Richard M Durbin

List of Publications by Year
in descending order

221 papers	244,327 citations	1094 112 h-index	1341 223 g-index
280 all docs	280 docs citations	280 times ranked	204813 citing authors

#	Article	IF	Citations
1	Ethical, legal, and social issues in the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2115859119.	3.3	8
2	The Earth BioGenome Project 2020: Starting the clock. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	124
3	Placing Ancient DNA Sequences into Reference Phylogenies. Molecular Biology and Evolution, 2022, 39, .	3.5	23
4	Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	33
5	Why sequence all eukaryotes?. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	51
6	Sequence locally, think globally: The Darwin Tree of Life Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	120
7	Genomic consequences of domestication of the Siamese fighting fish. Science Advances, 2022, 8, eabm4950.	4.7	20
8	A Theoretical Analysis of Taxonomic Binning Accuracy. Molecular Ecology Resources, 2022, , .	2.2	0
9	The complete sequence of a human genome. Science, 2022, 376, 44-53.	6.0	1,222
10	A high-quality, chromosome-level genome assembly of the Black Soldier Fly (Hermetia illucens) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.8	37
11	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. Genome Biology, 2021, 22, 120.	3.8	69
12	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	13.7	1,139
13	The genome sequence of the brown trout, Salmo trutta Linnaeus 1758. Wellcome Open Research, 2021, 6, 108.	0.9	15
14	The genome sequence of the European golden eagle, Aquila chrysaetos chrysaetos Linnaeus 1758. Wellcome Open Research, 2021, 6, 112.	0.9	3
15	Environmental genomics of Late Pleistocene black bears and giant short-faced bears. Current Biology, 2021, 31, 2728-2736.e8.	1.8	42
16	Late Quaternary dynamics of Arctic biota from ancient environmental genomics. Nature, 2021, 600, 86-92.	13.7	81
17	Mapping epigenetic divergence in the massive radiation of Lake Malawi cichlid fishes. Nature Communications, 2021, 12, 5870.	5.8	17
18	Efficient iterative Hi-C scaffolder based on N-best neighbors. BMC Bioinformatics, 2021, 22, 569.	1.2	12

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19	Haplotype-aware graph indexes. Bioinformatics, 2020, 36, 400-407.	1.8	59
20	Efficiently Inferring the Demographic History of Many Populations With Allele Count Data. Journal of the American Statistical Association, 2020, 115, 1472-1487.	1.8	90
21	A haplotype-awarede novoassembly of related individuals using pedigree sequence graph. Bioinformatics, 2020, 36, 2385-2392.	1.8	22
22	Ancestral Hybridization Facilitated Species Diversification in the Lake Malawi Cichlid Fish Adaptive Radiation. Molecular Biology and Evolution, 2020, 37, 1100-1113.	3.5	98
23	Removing reference bias and improving indel calling in ancient DNA data analysis by mapping to a sequence variation graph. Genome Biology, 2020, 21, 250.	3.8	44
24	A haplotype-resolved,de novogenome assembly for the wood tiger moth (Arctia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 Td	3.3	20
25	Souporcell: robust clustering of single-cell RNA-seq data by genotype without reference genotypes. Nature Methods, 2020, 17, 615-620.	9.0	232
26	Insights into human genetic variation and population history from 929 diverse genomes. Science, 2020, 367, .	6.0	534
27	Identifying and removing haplotypic duplication in primary genome assemblies. Bioinformatics, 2020, 36, 2896-2898.	1.8	1,221
28	The genome sequence of the Eurasian red squirrel, Sciurus vulgaris Linnaeus 1758. Wellcome Open Research, 2020, 5, 18.	0.9	3
29	The genome sequence of the eastern grey squirrel, Sciurus carolinensis Gmelin, 1788. Wellcome Open Research, 2020, 5, 27.	0.9	4
30	Population-scale proteome variation in human induced pluripotent stem cells. ELife, 2020, 9, .	2.8	40
31	The genome sequence of the Eurasian river otter, Lutra lutra Linnaeus 1758. Wellcome Open Research, 2020, 5, 33.	0.9	6
32	htsget: a protocol for securely streaming genomic data. Bioinformatics, 2019, 35, 119-121.	1.8	23
33	Crumble: reference free lossy compression of sequence quality values. Bioinformatics, 2019, 35, 337-339.	1.8	21
34	Viral coinfection analysis using a MinHash toolkit. BMC Bioinformatics, 2019, 20, 389.	1.2	3
35	A High-Quality De novo Genome Assembly from a Single Mosquito Using PacBio Sequencing. Genes, 2019, 10, 62.	1.0	121
36	The population history of northeastern Siberia since the Pleistocene. Nature, 2019, 570, 182-188.	13.7	259

