Ewan Birney

List of Publications by Year
in descending order

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232 papers	138,858 citations	1798 103 h-index	1048 234 g-index
264 all docs	264 docs citations	264 times ranked	138374 citing authors

#	Article	IF	Citations
1	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	13.7	21,074
2	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516
3	Velvet: Algorithms for de novo short read assembly using de Bruijn graphs. Genome Research, 2008, 18, 821-829.	2.4	8,699
4	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	13.7	6,319
5	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
6	AlphaFold Protein Structure Database: massively expanding the structural coverage of protein-sequence space with high-accuracy models. Nucleic Acids Research, 2022, 50, D439-D444.	6.5	3,692
7	A Draft Sequence of the Neandertal Genome. Science, 2010, 328, 710-722.	6.0	3,588
8	Mapping identifiers for the integration of genomic datasets with the R/Bioconductor package biomaRt. Nature Protocols, 2009, 4, 1184-1191.	5.5	3,084
9	Patterns of somatic mutation in human cancer genomes. Nature, 2007, 446, 153-158.	13.7	2,802
10	Automated generation of heuristics for biological sequence comparison. BMC Bioinformatics, 2005, 6, 31.	1.2	2,294
11	GeneWise and Genomewise. Genome Research, 2004, 14, 988-995.	2.4	2,128
12	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
13	The Pfam Protein Families Database. Nucleic Acids Research, 2002, 30, 276-280.	6.5	2,067
14	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	13.7	1,943
15	The Genome Sequence of the Malaria MosquitoAnopheles gambiae. Science, 2002, 298, 129-149.	6.0	1,859
16	Highly accurate protein structure prediction for the human proteome. Nature, 2021, 596, 590-596.	13.7	1,773
17	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	13.7	1,760
18	The genomic basis of adaptive evolution in threespine sticklebacks. Nature, 2012, 484, 55-61.	13.7	1,600

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19	Comparative Genomics of the Eukaryotes. Science, 2000, 287, 2204-2215.	6.0	1,573
20	Mouse genomic variation and its effect on phenotypes and gene regulation. Nature, 2011, 477, 289-294.	13.7	1,461
21	The Reactome pathway knowledgebase. Nucleic Acids Research, 2014, 42, D472-D477.	6.5	1,448
22	The Bioperl Toolkit: Perl Modules for the Life Sciences. Genome Research, 2002, 12, 1611-1618.	2.4	1,427
23	Reactome: a database of reactions, pathways and biological processes. Nucleic Acids Research, 2011, 39, D691-D697.	6.5	1,391
24	Ensembl 2016. Nucleic Acids Research, 2016, 44, D710-D716.	6.5	1,372
25	Oases: robust de novo RNA-seq assembly across the dynamic range of expression levels. Bioinformatics, 2012, 28, 1086-1092.	1.8	1,351
26	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	6.0	1,283
27	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	2.6	1,257
28	Ensembl 2014. Nucleic Acids Research, 2014, 42, D749-D755.	6.5	1,211
29	The Pfam Protein Families Database. Nucleic Acids Research, 2000, 28, 263-266.	6.5	1,173
30	Ensembl 2015. Nucleic Acids Research, 2015, 43, D662-D669.	6.5	1,145
31	EnsemblCompara GeneTrees: Complete, duplication-aware phylogenetic trees in vertebrates. Genome Research, 2009, 19, 327-335.	2.4	1,058
32	Genome Sequence of Aedes aegypti, a Major Arbovirus Vector. Science, 2007, 316, 1718-1723.	6.0	1,025
33	A high-resolution map of human evolutionary constraint using 29 mammals. Nature, 2011, 478, 476-482.	13.7	1,016
34	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
35	A small-cell lung cancer genome with complex signatures of tobacco exposure. Nature, 2010, 463, 184-190.	13.7	972
36	Ensembl 2013. Nucleic Acids Research, 2012, 41, D48-D55.	6.5	856

