

# David Haussler

## List of Publications by Year in descending order

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Version: 2024-02-01

92  
papers

64,279  
citations

31974

53  
h-index

58576

82  
g-index

106  
all docs

106  
docs citations

106  
times ranked

75111  
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	27.8	21,074
2	The Human Genome Browser at UCSC. <i>Genome Research</i> , 2002, 12, 996-1006.	5.5	8,776
3	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	27.8	6,319
4	GENCODE: The reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , 2012, 22, 1760-1774.	5.5	4,217
5	Visualizing and interpreting cancer genomics data via the Xena platform. <i>Nature Biotechnology</i> , 2020, 38, 675-678.	17.5	2,069
6	Using native and syntenically mapped cDNA alignments to improve <i>de novo</i> gene finding. <i>Bioinformatics</i> , 2008, 24, 637-644.	4.1	1,618
7	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	12.6	1,583
8	Aligning Multiple Genomic Sequences With the Threaded Blockset Aligner. <i>Genome Research</i> , 2004, 14, 708-715.	5.5	1,290
9	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	27.8	1,139
10	Human-Mouse Alignments with BLASTZ. <i>Genome Research</i> , 2003, 13, 103-107.	5.5	1,071
11	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	12.6	895
12	The UCSC Genome Browser database: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D670-D681.	14.5	891
13	Toil enables reproducible, open source, big biomedical data analyses. <i>Nature Biotechnology</i> , 2017, 35, 314-316.	17.5	873
14	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.	7.1	792
15	The UCSC Genome Browser database: 2019 update. <i>Nucleic Acids Research</i> , 2019, 47, D853-D858.	14.5	699
16	Chromosome-scale shotgun assembly using an in vitro method for long-range linkage. <i>Genome Research</i> , 2016, 26, 342-350.	5.5	679
17	Earth BioGenome Project: Sequencing life for the future of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4325-4333.	7.1	652
18	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	6.4	582

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19	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	27.8	541
20	Establishing Cerebral Organoids as Models of Human-Specific Brain Evolution. <i>Cell</i> , 2019, 176, 743-756.e17.	28.9	423
21	Rapid discrimination among individual DNA hairpin molecules at single-nucleotide resolution using an ion channel. <i>Nature Biotechnology</i> , 2001, 19, 248-252.	17.5	400
22	An evolutionary arms race between KRAB zinc-finger genes ZNF91/93 and SVA/L1 retrotransposons. <i>Nature</i> , 2014, 516, 242-245.	27.8	396
23	The UCSC Genome Browser database: 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, D717-D725.	14.5	376
24	Long-read sequence assembly of the gorilla genome. <i>Science</i> , 2016, 352, aae0344.	12.6	368
25	Human-Specific NOTCH2NL Genes Affect Notch Signaling and Cortical Neurogenesis. <i>Cell</i> , 2018, 173, 1356-1369.e22.	28.9	366
26	The UCSC Genome Browser database: 2021 update. <i>Nucleic Acids Research</i> , 2021, 49, D1046-D1057.	14.5	354
27	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. <i>Nature Biotechnology</i> , 2020, 38, 1044-1053.	17.5	344
28	High-resolution comparative analysis of great ape genomes. <i>Science</i> , 2018, 360, .	12.6	304
29	The Human Epigenome Browser at Washington University. <i>Nature Methods</i> , 2011, 8, 989-990.	19.0	302
30	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254449.	12.6	300
31	The UCSC Cancer Genomics Browser: update 2015. <i>Nucleic Acids Research</i> , 2015, 43, D812-D817.	14.5	300
32	Combining tumor genome simulation with crowdsourcing to benchmark somatic single-nucleotide-variant detection. <i>Nature Methods</i> , 2015, 12, 623-630.	19.0	282
33	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.	21.4	264
34	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. <i>Nature</i> , 2020, 587, 246-251.	27.8	256
35	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	27.8	251
36	Cactus: Algorithms for genome multiple sequence alignment. <i>Genome Research</i> , 2011, 21, 1512-1528.	5.5	245

