5	671
41	Five-Vertebrate ChIP-seq Reveals the Evolutionary Dynamics of Transcription Factor Binding. Science, 2010, 328, 1036-1040.	6.0	663
42	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	13.7	663
43	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	13.7	657
44	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	5.8	636
45	GENCODE 2021. Nucleic Acids Research, 2021, 49, D916-D923.	6.5	633
46	Ensembl 2011. Nucleic Acids Research, 2011, 39, D800-D806.	6.5	630
47	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. Nature Biotechnology, 2008, 26, 779-785.	9.4	619
48	Sequencing of the sea lamprey (Petromyzon marinus) genome provides insights into vertebrate evolution. Nature Genetics, 2013, 45, 415-421.	9.4	588
49	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	13.5	573
50	De novo assembly and genotyping of variants using colored de Bruijn graphs. Nature Genetics, 2012, 44, 226-232.	9.4	564
51	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	13.7	541
52	Ensembl 2017. Nucleic Acids Research, 2017, 45, D635-D642.	6.5	535
53	Waves of Retrotransposon Expansion Remodel Genome Organization and CTCF Binding in Multiple Mammalian Lineages. Cell, 2012, 148, 335-348.	13.5	528
54	Functional annotation of noncoding sequence variants. Nature Methods, 2014, 11, 294-296.	9.0	493

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55	Î²-Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. Cell, 2016, 167, 1354-1368.e14.	13.5	467
56	Modernizing Reference Genome Assemblies. PLoS Biology, 2011, 9, e1001091.	2.6	458
57	Ensembl 2008. Nucleic Acids Research, 2007, 36, D707-D714.	6.5	440
58	The sheep genome illuminates biology of the rumen and lipid metabolism. Science, 2014, 344, 1168-1173.	6.0	436
59	Ensembl Genomes 2020â€"enabling non-vertebrate genomic research. Nucleic Acids Research, 2020, 48, D689-D695.	6.5	416
60	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
61	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
62	Ensembl variation resources. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	377
63	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	6.0	358
64	The landscape of histone modifications across 1% of the human genome in five human cell lines. Genome Research, 2007, 17, 691-707.	2.4	353
65	An integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs). Genome Research, 2008, 18, 1518-1529.	2.4	350
66	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (Meleagris gallopavo): Genome Assembly and Analysis. PLoS Biology, 2010, 8, e1000475.	2.6	348
67	Ensembl comparative genomics resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav096.	1.4	344
68	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
69	The European Genome-phenome Archive of human data consented for biomedical research. Nature Genetics, 2015, 47, 692-695.	9.4	338
70	A CTCF-independent role for cohesin in tissue-specific transcription. Genome Research, 2010, 20, 578-588.	2.4	331
71	BLUEPRINT to decode the epigenetic signature written in blood. Nature Biotechnology, 2012, 30, 224-226.	9.4	323
72	Gibbon genome and the fast karyotype evolution of small apes. Nature, 2014, 513, 195-201.	13.7	320

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73	The 1000 Genomes Project: data management and community access. Nature Methods, 2012, 9, 459-462.	9.0	308
74	Sense from sequence reads: methods for alignment and assembly. Nature Methods, 2009, 6, S6-S12.	9.0	299
75	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. Genome Research, 2013, 23, 2066-2077.	2.4	282
76	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. Nature Genetics, 2015, 47, 746-756.	9.4	278
77	VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. Nucleic Acids Research, 2022, 50, D898-D911.	6.5	277
78	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. Nature Genetics, 2016, 48, 593-599.	9.4	273
79	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	6.0	253
80	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
81	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
82	Ensembl's 10th year. Nucleic Acids Research, 2010, 38, D557-D562.	6.5	251
83	The DNA sequence of human chromosome 7. Nature, 2003, 424, 157-164.	13.7	236
84	EGASP: the human ENCODE Genome Annotation Assessment Project. Genome Biology, 2006, 7, S2.	13.9	228
85	dbVar and DGVa: public archives for genomic structural variation. Nucleic Acids Research, 2012, 41, D936-D941.	6.5	222
86	The International Genome Sample Resource (IGSR) collection of open human genomic variation resources. Nucleic Acids Research, 2020, 48, D941-D947.	6.5	221
87	Convergent genomic signatures of domestication in sheep and goats. Nature Communications, 2018, 9, 813.	5.8	220
88	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. Nature Genetics, 2017, 49, 1231-1238.	9.4	216
89	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
90	CHD7 Targets Active Gene Enhancer Elements to Modulate ES Cell-Specific Gene Expression. PLoS Genetics, 2010, 6, e1001023.	1.5	213

