

Richard M Durbin

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

249 papers	167,841 citations	108 h-index	280 g-index
280 ext. papers	214,227 ext. citations	17 avg, IF	8.73 L-index

#	Paper	IF	Citations
249	Ethical, legal, and social issues in the Earth BioGenome Project.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	3
248	The Earth BioGenome Project 2020: Starting the clock.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	15
247	Placing ancient DNA sequences into reference phylogenies.. <i>Molecular Biology and Evolution</i> , 2022 ,	8.3	3
246	Standards recommendations for the Earth BioGenome Project.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	4
245	Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	6
244	Sequence locally, think globally: The Darwin Tree of Life Project.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	9
243	Genomic consequences of domestication of the Siamese fighting fish.. <i>Science Advances</i> , 2022 , 8, eabm4250,	4.5	3
242	The complete sequence of a human genome.. <i>Science</i> , 2022 , 376, 44-53	33.3	107
241	Efficient iterative Hi-C scaffold based on N-best neighbors. <i>BMC Bioinformatics</i> , 2021 , 22, 569	3.6	0
240	Late Quaternary dynamics of Arctic biota from ancient environmental genomics. <i>Nature</i> , 2021 , 600, 86-92,	30.4	12
239	Mapping epigenetic divergence in the massive radiation of Lake Malawi cichlid fishes. <i>Nature Communications</i> , 2021 , 12, 5870	17.4	2
238	A high-quality, chromosome-level genome assembly of the Black Soldier Fly (<i>Hermetia illucens</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	9
237	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. <i>Genome Biology</i> , 2021 , 22, 120	18.3	19
236	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737-746,	46.4	161
235	The genome sequence of the brown trout, Linnaeus 1758. <i>Wellcome Open Research</i> , 2021 , 6, 108	4.8	5
234	The genome sequence of the European golden eagle, Linnaeus 1758. <i>Wellcome Open Research</i> , 2021 , 6, 112	4.8	0
233	Environmental genomics of Late Pleistocene black bears and giant short-faced bears. <i>Current Biology</i> , 2021 , 31, 2728-2736.e8	6.3	6

232	Haplotype-aware graph indexes. <i>Bioinformatics</i> , 2020 , 36, 400-407	7.2	23
231	Souporcell: robust clustering of single-cell RNA-seq data by genotype without reference genotypes. <i>Nature Methods</i> , 2020 , 17, 615-620	21.6	69
230	Insights into human genetic variation and population history from 929 diverse genomes. <i>Science</i> , 2020 , 367,	33.3	196
229	Identifying and removing haplotypic duplication in primary genome assemblies. <i>Bioinformatics</i> , 2020 , 36, 2896-2898	7.2	222
228	The genome sequence of the Eurasian red squirrel, Linnaeus 1758. <i>Wellcome Open Research</i> , 2020 , 5, 18	4.8	2
227	The genome sequence of the eastern grey squirrel, Gmelin, 1788. <i>Wellcome Open Research</i> , 2020 , 5, 27	4.8	1
226	Population-scale proteome variation in human induced pluripotent stem cells. <i>ELife</i> , 2020 , 9,	8.9	16
225	The genome sequence of the Eurasian river otter, <i>Lutra lutra</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2020 , 5, 33	4.8	1
224	A haplotype-aware de novo assembly of related individuals using pedigree sequence graph. <i>Bioinformatics</i> , 2020 , 36, 2385-2392	7.2	9
223	Ancestral Hybridization Facilitated Species Diversification in the Lake Malawi Cichlid Fish Adaptive Radiation. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1100-1113	8.3	41
222	Removing reference bias and improving indel calling in ancient DNA data analysis by mapping to a sequence variation graph. <i>Genome Biology</i> , 2020 , 21, 250	18.3	9
221	A haplotype-resolved, de novo genome assembly for the wood tiger moth (<i>Arctia plantaginis</i>) through trio binning. <i>GigaScience</i> , 2020 , 9,	7.6	6
220	Efficiently inferring the demographic history of many populations with allele count data. <i>Journal of the American Statistical Association</i> , 2020 , 115, 1472-1487	2.8	33
219	A High-Quality Genome Assembly from a Single Mosquito Using PacBio Sequencing. <i>Genes</i> , 2019 , 10,	4.2	72
218	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , 2019 , 570, 182-188	50.4	137
217	htsget: a protocol for securely streaming genomic data. <i>Bioinformatics</i> , 2019 , 35, 119-121	7.2	13
216	Crumble: reference free lossy compression of sequence quality values. <i>Bioinformatics</i> , 2019 , 35, 337-339	7.2	11
215	Viral coinfection analysis using a MinHash toolkit. <i>BMC Bioinformatics</i> , 2019 , 20, 389	3.6	2

