

# Ewan Birney

## List of Publications by Citations

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235  
papers

106,543  
citations

99  
h-index

264  
g-index

264  
ext. papers

126,037  
ext. citations

20.4  
avg, IF

8.55  
L-index

#	Paper	IF	Citations
235	Initial sequencing and analysis of the human genome. <i>Nature</i> , <b>2001</b> , 409, 860-921	50.4	17366
234	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , <b>2012</b> , 489, 57-74	50.4	11449
233	Velvet: algorithms for de novo short read assembly using de Bruijn graphs. <i>Genome Research</i> , <b>2008</b> , 18, 821-9	9.7	7156
232	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , <b>2002</b> , 420, 520-62	50.4	5376
231	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , <b>2007</b> , 447, 799-816	50.4	4121
230	A draft sequence of the Neandertal genome. <i>Science</i> , <b>2010</b> , 328, 710-722	33.3	2599
229	Patterns of somatic mutation in human cancer genomes. <i>Nature</i> , <b>2007</b> , 446, 153-8	50.4	2400
228	The Pfam protein families database. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, 276-80	20.1	1839
227	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , <b>2004</b> , 428, 493-521	50.4	1689
226	Mapping identifiers for the integration of genomic datasets with the R/Bioconductor package biomaRt. <i>Nature Protocols</i> , <b>2009</b> , 4, 1184-91	18.8	1626
225	The genome sequence of the malaria mosquito <i>Anopheles gambiae</i> . <i>Science</i> , <b>2002</b> , 298, 129-49	33.3	1622
224	International network of cancer genome projects. <i>Nature</i> , <b>2010</b> , 464, 993-8	50.4	1613
223	Automated generation of heuristics for biological sequence comparison. <i>BMC Bioinformatics</i> , <b>2005</b> , 6, 31	3.6	1485
222	GeneWise and Genomewise. <i>Genome Research</i> , <b>2004</b> , 14, 988-95	9.7	1467
221	Comparative genomics of the eukaryotes. <i>Science</i> , <b>2000</b> , 287, 2204-15	33.3	1364
220	The Bioperl toolkit: Perl modules for the life sciences. <i>Genome Research</i> , <b>2002</b> , 12, 1611-8	9.7	1234
219	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , <b>2016</b> , 534, 47-54	50.4	1193

218	The Reactome pathway knowledgebase. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D472-7	20.1	1188
217	The genomic basis of adaptive evolution in threespine sticklebacks. <i>Nature</i> , <b>2012</b> , 484, 55-61	50.4	1187
216	Oases: robust de novo RNA-seq assembly across the dynamic range of expression levels. <i>Bioinformatics</i> , <b>2012</b> , 28, 1086-92	7.2	1129
215	Ensembl 2016. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D710-6	20.1	1094
214	Reactome: a database of reactions, pathways and biological processes. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D691-7	20.1	1090
213	Ensembl 2014. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D749-55	20.1	1087
212	Mouse genomic variation and its effect on phenotypes and gene regulation. <i>Nature</i> , <b>2011</b> , 477, 289-94	50.4	1087
211	The Pfam protein families database. <i>Nucleic Acids Research</i> , <b>2000</b> , 28, 263-6	20.1	1074
210	Evolutionary and biomedical insights from the rhesus macaque genome. <i>Science</i> , <b>2007</b> , 316, 222-34	33.3	1072
209	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , <b>2011</b> , 9, e1001046	9.7	1060
208	Ensembl 2015. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D662-9	20.1	1013
207	Genome sequence of <i>Aedes aegypti</i> , a major arbovirus vector. <i>Science</i> , <b>2007</b> , 316, 1718-23	33.3	867
206	A small-cell lung cancer genome with complex signatures of tobacco exposure. <i>Nature</i> , <b>2010</b> , 463, 184-90	50.4	852
205	EnsemblCompara GeneTrees: Complete, duplication-aware phylogenetic trees in vertebrates. <i>Genome Research</i> , <b>2009</b> , 19, 327-35	9.7	836
204	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , <b>2011</b> , 478, 476-82	50.4	802
203	Ensembl 2012. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D84-90	20.1	798
202	Ensembl 2013. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D48-55	20.1	797
201	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , <b>2015</b> , 526, 82-90	50.4	776