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91	Evolution of transcription factor binding in metazoans â€" mechanisms and functional implications. Nature Reviews Genetics, 2014, 15, 221-233.	7.7	207
92	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	13.7	192
93	Making sense of big data in health research: Towards an EU action plan. Genome Medicine, 2016, 8, 71.	3.6	190
94	An improved pig reference genome sequence to enable pig genetics and genomics research. GigaScience, 2020, 9, .	3.3	187
95	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. Nature Genetics, 2013, 45, 767-775.	9.4	176
96	The functional spectrum of low-frequency coding variation. Genome Biology, 2011, 12, R84.	13.9	173
97	SNP and haplotype mapping for genetic analysis in the rat. Nature Genetics, 2008, 40, 560-566.	9.4	172
98	Extensive compensatory cis-trans regulation in the evolution of mouse gene expression. Genome Research, 2012, 22, 2376-2384.	2.4	170
99	Ascl1 Coordinately Regulates Gene Expression and the Chromatin Landscape during Neurogenesis. Cell Reports, 2015, 10, 1544-1556.	2.9	169
100	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. Nature Genetics, 2018, 50, 1574-1583.	9.4	169
101	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
102	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
103	Genome-wide nucleotide-level mammalian ancestor reconstruction. Genome Research, 2008, 18, 1829-1843.	2.4	164
104	A joint NCBI and EMBL-EBI transcript set for clinical genomics and research. Nature, 2022, 604, 310-315.	13.7	162
105	Computational approaches to identify functional genetic variants in cancer genomes. Nature Methods, 2013, 10, 723-729.	9.0	161
106	The Ensembl REST API: Ensembl Data for Any Language. Bioinformatics, 2015, 31, 143-145.	1.8	161
107	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
108	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	15.2	157

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109	Genome Sequencing Reveals Loci under Artificial Selection that Underlie Disease Phenotypes in the Laboratory Rat. Cell, 2013, 154, 691-703.	13.5	154
110	Spatial enhancer clustering and regulation of enhancer-proximal genes by cohesin. Genome Research, 2015, 25, 504-513.	2.4	149
111	Cooperativity and Rapid Evolution of Cobound Transcription Factors in Closely Related Mammals. Cell, 2013, 154, 530-540.	13.5	148
112	Random Monoallelic Gene Expression Increases upon Embryonic Stem Cell Differentiation. Developmental Cell, 2014, 28, 351-365.	3.1	143
113	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. Nature Communications, 2016, 7, 13555.	5.8	142
114	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. Nucleic Acids Research, 2022, 50, D996-D1003.	6.5	141
115	Cohesin regulates tissue-specific expression by stabilizing highly occupied cis-regulatory modules. Genome Research, 2012, 22, 2163-2175.	2.4	140
116	Extending reference assembly models. Genome Biology, 2015, 16, 13.	3.8	139
117	WiggleTools: parallel processing of large collections of genome-wide datasets for visualization and statistical analysis. Bioinformatics, 2014, 30, 1008-1009.	1.8	134
118	Complexity and conservation of regulatory landscapes underlie evolutionary resilience of mammalian gene expression. Nature Ecology and Evolution, 2018, 2, 152-163.	3.4	131
119	Ensembl variation resources. BMC Genomics, 2010, 11, 293.	1.2	124
120	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
121	The BLUEPRINT Data Analysis Portal. Cell Systems, 2016, 3, 491-495.e5.	2.9	123
122	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
123	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
124	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
125	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. Genome Research, 2015, 25, 478-487.	2.4	118
126	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. Genome Research, 2008, 18, 393-403.	2.4	117

