

Angie S Hinrichs

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3207971/publications.pdf>

Version: 2024-02-01

47
papers

39,711
citations

70961

41
h-index

223531

46
g-index

54
all docs

54
docs citations

54
times ranked

54852
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	The UCSC Genome Browser database: 2021 update. <i>Nucleic Acids Research</i> , 2021, 49, D1046-D1057.	6.5	354
3	Ultrafast Sample placement on Existing tRees (USHER) enables real-time phylogenetics for the SARS-CoV-2 pandemic. <i>Nature Genetics</i> , 2021, 53, 809-816.	9.4	264
4	A Daily-Updated Database and Tools for Comprehensive SARS-CoV-2 Mutation-Annotated Trees. <i>Molecular Biology and Evolution</i> , 2021, 38, 5819-5824.	3.5	69
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	Stability of SARS-CoV-2 phylogenies. <i>PLoS Genetics</i> , 2020, 16, e1009175.	1.5	92
8	The UCSC Genome Browser database: 2019 update. <i>Nucleic Acids Research</i> , 2019, 47, D853-D858.	6.5	699
9	The UCSC Genome Browser database: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D762-D769.	6.5	476
10	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D626-D634.	6.5	308
11	The UCSC Genome Browser database: 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, D717-D725.	6.5	376
12	UCSC Data Integrator and Variant Annotation Integrator. <i>Bioinformatics</i> , 2016, 32, 1430-1432.	1.8	78
13	Navigating protected genomics data with UCSC Genome Browser in a Box. <i>Bioinformatics</i> , 2015, 31, 764-766.	1.8	49
14	The UCSC Genome Browser database: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D670-D681.	6.5	891
15	The UCSC Genome Browser database: 2014 update. <i>Nucleic Acids Research</i> , 2014, 42, D764-D770.	6.5	619
16	The UCSC Ebola Genome Portal. <i>PLOS Currents</i> , 2014, 6, .	1.4	6
17	The UCSC Genome Browser database: extensions and updates 2011. <i>Nucleic Acids Research</i> , 2012, 40, D918-D923.	6.5	294
18	The UCSC Genome Browser database: extensions and updates 2013. <i>Nucleic Acids Research</i> , 2012, 41, D64-D69.	6.5	732

#	ARTICLE	IF	CITATIONS
19	The UCSC Genome Browser. <i>Current Protocols in Bioinformatics</i> , 2012, 40, Unit1.4.	25.8	86
20	G-NEST: a gene neighborhood scoring tool to identify co-conserved, co-expressed genes. <i>BMC Bioinformatics</i> , 2012, 13, 253.	1.2	14
21	ENCODE whole-genome data in the UCSC Genome Browser: update 2012. <i>Nucleic Acids Research</i> , 2012, 40, D912-D917.	6.5	220
22	The UCSC Genome Browser. <i>Current Protocols in Human Genetics</i> , 2011, 71, Unit18.6.	3.5	38
23	The UCSC Genome Browser database: update 2011. <i>Nucleic Acids Research</i> , 2011, 39, D876-D882.	6.5	958
24	ENCODE whole-genome data in the UCSC genome browser (2011 update). <i>Nucleic Acids Research</i> , 2011, 39, D871-D875.	6.5	164
25	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010, 467, 1061-1073.	13.7	7,209
26	The UCSC Genome Browser database: update 2010. <i>Nucleic Acids Research</i> , 2010, 38, D613-D619.	6.5	537
27	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	6.0	912
28	ENCODE whole-genome data in the UCSC Genome Browser. <i>Nucleic Acids Research</i> , 2010, 38, D620-D625.	6.5	218
29	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	6.0	1,124
30	BigWig and BigBed: enabling browsing of large distributed datasets. <i>Bioinformatics</i> , 2010, 26, 2204-2207.	1.8	1,025
31	The UCSC Genome Browser Database: update 2009. <i>Nucleic Acids Research</i> , 2009, 37, D755-D761.	6.5	329
32	The UCSC Genome Browser. <i>Current Protocols in Bioinformatics</i> , 2009, 28, Unit1.4.	25.8	149
33	The bovine lactation genome: insights into the evolution of mammalian milk. <i>Genome Biology</i> , 2009, 10, R43.	13.9	164
34	The ENCODE Project at UC Santa Cruz. <i>Nucleic Acids Research</i> , 2007, 35, D663-D667.	6.5	92
35	The UCSC genome browser database: update 2007. <i>Nucleic Acids Research</i> , 2007, 35, D668-D673.	6.5	260
36	The UCSC Genome Browser Database: 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D773-D779.	6.5	459

#	ARTICLE	IF	CITATIONS
37	The UCSC Genome Browser. <i>Current Protocols in Bioinformatics</i> , 2007, 17, Unit 1.4.	25.8	41
38	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
39	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
40	Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007, 450, 219-232.	13.7	573
41	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
42	Comparative Genomic Analysis Using the UCSC Genome Browser. <i>Methods in Molecular Biology</i> , 2007, 395, 17-33.	0.4	23
43	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. <i>Genome Research</i> , 2005, 15, 1034-1050.	2.4	3,517
44	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
45	Evolution's cauldron: Duplication, deletion, and rearrangement in the mouse and human genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 11484-11489.	3.3	792
46	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319
47	Comparative Genomic Analysis Using the UCSC Genome Browser. , 0, , 17-34.		1