200	Immunity-related genes and gene families in <i>Anopheles gambiae</i> . <i>Science</i> , <b>2002</b> , 298, 159-65	33.3	743
199	Reactome knowledgebase of human biological pathways and processes. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D619-22	20.1	675
198	The International Protein Index: an integrated database for proteomics experiments. <i>Proteomics</i> , <b>2004</b> , 4, 1985-8	4.8	650
197	Analysis of the RNA-recognition motif and RS and RGG domains: conservation in metazoan pre-mRNA splicing factors. <i>Nucleic Acids Research</i> , <b>1993</b> , 21, 5803-16	20.1	610
196	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. <i>Genome Research</i> , <b>2012</b> , 22, 1798-812	9.7	596
195	Ensembl 2011. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D800-6	20.1	590
194	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , <b>2008</b> , 453, 175-83	50.4	545
193	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 779-85	44.5	533
192	Towards practical, high-capacity, low-maintenance information storage in synthesized DNA. <i>Nature</i> , <b>2013</b> , 494, 77-80	50.4	501
191	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 935-42	44.5	499
190	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 6131-8	11.5	490
189	Comparative genome and proteome analysis of <i>Anopheles gambiae</i> and <i>Drosophila melanogaster</i> . <i>Science</i> , <b>2002</b> , 298, 149-59	33.3	455
188	Reactome: a knowledge base of biologic pathways and processes. <i>Genome Biology</i> , <b>2007</b> , 8, R39	18.3	454
187	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. <i>Nature Medicine</i> , <b>2017</b> , 23, 517-525	50.5	444
186	The consensus coding sequence (CCDS) project: Identifying a common protein-coding gene set for the human and mouse genomes. <i>Genome Research</i> , <b>2009</b> , 19, 1316-23	9.7	415
185	Highly accurate protein structure prediction for the human proteome. <i>Nature</i> , <b>2021</b> , 596, 590-596	50.4	399
184	Open chromatin defined by DNaseI and FAIRE identifies regulatory elements that shape cell-type identity. <i>Genome Research</i> , <b>2011</b> , 21, 1757-67	9.7	391
183	Integrative annotation of chromatin elements from ENCODE data. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 827-40.1	40.1	383

182	The European Nucleotide Archive. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D28-31	20.1	322
181	An overview of Ensembl. <i>Genome Research</i> , <b>2004</b> , 14, 925-8	9.7	316
180	The landscape of histone modifications across 1% of the human genome in five human cell lines. <i>Genome Research</i> , <b>2007</b> , 17, 691-707	9.7	315
179	EnSMart: a generic system for fast and flexible access to biological data. <i>Genome Research</i> , <b>2004</b> , 14, 160-9	9.7	306
178	PH domain: the first anniversary. <i>Trends in Biochemical Sciences</i> , <b>1994</b> , 19, 349-53	10.3	306
177	An integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs). <i>Genome Research</i> , <b>2008</b> , 18, 1518-29	9.7	304
176	Common genetic variation drives molecular heterogeneity in human iPSCs. <i>Nature</i> , <b>2017</b> , 546, 370-375	50.4	294
175	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , <b>2015</b> , 47, 1415-25	36.3	292
174	AlphaFold Protein Structure Database: massively expanding the structural coverage of protein-sequence space with high-accuracy models. <i>Nucleic Acids Research</i> , <b>2021</b> ,	20.1	285
173	A physical map of the mouse genome. <i>Nature</i> , <b>2002</b> , 418, 743-50	50.4	282
172	Challenges and standards in integrating surveys of structural variation. <i>Nature Genetics</i> , <b>2007</b> , 39, S7-15	36.3	279
171	Genome-wide meta-analysis identifies new susceptibility loci for migraine. <i>Nature Genetics</i> , <b>2013</b> , 45, 912-917	36.3	276
170	Using GeneWise in the Drosophila annotation experiment. <i>Genome Research</i> , <b>2000</b> , 10, 547-8	9.7	263
169	Sense from sequence reads: methods for alignment and assembly. <i>Nature Methods</i> , <b>2009</b> , 6, S6-S12	21.6	261
168	Heritable individual-specific and allele-specific chromatin signatures in humans. <i>Science</i> , <b>2010</b> , 328, 235-239	33.3	260
167	High-resolution genome-wide in vivo footprinting of diverse transcription factors in human cells. <i>Genome Research</i> , <b>2011</b> , 21, 456-64	9.7	250
166	Open Targets: a platform for therapeutic target identification and validation. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D985-D994	20.1	241
165	Ensembl's 10th year. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D557-62	20.1	240