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37	Immunity-Related Genes and Gene Families inAnopheles gambiae. Science, 2002, 298, 159-165.	6.0	845
38	Ensembl 2012. Nucleic Acids Research, 2012, 40, D84-D90.	6.5	840
39	Towards practical, high-capacity, low-maintenance information storage in synthesized DNA. Nature, 2013, 494, 77-80.	13.7	787
40	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. Nature Medicine, 2017, 23, 517-525.	15.2	769
41	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. Genome Research, 2012, 22, 1798-1812.	2.4	762
42	Reactome knowledgebase of human biological pathways and processes. Nucleic Acids Research, 2009, 37, D619-D622.	6.5	760
43	The International Protein Index: An integrated database for proteomics experiments. Proteomics, 2004, 4, 1985-1988.	1.3	685
44	Analysis of the RNA-recognition motif and RS and RGG domains: conservation in metazoan pre-mRNA splicing factors. Nucleic Acids Research, 1993, 21, 5803-5816.	6.5	661
45	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	13.7	657
46	Defining functional DNA elements in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6131-6138.	3.3	635
47	Ensembl 2011. Nucleic Acids Research, 2011, 39, D800-D806.	6.5	630
48	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. Nature Biotechnology, 2008, 26, 779-785.	9.4	619
49	The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942.	9.4	613
50	Reactome: a knowledge base of biologic pathways and processes. Genome Biology, 2007, 8, R39.	13.9	539
51	Comparative Genome and Proteome Analysis ofAnopheles gambiaeandDrosophila melanogaster. Science, 2002, 298, 149-159.	6.0	531
52	Common genetic variation drives molecular heterogeneity in human iPSCs. Nature, 2017, 546, 370-375.	13.7	491
53	Integrative annotation of chromatin elements from ENCODE data. Nucleic Acids Research, 2013, 41, 827-841.	6.5	490
54	The consensus coding sequence (CCDS) project: Identifying a common protein-coding gene set for the human and mouse genomes. Genome Research, 2009, 19, 1316-1323.	2.4	476

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55	The European Nucleotide Archive. Nucleic Acids Research, 2011, 39, D28-D31.	6.5	471
56	Open chromatin defined by DNaseI and FAIRE identifies regulatory elements that shape cell-type identity. Genome Research, 2011, 21, 1757-1767.	2.4	449
57	An Overview of Ensembl. Genome Research, 2004, 14, 925-928.	2.4	391
58	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
59	Open Targets: a platform for therapeutic target identification and validation. Nucleic Acids Research, 2017, 45, D985-D994.	6.5	355
60	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
61	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
62	EnsMart: A Generic System for Fast and Flexible Access to Biological Data. Genome Research, 2003, 14, 160-169.	2.4	348
63	Using GeneWise in the Drosophila Annotation Experiment. Genome Research, 2000, 10, 547-548.	2.4	338
64	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	9.4	338
65	PH domain: the first anniversary. Trends in Biochemical Sciences, 1994, 19, 349-353.	3.7	332
66	Challenges and standards in integrating surveys of structural variation. Nature Genetics, 2007, 39, S7-S15.	9.4	331
67	Efficient storage of high throughput DNA sequencing data using reference-based compression. Genome Research, 2011, 21, 734-740.	2.4	329
68	A physical map of the mouse genome. Nature, 2002, 418, 743-750.	13.7	316
69	Heritable Individual-Specific and Allele-Specific Chromatin Signatures in Humans. Science, 2010, 328, 235-239.	6.0	304
70	Sense from sequence reads: methods for alignment and assembly. Nature Methods, 2009, 6, S6-S12.	9.0	299
71	High-resolution genome-wide in vivo footprinting of diverse transcription factors in human cells. Genome Research, 2011, 21, 456-464.	2.4	286
72	Factorbook.org: a Wiki-based database for transcription factor-binding data generated by the ENCODE consortium. Nucleic Acids Research, 2013, 41, D171-D176.	6.5	274

