Ewan Birney

List of Publications by Year
in descending order

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232	138,858	2091	1213
papers	citations	103 h-index	234 g-index

264	264	264	153367
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	The European Bioinformatics Institute (EMBL-EBI) in 2021. Nucleic Acids Research, 2022, 50, D11-D19.	6.5	34
3	The Medaka Inbred Kiyosu-Karlsruhe (MIKK) panel. Genome Biology, 2022, 23, 59.	3.8	6
4	Genomic variations and epigenomic landscape of the Medaka Inbred Kiyosu-Karlsruhe (MIKK) panel. Genome Biology, 2022, 23, 58.	3.8	5
5	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
6	A joint NCBI and EMBL-EBI transcript set for clinical genomics and research. Nature, 2022, 604, 310-315.	13.7	162
7	Selective clonal persistence of human retroviruses in vivo: Radial chromatin organization, integration site, and host transcription. Science Advances, 2022, 8, eabm6210.	4.7	15
8	The Gene Curation Coalition: A global effort to harmonize geneâ€“disease evidence resources. Genetics in Medicine, 2022, 24, 1732-1742.	1.1	56
9	The contribution of common regulatory and protein-coding TYR variants to the genetic architecture of albinism. Nature Communications, 2022, 13, .	5.8	17
10	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. Nature Communications, 2021, 12, 1258.	5.8	196
11	Genetic variation affects morphological retinal phenotypes extracted from UK Biobank optical coherence tomography images. PLoS Genetics, 2021, 17, e1009497.	1.5	50
12	REMBI: Recommended Metadata for Biological Imagesâ€”enabling reuse of microscopy data in biology. Nature Methods, 2021, 18, 1418-1422.	9.0	63
13	Highly accurate protein structure prediction for the human proteome. Nature, 2021, 596, 590-596.	13.7	1,773
14	The International Human Genome Project. Human Molecular Genetics, 2021, 30, R161-R163.	1.4	9
15	Personalized profiles for disease risk must capture all facets of health. Nature, 2021, 597, 175-177.	13.7	28
16	The European Bioinformatics Institute: empowering cooperation in response to a global health crisis. Nucleic Acids Research, 2021, 49, D29-D37.	6.5	22
17	Genomic reconstruction of the SARS-CoV-2 epidemic in England. Nature, 2021, 600, 506-511.	13.7	80
18	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	3.0	94

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19	RNA modifications detection by comparative Nanopore direct RNA sequencing. Nature Communications, 2021, 12, 7198.	5.8	163
20	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
21	Comparison of Associations with Different Macular Inner Retinal Thickness Parameters in a Large Cohort. Ophthalmology, 2020, 127, 62-71.	2.5	64
22	Genetic and functional insights into the fractal structure of the heart. Nature, 2020, 584, 589-594.	13.7	86
23	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	7.7	69
24	GARFIELD classifies disease-relevant genomic features through integration of functional annotations with association signals. Nature Genetics, 2019, 51, 343-353.	9.4	147
25	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
26	Biomolecular Data Resources: Bioinformatics Infrastructure for Biomedical Data Science. Annual Review of Biomedical Data Science, 2019, 2, 199-222.	2.8	8
27	The Convergence of Research and Clinical Genomics. American Journal of Human Genetics, 2019, 104, 781-783.	2.6	12
28	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
29	The European Bioinformatics Institute in 2018: tools, infrastructure and training. Nucleic Acids Research, 2019, 47, D15-D22.	6.5	33
30	Integrating Genomics into Healthcare: A Global Responsibility. American Journal of Human Genetics, 2019, 104, 13-20.	2.6	264
31	The European Bioinformatics Institute in 2017: data coordination and integration. Nucleic Acids Research, 2018, 46, D21-D29.	6.5	56
32	A call for public archives for biological image data. Nature Methods, 2018, 15, 849-854.	9.0	99
33	The human leukemia virus HTLV-1 alters the structure and transcription of host chromatin in cis. ELife, 2018, 7, .	2.8	64
34	Interactions between genetic variation and cellular environment in skeletal muscle gene expression. PLoS ONE, 2018, 13, e0195788.	1.1	18
35	A roadmap for restoring trust in Big Data. Lancet Oncology, The, 2018, 19, 1014-1015.	5.1	13
36	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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37	ChromoTrace: Computational reconstruction of 3D chromosome configurations for super-resolution microscopy. PLoS Computational Biology, 2018, 14, e1006002.	1.5	5
38	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
39	Promoter shape varies across populations and affects promoter evolution and expression noise. Nature Genetics, 2017, 49, 550-558.	9.4	74
40	Common genetic variation drives molecular heterogeneity in human iPSCs. Nature, 2017, 546, 370-375.	13.7	491
41	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. Nature Medicine, 2017, 23, 517-525.	15.2	769
42	Genetic variants regulating expression levels and isoform diversity during embryogenesis. Nature, 2017, 541, 402-406.	13.7	56
43	Open Targets: a platform for therapeutic target identification and validation. Nucleic Acids Research, 2017, 45, D985-D994.	6.5	355
44	MinION Analysis and Reference Consortium: Phase 2 data release and analysis of R9.0 chemistry. F1000Research, 2017, 6, 760.	0.8	107
45	Ensembl regulation resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav119.	1.4	45
46	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	13.7	1,760
47	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. Cell Reports, 2016, 17, 2137-2150.	2.9	102
48	The topography of mutational processes in breast cancer genomes. Nature Communications, 2016, 7, 11383.	5.8	235
49	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. Nature Communications, 2016, 7, 12910.	5.8	119
50	Development of integrated high-resolution three-dimensional MRI and computational modelling techniques to identify novel genetic and anthropometric determinants of cardiac form and function. Lancet, The, 2016, 387, S36.	6.3	1
51	Ensembl 2016. Nucleic Acids Research, 2016, 44, D710-D716.	6.5	1,372
52	The European Bioinformatics Institute in 2016: Data growth and integration. Nucleic Acids Research, 2016, 44, D20-D26.	6.5	108
53	Epigenome-wide Association Studies and the Interpretation of Disease -Omics. PLoS Genetics, 2016, 12, e1006105.	1.5	194
54	The Mighty Fruit Fly Moves into Outbred Genetics. PLoS Genetics, 2016, 12, e1006388.	1.5	3