214	GFAKluge: A C++ library and command line utilities for the Graphical Fragment Assembly formats. <i>Journal of Open Source Software</i> , 2019 , 4,	5.2	2
213	Identifying Extrinsic versus Intrinsic Drivers of Variation in Cell Behavior in Human iPSC Lines from Healthy Donors. <i>Cell Reports</i> , 2019 , 26, 2078-2087.e3	10.6	16
212	Earth BioGenome Project: Sequencing life for the future of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 4325-4333	11.5	334
211	Did Our Species Evolve in Subdivided Populations across Africa, and Why Does It Matter?. <i>Trends in Ecology and Evolution</i> , 2018 , 33, 582-594	10.9	200
210	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018 , 360,	33.3	162
209	Variation graph toolkit improves read mapping by representing genetic variation in the reference. <i>Nature Biotechnology</i> , 2018 , 36, 875-879	44.5	223
208	Whole-genome sequences of Malawi cichlids reveal multiple radiations interconnected by gene flow. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1940-1955	12.3	160
207	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. <i>Nature Genetics</i> , 2018 , 50, 1574-1583	36.3	91
206	Detecting archaic introgression using an unadmixed outgroup. <i>PLoS Genetics</i> , 2018 , 14, e1007641	6	42
205	A graph-based approach to diploid genome assembly. <i>Bioinformatics</i> , 2018 , 34, i105-i114	7.2	36
204	Whole-genome view of the consequences of a population bottleneck using 2926 genome sequences from Finland and United Kingdom. <i>European Journal of Human Genetics</i> , 2017 , 25, 477-484	5.3	41
203	Whole-exome sequencing of 228 patients with sporadic Parkinson's disease. <i>Scientific Reports</i> , 2017 , 7, 41188	4.9	21
202	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. <i>Genome Research</i> , 2017 , 27, 849-864	9.7	365
201	Contrasting evolutionary genome dynamics between domesticated and wild yeasts. <i>Nature Genetics</i> , 2017 , 49, 913-924	36.3	178
200	Common genetic variation drives molecular heterogeneity in human iPSCs. <i>Nature</i> , 2017 , 546, 370-375	50.4	294
199	De novo yeast genome assemblies from MinION, PacBio and MiSeq platforms. <i>Scientific Reports</i> , 2017 , 7, 3935	4.9	101
198	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. <i>American Journal of Human Genetics</i> , 2017 , 100, 865-884	11	74
197	Using reference-free compressed data structures to analyze sequencing reads from thousands of human genomes. <i>Genome Research</i> , 2017 , 27, 300-309	9.7	15

196	Estimating the human mutation rate from autozygous segments reveals population differences in human mutational processes. <i>Nature Communications</i> , 2017 , 8, 303	17.4	52
195	No evidence for maintenance of a sympatric species barrier by chromosomal inversions. <i>Evolution Letters</i> , 2017 , 1, 138-154	5.3	49
194	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. <i>Nature Communications</i> , 2017 , 8, 15927	17.4	37
193	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016 , 48, 1279-83	36.3	1447
192	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016 , 538, 207-214	50.4	268
191	Deficient methylation and formylation of mt-tRNA(Met) wobble cytosine in a patient carrying mutations in NSUN3. <i>Nature Communications</i> , 2016 , 7, 12039	17.4	124
190	Whole-exome sequencing in an isolated population from the Dalmatian island of Vis. <i>European Journal of Human Genetics</i> , 2016 , 24, 1479-87	5.3	5
189	Iron Age and Anglo-Saxon genomes from East England reveal British migration history. <i>Nature Communications</i> , 2016 , 7, 10408	17.4	100
188	Bi-allelic Truncating Mutations in TANGO2 Cause Infancy-Onset Recurrent Metabolic Crises with Encephalocardiomyopathy. <i>American Journal of Human Genetics</i> , 2016 , 98, 358-62	11	49
187	Health and population effects of rare gene knockouts in adult humans with related parents. <i>Science</i> , 2016 , 352, 474-7	33.3	185
186	DNAH11 Localization in the Proximal Region of Respiratory Cilia Defines Distinct Outer Dynein Arm Complexes. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2016 , 55, 213-24	5.7	79
185	A high-content platform to characterise human induced pluripotent stem cell lines. <i>Methods</i> , 2016 , 96, 85-96	4.6	28
184	A Method for Checking Genomic Integrity in Cultured Cell Lines from SNP Genotyping Data. <i>PLoS ONE</i> , 2016 , 11, e0155014	3.7	16
183	BCFtools/RoH: a hidden Markov model approach for detecting autozygosity from next-generation sequencing data. <i>Bioinformatics</i> , 2016 , 32, 1749-51	7.2	256
182	Reference-based phasing using the Haplotype Reference Consortium panel. <i>Nature Genetics</i> , 2016 , 48, 1443-1448	36.3	699
181	TTC25 Deficiency Results in Defects of the Outer Dynein Arm Docking Machinery and Primary Ciliary Dyskinesia with Left-Right Body Asymmetry Randomization. <i>American Journal of Human Genetics</i> , 2016 , 99, 460-9	11	58
180	POPULATION GENETICS. Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015 , 349, aab3884	33.3	317
179	Extending reference assembly models. <i>Genome Biology</i> , 2015 , 16, 13	18.3	107