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37	The Human Pangenome Project: a global resource to map genomic diversity. <i>Nature</i> , 2022, 604, 437-446.	27.8	192
38	The UCSC Genome Browser database: 2022 update. <i>Nucleic Acids Research</i> , 2022, 50, D1115-D1122.	14.5	175
39	HAL: a hierarchical format for storing and analyzing multiple genome alignments. <i>Bioinformatics</i> , 2013, 29, 1341-1342.	4.1	164
40	BRCA Challenge: BRCA Exchange as a global resource for variants in BRCA1 and BRCA2. <i>PLoS Genetics</i> , 2018, 14, e1007752.	3.5	148
41	The Cancer Genomics Hub (CGHub): overcoming cancer through the power of torrential data. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau093-bau093.	3.0	133
42	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. <i>Science</i> , 2021, 374, abg8871.	12.6	132
43	The Earth BioGenome Project 2020: Starting the clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	124
44	Comparative Genomics Search for Losses of Long-Established Genes on the Human Lineage. <i>PLoS Computational Biology</i> , 2007, 3, e247.	3.2	103
45	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. <i>Cell Reports</i> , 2019, 29, 1675-1689.e9.	6.4	103
46	Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , 2014, 24, 2077-2089.	5.5	102
47	GA4GH: International policies and standards for data sharing across genomic research and healthcare. <i>Cell Genomics</i> , 2021, 1, 100029.	6.5	94
48	Cactus Graphs for Genome Comparisons. <i>Journal of Computational Biology</i> , 2011, 18, 469-481.	1.6	93
49	Stability of SARS-CoV-2 phylogenies. <i>PLoS Genetics</i> , 2020, 16, e1009175.	3.5	92
50	RADIA: RNA and DNA Integrated Analysis for Somatic Mutation Detection. <i>PLoS ONE</i> , 2014, 9, e111516.	2.5	90
51	Comparative Annotation Toolkit (CAT)â€™ simultaneous clade and personal genome annotation. <i>Genome Research</i> , 2018, 28, 1029-1038.	5.5	86
52	The UCSC SARS-CoV-2 Genome Browser. <i>Nature Genetics</i> , 2020, 52, 991-998.	21.4	79
53	UCSC Data Integrator and Variant Annotation Integrator. <i>Bioinformatics</i> , 2016, 32, 1430-1432.	4.1	78
54	Federated discovery and sharing of genomic data using Beacons. <i>Nature Biotechnology</i> , 2019, 37, 220-224.	17.5	75

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55	A Daily-Updated Database and Tools for Comprehensive SARS-CoV-2 Mutation-Annotated Trees. <i>Molecular Biology and Evolution</i> , 2021, 38, 5819-5824.	8.9	69
56	TumorMap: Exploring the Molecular Similarities of Cancer Samples in an Interactive Portal. <i>Cancer Research</i> , 2017, 77, e111-e114.	0.9	59
57	Feather Development Genes and Associated Regulatory Innovation Predate the Origin of Dinosauria. <i>Molecular Biology and Evolution</i> , 2015, 32, 23-28.	8.9	57
58	Structurally Conserved Primate LncRNAs Are Transiently Expressed during Human Cortical Differentiation and Influence Cell-Type-Specific Genes. <i>Stem Cell Reports</i> , 2019, 12, 245-257.	4.8	53
59	Navigating protected genomics data with UCSC Genome Browser in a Box. <i>Bioinformatics</i> , 2015, 31, 764-766.	4.1	49
60	Building a Pan-Genome Reference for a Population. <i>Journal of Computational Biology</i> , 2015, 22, 387-401.	1.6	48
61	Combining accurate tumor genome simulation with crowdsourcing to benchmark somatic structural variant detection. <i>Genome Biology</i> , 2018, 19, 188.	8.8	42
62	Comparative Tumor RNA Sequencing Analysis for Difficult-to-Treat Pediatric and Young Adult Patients With Cancer. <i>JAMA Network Open</i> , 2019, 2, e1913968.	5.9	38
63	A Recurrent Mutation in Anaplastic Lymphoma Kinase with Distinct Neoepitope Conformations. <i>Frontiers in Immunology</i> , 2018, 9, 99.	4.8	35
64	Comparative assembly hubs: Web-accessible browsers for comparative genomics. <i>Bioinformatics</i> , 2014, 30, 3293-3301.	4.1	33
65	The NIH BD2K center for big data in translational genomics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1143-1147.	4.4	30
66	Blockchain-Authenticated Sharing of Genomic and Clinical Outcomes Data of Patients With Cancer: A Prospective Cohort Study. <i>Journal of Medical Internet Research</i> , 2020, 22, e16810.	4.3	29
67	A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , 2020, 11, 3400.	12.8	23
68	Picoscope: low-cost system for simultaneous longitudinal biological imaging. <i>Communications Biology</i> , 2021, 4, 1261.	4.4	23
69	Barriers to accessing public cancer genomic data. <i>Scientific Data</i> , 2019, 6, 98.	5.3	22
70	Positive selection in noncoding genomic regions of vocal learning birds is associated with genes implicated in vocal learning and speech functions in humans. <i>Genome Research</i> , 2021, 31, 2035-2049.	5.5	16
71	The birds of Genome10K. <i>GigaScience</i> , 2014, 3, 32.	6.4	15
72	ProTECT—Prediction of T-Cell Epitopes for Cancer Therapy. <i>Frontiers in Immunology</i> , 2020, 11, 483296.	4.8	14

