Mark E Diekhans

List of Publications by Year
in descending order

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64 papers	29,083 citations	41344 49 h-index	114465 63 g-index
74 all docs	74 docs citations	74 times ranked	46157 citing authors

#	Article	IF	Citations
1	The UCSC Genome Browser database: 2022 update. Nucleic Acids Research, 2022, 50, D1115-D1122.	14.5	175
2	Identification of high-confidence human poly(A) RNA isoform scaffolds using nanopore sequencing. Rna, 2022, 28, 162-176.	3.5	12
3	Complete genomic and epigenetic maps of human centromeres. Science, 2022, 376, eabl4178.	12.6	204
4	The complete sequence of a human genome. Science, 2022, 376, 44-53.	12.6	1,222
5	Segmental duplications and their variation in a complete human genome. Science, 2022, 376, eabj6965.	12.6	130
6	GENCODE 2021. Nucleic Acids Research, 2021, 49, D916-D923.	14.5	633
7	The UCSC Genome Browser database: 2021 update. Nucleic Acids Research, 2021, 49, D1046-D1057.	14.5	354
8	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	27.8	1,139
9	A high-quality bonobo genome refines the analysis of hominid evolution. Nature, 2021, 594, 77-81.	27.8	39
10	UCSC Genome Browser enters 20th year. Nucleic Acids Research, 2020, 48, D756-D761.	14.5	138
11	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. Nature, 2020, 587, 246-251.	27.8	256
12	Dense sampling of bird diversity increases power of comparative genomics. Nature, 2020, 587, 252-257.	27.8	251
13	Transcriptional activity and strain-specific history of mouse pseudogenes. Nature Communications, 2020, 11, 3695.	12.8	17
14	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
15	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. Science, 2020, 370, .	12.6	105
16	AMELIE speeds Mendelian diagnosis by matching patient phenotype and genotype to primary literature. Science Translational Medicine, 2020, 12, .	12.4	60
17	halSynteny: a fast, easy-to-use conserved synteny block construction method for multiple whole-genome alignments. GigaScience, 2020, 9, .	6.4	10
18	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmasks de novo variants in SCN1A. Npj Genomic Medicine, 2019, 4, 31.	3.8	27

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19	The UCSC Genome Browser database: 2019 update. Nucleic Acids Research, 2019, 47, D853-D858.	14.5	699
20	GENCODE reference annotation for the human and mouse genomes. Nucleic Acids Research, 2019, 47, D766-D773.	14.5	2,350
21	Whole-Genome Alignment and Comparative Annotation. Annual Review of Animal Biosciences, 2019, 7, 41-64.	7.4	62
22	Consensus coding sequence (CCDS) database: a standardized set of human and mouse protein-coding regions supported by expert curation. Nucleic Acids Research, 2018, 46, D221-D228.	14.5	97
23	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. Nature Genetics, 2018, 50, 1574-1583.	21.4	169
24	The UCSC Genome Browser database: 2018 update. Nucleic Acids Research, 2018, 46, D762-D769.	14.5	476
25	Evaluating recovery potential of the northern white rhinoceros from cryopreserved somatic cells. Genome Research, 2018, 28, 780-788.	5.5	39
26	High-resolution comparative analysis of great ape genomes. Science, 2018, 360, .	12.6	304
27	Comparative Annotation Toolkit (CAT)â€”simultaneous clade and personal genome annotation. Genome Research, 2018, 28, 1029-1038.	5.5	86
28	OUP accepted manuscript. Nucleic Acids Research, 2017, 45, D626-D634.	14.5	308
29	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. Human Mutation, 2017, 38, 1266-1276.	2.5	14
30	Long-read sequence assembly of the gorilla genome. Science, 2016, 352, aae0344.	12.6	368
31	The UCSC Genome Browser database: 2016 update. Nucleic Acids Research, 2016, 44, D717-D725.	14.5	376
32	Genomic legacy of the African cheetah, Acinonyx jubatus. Genome Biology, 2015, 16, 277.	8.8	167
33	The UCSC Cancer Genomics Browser: update 2015. Nucleic Acids Research, 2015, 43, D812-D817.	14.5	300
34	The NIH BD2K center for big data in translational genomics. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1143-1147.	4.4	30
35	The UCSC Genome Browser database: 2015 update. Nucleic Acids Research, 2015, 43, D670-D681.	14.5	891
36	The UCSC Genome Browser database: 2014 update. Nucleic Acids Research, 2014, 42, D764-D770.	14.5	619

