

Hiram Clawson

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

24,330
citations

126708

33
h-index

288905

40
g-index

42
all docs

42
docs citations

42
times ranked

37331
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	Euarchontoglires Challenged by Incomplete Lineage Sorting. <i>Genes</i> , 2022, 13, 774.	1.0	2
3	The UCSC Genome Browser database: 2021 update. <i>Nucleic Acids Research</i> , 2021, 49, D1046-D1057.	6.5	354
4	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	13.7	1,139
5	UCSC Genome Browser enters 20th year. <i>Nucleic Acids Research</i> , 2020, 48, D756-D761.	6.5	138
6	The UCSC SARS-CoV-2 Genome Browser. <i>Nature Genetics</i> , 2020, 52, 991-998.	9.4	79
7	The UCSC repeat browser allows discovery and visualization of evolutionary conflict across repeat families. <i>Mobile DNA</i> , 2020, 11, 13.	1.3	31
8	The UCSC Genome Browser database: 2019 update. <i>Nucleic Acids Research</i> , 2019, 47, D853-D858.	6.5	699
9	True Homoplasy of Retrotransposon Insertions in Primates. <i>Systematic Biology</i> , 2019, 68, 482-493.	2.7	30
10	The UCSC Genome Browser database: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D762-D769.	6.5	476
11	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D626-D634.	6.5	308
12	Speciation network in Laurasiatheria: retrophylogenomic signals. <i>Genome Research</i> , 2017, 27, 997-1003.	2.4	38
13	Genome sequence of the basal haplorrhine primate <i>Tarsius syrichta</i> reveals unusual insertions. <i>Nature Communications</i> , 2016, 7, 12997.	5.8	32
14	The UCSC Genome Browser database: 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, D717-D725.	6.5	376
15	Navigating protected genomics data with UCSC Genome Browser in a Box. <i>Bioinformatics</i> , 2015, 31, 764-766.	1.8	49
16	The UCSC Genome Browser database: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D670-D681.	6.5	891
17	Exploring Massive Incomplete Lineage Sorting in Arctoids (Laurasiatheria, Carnivora). <i>Molecular Biology and Evolution</i> , 2015, 32, msv188.	3.5	48
18	The UCSC Genome Browser database: 2014 update. <i>Nucleic Acids Research</i> , 2014, 42, D764-D770.	6.5	619

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19	Track data hubs enable visualization of user-defined genome-wide annotations on the UCSC Genome Browser. <i>Bioinformatics</i> , 2014, 30, 1003-1005.	1.8	375
20	Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , 2014, 24, 2077-2089.	2.4	102
21	Comparative assembly hubs: Web-accessible browsers for comparative genomics. <i>Bioinformatics</i> , 2014, 30, 3293-3301.	1.8	33
22	The UCSC Ebola Genome Portal. <i>PLOS Currents</i> , 2014, 6, .	1.4	6
23	The UCSC Genome Browser database: extensions and updates 2011. <i>Nucleic Acids Research</i> , 2012, 40, D918-D923.	6.5	294
24	The UCSC Genome Browser database: extensions and updates 2013. <i>Nucleic Acids Research</i> , 2012, 41, D64-D69.	6.5	732
25	ENCODE whole-genome data in the UCSC Genome Browser: update 2012. <i>Nucleic Acids Research</i> , 2012, 40, D912-D917.	6.5	220
26	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	13.7	1,016
27	The UCSC Genome Browser database: update 2011. <i>Nucleic Acids Research</i> , 2011, 39, D876-D882.	6.5	958
28	ENCODE whole-genome data in the UCSC genome browser (2011 update). <i>Nucleic Acids Research</i> , 2011, 39, D871-D875.	6.5	164
29	The UCSC Genome Browser database: update 2010. <i>Nucleic Acids Research</i> , 2010, 38, D613-D619.	6.5	537
30	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	6.0	912
31	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	6.0	1,124
32	The ENCODE Project at UC Santa Cruz. <i>Nucleic Acids Research</i> , 2007, 35, D663-D667.	6.5	92
33	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007, 17, 760-774.	2.4	184
34	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
35	The UCSC Known Genes. <i>Bioinformatics</i> , 2006, 22, 1036-1046.	1.8	462
36	Intronic Alternative Splicing Regulators Identified by Comparative Genomics in Nematodes. <i>PLoS Computational Biology</i> , 2006, 2, e86.	1.5	86

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37	Exploring relationships and mining data with the UCSC Gene Sorter. <i>Genome Research</i> , 2005, 15, 737-741.	2.4	77
38	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. <i>Genome Research</i> , 2005, 15, 1034-1050.	2.4	3,517
39	Aligning Multiple Genomic Sequences With the Threaded Blockset Aligner. <i>Genome Research</i> , 2004, 14, 708-715.	2.4	1,290
40	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943