David Haussler

List of Publications by Citations

96 papers	**45,692** citations	**44** h-index	**106** g-index
106 ext. papers	**55,576** ext. citations	**18.7** avg, IF	**6.29** L-index

#	Paper	IF	Citations
96	Initial sequencing and analysis of the human genome. *Nature*, **2001**, 409, 860-921	50.4	17366
95	The human genome browser at UCSC. *Genome Research*, **2002**, 12, 996-1006	9.7	5840
94	Initial sequencing and comparative analysis of the mouse genome. *Nature*, **2002**, 420, 520-62	50.4	5376
93	GENCODE: the reference human genome annotation for The ENCODE Project. *Genome Research*, **2012**, 22, 1760-74	9.7	3142
92	Whole-genome analyses resolve early branches in the tree of life of modern birds. *Science*, **2014**, 346, 1320-31	33.3	1182
91	Aligning multiple genomic sequences with the threaded blockset aligner. *Genome Research*, **2004**, 14, 708-15	9.7	1006
90	Human-mouse alignments with BLASTZ. *Genome Research*, **2003**, 13, 103-7	9.7	920
89	Using native and syntenically mapped cDNA alignments to improve de novo gene finding. *Bioinformatics*, **2008**, 24, 637-44	7.2	871
88	The UCSC Genome Browser database: 2015 update. *Nucleic Acids Research*, **2015**, 43, D670-81	20.1	712
87	Visualizing and interpreting cancer genomics data via the Xena platform. *Nature Biotechnology*, **2020**, 38, 675-678	44.5	676
86	Comparative genomics reveals insights into avian genome evolution and adaptation. *Science*, **2014**, 346, 1311-20	33.3	628
85	Evolution's cauldron: duplication, deletion, and rearrangement in the mouse and human genomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 11484-9	11.5	624
84	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. *GigaScience*, **2013**, 2, 10	7.6	461
83	The UCSC Genome Browser database: 2019 update. *Nucleic Acids Research*, **2019**, 47, D853-D858	20.1	456
82	Comparative and demographic analysis of orang-utan genomes. *Nature*, **2011**, 469, 529-33	50.4	431
81	Chromosome-scale shotgun assembly using an in vitro method for long-range linkage. *Genome Research*, **2016**, 26, 342-50	9.7	415
80	Toil enables reproducible, open source, big biomedical data analyses. *Nature Biotechnology*, **2017**, 35, 314-316	44.5	387

79	Rapid discrimination among individual DNA hairpin molecules at single-nucleotide resolution using an ion channel. *Nature Biotechnology*, **2001**, 19, 248-52	44.5	350
78	Earth BioGenome Project: Sequencing life for the future of life. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 4325-4333	11.5	334
77	The UCSC Genome Browser database: 2016 update. *Nucleic Acids Research*, **2016**, 44, D717-25	20.1	317
76	Long-read sequence assembly of the gorilla genome. *Science*, **2016**, 352, aae0344	33.3	282
75	An evolutionary arms race between KRAB zinc-finger genes ZNF91/93 and SVA/L1 retrotransposons. *Nature*, **2014**, 516, 242-5	50.4	281
74	The Human Epigenome Browser at Washington University. *Nature Methods*, **2011**, 8, 989-90	21.6	240
73	Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. *Science*, **2014**, 346, 1254449	33.3	231
72	The UCSC Cancer Genomics Browser: update 2015. *Nucleic Acids Research*, **2015**, 43, D812-7	20.1	223
71	Establishing Cerebral Organoids as Models of Human-Specific Brain Evolution. *Cell*, **2019**, 176, 743-756.e17	56.2	217
70	Human-Specific NOTCH2NL Genes Affect Notch Signaling and Cortical Neurogenesis. *Cell*, **2018**, 173, 1356-1369.e22	56.2	217
69	Combining tumor genome simulation with crowdsourcing to benchmark somatic single-nucleotide-variant detection. *Nature Methods*, **2015**, 12, 623-30	21.6	201
68	High-resolution comparative analysis of great ape genomes. *Science*, **2018**, 360,	33.3	178
67	Cactus: Algorithms for genome multiple sequence alignment. *Genome Research*, **2011**, 21, 1512-28	9.7	170
66	Towards complete and error-free genome assemblies of all vertebrate species. *Nature*, **2021**, 592, 737-746	50.4	161
65	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. *Nature Biotechnology*, **2020**, 38, 1044-1053	44.5	143
64	The Cancer Genomics Hub (CGHub): overcoming cancer through the power of torrential data. *Database: the Journal of Biological Databases and Curation*, **2014**, 2014,	5	115
63	The UCSC Genome Browser database: 2021 update. *Nucleic Acids Research*, **2021**, 49, D1046-D1057	20.1	106
62	Comparative genomics search for losses of long-established genes on the human lineage. *PLoS Computational Biology*, **2007**, 3, e247	5	93