178	Pathway-based factor analysis of gene expression data produces highly heritable phenotypes that associate with age. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 839-47	3.2	5
177	A global reference for human genetic variation. <i>Nature</i> , 2015 , 526, 68-74	50.4	8599
176	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. <i>Nature</i> , 2015 , 526, 112-7	50.4	308
175	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015 , 526, 82-90	50.4	776
174	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. <i>Nature Communications</i> , 2015 , 6, 8111	17.4	186
173	Gene-gene and gene-environment interactions detected by transcriptome sequence analysis in twins. <i>Nature Genetics</i> , 2015 , 47, 88-91	36.3	140
172	Deficiency of ECHS1 causes mitochondrial encephalopathy with cardiac involvement. <i>Annals of Clinical and Translational Neurology</i> , 2015 , 2, 492-509	5.3	69
171	Whole-genome sequence-based analysis of thyroid function. <i>Nature Communications</i> , 2015 , 6, 5681	17.4	56
170	Immunofluorescence Analysis and Diagnosis of Primary Ciliary Dyskinesia with Radial Spoke Defects. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2015 , 53, 563-73	5.7	90
169	Tracing the route of modern humans out of Africa by using 225 human genome sequences from Ethiopians and Egyptians. <i>American Journal of Human Genetics</i> , 2015 , 96, 986-91	11	107
168	Homozygous loss-of-function variants in European cosmopolitan and isolate populations. <i>Human Molecular Genetics</i> , 2015 , 24, 5464-74	5.6	18
167	Genomic islands of speciation separate cichlid ecomorphs in an East African crater lake. <i>Science</i> , 2015 , 350, 1493-1498	33.3	204
166	The genomic and phenotypic diversity of <i>Schizosaccharomyces pombe</i> . <i>Nature Genetics</i> , 2015 , 47, 235-41	36.3	111
165	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. <i>Nature Communications</i> , 2014 , 5, 4871	17.4	46
164	Managing clinically significant findings in research: the UK10K example. <i>European Journal of Human Genetics</i> , 2014 , 22, 1100-4	5.3	33
163	Inferring human population size and separation history from multiple genome sequences. <i>Nature Genetics</i> , 2014 , 46, 919-25	36.3	569
162	Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. <i>Genome Biology</i> , 2014 , 15, R88	18.3	51
161	Quantitative genetics of CTCF binding reveal local sequence effects and different modes of X-chromosome association. <i>PLoS Genetics</i> , 2014 , 10, e1004798	6	38