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73	MinION Analysis and Reference Consortium: Phase 1 data release and analysis. F1000Research, 2015, 4, 1075.	0.8	270
74	Integrating Genomics into Healthcare: A Global Responsibility. American Journal of Human Genetics, 2019, 104, 13-20.	2.6	264
75	Ensembl's 10th year. Nucleic Acids Research, 2010, 38, D557-D562.	6.5	251
76	Enredo and Pecan: Genome-wide mammalian consistency-based multiple alignment with paralogs. Genome Research, 2008, 18, 1814-1828.	2.4	249
77	Prepublication data sharing. Nature, 2009, 461, 168-170.	13.7	243
78	A Transcription Factor Collective Defines Cardiac Cell Fate and Reflects Lineage History. Cell, 2012, 148, 473-486.	13.5	239
79	The topography of mutational processes in breast cancer genomes. Nature Communications, 2016, 7, 11383.	5.8	235
80	VectorBase: a data resource for invertebrate vector genomics. Nucleic Acids Research, 2009, 37, D583-D587.	6.5	234
81	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. Genome Biology, 2012, 13, R48.	13.9	233
82	Identification of novel peptide hormones in the human proteome by hidden Markov model screening. Genome Research, 2007, 17, 320-327.	2.4	231
83	Modeling gene expression using chromatin features in various cellular contexts. Genome Biology, 2012, 13, R53.	13.9	231
84	EGASP: the human ENCODE Genome Annotation Assessment Project. Genome Biology, 2006, 7, S2.	13.9	228
85	The implications of alternative splicing in the ENCODE protein complement. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5495-5500.	3.3	206
86	Comparative genomics: genome-wide analysis in metazoan eukaryotes. Nature Reviews Genetics, 2003, 4, 251-262.	7.7	203
87	Pebble and Rock Band: Heuristic Resolution of Repeats and Scaffolding in the Velvet Short-Read de Novo Assembler. PLoS ONE, 2009, 4, e8407.	1.1	196
88	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. Nature Communications, 2021, 12, 1258.	5.8	196
89	The HGNC Database in 2008: a resource for the human genome. Nucleic Acids Research, 2007, 36, D445-D448.	6.5	194
90	Epigenome-wide Association Studies and the Interpretation of Disease -Omics. PLoS Genetics, 2016, 12, e1006105.	1.5	194

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91	The EBI RDF platform: linked open data for the life sciences. Bioinformatics, 2014, 30, 1338-1339.	1.8	190
92	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	2.4	184
93	Comparative Analysis of Noncoding Regions of 77 Orthologous Mouse and Human Gene Pairs. Genome Research, 1999, 9, 815-824.	2.4	180
94	Ensembl Genomes: an integrative resource for genome-scale data from non-vertebrate species. Nucleic Acids Research, 2012, 40, D91-D97.	6.5	179
95	SNP and haplotype mapping for genetic analysis in the rat. Nature Genetics, 2008, 40, 560-566.	9.4	172
96	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. Genome Research, 2012, 22, 1658-1667.	2.4	166
97	Genome-wide nucleotide-level mammalian ancestor reconstruction. Genome Research, 2008, 18, 1829-1843.	2.4	164
98	RNA modifications detection by comparative Nanopore direct RNA sequencing. Nature Communications, 2021, 12, 7198.	5.8	163
99	A joint NCBI and EMBL-EBI transcript set for clinical genomics and research. Nature, 2022, 604, 310-315.	13.7	162
100	GARFIELD classifies disease-relevant genomic features through integration of functional annotations with association signals. Nature Genetics, 2019, 51, 343-353.	9.4	147
101	Cancer and genomics. Nature, 2001, 409, 850-852.	13.7	140
102	Update of the Anopheles gambiae PEST genome assembly. Genome Biology, 2007, 8, R5.	13.9	127
103	Ensembl variation resources. BMC Genomics, 2010, 11, 293.	1.2	124
104	Cell-type specific and combinatorial usage of diverse transcription factors revealed by genome-wide binding studies in multiple human cells. Genome Research, 2012, 22, 9-24.	2.4	119
105	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. Nature Communications, 2016, 7, 12910.	5.8	119
106	The Ensembl Core Software Libraries. Genome Research, 2004, 14, 929-933.	2.4	116
107	Integrative analysis of gene expression, DNA methylation, physiological traits, and genetic variation in human skeletal muscle. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10883-10888.	3.3	114
108	The European Bioinformatics Institute in 2016: Data growth and integration. Nucleic Acids Research, 2016, 44, D20-D26.	6.5	108

