

Mark E Diekhans

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

29,083
citations

41258

49
h-index

114278

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. <i>Nucleic Acids Research</i> , 2022, 50, D1115-D1122.	6.5	175
2	Identification of high-confidence human poly(A) RNA isoform scaffolds using nanopore sequencing. <i>Rna</i> , 2022, 28, 162-176.	1.6	12
3	Complete genomic and epigenetic maps of human centromeres. <i>Science</i> , 2022, 376, eabl4178.	6.0	204
4	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	6.0	1,222
5	Segmental duplications and their variation in a complete human genome. <i>Science</i> , 2022, 376, eabj6965.	6.0	130
6	GENCODE 2021. <i>Nucleic Acids Research</i> , 2021, 49, D916-D923.	6.5	633
7	The UCSC Genome Browser database: 2021 update. <i>Nucleic Acids Research</i> , 2021, 49, D1046-D1057.	6.5	354
8	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	13.7	1,139
9	A high-quality bonobo genome refines the analysis of hominid evolution. <i>Nature</i> , 2021, 594, 77-81.	13.7	39
10	UCSC Genome Browser enters 20th year. <i>Nucleic Acids Research</i> , 2020, 48, D756-D761.	6.5	138
11	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. <i>Nature</i> , 2020, 587, 246-251.	13.7	256
12	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	13.7	251
13	Transcriptional activity and strain-specific history of mouse pseudogenes. <i>Nature Communications</i> , 2020, 11, 3695.	5.8	17
14	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
15	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. <i>Science</i> , 2020, 370, .	6.0	105
16	AMELIE speeds Mendelian diagnosis by matching patient phenotype and genotype to primary literature. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	60
17	halSynteny: a fast, easy-to-use conserved synteny block construction method for multiple whole-genome alignments. <i>GigaScience</i> , 2020, 9, .	3.3	10
18	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmasks de novo variants in SCN1A. <i>Npj Genomic Medicine</i> , 2019, 4, 31.	1.7	27

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19	The UCSC Genome Browser database: 2019 update. <i>Nucleic Acids Research</i> , 2019, 47, D853-D858.	6.5	699
20	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019, 47, D766-D773.	6.5	2,350
21	Whole-Genome Alignment and Comparative Annotation. <i>Annual Review of Animal Biosciences</i> , 2019, 7, 41-64.	3.6	62
22	Consensus coding sequence (CCDS) database: a standardized set of human and mouse protein-coding regions supported by expert curation. <i>Nucleic Acids Research</i> , 2018, 46, D221-D228.	6.5	97
23	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. <i>Nature Genetics</i> , 2018, 50, 1574-1583.	9.4	169
24	The UCSC Genome Browser database: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D762-D769.	6.5	476
25	Evaluating recovery potential of the northern white rhinoceros from cryopreserved somatic cells. <i>Genome Research</i> , 2018, 28, 780-788.	2.4	39
26	High-resolution comparative analysis of great ape genomes. <i>Science</i> , 2018, 360, .	6.0	304
27	Comparative Annotation Toolkit (CAT) simultaneous clade and personal genome annotation. <i>Genome Research</i> , 2018, 28, 1029-1038.	2.4	86
28	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D626-D634.	6.5	308
29	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. <i>Human Mutation</i> , 2017, 38, 1266-1276.	1.1	14
30	Long-read sequence assembly of the gorilla genome. <i>Science</i> , 2016, 352, aae0344.	6.0	368
31	The UCSC Genome Browser database: 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, D717-D725.	6.5	376
32	Genomic legacy of the African cheetah, <i>Acinonyx jubatus</i> . <i>Genome Biology</i> , 2015, 16, 277.	3.8	167
33	The UCSC Cancer Genomics Browser: update 2015. <i>Nucleic Acids Research</i> , 2015, 43, D812-D817.	6.5	300
34	The NIH BD2K center for big data in translational genomics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1143-1147.	2.2	30
35	The UCSC Genome Browser database: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D670-D681.	6.5	891
36	The UCSC Genome Browser database: 2014 update. <i>Nucleic Acids Research</i> , 2014, 42, D764-D770.	6.5	619

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37	Current status and new features of the Consensus Coding Sequence database. <i>Nucleic Acids Research</i> , 2014, 42, D865-D872.	6.5	140
38	Comparative analysis of pseudogenes across three phyla. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13361-13366.	3.3	72
39	Multiple evidence strands suggest that there may be as few as 19 000 human protein-coding genes. <i>Human Molecular Genetics</i> , 2014, 23, 5866-5878.	1.4	463
40	MuPIT interactive: webserver for mapping variant positions to annotated, interactive 3D structures. <i>Human Genetics</i> , 2013, 132, 1235-1243.	1.8	68
41	The UCSC Cancer Genomics Browser: update 2013. <i>Nucleic Acids Research</i> , 2013, 41, D949-D954.	6.5	172
42	The UCSC Genome Browser database: extensions and updates 2011. <i>Nucleic Acids Research</i> , 2012, 40, D918-D923.	6.5	294
43	The GENCODE pseudogene resource. <i>Genome Biology</i> , 2012, 13, R51.	13.9	273
44	GENCODE: The reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , 2012, 22, 1760-1774.	2.4	4,217
45	ENCODE whole-genome data in the UCSC Genome Browser: update 2012. <i>Nucleic Acids Research</i> , 2012, 40, D912-D917.	6.5	220
46	Cactus Graphs for Genome Comparisons. <i>Journal of Computational Biology</i> , 2011, 18, 469-481.	0.8	93
47	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	2.4	443
48	Cactus: Algorithms for genome multiple sequence alignment. <i>Genome Research</i> , 2011, 21, 1512-1528.	2.4	245
49	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, 1316-1323.	2.4	476
50	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2009, 19, 2324-2333.	2.4	125
51	Retrocopy contributions to the evolution of the human genome. <i>BMC Genomics</i> , 2008, 9, 466.	1.2	93
52	Using native and syntenically mapped cDNA alignments to improve <i>de novo</i> gene finding. <i>Bioinformatics</i> , 2008, 24, 637-644.	1.8	1,618
53	Targeted discovery of novel human exons by comparative genomics. <i>Genome Research</i> , 2007, 17, 1763-1773.	2.4	42
54	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , 2007, 17, 1797-1808.	2.4	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.	1.5	103
56	Regions of extreme synonymous codon selection in mammalian genes. Nucleic Acids Research, 2006, 34, 1700-1710.	6.5	47
57	Analysis of Human mRNAs With the Reference Genome Sequence Reveals Potential Errors, Polymorphisms, and RNA Editing. Genome Research, 2004, 14, 2034-2040.	2.4	26
58	Score Functions for Determining Regional Conservation in Two-Species Local Alignments. Journal of Computational Biology, 2004, 11, 395-411.	0.8	2
59	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. Genome Research, 2003, 13, 13-26.	2.4	263
60	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	13.7	6,319
61	A Discriminative Framework for Detecting Remote Protein Homologies. Journal of Computational Biology, 2000, 7, 95-114.	0.8	370
62	Predicting protein structure using only sequence information. Proteins: Structure, Function and Bioinformatics, 1999, 37, 121-125.	1.5	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, Suppl 3, 121-5.	1.5	52