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127	A large scale hearing loss screen reveals an extensive unexplored genetic landscape for auditory dysfunction. Nature Communications, 2017, 8, 886.	5.8	116
128	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, 3829-3834.	3.3	109
129	A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. Nature Communications, 2021, 12, 463.	5.8	109
130	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
131	The tuatara genome reveals ancient features of amniote evolution. Nature, 2020, 584, 403-409.	13.7	105
132	Functional annotations of three domestic animal genomes provide vital resources for comparative and agricultural research. Nature Communications, 2021, 12, 1821.	5.8	105
133	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. Cell Reports, 2018, 24, 2784-2794.	2.9	104
134	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
135	Locus Reference Genomic sequences: an improved basis for describing human DNA variants. Genome Medicine, 2010, 2, 24.	3.6	100
136	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
137	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	0.6	97
138	Chromosome assembly of large and complex genomes using multiple references. Genome Research, 2018, 28, 1720-1732.	2.4	94
139	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	13.5	94
140	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	3.0	94
141	Clustered CTCF binding is an evolutionary mechanism to maintain topologically associating domains. Genome Biology, 2020, 21, 5.	3.8	89
142	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.	2.4	88
143	Standardized annotation of translated open reading frames. Nature Biotechnology, 2022, 40, 994-999.	9.4	86
144	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. Genome Research, 2010, 20, 791-803.	2.4	84

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145	Multi-species, multi-transcription factor binding highlights conserved control of tissue-specific biological pathways. ELife, 2014, 3, e02626.	2.8	84
146	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
147	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
148	Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. Nucleic Acids Research, 2021, 49, D1452-D1463.	6.5	83
149	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
150	The human-induced pluripotent stem cell initiativeâ€"data resources for cellular genetics. Nucleic Acids Research, 2017, 45, D691-D697.	6.5	81
151	A standard variation file format for human genome sequences. Genome Biology, 2010, 11, R88.	13.9	79
152	Federated discovery and sharing of genomic data using Beacons. Nature Biotechnology, 2019, 37, 220-224.	9.4	75
153	Functional diversity for REST (NRSF) is defined by in vivo binding affinity hierarchies at the DNA sequence level. Genome Research, 2009, 19, 994-1005.	2.4	73
154	Locus Reference Genomic: reference sequences for the reporting of clinically relevant sequence variants. Nucleic Acids Research, 2014, 42, D873-D878.	6.5	73
155	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
156	Public data archives for genomic structural variation. Nature Genetics, 2010, 42, 813-814.	9.4	71
157	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
158	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	7.7	69
159	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
160	The Human Variome Project. Science, 2008, 322, 861-862.	6.0	63
161	Latent Regulatory Potential of Human-Specific Repetitive Elements. Molecular Cell, 2013, 49, 262-272.	4.5	62
162	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