160	Distribution and medical impact of loss-of-function variants in the Finnish founder population. <i>PLoS Genetics</i> , 2014 , 10, e1004494	6	243
159	Estimation of epistatic variance components and heritability in founder populations and crosses. <i>Genetics</i> , 2014 , 198, 1405-16	4	19
158	Estimating telomere length from whole genome sequence data. <i>Nucleic Acids Research</i> , 2014 , 42, e75	20.1	85
157	Efficient haplotype matching and storage using the positional Burrows-Wheeler transform (PBWT). <i>Bioinformatics</i> , 2014 , 30, 1266-72	7.2	241
156	A high-definition view of functional genetic variation from natural yeast genomes. <i>Molecular Biology and Evolution</i> , 2014 , 31, 872-88	8.3	206
155	Genetic interactions affecting human gene expression identified by variance association mapping. <i>ELife</i> , 2014 , 3, e01381	8.9	86
154	The anatomy of successful computational biology software. <i>Nature Biotechnology</i> , 2013 , 31, 894-7	44.5	18
153	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013 , 2, 10	7.6	461
152	Global analysis of DNA methylation variation in adipose tissue from twins reveals links to disease-associated variants in distal regulatory elements. <i>American Journal of Human Genetics</i> , 2013 , 93, 876-90	11	269
151	High-resolution mapping of complex traits with a four-parent advanced intercross yeast population. <i>Genetics</i> , 2013 , 195, 1141-55	4	91
150	Gene expression changes with age in skin, adipose tissue, blood and brain. <i>Genome Biology</i> , 2013 , 14, R75	18.3	185
149	A genome-wide survey of genetic variation in gorillas using reduced representation sequencing. <i>PLoS ONE</i> , 2013 , 8, e65066	3.7	16
148	High levels of RNA-editing site conservation amongst 15 laboratory mouse strains. <i>Genome Biology</i> , 2012 , 13, 26	18.3	122
147	Using probabilistic estimation of expression residuals (PEER) to obtain increased power and interpretability of gene expression analyses. <i>Nature Protocols</i> , 2012 , 7, 500-7	18.8	460
146	Ensembl 2012. <i>Nucleic Acids Research</i> , 2012 , 40, D84-90	20.1	798
145	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012 , 491, 56-65	50.4	6049
144	Revising the human mutation rate: implications for understanding human evolution. <i>Nature Reviews Genetics</i> , 2012 , 13, 745-53	30.1	369
143	Mapping cis- and trans-regulatory effects across multiple tissues in twins. <i>Nature Genetics</i> , 2012 , 44, 1084-93	36.3	572

142	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012 , 483, 169-75	50.4	517
141	WormBase: Annotating many nematode genomes. <i>Worm</i> , 2012 , 1, 15-21		11
140	Extent, causes, and consequences of small RNA expression variation in human adipose tissue. <i>PLoS Genetics</i> , 2012 , 8, e1002704	6	43
139	Patterns of cis regulatory variation in diverse human populations. <i>PLoS Genetics</i> , 2012 , 8, e1002639	6	361
138	Efficient de novo assembly of large genomes using compressed data structures. <i>Genome Research</i> , 2012 , 22, 549-56	9.7	501
137	WormBase 2012: more genomes, more data, new website. <i>Nucleic Acids Research</i> , 2012 , 40, D735-41	20.1	159
136	Inference of human population history from individual whole-genome sequences. <i>Nature</i> , 2011 , 475, 493-6	50.4	1299
135	Mouse genomic variation and its effect on phenotypes and gene regulation. <i>Nature</i> , 2011 , 477, 289-94	50.4	1087
134	Identity-by-descent-based phasing and imputation in founder populations using graphical models. <i>Genetic Epidemiology</i> , 2011 , 35, 853-60	2.6	26
133	Dindel: accurate indel calls from short-read data. <i>Genome Research</i> , 2011 , 21, 961-73	9.7	341
132	The variant call format and VCFtools. <i>Bioinformatics</i> , 2011 , 27, 2156-8	7.2	6200
131	Revealing the genetic structure of a trait by sequencing a population under selection. <i>Genome Research</i> , 2011 , 21, 1131-8	9.7	185
130	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41	9.7	364
129	Ensembl 2011. <i>Nucleic Acids Research</i> , 2011 , 39, D800-6	20.1	590
128	SNP detection and genotyping from low-coverage sequencing data on multiple diploid samples. <i>Genome Research</i> , 2011 , 21, 952-60	9.7	117
127	Joint genetic analysis of gene expression data with inferred cellular phenotypes. <i>PLoS Genetics</i> , 2011 , 7, e1001276	6	57
126	The architecture of gene regulatory variation across multiple human tissues: the MuTHER study. <i>PLoS Genetics</i> , 2011 , 7, e1002003	6	336
125	Trait variation in yeast is defined by population history. <i>PLoS Genetics</i> , 2011 , 7, e1002111	6	230