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109	VectorBase: a home for invertebrate vectors of human pathogens. Nucleic Acids Research, 2007, 35, D503-D505.	6.5	107
110	MinION Analysis and Reference Consortium: Phase 2 data release and analysis of R9.0 chemistry. F1000Research, 2017, 6, 760.	0.8	107
111	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. Cell Reports, 2016, 17, 2137-2150.	2.9	102
112	Locus Reference Genomic sequences: an improved basis for describing human DNA variants. Genome Medicine, 2010, 2, 24.	3.6	100
113	A call for public archives for biological image data. Nature Methods, 2018, 15, 849-854.	9.0	99
114	Lessons for big-data projects. Nature, 2012, 489, 49-51.	13.7	95
115	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	3.0	94
116	A survey of homozygous deletions in human cancer genomes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4542-4547.	3.3	90
117	Integrating biological data â€“ the Distributed Annotation System. BMC Bioinformatics, 2008, 9, S3.	1.2	87
118	Genetic and functional insights into the fractal structure of the heart. Nature, 2020, 584, 589-594.	13.7	86
119	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. Genome Research, 2010, 20, 791-803.	2.4	84
120	Evolutionary Constraints of Phosphorylation in Eukaryotes, Prokaryotes, and Mitochondria. Molecular and Cellular Proteomics, 2010, 9, 2642-2653.	2.5	83
121	Analysis of variation at transcription factor binding sites in Drosophila and humans. Genome Biology, 2012, 13, R49.	13.9	83
122	Petabyte-scale innovations at the European Nucleotide Archive. Nucleic Acids Research, 2009, 37, D19-D25.	6.5	82
123	Confounding between recombination and selection, and the Ped/Pop method for detecting selection. Genome Research, 2008, 18, 1304-1313.	2.4	81
124	Genomic reconstruction of the SARS-CoV-2 epidemic in England. Nature, 2021, 600, 506-511.	13.7	80
125	Transcriptome analysis for the chicken based on 19,626 finished cDNA sequences and 485,337 expressed sequence tags. Genome Research, 2005, 15, 174-183.	2.4	79
126	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. Nature Genetics, 2017, 49, 341-348.	9.4	75

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127	Promoter shape varies across populations and affects promoter evolution and expression noise. Nature Genetics, 2017, 49, 550-558.	9.4	74
128	Trawler: de novo regulatory motif discovery pipeline for chromatin immunoprecipitation. Nature Methods, 2007, 4, 563-565.	9.0	71
129	The European Bioinformatics Instituteâ€™s data resources 2014. Nucleic Acids Research, 2014, 42, D18-D25.	6.5	71
130	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	7.7	69
131	Comparison of Human Chromosome 21 Conserved Nongenic Sequences (CNGs) With the Mouse and Dog Genomes Shows That Their Selective Constraint Is Independent of Their Genic Environment. Genome Research, 2004, 14, 852-859.	2.4	68
132	Improvements to services at the European Nucleotide Archive. Nucleic Acids Research, 2010, 38, D39-D45.	6.5	67
133	RNAcentral: A vision for an international database of RNA sequences. Rna, 2011, 17, 1941-1946.	1.6	67
134	Genome information resources â€“ developments at Ensembl. Trends in Genetics, 2004, 20, 268-272.	2.9	65
135	The human leukemia virus HTLV-1 alters the structure and transcription of host chromatin in cis. ELife, 2018, 7, .	2.8	64
136	Comparison of Associations with Different Macular Inner Retinal Thickness Parameters in a Large Cohort. Ophthalmology, 2020, 127, 62-71.	2.5	64
137	REMBI: Recommended Metadata for Biological Imagesâ€”enabling reuse of microscopy data in biology. Nature Methods, 2021, 18, 1418-1422.	9.0	63
138	The Anopheles gambiae genome: an update. Trends in Parasitology, 2004, 20, 49-52.	1.5	62
139	The end of the start for population sequencing. Nature, 2015, 526, 52-53.	13.7	62
140	Mining the draft human genome. Nature, 2001, 409, 827-828.	13.7	58
141	The European Bioinformatics Institute's data resources. Nucleic Acids Research, 2003, 31, 43-50.	6.5	56
142	Genetic variants regulating expression levels and isoform diversity during embryogenesis. Nature, 2017, 541, 402-406.	13.7	56
143	The European Bioinformatics Institute in 2017: data coordination and integration. Nucleic Acids Research, 2018, 46, D21-D29.	6.5	56
144	The Gene Curation Coalition: A global effort to harmonize geneâ€“disease evidence resources. Genetics in Medicine, 2022, 24, 1732-1742.	1.1	56