164	Efficient storage of high throughput DNA sequencing data using reference-based compression. <i>Genome Research</i> , <b>2011</b> , 21, 734-40	9.7	233
163	Enredo and Pecan: genome-wide mammalian consistency-based multiple alignment with paralogs. <i>Genome Research</i> , <b>2008</b> , 18, 1814-28	9.7	218
162	Factorbook.org: a Wiki-based database for transcription factor-binding data generated by the ENCODE consortium. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D171-6	20.1	212
161	MinION Analysis and Reference Consortium: Phase 1 data release and analysis. <i>F1000Research</i> , <b>2015</b> , 4, 1075	3.6	210
160	VectorBase: a data resource for invertebrate vector genomics. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D583-7	20.1	200
159	Prepublication data sharing. <i>Nature</i> , <b>2009</b> , 461, 168-70	50.4	197
158	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. <i>Genome Biology</i> , <b>2012</b> , 13, R48	18.3	194
157	A transcription factor collective defines cardiac cell fate and reflects lineage history. <i>Cell</i> , <b>2012</b> , 148, 473-86	56.2	191
156	EGASP: the human ENCODE Genome Annotation Assessment Project. <i>Genome Biology</i> , <b>2006</b> , 7 Suppl 1, S2.1-31	18.3	187
155	Modeling gene expression using chromatin features in various cellular contexts. <i>Genome Biology</i> , <b>2012</b> , 13, R53	18.3	182
154	The implications of alternative splicing in the ENCODE protein complement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 5495-500	11.5	177
153	The topography of mutational processes in breast cancer genomes. <i>Nature Communications</i> , <b>2016</b> , 7, 11383	17.4	172
152	Comparative genomics: genome-wide analysis in metazoan eukaryotes. <i>Nature Reviews Genetics</i> , <b>2003</b> , 4, 251-62	30.1	172
151	Identification of novel peptide hormones in the human proteome by hidden Markov model screening. <i>Genome Research</i> , <b>2007</b> , 17, 320-7	9.7	170
150	Integrating Genomics into Healthcare: A Global Responsibility. <i>American Journal of Human Genetics</i> , <b>2019</b> , 104, 13-20	11	166
149	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , <b>2007</b> , 17, 760-74	9.7	163
148	The HGNC Database in 2008: a resource for the human genome. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D445-8	20.1	163
147	The EBI RDF platform: linked open data for the life sciences. <i>Bioinformatics</i> , <b>2014</b> , 30, 1338-9	7.2	160

146	Pebble and rock band: heuristic resolution of repeats and scaffolding in the velvet short-read de novo assembler. <i>PLoS ONE</i> , <b>2009</b> , 4, e8407	3.7	151
145	SNP and haplotype mapping for genetic analysis in the rat. <i>Nature Genetics</i> , <b>2008</b> , 40, 560-6	36.3	150
144	Ensembl Genomes: an integrative resource for genome-scale data from non-vertebrate species. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D91-7	20.1	141
143	Comparative analysis of noncoding regions of 77 orthologous mouse and human gene pairs. <i>Genome Research</i> , <b>1999</b> , 9, 815-24	9.7	141
142	Epigenome-wide Association Studies and the Interpretation of Disease -Omics. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1006105	6	137
141	Genome-wide nucleotide-level mammalian ancestor reconstruction. <i>Genome Research</i> , <b>2008</b> , 18, 1829-43	3.7	136
140	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , <b>2012</b> , 22, 1658-67	9.7	133
139	Cancer and genomics. <i>Nature</i> , <b>2001</b> , 409, 850-2	50.4	108
138	Ensembl variation resources. <i>BMC Genomics</i> , <b>2010</b> , 11, 293	4.5	104
137	The Ensembl core software libraries. <i>Genome Research</i> , <b>2004</b> , 14, 929-33	9.7	100
136	VectorBase: a home for invertebrate vectors of human pathogens. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D503-5	3.1	97
135	The European Bioinformatics Institute in 2016: Data growth and integration. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D20-6	20.1	91
134	Locus Reference Genomic sequences: an improved basis for describing human DNA variants. <i>Genome Medicine</i> , <b>2010</b> , 2, 24	14.4	86
133	Cell-type specific and combinatorial usage of diverse transcription factors revealed by genome-wide binding studies in multiple human cells. <i>Genome Research</i> , <b>2012</b> , 22, 9-24	9.7	86
132	Update of the <i>Anopheles gambiae</i> PEST genome assembly. <i>Genome Biology</i> , <b>2007</b> , 8, R5	18.3	82
131	MinION Analysis and Reference Consortium: Phase 2 data release and analysis of R9.0 chemistry. <i>F1000Research</i> , <b>2017</b> , 6, 760	3.6	79
130	The making of ENCODE: Lessons for big-data projects. <i>Nature</i> , <b>2012</b> , 489, 49-51	50.4	77
129	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. <i>Genome Research</i> , <b>2010</b> , 20, 791-803	9.7	77