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37	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
38	GFAKluge: A C++ library and command line utilities for the Graphical Fragment Assembly formats. Journal of Open Source Software, 2019, 4, 1083.	2.0	4
39	Earth BioGenome Project: Sequencing life for the future of life. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4325-4333.	3.3	652
40	Whole-genome sequences of Malawi cichlids reveal multiple radiations interconnected by gene flow. Nature Ecology and Evolution, 2018, 2, 1940-1955.	3.4	358
41	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. Nature Genetics, 2018, 50, 1574-1583.	9.4	169
42	Detecting archaic introgression using an unadmixed outgroup. PLoS Genetics, 2018, 14, e1007641.	1.5	78
43	A graph-based approach to diploid genome assembly. Bioinformatics, 2018, 34, i105-i114.	1.8	59
44	Did Our Species Evolve in Subdivided Populations across Africa, and Why Does It Matter?. Trends in Ecology and Evolution, 2018, 33, 582-594.	4.2	315
45	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. Science, 2018, 360, .	6.0	262
46	Variation graph toolkit improves read mapping by representing genetic variation in the reference. Nature Biotechnology, 2018, 36, 875-879.	9.4	435
47	Abstract 3273: rkmh: A MinHash toolbox for analyzing HPV coinfections. , 2018, , .		0
48	Whole-genome view of the consequences of a population bottleneck using 2926 genome sequences from Finland and United Kingdom. European Journal of Human Genetics, 2017, 25, 477-484.	1.4	60
49	Whole-exome sequencing of 228 patients with sporadic Parkinsonâ€™s disease. Scientific Reports, 2017, 7, 41188.	1.6	27
50	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. Genome Research, 2017, 27, 849-864.	2.4	728
51	Contrasting evolutionary genome dynamics between domesticated and wild yeasts. Nature Genetics, 2017, 49, 913-924.	9.4	340
52	Common genetic variation drives molecular heterogeneity in human iPSCs. Nature, 2017, 546, 370-375.	13.7	491
53	De novo yeast genome assemblies from MinION, PacBio and MiSeq platforms. Scientific Reports, 2017, 7, 3935.	1.6	146
54	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	2.6	131

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55	Using reference-free compressed data structures to analyze sequencing reads from thousands of human genomes. Genome Research, 2017, 27, 300-309.	2.4	19
56	Estimating the human mutation rate from autozygous segments reveals population differences in human mutational processes. Nature Communications, 2017, 8, 303.	5.8	81
57	No evidence for maintenance of a sympatricHeliconiusspecies barrier by chromosomal inversions. Evolution Letters, 2017, 1, 138-154.	1.6	90
58	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. Nature Communications, 2017, 8, 15927.	5.8	64
59	BCFtools/RoH: a hidden Markov model approach for detecting autozygosity from next-generation sequencing data. Bioinformatics, 2016, 32, 1749-1751.	1.8	506
60	Reference-based phasing using the Haplotype Reference Consortium panel. Nature Genetics, 2016, 48, 1443-1448.	9.4	1,357
61	TTC25 Deficiency Results in Defects of the Outer Dynein Arm Docking Machinery and Primary Ciliary Dyskinesia with Left-Right Body Asymmetry Randomization. American Journal of Human Genetics, 2016, 99, 460-469.	2.6	88
62	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
63	A genomic history of Aboriginal Australia. Nature, 2016, 538, 207-214.	13.7	439
64	Deficient methylation and formylation of mt-tRNAMet wobble cytosine in a patient carrying mutations in NSUN3. Nature Communications, 2016, 7, 12039.	5.8	178
65	Whole-exome sequencing in an isolated population from the Dalmatian island of Vis. European Journal of Human Genetics, 2016, 24, 1479-1487.	1.4	11
66	Iron Age and Anglo-Saxon genomes from East England reveal British migration history. Nature Communications, 2016, 7, 10408.	5.8	144
67	Bi-allelic Truncating Mutations in TANGO2 Cause Infancy-Onset Recurrent Metabolic Crises with Encephalocardiomyopathy. American Journal of Human Genetics, 2016, 98, 358-362.	2.6	77
68	Health and population effects of rare gene knockouts in adult humans with related parents. Science, 2016, 352, 474-477.	6.0	272
69	DNAH11 Localization in the Proximal Region of Respiratory Cilia Defines Distinct Outer Dynein Arm Complexes. American Journal of Respiratory Cell and Molecular Biology, 2016, 55, 213-224.	1.4	107
70	A high-content platform to characterise human induced pluripotent stem cell lines. Methods, 2016, 96, 85-96.	1.9	41
71	A Method for Checking Genomic Integrity in Cultured Cell Lines from SNP Genotyping Data. PLoS ONE, 2016, 11, e0155014.	1.1	26
72	Deficiency of <scp>ECHS</scp>1 causes mitochondrial encephalopathy with cardiac involvement. Annals of Clinical and Translational Neurology, 2015, 2, 492-509.	1.7	90