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145	Approaches to comparative sequence analysis: towards a functional view of vertebrate genomes. Nature Reviews Genetics, 2008, 9, 303-313.	7.7	55
146	Quantitative Genetics of CTCF Binding Reveal Local Sequence Effects and Different Modes of X-Chromosome Association. PLoS Genetics, 2014, 10, e1004798.	1.5	55
147	Genomic and Phenotypic Characterization of a Wild Medaka Population: Towards the Establishment of an Isogenic Population Genetic Resource in Fish. G3: Genes, Genomes, Genetics, 2014, 4, 433-445.	0.8	54
148	Optimized design and assessment of whole genome tiling arrays. Bioinformatics, 2007, 23, i195-i204.	1.8	53
149	Arabidopsis Reactome: A Foundation Knowledgebase for Plant Systems Biology. Plant Cell, 2008, 20, 1426-1436.	3.1	52
150	A SNP Map of the Rat Genome Generated from cDNA Sequences. Science, 2004, 303, 807-807.	6.0	51
151	Policy challenges of clinical genome sequencing. BMJ, The, 2013, 347, f6845-f6845.	3.0	50
152	Genetic variation affects morphological retinal phenotypes extracted from UK Biobank optical coherence tomography images. PLoS Genetics, 2021, 17, e1009497.	1.5	50
153	Sequence progressive alignment, a framework for practical large-scale probabilistic consistency alignment. Bioinformatics, 2009, 25, 295-301.	1.8	47
154	Priorities for nucleotide trace, sequence and annotation data capture at the Ensembl Trace Archive and the EMBL Nucleotide Sequence Database. Nucleic Acids Research, 2007, 36, D5-D12.	6.5	46
155	The discovery, positioning and verification of a set of transcription-associated motifs in vertebrates. Genome Biology, 2005, 6, R104.	13.9	45
156	In Vivo Validation of a Computationally Predicted Conserved Ath5 Target Gene Set. PLoS Genetics, 2007, 3, e159.	1.5	45
157	Ensembl regulation resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav119.	1.4	45
158	Paralogous annotation of disease-causing variants in long QT syndrome genes. Human Mutation, 2012, 33, 1188-1191.	1.1	44
159	What everybody should know about the rat genome and its online resources. Nature Genetics, 2008, 40, 523-527.	9.4	43
160	EMMA--mouse mutant resources for the international scientific community. Nucleic Acids Research, 2010, 38, D570-D576.	6.5	39
161	Identifying Extrinsic versus Intrinsic Drivers of Variation in Cell Behavior in Human iPSC Lines from Healthy Donors. Cell Reports, 2019, 26, 2078-2087.e3.	2.9	36
162	PhenotypeSimulator: A comprehensive framework for simulating multi-trait, multi-locus genotype to phenotype relationships. Bioinformatics, 2018, 34, 2951-2956.	1.8	35

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163	Gene finding in the chicken genome. BMC Bioinformatics, 2005, 6, 131.	1.2	34
164	The European Bioinformatics Institute (EMBL-EBI) in 2021. Nucleic Acids Research, 2022, 50, D11-D19.	6.5	34
165	Genome annotation techniques: new approaches and challenges. Drug Discovery Today, 2002, 7, S70-S76.	3.2	33
166	A database and API for variation, dense genotyping and resequencing data. BMC Bioinformatics, 2010, 11, 238.	1.2	33
167	The European Bioinformatics Institute in 2018: tools, infrastructure and training. Nucleic Acids Research, 2019, 47, D15-D22.	6.5	33
168	Major submissions tool developments at the European nucleotide archive. Nucleic Acids Research, 2012, 40, D43-D47.	6.5	32
169	Open annotation offers a democratic solution to genome sequencing. Nature, 2000, 403, 825-825.	13.7	31
170	Genome browsing with Ensembl: a practical overview. Briefings in Functional Genomics & Proteomics, 2007, 6, 202-219.	3.8	31
171	Ensembl Genome Browser. , 2010, , 923-939.		31
172	Sockeye: A 3D Environment for Comparative Genomics. Genome Research, 2004, 14, 956-962.	2.4	30
173	Estimating the Neutral Rate of Nucleotide Substitution Using Introns. Molecular Biology and Evolution, 2006, 24, 522-531.	3.5	29
174	Allele-specific and heritable chromatin signatures in humans. Human Molecular Genetics, 2010, 19, R204-R209.	1.4	28
175	A new strategy for genome assembly using short sequence reads and reduced representation libraries. Genome Research, 2010, 20, 249-256.	2.4	28
176	Personalized profiles for disease risk must capture all facets of health. Nature, 2021, 597, 175-177.	13.7	28
177	Assemblies: the good, the bad, the ugly. Nature Methods, 2011, 8, 59-60.	9.0	26
178	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3366.	3.3	25
179	Using human genetics to make new medicines. Nature Reviews Genetics, 2015, 16, 561-562.	7.7	25
180	The European Bioinformatics Institute in 2020: building a global infrastructure of interconnected data resources for the life sciences. Nucleic Acids Research, 2020, 48, D17-D23.	6.5	25