124	Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. <i>Nature</i> , 2010 , 464, 721-7	50.4	668
123	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010 , 467, 1061-73	50.4	6142
122	Efficient construction of an assembly string graph using the FM-index. <i>Bioinformatics</i> , 2010 , 26, i367-73	7.2	164
121	WormBase: a comprehensive resource for nematode research. <i>Nucleic Acids Research</i> , 2010 , 38, D463-7	20.1	289
120	Ensembl@ 10th year. <i>Nucleic Acids Research</i> , 2010 , 38, D557-62	20.1	240
119	Copy number variant detection in inbred strains from short read sequence data. <i>Bioinformatics</i> , 2010 , 26, 565-7	7.2	40
118	A Bayesian framework to account for complex non-genetic factors in gene expression levels greatly increases power in eQTL studies. <i>PLoS Computational Biology</i> , 2010 , 6, e1000770	5	295
117	Systematic analysis of human protein complexes identifies chromosome segregation proteins. <i>Science</i> , 2010 , 328, 593-9	33.3	419
116	Fast and accurate long-read alignment with Burrows-Wheeler transform. <i>Bioinformatics</i> , 2010 , 26, 589-95	7.2	6791
115	The consensus coding sequence (CCDS) project: Identifying a common protein-coding gene set for the human and mouse genomes. <i>Genome Research</i> , 2009 , 19, 1316-23	9.7	415
114	Population genomics of domestic and wild yeasts. <i>Nature</i> , 2009 , 458, 337-41	50.4	1073
113	Prepublication data sharing. <i>Nature</i> , 2009 , 461, 168-70	50.4	197
112	The Sequence Alignment/Map format and SAMtools. <i>Bioinformatics</i> , 2009 , 25, 2078-9	7.2	30805
111	Fast and accurate short read alignment with Burrows-Wheeler transform. <i>Bioinformatics</i> , 2009 , 25, 1754-60	7.2	26095
110	Deep short-read sequencing of chromosome 17 from the mouse strains A/J and CAST/Ei identifies significant germline variation and candidate genes that regulate liver triglyceride levels. <i>Genome Biology</i> , 2009 , 10, R112	18.3	32
109	EnsemblCompara GeneTrees: Complete, duplication-aware phylogenetic trees in vertebrates. <i>Genome Research</i> , 2009 , 19, 327-35	9.7	836
108	Inferring selection on amino acid preference in protein domains. <i>Molecular Biology and Evolution</i> , 2009 , 26, 527-36	8.3	7
107	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008 , 456, 60-5	50.4	744

106	Accurate whole human genome sequencing using reversible terminator chemistry. <i>Nature</i> , 2008 , 456, 53-9	50.4	2615
105	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. <i>Nature Biotechnology</i> , 2008 , 26, 779-85	44.5	533
104	Identification of somatically acquired rearrangements in cancer using genome-wide massively parallel paired-end sequencing. <i>Nature Genetics</i> , 2008 , 40, 722-9	36.3	666
103	BAC TransgeneOmics: a high-throughput method for exploration of protein function in mammals. <i>Nature Methods</i> , 2008 , 5, 409-15	21.6	484
102	A large genome center@improvements to the Illumina sequencing system. <i>Nature Methods</i> , 2008 , 5, 1005-10	21.6	575
101	Mapping short DNA sequencing reads and calling variants using mapping quality scores. <i>Genome Research</i> , 2008 , 18, 1851-8	9.7	2002
100	Accounting for Non-genetic Factors Improves the Power of eQTL Studies 2008 , 411-422		13
99	WormBase 2007. <i>Nucleic Acids Research</i> , 2008 , 36, D612-7	20.1	91
98	TreeFam: 2008 Update. <i>Nucleic Acids Research</i> , 2008 , 36, D735-40	20.1	234
97	Regulatory evolution in proteins by turnover and lineage-specific changes of cyclin-dependent kinase consensus sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 17713-8	11.5	56
96	Genomix: a method for combining gene-finders@predictions, which uses evolutionary conservation of sequence and intron-exon structure. <i>Bioinformatics</i> , 2007 , 23, 1468-75	7.2	10
95	WormBase: new content and better access. <i>Nucleic Acids Research</i> , 2007 , 35, D506-10	20.1	76
94	A systematic comparative and structural analysis of protein phosphorylation sites based on the mtcPTM database. <i>Genome Biology</i> , 2007 , 8, R90	18.3	53
93	Clustering of phosphorylation site recognition motifs can be exploited to predict the targets of cyclin-dependent kinase. <i>Genome Biology</i> , 2007 , 8, R23	18.3	60
92	[X]uniqMAP: unique gene sequence regions in the human and mouse genomes. <i>BMC Genomics</i> , 2006 , 7, 249	4.5	0
91	WormBase: better software, richer content. <i>Nucleic Acids Research</i> , 2006 , 34, D475-8	20.1	68
90	A conserved sequence motif in 3@untranslated regions of ribosomal protein mRNAs in nematodes. <i>Rna</i> , 2006 , 12, 1786-9	5.8	7
89	TreeFam: a curated database of phylogenetic trees of animal gene families. <i>Nucleic Acids Research</i> , 2006 , 34, D572-80	20.1	383