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37	Current status and new features of the Consensus Coding Sequence database. Nucleic Acids Research, 2014, 42, D865-D872.	14.5	140
38	Comparative analysis of pseudogenes across three phyla. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13361-13366.	7.1	72
39	Multiple evidence strands suggest that there may be as few as 19 000 human protein-coding genes. Human Molecular Genetics, 2014, 23, 5866-5878.	2.9	463
40	MuPIT interactive: webserver for mapping variant positions to annotated, interactive 3D structures. Human Genetics, 2013, 132, 1235-1243.	3.8	68
41	The UCSC Cancer Genomics Browser: update 2013. Nucleic Acids Research, 2013, 41, D949-D954.	14.5	172
42	The UCSC Genome Browser database: extensions and updates 2011. Nucleic Acids Research, 2012, 40, D918-D923.	14.5	294
43	The GENCODE pseudogene resource. Genome Biology, 2012, 13, R51.	9.6	273
44	GENCODE: The reference human genome annotation for The ENCODE Project. Genome Research, 2012, 22, 1760-1774.	5.5	4,217
45	ENCODE whole-genome data in the UCSC Genome Browser: update 2012. Nucleic Acids Research, 2012, 40, D912-D917.	14.5	220
46	Cactus Graphs for Genome Comparisons. Journal of Computational Biology, 2011, 18, 469-481.	1.6	93
47	Assemblathon 1: A competitive assessment of de novo short read assembly methods. Genome Research, 2011, 21, 2224-2241.	5.5	443
48	Cactus: Algorithms for genome multiple sequence alignment. Genome Research, 2011, 21, 1512-1528.	5.5	245
49	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.	5.5	476
50	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	5.5	125
51	Retrocopy contributions to the evolution of the human genome. BMC Genomics, 2008, 9, 466.	2.8	93
52	Using native and syntenically mapped cDNA alignments to improve de novo gene finding. Bioinformatics, 2008, 24, 637-644.	4.1	1,618
53	Targeted discovery of novel human exons by comparative genomics. Genome Research, 2007, 17, 1763-1773.	5.5	42
54	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	5.5	237

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55	Comparative Genomics Search for Losses of Long-Established Genes on the Human Lineage. PLoS Computational Biology, 2007, 3, e247.	3.2	103
56	Regions of extreme synonymous codon selection in mammalian genes. Nucleic Acids Research, 2006, 34, 1700-1710.	14.5	47
57	Analysis of Human mRNAs With the Reference Genome Sequence Reveals Potential Errors, Polymorphisms, and RNA Editing. Genome Research, 2004, 14, 2034-2040.	5.5	26
58	Score Functions for Determining Regional Conservation in Two-Species Local Alignments. Journal of Computational Biology, 2004, 11, 395-411.	1.6	2
59	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. Genome Research, 2003, 13, 13-26.	5.5	263
60	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
61	A Discriminative Framework for Detecting Remote Protein Homologies. Journal of Computational Biology, 2000, 7, 95-114.	1.6	370
62	Predicting protein structure using only sequence information. Proteins: Structure, Function and Bioinformatics, 1999, 37, 121-125.	2.6	76
63	Predicting protein structure using only sequence information. , 1999, 37, 121.		1
64	Predicting protein structure using only sequence information. Proteins: Structure, Function and Bioinformatics, 1999, 37, 121-125.	2.6	52