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181	An effective model for natural selection in promoters. Genome Research, 2010, 20, 685-692.	2.4	24
182	The systematic annotation of the three main GPCR families in Reactome. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq018-baq018.	1.4	24
183	Highly conserved elements discovered in vertebrates are present in non-syntenic loci of tunicates, act as enhancers and can be transcribed during development. Nucleic Acids Research, 2013, 41, 3600-3618.	6.5	24
184	DATABASES ANDTOOLS FORBROWSINGGENOMES. Annual Review of Genomics and Human Genetics, 2002, 3, 293-310.	2.5	23
185	An International Bioinformatics Infrastructure to Underpin the Arabidopsis Community. Plant Cell, 2010, 22, 2530-2536.	3.1	23
186	The future of DNA sequence archiving. GigaScience, 2012, 1, 2.	3.3	23
187	The European Bioinformatics Institute: empowering cooperation in response to a global health crisis. Nucleic Acids Research, 2021, 49, D29-D37.	6.5	22
188	Chromatin and heritability: how epigenetic studies can complement genetic approaches. Trends in Genetics, 2011, 27, 172-176.	2.9	20
189	Discovering Novel cis-Regulatory Motifs Using Functional Networks. Genome Research, 2003, 13, 883-895.	2.4	19
190	Come fly with us. Nature, 2007, 450, 184-185.	13.7	19
191	Genomic information infrastructure after the deluge. Genome Biology, 2010, 11, 402.	13.9	19
192	Searching databases to find protein domain organization. Advances in Protein Chemistry, 2000, 54, 137-157.	4.4	18
193	Progress in sequencing the mouse genome. Genesis, 2001, 31, 137-141.	0.8	18
194	MAPU 2.0: high-accuracy proteomes mapped to genomes. Nucleic Acids Research, 2009, 37, D902-D906.	6.5	18
195	Interactions between genetic variation and cellular environment in skeletal muscle gene expression. PLoS ONE, 2018, 13, e0195788.	1.1	18
196	Dry work in a wet world: computation in systems biology. Molecular Systems Biology, 2006, 2, 40.	3.2	17
197	The contribution of common regulatory and protein-coding TYR variants to the genetic architecture of albinism. Nature Communications, 2022, 13, .	5.8	17
198	Biological database design and implementation. Briefings in Bioinformatics, 2004, 5, 31-38.	3.2	16

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199	FORGE: A tool to discover cell specific enrichments of GWAS associated SNPs in regulatory regions. F1000Research, 0, 4, 18.	0.8	16
200	The consequence of natural selection on genetic variation in the mouse. Genomics, 2010, 95, 196-202.	1.3	15
201	Selective clonal persistence of human retroviruses in vivo: Radial chromatin organization, integration site, and host transcription. Science Advances, 2022, 8, eabm6210.	4.7	15
202	TranscriptSNPView: a genome-wide catalog of mouse coding variation. Nature Genetics, 2006, 38, 853-853.	9.4	14
203	Advanced Genomic Data Mining. PLoS Computational Biology, 2008, 4, e1000121.	1.5	13
204	A roadmap for restoring trust in Big Data. Lancet Oncology, The, 2018, 19, 1014-1015.	5.1	13
205	Finding and sharing: new approaches to registries of databases and services for the biomedical sciences. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq014-baq014.	1.4	12
206	Integrative knowledge management to enhance pharmaceutical R&D. Nature Reviews Drug Discovery, 2014, 13, 239-240.	21.5	12
207	The Convergence of Research and Clinical Genomics. American Journal of Human Genetics, 2019, 104, 781-783.	2.6	12
208	Nanopore ReCappable sequencing maps SARS-CoV-2 5â€² capping sites and provides new insights into the structure of sgRNAs. Nucleic Acids Research, 2022, 50, 3475-3489.	6.5	12
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