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73	A hidden layer of structural variation in transposable elements reveals potential genetic modifiers in human disease-risk loci. <i>Genome Research</i> , 2022, 32, 656-670.	5.5	13
74	Low cost cloud based remote microscopy for biological sciences. <i>Internet of Things (Netherlands)</i> , 2022, 18, 100454.	7.7	12
75	Cancer microenvironment and genomics: evolution in process. <i>Clinical and Experimental Metastasis</i> , 2022, 39, 85-99.	3.3	11
76	Spiking neural state machine for gait frequency entrainment in a flexible modular robot. <i>PLoS ONE</i> , 2020, 15, e0240267.	2.5	9
77	Identification of a differentiation stall in epithelial mesenchymal transition in histone H3â€“mutant diffuse midline glioma. <i>GigaScience</i> , 2020, 9, .	6.4	8
78	Neuromorphic Closed-Loop Control of a Flexible Modular Robot by a Simulated Spiking Central Pattern Generator. , 2020, , .		8
79	Light-weight electrophysiology hardware and software platform for cloud-based neural recording experiments. <i>Journal of Neural Engineering</i> , 2021, 18, 066004.	3.5	7
80	Representing and decomposing genomic structural variants as balanced integer flows on sequence graphs. <i>BMC Bioinformatics</i> , 2016, 17, 400.	2.6	6
81	The case for using mapped exonic non-duplicate reads when reporting RNA-sequencing depth: examples from pediatric cancer datasets. <i>GigaScience</i> , 2021, 10, .	6.4	2
82	Hydra: A mixture modeling framework for subtyping pediatric cancer cohorts using multimodal gene expression signatures. <i>PLoS Computational Biology</i> , 2020, 16, e1007753.	3.2	1
83	The Human Epigenome Browser at Washington University. , 0, .		1
84	Detecting the Coevolution in and among Protein Domains. <i>PLoS Computational Biology</i> , 2005, preprint, e211.	3.2	1
85	Computing how we became human. , 2008, , .		0
86	Title is missing!. , 2020, 16, e1007753.		0
87	Title is missing!. , 2020, 16, e1007753.		0
88	Title is missing!. , 2020, 16, e1007753.		0
89	Spiking neural state machine for gait frequency entrainment in a flexible modular robot. , 2020, 15, e0240267.		0
90	Spiking neural state machine for gait frequency entrainment in a flexible modular robot. , 2020, 15, e0240267.		0

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91	Spiking neural state machine for gait frequency entrainment in a flexible modular robot. , 2020, 15, e0240267.		0
92	Spiking neural state machine for gait frequency entrainment in a flexible modular robot. , 2020, 15, e0240267.		0