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55	The EMBL-EBI channel. F1000Research, 2016, 5, 52.	0.8	1
56	MinION Analysis and Reference Consortium: Phase 1 data release and analysis. F1000Research, 2015, 4, 1075.	0.8	270
57	Progress in Medicine: Experts Take Stock. PLoS Medicine, 2015, 12, e1001933.	3.9	2
58	The end of the start for population sequencing. Nature, 2015, 526, 52-53.	13.7	62
59	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
60	Using human genetics to make new medicines. Nature Reviews Genetics, 2015, 16, 561-562.	7.7	25
61	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
62	Ensembl 2015. Nucleic Acids Research, 2015, 43, D662-D669.	6.5	1,145
63	Ensembl 2014. Nucleic Acids Research, 2014, 42, D749-D755.	6.5	1,211
64	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
65	The Reactome pathway knowledgebase. Nucleic Acids Research, 2014, 42, D472-D477.	6.5	1,448
66	Quantitative Genetics of CTCF Binding Reveal Local Sequence Effects and Different Modes of X-Chromosome Association. PLoS Genetics, 2014, 10, e1004798.	1.5	55
67	The EBI RDF platform: linked open data for the life sciences. Bioinformatics, 2014, 30, 1338-1339.	1.8	190
68	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
69	Integrative knowledge management to enhance pharmaceutical R&D. Nature Reviews Drug Discovery, 2014, 13, 239-240.	21.5	12
70	Four makes a party. Nature, 2014, 505, 32-33.	13.7	4
71	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
72	The European Bioinformatics Instituteâ€™s data resources 2014. Nucleic Acids Research, 2014, 42, D18-D25.	6.5	71

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73	Integrative annotation of chromatin elements from ENCODE data. Nucleic Acids Research, 2013, 41, 827-841.	6.5	490
74	Towards practical, high-capacity, low-maintenance information storage in synthesized DNA. Nature, 2013, 494, 77-80.	13.7	787
75	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	9.4	338
76	Policy challenges of clinical genome sequencing. BMJ, The, 2013, 347, f6845-f6845.	3.0	50
77	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
78	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
79	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
80	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. Genome Research, 2012, 22, 1798-1812.	2.4	762
81	Ensembl Genomes: an integrative resource for genome-scale data from non-vertebrate species. Nucleic Acids Research, 2012, 40, D91-D97.	6.5	179
82	Major submissions tool developments at the European nucleotide archive. Nucleic Acids Research, 2012, 40, D43-D47.	6.5	32
83	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
84	Analysis of variation at transcription factor binding sites in Drosophila and humans. Genome Biology, 2012, 13, R49.	13.9	83
85	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516
86	Ensembl 2012. Nucleic Acids Research, 2012, 40, D84-D90.	6.5	840
87	Oases: robust de novo RNA-seq assembly across the dynamic range of expression levels. Bioinformatics, 2012, 28, 1086-1092.	1.8	1,351
88	Ensembl 2013. Nucleic Acids Research, 2012, 41, D48-D55.	6.5	856
89	Modeling gene expression using chromatin features in various cellular contexts. Genome Biology, 2012, 13, R53.	13.9	231
90	A Transcription Factor Collective Defines Cardiac Cell Fate and Reflects Lineage History. Cell, 2012, 148, 473-486.	13.5	239