88	Pfam: clans, web tools and services. <i>Nucleic Acids Research</i> , 2006 , 34, D247-51	20.1	1784
87	Vertebrate gene finding from multiple-species alignments using a two-level strategy. <i>Genome Biology</i> , 2006 , 7 Suppl 1, S6.1-12	18.3	11
86	Mapping trait loci by use of inferred ancestral recombination graphs. <i>American Journal of Human Genetics</i> , 2006 , 79, 910-22	11	87
85	The Sequence Ontology: a tool for the unification of genome annotations. <i>Genome Biology</i> , 2005 , 6, R44	18.3	492
84	WormBase: a comprehensive data resource for <i>Caenorhabditis</i> biology and genomics. <i>Nucleic Acids Research</i> , 2005 , 33, D383-9	20.1	140
83	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2005 , 33, D201-5	20.1	426
82	The DNA sequence of the human X chromosome. <i>Nature</i> , 2005 , 434, 325-37	50.4	822
81	A probabilistic model of 3Qend formation in <i>Caenorhabditis elegans</i> . <i>Nucleic Acids Research</i> , 2004 , 32, 3392-9	20.1	40
80	Gene structure conservation aids similarity based gene prediction. <i>Nucleic Acids Research</i> , 2004 , 32, 776-83	20.1	62
79	An overview of Ensembl. <i>Genome Research</i> , 2004 , 14, 925-8	9.7	316
78	GeneWise and Genomewise. <i>Genome Research</i> , 2004 , 14, 988-95	9.7	1467
77	WormBase: a multi-species resource for nematode biology and genomics. <i>Nucleic Acids Research</i> , 2004 , 32, D411-7	20.1	543
76	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521	50.4	1689
75	Enhanced protein domain discovery using taxonomy. <i>BMC Bioinformatics</i> , 2004 , 5, 56	3.6	14
74	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2004 , 32, D138-41	20.1	2720
73	WormBase: a cross-species database for comparative genomics. <i>Nucleic Acids Research</i> , 2003 , 31, 133-7	20.1	90
72	Enhanced protein domain discovery by using language modeling techniques from speech recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 4516-20	11.5	42
71	The genome sequence of <i>Caenorhabditis briggsae</i> : a platform for comparative genomics. <i>PLoS Biology</i> , 2003 , 1, E45	9.7	677

70	Systematic functional analysis of the <i>Caenorhabditis elegans</i> genome using RNAi. <i>Nature</i> , 2003 , 421, 231-7	50.4	2758
69	A table-driven, full-sensitivity similarity search algorithm. <i>Journal of Computational Biology</i> , 2003 , 10, 103-17	1.7	9
68	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003 , 31, 315-8	20.1	556
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26	Reference-based phasing using the Haplotype Reference Consortium panel		3
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24	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly		13
23	The rate of false polymorphisms introduced when imputing genotypes from global imputation panels		6
22	Genome Graphs		34
21	Whole genome sequences of Malawi cichlids reveal multiple radiations interconnected by gene flow		17
20	Towards complete and error-free genome assemblies of all vertebrate species		38
19	Complete vertebrate mitogenomes reveal widespread gene duplications and repeats		5
18	Mapping epigenetic divergence in the massive radiation of Lake Malawi cichlid fishes		1
17	Placing ancient DNA sequences into reference phylogenies		2

16	Sequence variation aware genome references and read mapping with the variation graph toolkit		11
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8	Removing reference bias and improving indel calling in ancient DNA data analysis by mapping to a sequence variation graph		5
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1	Differential use of multiple genetic sex determination systems in divergent ecomorphs of an African crater lake cichlid		1