128	Integrating biological data--the Distributed Annotation System. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 8, S3	3.6	77
127	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , <b>2016</b> , 7, 12910	17.4	74
126	Petabyte-scale innovations at the European Nucleotide Archive. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D19-25	20.1	72
125	GARFIELD classifies disease-relevant genomic features through integration of functional annotations with association signals. <i>Nature Genetics</i> , <b>2019</b> , 51, 343-353	36.3	71
124	Analysis of variation at transcription factor binding sites in Drosophila and humans. <i>Genome Biology</i> , <b>2012</b> , 13, R49	18.3	71
123	Transcriptome analysis for the chicken based on 19,626 finished cDNA sequences and 485,337 expressed sequence tags. <i>Genome Research</i> , <b>2005</b> , 15, 174-83	9.7	71
122	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. <i>Cell Reports</i> , <b>2016</b> , 17, 2137-2150	21.6	70
121	Evolutionary constraints of phosphorylation in eukaryotes, prokaryotes, and mitochondria. <i>Molecular and Cellular Proteomics</i> , <b>2010</b> , 9, 2642-53	7.6	70
120	A survey of homozygous deletions in human cancer genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 4542-7	11.5	70
119	Trawler: de novo regulatory motif discovery pipeline for chromatin immunoprecipitation. <i>Nature Methods</i> , <b>2007</b> , 4, 563-5	21.6	66
118	A call for public archives for biological image data. <i>Nature Methods</i> , <b>2018</b> , 15, 849-854	21.6	61
117	The Anopheles gambiae genome: an update. <i>Trends in Parasitology</i> , <b>2004</b> , 20, 49-52	6.4	56
116	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. <i>Genome Research</i> , <b>2004</b> , 14, 852-9	9.7	55
115	Genome information resources - developments at Ensembl. <i>Trends in Genetics</i> , <b>2004</b> , 20, 268-72	8.5	55
114	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. <i>Nature Genetics</i> , <b>2017</b> , 49, 341-348	36.3	54
113	Integrative analysis of gene expression, DNA methylation, physiological traits, and genetic variation in human skeletal muscle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 10883-10888	11.5	54
112	The European Bioinformatics Institute's data resources 2014. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D18-25	20.1	54
111	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , <b>2011</b> , 17, 1941-6	5.8	54