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91	The future of DNA sequence archiving. GigaScience, 2012, 1, 2.	3.3	23
92	Lessons for big-data projects. Nature, 2012, 489, 49-51.	13.7	95
93	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. Genome Research, 2012, 22, 1658-1667.	2.4	166
94	The genomic basis of adaptive evolution in threespine sticklebacks. Nature, 2012, 484, 55-61.	13.7	1,600
95	Paralogous annotation of disease-causing variants in long QT syndrome genes. Human Mutation, 2012, 33, 1188-1191.	1.1	44
96	Reactome: a database of reactions, pathways and biological processes. Nucleic Acids Research, 2011, 39, D691-D697.	6.5	1,391
97	Considerations for the inclusion of 2x mammalian genomes in phylogenetic analyses. Genome Biology, 2011, 12, 401.	13.9	7
98	Mouse genomic variation and its effect on phenotypes and gene regulation. Nature, 2011, 477, 289-294.	13.7	1,461
99	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	2.6	1,257
100	Strengths and Weaknesses of Selected Modeling Methods Used in Systems Biology. , 2011, , .		2
101	Assemblies: the good, the bad, the ugly. Nature Methods, 2011, 8, 59-60.	9.0	26
102	Chromatin and heritability: how epigenetic studies can complement genetic approaches. Trends in Genetics, 2011, 27, 172-176.	2.9	20
103	A high-resolution map of human evolutionary constraint using 29 mammals. Nature, 2011, 478, 476-482.	13.7	1,016
104	High-resolution genome-wide in vivo footprinting of diverse transcription factors in human cells. Genome Research, 2011, 21, 456-464.	2.4	286
105	Efficient storage of high throughput DNA sequencing data using reference-based compression. Genome Research, 2011, 21, 734-740.	2.4	329
106	The European Nucleotide Archive. Nucleic Acids Research, 2011, 39, D28-D31.	6.5	471
107	Ensembl 2011. Nucleic Acids Research, 2011, 39, D800-D806.	6.5	630
108	RNAcentral: A vision for an international database of RNA sequences. Rna, 2011, 17, 1941-1946.	1.6	67

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109	Open chromatin defined by DNaseI and FAIRE identifies regulatory elements that shape cell-type identity. Genome Research, 2011, 21, 1757-1767.	2.4	449
110	A Draft Sequence of the Neandertal Genome. Science, 2010, 328, 710-722.	6.0	3,588
111	Heritable Individual-Specific and Allele-Specific Chromatin Signatures in Humans. Science, 2010, 328, 235-239.	6.0	304
112	A database and API for variation, dense genotyping and resequencing data. BMC Bioinformatics, 2010, 11, 238.	1.2	33
113	Ensembl variation resources. BMC Genomics, 2010, 11, 293.	1.2	124
114	A small-cell lung cancer genome with complex signatures of tobacco exposure. Nature, 2010, 463, 184-190.	13.7	972
115	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
116	The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942.	9.4	613
117	An International Bioinformatics Infrastructure to Underpin the Arabidopsis Community. Plant Cell, 2010, 22, 2530-2536.	3.1	23
118	Improvements to services at the European Nucleotide Archive. Nucleic Acids Research, 2010, 38, D39-D45.	6.5	67
119	Ensembl's 10th year. Nucleic Acids Research, 2010, 38, D557-D562.	6.5	251
120	Allele-specific and heritable chromatin signatures in humans. Human Molecular Genetics, 2010, 19, R204-R209.	1.4	28
121	A new strategy for genome assembly using short sequence reads and reduced representation libraries. Genome Research, 2010, 20, 249-256.	2.4	28
122	EMMA--mouse mutant resources for the international scientific community. Nucleic Acids Research, 2010, 38, D570-D576.	6.5	39
123	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
124	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. Genome Research, 2010, 20, 791-803.	2.4	84
125	Evolutionary Constraints of Phosphorylation in Eukaryotes, Prokaryotes, and Mitochondria. Molecular and Cellular Proteomics, 2010, 9, 2642-2653.	2.5	83
126	An effective model for natural selection in promoters. Genome Research, 2010, 20, 685-692.	2.4	24

