

# Angie S Hinrichs

## List of Publications by Year in descending order

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Version: 2024-02-01

47  
papers

39,711  
citations

81434

41  
h-index

252626

46  
g-index

54  
all docs

54  
docs citations

54  
times ranked

61408  
citing authors

#	ARTICLE	IF	CITATIONS
1	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010, 467, 1061-1073.	13.7	7,209
2	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319
3	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
4	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. <i>Genome Research</i> , 2005, 15, 1034-1050.	2.4	3,517
5	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
6	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
7	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	6.0	1,124
8	BigWig and BigBed: enabling browsing of large distributed datasets. <i>Bioinformatics</i> , 2010, 26, 2204-2207.	1.8	1,025
9	The UCSC Genome Browser database: update 2011. <i>Nucleic Acids Research</i> , 2011, 39, D876-D882.	6.5	958
10	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	6.0	912
11	The UCSC Genome Browser database: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D670-D681.	6.5	891
12	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
13	The UCSC Genome Browser database: extensions and updates 2013. <i>Nucleic Acids Research</i> , 2012, 41, D64-D69.	6.5	732
14	The UCSC Genome Browser database: 2019 update. <i>Nucleic Acids Research</i> , 2019, 47, D853-D858.	6.5	699
15	The UCSC Genome Browser database: 2014 update. <i>Nucleic Acids Research</i> , 2014, 42, D764-D770.	6.5	619
16	Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007, 450, 219-232.	13.7	573
17	The UCSC Genome Browser database: update 2010. <i>Nucleic Acids Research</i> , 2010, 38, D613-D619.	6.5	537
18	The UCSC Genome Browser database: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D762-D769.	6.5	476

#	ARTICLE	IF	CITATIONS
19	The UCSC Genome Browser Database: 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D773-D779.	6.5	459
20	The UCSC Genome Browser database: 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, D717-D725.	6.5	376
21	The UCSC Genome Browser database: 2021 update. <i>Nucleic Acids Research</i> , 2021, 49, D1046-D1057.	6.5	354
22	The UCSC Genome Browser Database: update 2009. <i>Nucleic Acids Research</i> , 2009, 37, D755-D761.	6.5	329
23	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D626-D634.	6.5	308
24	The UCSC Genome Browser database: extensions and updates 2011. <i>Nucleic Acids Research</i> , 2012, 40, D918-D923.	6.5	294
25	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
26	The UCSC genome browser database: update 2007. <i>Nucleic Acids Research</i> , 2007, 35, D668-D673.	6.5	260
27	ENCODE whole-genome data in the UCSC Genome Browser: update 2012. <i>Nucleic Acids Research</i> , 2012, 40, D912-D917.	6.5	220
28	ENCODE whole-genome data in the UCSC Genome Browser. <i>Nucleic Acids Research</i> , 2010, 38, D620-D625.	6.5	218
29	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
30	The UCSC Genome Browser database: 2022 update. <i>Nucleic Acids Research</i> , 2022, 50, D1115-D1122.	6.5	175
31	The bovine lactation genome: insights into the evolution of mammalian milk. <i>Genome Biology</i> , 2009, 10, R43.	13.9	164
32	ENCODE whole-genome data in the UCSC genome browser (2011 update). <i>Nucleic Acids Research</i> , 2011, 39, D871-D875.	6.5	164
33	The UCSC Genome Browser. <i>Current Protocols in Bioinformatics</i> , 2009, 28, Unit1.4.	25.8	149
34	UCSC Genome Browser enters 20th year. <i>Nucleic Acids Research</i> , 2020, 48, D756-D761.	6.5	138
35	The ENCODE Project at UC Santa Cruz. <i>Nucleic Acids Research</i> , 2007, 35, D663-D667.	6.5	92
36	Stability of SARS-CoV-2 phylogenies. <i>PLoS Genetics</i> , 2020, 16, e1009175.	1.5	92

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37	The UCSC Genome Browser. Current Protocols in Bioinformatics, 2012, 40, Unit1.4.	25.8	86
38	The UCSC SARS-CoV-2 Genome Browser. Nature Genetics, 2020, 52, 991-998.	9.4	79
39	UCSC Data Integrator and Variant Annotation Integrator. Bioinformatics, 2016, 32, 1430-1432.	1.8	78
40	A Daily-Updated Database and Tools for Comprehensive SARS-CoV-2 Mutation-Annotated Trees. Molecular Biology and Evolution, 2021, 38, 5819-5824.	3.5	69
41	Navigating protected genomics data with UCSC Genome Browser in a Box. Bioinformatics, 2015, 31, 764-766.	1.8	49
42	The UCSC Genome Browser. Current Protocols in Bioinformatics, 2007, 17, Unit 1.4.	25.8	41
43	The UCSC Genome Browser. Current Protocols in Human Genetics, 2011, 71, Unit18.6.	3.5	38
44	Comparative Genomic Analysis Using the UCSC Genome Browser. Methods in Molecular Biology, 2007, 395, 17-33.	0.4	23
45	G-NEST: a gene neighborhood scoring tool to identify co-conserved, co-expressed genes. BMC Bioinformatics, 2012, 13, 253.	1.2	14
46	The UCSC Ebola Genome Portal. PLOS Currents, 2014, 6, .	1.4	6
47	Comparative Genomic Analysis Using the UCSC Genome Browser. , 0, , 17-34.		1