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73	Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681.	5.8	75
74	Immunofluorescence Analysis and Diagnosis of Primary Ciliary Dyskinesia with Radial Spoke Defects. American Journal of Respiratory Cell and Molecular Biology, 2015, 53, 563-573.	1.4	120
75	Tracing the Route of Modern Humans out of Africa by Using 225 Human Genome Sequences from Ethiopians and Egyptians. American Journal of Human Genetics, 2015, 96, 986-991.	2.6	152
76	Homozygous loss-of-function variants in European cosmopolitan and isolate populations. Human Molecular Genetics, 2015, 24, 5464-5474.	1.4	27
77	Genomic islands of speciation separate cichlid ecomorphs in an East African crater lake. Science, 2015, 350, 1493-1498.	6.0	330
78	The genomic and phenotypic diversity of Schizosaccharomyces pombe. Nature Genetics, 2015, 47, 235-241.	9.4	174
79	Genomic evidence for the Pleistocene and recent population history of Native Americans. Science, 2015, 349, aab3884.	6.0	449
80	Extending reference assembly models. Genome Biology, 2015, 16, 13.	3.8	139
81	Pathway-Based Factor Analysis of Gene Expression Data Produces Highly Heritable Phenotypes That Associate with Age. G3: Genes, Genomes, Genetics, 2015, 5, 839-847.	0.8	7
82	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
83	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	13.7	483
84	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
85	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. Nature Communications, 2015, 6, 8111.	5.8	300
86	Gene-gene and gene-environment interactions detected by transcriptome sequence analysis in twins. Nature Genetics, 2015, 47, 88-91.	9.4	215
87	Quantitative Genetics of CTCF Binding Reveal Local Sequence Effects and Different Modes of X-Chromosome Association. PLoS Genetics, 2014, 10, e1004798.	1.5	55
88	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	1.5	351
89	Estimation of Epistatic Variance Components and Heritability in Founder Populations and Crosses. Genetics, 2014, 198, 1405-1416.	1.2	27
90	Estimating telomere length from whole genome sequence data. Nucleic Acids Research, 2014, 42, e75-e75.	6.5	151

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91	Efficient haplotype matching and storage using the positional Burrowsâ€“Wheeler transform (PBWT). Bioinformatics, 2014, 30, 1266-1272.	1.8	387
92	A High-Definition View of Functional Genetic Variation from Natural Yeast Genomes. Molecular Biology and Evolution, 2014, 31, 872-888.	3.5	328
93	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871.	5.8	62
94	Managing clinically significant findings in research: the UK10K example. European Journal of Human Genetics, 2014, 22, 1100-1104.	1.4	38
95	Inferring human population size and separation history from multiple genome sequences. Nature Genetics, 2014, 46, 919-925.	9.4	870
96	Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. Genome Biology, 2014, 15, R88.	13.9	72
97	Genetic interactions affecting human gene expression identified by variance association mapping. ELife, 2014, 3, e01381.	2.8	137
98	The anatomy of successful computational biology software. Nature Biotechnology, 2013, 31, 894-897.	9.4	25
99	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	3.3	582
100	Global Analysis of DNA Methylation Variation in Adipose Tissue from Twins Reveals Links to Disease-Associated Variants in Distal Regulatory Elements. American Journal of Human Genetics, 2013, 93, 876-890.	2.6	330
101	High-Resolution Mapping of Complex Traits with a Four-Parent Advanced Intercross Yeast Population. Genetics, 2013, 195, 1141-1155.	1.2	164
102	Gene expression changes with age in skin, adipose tissue, blood and brain. Genome Biology, 2013, 14, R75.	13.9	263
103	A Genome-Wide Survey of Genetic Variation in Gorillas Using Reduced Representation Sequencing. PLoS ONE, 2013, 8, e65066.	1.1	23
104	WormBase. Worm, 2012, 1, 15-21.	1.0	14
105	Extent, Causes, and Consequences of Small RNA Expression Variation in Human Adipose Tissue. PLoS Genetics, 2012, 8, e1002704.	1.5	48
106	Patterns of Cis Regulatory Variation in Diverse Human Populations. PLoS Genetics, 2012, 8, e1002639.	1.5	439
107	Efficient de novo assembly of large genomes using compressed data structures. Genome Research, 2012, 22, 549-556.	2.4	649
108	WormBase 2012: more genomes, more data, new website. Nucleic Acids Research, 2012, 40, D735-D741.	6.5	175