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163	nGASP â€“ the nematode genome annotation assessment project. BMC Bioinformatics, 2008, 9, 549.	1.2	61
164	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
165	Interplay of cis and trans mechanisms driving transcription factor binding and gene expression evolution. Nature Communications, 2017, 8, 1092.	5.8	60
166	Identification of genetic elements in metabolism by high-throughput mouse phenotyping. Nature Communications, 2018, 9, 288.	5.8	59
167	Divergence in gene expression within and between two closely related flycatcher species. Molecular Ecology, 2016, 25, 2015-2028.	2.0	57
168	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. Nature Genetics, 2017, 49, 1714-1721.	9.4	57
169	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
170	The European Genome-phenome Archive in 2021. Nucleic Acids Research, 2022, 50, D980-D987.	6.5	55
171	Decoupling of evolutionary changes in transcription factor binding and gene expression in mammals. Genome Research, 2015, 25, 167-178.	2.4	54
172	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. Cell Reports, 2016, 17, 2101-2111.	2.9	54
173	Optimized design and assessment of whole genome tiling arrays. Bioinformatics, 2007, 23, i195-i204.	1.8	53
174	Characterizing genetic variants for clinical action. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2014, 166, 93-104.	0.7	50
175	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. Nature Communications, 2017, 8, 16058.	5.8	50
176	The European Variation Archive: a FAIR resource of genomic variation for all species. Nucleic Acids Research, 2022, 50, D1216-D1220.	6.5	50
177	Alignment of 1000 Genomes Project reads to reference assembly GRCh38. GigaScience, 2017, 6, 1-8.	3.3	49
178	Ensembl regulation resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav119.	1.4	45
179	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
180	Strand selective generation of endo-siRNAs from the Na/phosphate transporter gene Slc34a1 in murine tissues. Nucleic Acids Research, 2009, 37, 2274-2282.	6.5	39

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181	Getting the Entire Message: Progress in Isoform Sequencing. Frontiers in Genetics, 2019, 10, 709.	1.1	39
182	CTCF maintains regulatory homeostasis of cancer pathways. Genome Biology, 2018, 19, 106.	3.8	38
183	LINE retrotransposons characterize mammalian tissue-specific and evolutionarily dynamic regulatory regions. Genome Biology, 2021, 22, 62.	3.8	38
184	eHive: An Artificial Intelligence workflow system for genomic analysis. BMC Bioinformatics, 2010, 11, 240.	1.2	37
185	Accessing data from the International Mouse Phenotyping Consortium: state of the art and future plans. Mammalian Genome, 2012, 23, 641-652.	1.0	37
186	Identification of genes required for eye development by high-throughput screening of mouse knockouts. Communications Biology, 2018, 1, 236.	2.0	37
187	Pervasive lesion segregation shapes cancer genome evolution. Nature, 2020, 583, 265-270.	13.7	36
188	Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma. Genome Research, 2020, 30, 1217-1227.	2.4	35
189	Gene finding in the chicken genome. BMC Bioinformatics, 2005, 6, 131.	1.2	34
190	CAST-ChIP Maps Cell-Type-Specific Chromatin States in the Drosophila Central Nervous System. Cell Reports, 2013, 5, 271-282.	2.9	34
191	Epigenome data release: a participant-centered approach to privacy protection. Genome Biology, 2015, 16, 142.	3.8	34
192	The European Bioinformatics Institute (EMBL-EBI) in 2021. Nucleic Acids Research, 2022, 50, D11-D19.	6.5	34
193	A database and API for variation, dense genotyping and resequencing data. BMC Bioinformatics, 2010, 11, 238.	1.2	33
194	Computational approaches to interpreting genomic sequence variation. Genome Medicine, 2014, 6, 87.	3.6	33
195	Registered access: authorizing data access. European Journal of Human Genetics, 2018, 26, 1721-1731.	1.4	33
196	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
197	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
198	Uncovering information on expression of natural antisense transcripts in Affymetrix MOE430 datasets. BMC Genomics, 2007, 8, 200.	1.2	32

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199	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. Nature Communications, 2021, 12, 2298.	5.8	32
200	An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. Molecular Ecology Resources, 2019, 19, 1497-1515.	2.2	31
201	Applications of the 1000 Genomes Project resources. Briefings in Functional Genomics, 2017, 16, elw027.	1.3	30
202	The Deep Genome Project. Genome Biology, 2020, 21, 18.	3.8	30
203	Annotating and prioritizing genomic variants using the Ensembl Variant Effect Predictorâ€"A tutorial. Human Mutation, 2022, 43, 986-997.	1.1	30
204	Closure of the NCBI SRA and implications for the long-term future of genomics data storage. Genome Biology, 2011, 12, 402.	3.8	29
205	Avianbase: a community resource for bird genomics. Genome Biology, 2015, 16, 21.	3.8	28
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