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127	Ensembl Genome Browser. , 2010, , 923-939.		31
128	The consequence of natural selection on genetic variation in the mouse. Genomics, 2010, 95, 196-202.	1.3	15
129	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
130	Genomic information infrastructure after the deluge. Genome Biology, 2010, 11, 402.	13.9	19
131	Locus Reference Genomic sequences: an improved basis for describing human DNA variants. Genome Medicine, 2010, 2, 24.	3.6	100
132	EnsemblCompara GeneTrees: Complete, duplication-aware phylogenetic trees in vertebrates. Genome Research, 2009, 19, 327-335.	2.4	1,058
133	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
134	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
135	VectorBase: a data resource for invertebrate vector genomics. Nucleic Acids Research, 2009, 37, D583-D587.	6.5	234
136	Petabyte-scale innovations at the European Nucleotide Archive. Nucleic Acids Research, 2009, 37, D19-D25.	6.5	82
137	MAPU 2.0: high-accuracy proteomes mapped to genomes. Nucleic Acids Research, 2009, 37, D902-D906.	6.5	18
138	Sequence progressive alignment, a framework for practical large-scale probabilistic consistency alignment. Bioinformatics, 2009, 25, 295-301.	1.8	47
139	Prepublication data sharing. Nature, 2009, 461, 168-170.	13.7	243
140	Sense from sequence reads: methods for alignment and assembly. Nature Methods, 2009, 6, S6-S12.	9.0	299
141	Mapping identifiers for the integration of genomic datasets with the R/Bioconductor package biomaRt. Nature Protocols, 2009, 4, 1184-1191.	5.5	3,084
142	Reactome knowledgebase of human biological pathways and processes. Nucleic Acids Research, 2009, 37, D619-D622.	6.5	760
143	ENFIN â€“ A European network for integrative systems biology. Comptes Rendus - Biologies, 2009, 332, 1050-1058.	0.1	6
144	Visualising the Epigenome. , 2009, , 55-66.		0

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145	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	13.7	657
146	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. Nature Biotechnology, 2008, 26, 779-785.	9.4	619
147	SNP and haplotype mapping for genetic analysis in the rat. Nature Genetics, 2008, 40, 560-566.	9.4	172
148	What everybody should know about the rat genome and its online resources. Nature Genetics, 2008, 40, 523-527.	9.4	43
149	Levers and fulcrums: progress in cis-regulatory motif models. Nature Methods, 2008, 5, 297-298.	9.0	0
150	Approaches to comparative sequence analysis: towards a functional view of vertebrate genomes. Nature Reviews Genetics, 2008, 9, 303-313.	7.7	55
151	Integrating biological data â€“ the Distributed Annotation System. BMC Bioinformatics, 2008, 9, S3.	1.2	87
152	Confounding between recombination and selection, and the Ped/Pop method for detecting selection. Genome Research, 2008, 18, 1304-1313.	2.4	81
153	Advanced Genomic Data Mining. PLoS Computational Biology, 2008, 4, e1000121.	1.5	13
154	Arabidopsis Reactome: A Foundation Knowledgebase for Plant Systems Biology. Plant Cell, 2008, 20, 1426-1436.	3.1	52
155	Genome-wide nucleotide-level mammalian ancestor reconstruction. Genome Research, 2008, 18, 1829-1843.	2.4	164
156	Enredo and Pecan: Genome-wide mammalian consistency-based multiple alignment with paralogs. Genome Research, 2008, 18, 1814-1828.	2.4	249
157	Velvet: Algorithms for de novo short read assembly using de Bruijn graphs. Genome Research, 2008, 18, 821-829.	2.4	8,699
158	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
159	ENFIN - An Integrative Structure for Systems Biology. Lecture Notes in Computer Science, 2008, , 132-143.	1.0	0
160	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
161	The HGNC Database in 2008: a resource for the human genome. Nucleic Acids Research, 2007, 36, D445-D448.	6.5	194
162	Genome browsing with Ensembl: a practical overview. Briefings in Functional Genomics & Proteomics, 2007, 6, 202-219.	3.8	31