110	Confounding between recombination and selection, and the Ped/Pop method for detecting selection. <i>Genome Research</i> , <b>2008</b> , 18, 1304-13	9.7	52
109	Promoter shape varies across populations and affects promoter evolution and expression noise. <i>Nature Genetics</i> , <b>2017</b> , 49, 550-558	36.3	51
108	Mining the draft human genome. <i>Nature</i> , <b>2001</b> , 409, 827-8	50.4	51
107	Human genomics: The end of the start for population sequencing. <i>Nature</i> , <b>2015</b> , 526, 52-3	50.4	48
106	Improvements to services at the European Nucleotide Archive. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D39-45	20.1	47
105	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. <i>Nature Communications</i> , <b>2021</b> , 12, 1258	17.4	47
104	Optimized design and assessment of whole genome tiling arrays. <i>Bioinformatics</i> , <b>2007</b> , 23, i195-204	7.2	46
103	Policy challenges of clinical genome sequencing. <i>BMJ, The</i> , <b>2013</b> , 347, f6845	5.9	44
102	Arabidopsis reactome: a foundation knowledgebase for plant systems biology. <i>Plant Cell</i> , <b>2008</b> , 20, 1426-1436	13.6	44
101	A SNP map of the rat genome generated from cDNA sequences. <i>Science</i> , <b>2004</b> , 303, 807	33.3	44
100	Sequence progressive alignment, a framework for practical large-scale probabilistic consistency alignment. <i>Bioinformatics</i> , <b>2009</b> , 25, 295-301	7.2	42
99	Approaches to comparative sequence analysis: towards a functional view of vertebrate genomes. <i>Nature Reviews Genetics</i> , <b>2008</b> , 9, 303-13	30.1	42
98	Genetic variants regulating expression levels and isoform diversity during embryogenesis. <i>Nature</i> , <b>2017</b> , 541, 402-406	50.4	39
97	Priorities for nucleotide trace, sequence and annotation data capture at the Ensembl Trace Archive and the EMBL Nucleotide Sequence Database. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D5-12	20.1	39
96	Quantitative genetics of CTCF binding reveal local sequence effects and different modes of X-chromosome association. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004798	6	38
95	EMMA--mouse mutant resources for the international scientific community. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D570-6	20.1	38
94	In vivo validation of a computationally predicted conserved Ath5 target gene set. <i>PLoS Genetics</i> , <b>2007</b> , 3, 1661-71	6	38
93	The discovery, positioning and verification of a set of transcription-associated motifs in vertebrates. <i>Genome Biology</i> , <b>2005</b> , 6, R104	18.3	38

92	The European Bioinformatics Institute's data resources. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 43-50	20.1	38
91	Genomics in healthcare: GA4GH looks to 2022		38
90	What everybody should know about the rat genome and its online resources. <i>Nature Genetics</i> , <b>2008</b> , 40, 523-7	36.3	37
89	Leveraging European infrastructures to access 1 million human genomes by 2022. <i>Nature Reviews Genetics</i> , <b>2019</b> , 20, 693-701	30.1	36
88	The European Bioinformatics Institute in 2017: data coordination and integration. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D21-D29	20.1	36
87	Genomic and phenotypic characterization of a wild medaka population: towards the establishment of an isogenic population genetic resource in fish. <i>G3: Genes, Genomes, Genetics</i> , <b>2014</b> , 4, 433-45	3.2	34
86	RNA modifications detection by comparative Nanopore direct RNA sequencing		33
85	Ensembl regulation resources. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	33
84	The human leukemia virus HTLV-1 alters the structure and transcription of host chromatin in cis. <i>ELife</i> , <b>2018</b> , 7,	8.9	30
83	Major submissions tool developments at the European Nucleotide Archive. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D43-7	20.1	27
82	Genome browsing with Ensembl: a practical overview. <i>Briefings in Functional Genomics &amp; Proteomics</i> , <b>2007</b> , 6, 202-19		27
81	Paralogous annotation of disease-causing variants in long QT syndrome genes. <i>Human Mutation</i> , <b>2012</b> , 33, 1188-1191	4.7	26
80	A database and API for variation, dense genotyping and resequencing data. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 238	3.6	26
79	Gene finding in the chicken genome. <i>BMC Bioinformatics</i> , <b>2005</b> , 6, 131	3.6	26
78	Open annotation offers a democratic solution to genome sequencing. <i>Nature</i> , <b>2000</b> , 403, 825	50.4	26
77	Genetic and functional insights into the fractal structure of the heart. <i>Nature</i> , <b>2020</b> , 584, 589-594	50.4	26
76	Estimating the neutral rate of nucleotide substitution using introns. <i>Molecular Biology and Evolution</i> , <b>2007</b> , 24, 522-31	8.3	25
75	Assemblies: the good, the bad, the ugly. <i>Nature Methods</i> , <b>2011</b> , 8, 59-60	21.6	24

74	Allele-specific and heritable chromatin signatures in humans. <i>Human Molecular Genetics</i> , <b>2010</b> , 19, R204-9.6	9.6	24
73	A new strategy for genome assembly using short sequence reads and reduced representation libraries. <i>Genome Research</i> , <b>2010</b> , 20, 249-56	9.7	24
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