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109	High levels of RNA-editing site conservation amongst 15 laboratory mouse strains. Genome Biology, 2012, 13, R26.	13.9	149
110	Using probabilistic estimation of expression residuals (PEER) to obtain increased power and interpretability of gene expression analyses. Nature Protocols, 2012, 7, 500-507.	5.5	799
111	Ensembl 2012. Nucleic Acids Research, 2012, 40, D84-D90.	6.5	840
112	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
113	Revising the human mutation rate: implications for understanding human evolution. Nature Reviews Genetics, 2012, 13, 745-753.	7.7	483
114	Mapping cis- and trans-regulatory effects across multiple tissues in twins. Nature Genetics, 2012, 44, 1084-1089.	9.4	701
115	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	13.7	663
116	Dindel: Accurate indel calls from short-read data. Genome Research, 2011, 21, 961-973.	2.4	383
117	The variant call format and VCFtools. Bioinformatics, 2011, 27, 2156-2158.	1.8	11,326
118	Inference of human population history from individual whole-genome sequences. Nature, 2011, 475, 493-496.	13.7	2,053
119	Mouse genomic variation and its effect on phenotypes and gene regulation. Nature, 2011, 477, 289-294.	13.7	1,461
120	Identityâ€byâ€descentâ€based phasing and imputation in founder populations using graphical models. Genetic Epidemiology, 2011, 35, 853-860.	0.6	31
121	Revealing the genetic structure of a trait by sequencing a population under selection. Genome Research, 2011, 21, 1131-1138.	2.4	263
122	Assemblathon 1: A competitive assessment of de novo short read assembly methods. Genome Research, 2011, 21, 2224-2241.	2.4	443
123	Ensembl 2011. Nucleic Acids Research, 2011, 39, D800-D806.	6.5	630
124	SNP detection and genotyping from low-coverage sequencing data on multiple diploid samples. Genome Research, 2011, 21, 952-960.	2.4	142
125	Joint Genetic Analysis of Gene Expression Data with Inferred Cellular Phenotypes. PLoS Genetics, 2011, 7, e1001276.	1.5	76
126	The Architecture of Gene Regulatory Variation across Multiple Human Tissues: The MuTHER Study. PLoS Genetics, 2011, 7, e1002003.	1.5	392