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163	In Vivo Validation of a Computationally Predicted Conserved Ath5 Target Gene Set. PLoS Genetics, 2007, 3, e159.	1.5	45
164	VectorBase: a home for invertebrate vectors of human pathogens. Nucleic Acids Research, 2007, 35, D503-D505.	6.5	107
165	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
166	Identification of novel peptide hormones in the human proteome by hidden Markov model screening. Genome Research, 2007, 17, 320-327.	2.4	231
167	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
168	Optimized design and assessment of whole genome tiling arrays. Bioinformatics, 2007, 23, i195-i204.	1.8	53
169	Reactome: An integrated expert model of human molecular processes and access toolkit. Journal of Integrative Bioinformatics, 2007, 4, 286-296.	1.0	0
170	Reactome: a knowledge base of biologic pathways and processes. Genome Biology, 2007, 8, R39.	13.9	539
171	Update of the Anopheles gambiae PEST genome assembly. Genome Biology, 2007, 8, R5.	13.9	127
172	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	6.0	1,283
173	Genome Sequence of Aedes aegypti, a Major Arbovirus Vector. Science, 2007, 316, 1718-1723.	6.0	1,025
174	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	2.4	184
175	Come fly with us. Nature, 2007, 450, 184-185.	13.7	19
176	Double Dutch for duplications. Nature Genetics, 2007, 39, 1303-1304.	9.4	1
177	Challenges and standards in integrating surveys of structural variation. Nature Genetics, 2007, 39, S7-S15.	9.4	331
178	Trawler: de novo regulatory motif discovery pipeline for chromatin immunoprecipitation. Nature Methods, 2007, 4, 563-565.	9.0	71
179	Patterns of somatic mutation in human cancer genomes. Nature, 2007, 446, 153-158.	13.7	2,802
180	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

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181	Optimising oligonucleotide array design for ChIP-on-chip. BMC Bioinformatics, 2007, 8, .	1.2	1
182	ENFIN a Network to Enhance Integrative Systems Biology. Annals of the New York Academy of Sciences, 2007, 1115, 23-31.	1.8	8
183	EGASP: the human ENCODE Genome Annotation Assessment Project. Genome Biology, 2006, 7, S2.	13.9	228
184	Picking Pyknons out of the Human Genome. Cell, 2006, 125, 836-838.	13.5	9
185	TranscriptSNPView: a genome-wide catalog of mouse coding variation. Nature Genetics, 2006, 38, 853-853.	9.4	14
186	Estimating the Neutral Rate of Nucleotide Substitution Using Introns. Molecular Biology and Evolution, 2006, 24, 522-531.	3.5	29
187	Dry work in a wet world: computation in systems biology. Molecular Systems Biology, 2006, 2, 40.	3.2	17
188	Gene finding in the chicken genome. BMC Bioinformatics, 2005, 6, 131.	1.2	34
189	Automated generation of heuristics for biological sequence comparison. BMC Bioinformatics, 2005, 6, 31.	1.2	2,294
190	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
191	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
192	The discovery, positioning and verification of a set of transcription-associated motifs in vertebrates. Genome Biology, 2005, 6, R104.	13.9	45
193	Sockeye: A 3D Environment for Comparative Genomics. Genome Research, 2004, 14, 956-962.	2.4	30
194	Biological database design and implementation. Briefings in Bioinformatics, 2004, 5, 31-38.	3.2	16
195	The Ensembl Core Software Libraries. Genome Research, 2004, 14, 929-933.	2.4	116
196	A SNP Map of the Rat Genome Generated from cDNA Sequences. Science, 2004, 303, 807-807.	6.0	51
197	An Overview of Ensembl. Genome Research, 2004, 14, 925-928.	2.4	391
198	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

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199	GeneWise and Genomewise. Genome Research, 2004, 14, 988-995.	2.4	2,128
200	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	13.7	1,943
201	Genome information resources â€“ developments at Ensembl. Trends in Genetics, 2004, 20, 268-272.	2.9	65
202	The Anopheles gambiae genome: an update. Trends in Parasitology, 2004, 20, 49-52.	1.5	62
203	The International Protein Index: An integrated database for proteomics experiments. Proteomics, 2004, 4, 1985-1988.	1.3	685
204	Unrestricted free access works and must continue. Nature, 2003, 422, 801-801.	13.7	6
205	Comparative genomics: genome-wide analysis in metazoan eukaryotes. Nature Reviews Genetics, 2003, 4, 251-262.	7.7	203
206	EnsMart: A Generic System for Fast and Flexible Access to Biological Data. Genome Research, 2003, 14, 160-169.	2.4	348
207	Discovering Novel cis-Regulatory Motifs Using Functional Networks. Genome Research, 2003, 13, 883-895.	2.4	19
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