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127	Trait Variation in Yeast Is Defined by Population History. PLoS Genetics, 2011, 7, e1002111.	1.5	311
128	Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. Nature, 2010, 464, 721-727.	13.7	768
129	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
130	Efficient construction of an assembly string graph using the FM-index. Bioinformatics, 2010, 26, i367-i373.	1.8	198
131	WormBase: a comprehensive resource for nematode research. Nucleic Acids Research, 2010, 38, D463-D467.	6.5	325
132	Ensembl's 10th year. Nucleic Acids Research, 2010, 38, D557-D562.	6.5	251
133	Copy number variant detection in inbred strains from short read sequence data. Bioinformatics, 2010, 26, 565-567.	1.8	47
134	A Bayesian Framework to Account for Complex Non-Genetic Factors in Gene Expression Levels Greatly Increases Power in eQTL Studies. PLoS Computational Biology, 2010, 6, e1000770.	1.5	408
135	Systematic Analysis of Human Protein Complexes Identifies Chromosome Segregation Proteins. Science, 2010, 328, 593-599.	6.0	465
136	Fast and accurate long-read alignment with Burrowsâ€“Wheeler transform. Bioinformatics, 2010, 26, 589-595.	1.8	10,002
137	EnsemblCompara GeneTrees: Complete, duplication-aware phylogenetic trees in vertebrates. Genome Research, 2009, 19, 327-335.	2.4	1,058
138	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
139	Population genomics of domestic and wild yeasts. Nature, 2009, 458, 337-341.	13.7	1,391
140	Prepublication data sharing. Nature, 2009, 461, 168-170.	13.7	243
141	The Sequence Alignment/Map format and SAMtools. Bioinformatics, 2009, 25, 2078-2079.	1.8	49,124
142	Fast and accurate short read alignment with Burrowsâ€“Wheeler transform. Bioinformatics, 2009, 25, 1754-1760.	1.8	43,062
143	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. Genome Biology, 2009, 10, R112.	13.9	36
144	The diploid genome sequence of an Asian individual. Nature, 2008, 456, 60-65.	13.7	834

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145	Accurate whole human genome sequencing using reversible terminator chemistry. Nature, 2008, 456, 53-59.	13.7	3,118
146	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. Nature Biotechnology, 2008, 26, 779-785.	9.4	619
147	Identification of somatically acquired rearrangements in cancer using genome-wide massively parallel paired-end sequencing. Nature Genetics, 2008, 40, 722-729.	9.4	736
148	BAC TransgeneOmics: a high-throughput method for exploration of protein function in mammals. Nature Methods, 2008, 5, 409-415.	9.0	568
149	A large genome center's improvements to the Illumina sequencing system. Nature Methods, 2008, 5, 1005-1010.	9.0	656
150	Mapping short DNA sequencing reads and calling variants using mapping quality scores. Genome Research, 2008, 18, 1851-1858.	2.4	2,275
151	Accounting for Non-genetic Factors Improves the Power of eQTL Studies. Lecture Notes in Computer Science, 2008, , 411-422.	1.0	16
152	Inferring Selection on Amino Acid Preference in Protein Domains. Molecular Biology and Evolution, 2008, 26, 527-536.	3.5	9
153	Regulatory evolution in proteins by turnover and lineage-specific changes of cyclin-dependent kinase consensus sites. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17713-17718.	3.3	62
154	Genomix: a method for combining gene-finders' predictions, which uses evolutionary conservation of sequence and intronâ€“exon structure. Bioinformatics, 2007, 23, 1468-1475.	1.8	12
155	WormBase: new content and better access. Nucleic Acids Research, 2007, 35, D506-D510.	6.5	80
156	WormBase 2007. Nucleic Acids Research, 2007, 36, D612-D617.	6.5	95
157	TreeFam: 2008 Update. Nucleic Acids Research, 2007, 36, D735-D740.	6.5	294
158	A systematic comparative and structural analysis of protein phosphorylation sites based on the mtcPTM database. Genome Biology, 2007, 8, R90.	13.9	62
159	Clustering of phosphorylation site recognition motifs can be exploited to predict the targets of cyclin-dependent kinase. Genome Biology, 2007, 8, R23.	13.9	74
160	Vertebrate gene finding from multiple-species alignments using a two-level strategy. Genome Biology, 2006, 7, S6.	13.9	14
161	Mapping Trait Loci by Use of Inferred Ancestral Recombination Graphs. American Journal of Human Genetics, 2006, 79, 910-922.	2.6	105
162	[X]uniqMAP: unique gene sequence regions in the human and mouse genomes. BMC Genomics, 2006, 7, 249.	1.2	1

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163	WormBase: better software, richer content. Nucleic Acids Research, 2006, 34, D475-D478.	6.5	74
164	A conserved sequence motif in 3' untranslated regions of ribosomal protein mRNAs in nematodes. Rna, 2006, 12, 1786-1789.	1.6	7
165	TreeFam: a curated database of phylogenetic trees of animal gene families. Nucleic Acids Research, 2006, 34, D572-D580.	6.5	465
166	Pfam: clans, web tools and services. Nucleic Acids Research, 2006, 34, D247-D251.	6.5	2,030
167	The DNA sequence of the human X chromosome. Nature, 2005, 434, 325-337.	13.7	985
168	The Sequence Ontology: a tool for the unification of genome annotations. Genome Biology, 2005, 6, R44.	13.9	638
169	A probabilistic model of 3' end formation in Caenorhabditis elegans. Nucleic Acids Research, 2004, 32, 3392-3399.	6.5	50
170	Gene structure conservation aids similarity based gene prediction. Nucleic Acids Research, 2004, 32, 776-783.	6.5	79
171	WormBase: a comprehensive data resource for Caenorhabditis biology and genomics. Nucleic Acids Research, 2004, 33, D383-D389.	6.5	155
172	InterPro, progress and status in 2005. Nucleic Acids Research, 2004, 33, D201-D205.	6.5	478
173	An Overview of Ensembl. Genome Research, 2004, 14, 925-928.	2.4	391
174	GeneWise and Genomewise. Genome Research, 2004, 14, 988-995.	2.4	2,128
175	WormBase: a multi-species resource for nematode biology and genomics. Nucleic Acids Research, 2004, 32, 411D-417.	6.5	610
176	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	13.7	1,943
177	Enhanced protein domain discovery using taxonomy. BMC Bioinformatics, 2004, 5, 56.	1.2	18
178	The Pfam protein families database. Nucleic Acids Research, 2004, 32, 138D-141.	6.5	3,084
179	Systematic functional analysis of the Caenorhabditis elegans genome using RNAi. Nature, 2003, 421, 231-237.	13.7	3,343
180	A Table-Driven, Full-Sensitivity Similarity Search Algorithm. Journal of Computational Biology, 2003, 10, 103-117.	0.8	9

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181	The InterPro Database, 2003 brings increased coverage and new features. Nucleic Acids Research, 2003, 31, 315-318.	6.5	640
182	WormBase: a cross-species database for comparative genomics. Nucleic Acids Research, 2003, 31, 133-137.	6.5	107
183	Enhanced protein domain discovery by using language modeling techniques from speech recognition. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 4516-4520.	3.3	47
184	The Genome Sequence of Caenorhabditis briggsae: A Platform for Comparative Genomics. PLoS Biology, 2003, 1, e45.	2.6	812
185	InterPro: An integrated documentation resource for protein families, domains and functional sites. Briefings in Bioinformatics, 2002, 3, 225-235.	3.2	155
186	QuickTree: building huge Neighbour-Joining trees of protein sequences. Bioinformatics, 2002, 18, 1546-1547.	1.8	249
187	Comparative ab initio prediction of gene structures using pair HMMs. Bioinformatics, 2002, 18, 1309-1318.	1.8	114
188	GAZE: A Generic Framework for the Integration of Gene-Prediction Data by Dynamic Programming. Genome Research, 2002, 12, 1418-1427.	2.4	82
189	The Pfam Protein Families Database. Nucleic Acids Research, 2002, 30, 276-280.	6.5	2,067
190	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	13.7	21,074
191	A computational scan for U12-dependent introns in the human genome sequence. Nucleic Acids Research, 2001, 29, 4006-4013.	6.5	127
192	Alfresco---A Workbench for Comparative Genomic Sequence Analysis. Genome Research, 2000, 10, 1148-1157.	2.4	35
193	Using GeneWise in the Drosophila Annotation Experiment. Genome Research, 2000, 10, 547-548.	2.4	338
194	The Pfam Protein Families Database. Nucleic Acids Research, 2000, 28, 263-266.	6.5	1,173
195	Comparative Analysis of Noncoding Regions of 77 Orthologous Mouse and Human Gene Pairs. Genome Research, 1999, 9, 815-824.	2.4	180
196	Dynamic Programming Alignment Accuracy. Journal of Computational Biology, 1998, 5, 493-504.	0.8	97
197	Sequence Assembly withâ€‰CAFTOOLS. Genome Research, 1998, 8, 260-267.	2.4	16
198	Base Qualities Help Sequencingâ€‰Software. Genome Research, 1998, 8, 161-162.	2.4	8

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199	Analysis of Protein Domain Families inCaenorhabditis elegans. Genomics, 1997, 46, 200-216.	1.3	129
200	Gene expression and development databases forC. elegans. Seminars in Cell and Developmental Biology, 1997, 8, 459-467.	2.3	18
201	Pfam: A comprehensive database of protein domain families based on seed alignments. , 1997, 28, 405-420.		1,036
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