61	BRCA Challenge: BRCA Exchange as a global resource for variants in BRCA1 and BRCA2. *PLoS Genetics*, **2018**, 14, e1007752	6	90
60	Dense sampling of bird diversity increases power of comparative genomics. *Nature*, **2020**, 587, 252-257	50.4	89
59	HAL: a hierarchical format for storing and analyzing multiple genome alignments. *Bioinformatics*, **2013**, 29, 1341-2	7.2	78
58	Alignathon: a competitive assessment of whole-genome alignment methods. *Genome Research*, **2014**, 24, 2077-89	9.7	74
57	Cactus graphs for genome comparisons. *Journal of Computational Biology*, **2011**, 18, 469-81	1.7	66
56	RADIA: RNA and DNA integrated analysis for somatic mutation detection. *PLoS ONE*, **2014**, 9, e111516	3.7	59
55	Ultrafast Sample placement on Existing tRees (UShER) enables real-time phylogenetics for the SARS-CoV-2 pandemic. *Nature Genetics*, **2021**, 53, 809-816	36.3	58
54	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. *Nature*, **2020**, 587, 246-251	50.4	53
53	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. *Cell Reports*, **2019**, 29, 1675-1689.e9	10.6	51
52	The UCSC SARS-CoV-2 Genome Browser. *Nature Genetics*, **2020**, 52, 991-998	36.3	44
51	TumorMap: Exploring the Molecular Similarities of Cancer Samples in an Interactive Portal. *Cancer Research*, **2017**, 77, e111-e114	10.1	43
50	Stability of SARS-CoV-2 phylogenies. *PLoS Genetics*, **2020**, 16, e1009175	6	43
49	Federated discovery and sharing of genomic data using Beacons. *Nature Biotechnology*, **2019**, 37, 220-224	54.5	42
48	Feather development genes and associated regulatory innovation predate the origin of Dinosauria. *Molecular Biology and Evolution*, **2015**, 32, 23-8	8.3	42
47	Building a pan-genome reference for a population. *Journal of Computational Biology*, **2015**, 22, 387-401	1.7	41
46	UCSC Data Integrator and Variant Annotation Integrator. *Bioinformatics*, **2016**, 32, 1430-2	7.2	38
45	Comparative Annotation Toolkit (CAT)-simultaneous clade and personal genome annotation. *Genome Research*, **2018**, 28, 1029-1038	9.7	33
44	Navigating protected genomics data with UCSC Genome Browser in a Box. *Bioinformatics*, **2015**, 31, 764-6	7.2	33

43	Efficient de novo assembly of eleven human genomes using PromethION sequencing and a novel nanopore toolkit		29
42	Combining accurate tumor genome simulation with crowdsourcing to benchmark somatic structural variant detection. *Genome Biology*, **2018**, 19, 188	18.3	29
41	Structurally Conserved Primate LncRNAs Are Transiently Expressed during Human Cortical Differentiation and Influence Cell-Type-Specific Genes. *Stem Cell Reports*, **2019**, 12, 245-257	8	28
40	The NIH BD2K center for big data in translational genomics. *Journal of the American Medical Informatics Association: JAMIA*, **2015**, 22, 1143-7	8.6	24
39	Comparative Tumor RNA Sequencing Analysis for Difficult-to-Treat Pediatric and Young Adult Patients With Cancer. *JAMA Network Open*, **2019**, 2, e1913968	10.4	22
38	Comparative assembly hubs: web-accessible browsers for comparative genomics. *Bioinformatics*, **2014**, 30, 3293-301	7.2	22
37	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. *Cell Genomics*, **2021**, 1, 100029-100029		20
36	A Recurrent Mutation in Anaplastic Lymphoma Kinase with Distinct Neoepitope Conformations. *Frontiers in Immunology*, **2018**, 9, 99	8.4	16
35	Pandemic-Scale Phylogenomics Reveals Elevated Recombination Rates in the SARS-CoV-2 Spike Region		16
34	The Earth BioGenome Project 2020: Starting the clock.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	15
33	The UCSC Genome Browser database: 2022 update. *Nucleic Acids Research*, **2021**,	20.1	15
32	Progressive alignment with Cactus: a multiple-genome aligner for the thousand-genome era		15
31	Barriers to accessing public cancer genomic data. *Scientific Data*, **2019**, 6, 98	8.2	13
30	Blockchain-Authenticated Sharing of Genomic and Clinical Outcomes Data of Patients With Cancer: A Prospective Cohort Study. *Journal of Medical Internet Research*, **2020**, 22, e16810	7.6	12
29	A Daily-Updated Database and Tools for Comprehensive SARS-CoV-2 Mutation-Annotated Trees. *Molecular Biology and Evolution*, **2021**, 38, 5819-5824	8.3	12
28	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes.. *Science*, **2021**, 374, abg8871	33.3	11
27	A user guide for the online exploration and visualization of PCAWG data. *Nature Communications*, **2020**, 11, 3400	17.4	7
26	Comparative Annotation Toolkit (CAT) - simultaneous clade and personal genome annotation		7

25	The Human Pangenome Project: a global resource to map genomic diversity.. *Nature*, **2022**, 604, 437-446	50.4	7
24	Representing and decomposing genomic structural variants as balanced integer flows on sequence graphs. *BMC Bioinformatics*, **2016**, 17, 400	3.6	6
23	The birds of Genome10K. *GigaScience*, **2014**, 3, 32	7.6	6
22	ProTECT-Prediction of T-Cell Epitopes for Cancer Therapy. *Frontiers in Immunology*, **2020**, 11, 483296	8.4	5
21	A daily-updated database and tools for comprehensive SARS-CoV-2 mutation-annotated trees **2021** ,		4
20	Neuromorphic Closed-Loop Control of a Flexible Modular Robot by a Simulated Spiking Central Pattern Generator **2020**,		3
19	Automated assembly of high-quality diploid human reference genomes		3
18	Spiking neural state machine for gait frequency entrainment in a flexible modular robot. *PLoS ONE*, **2020**, 15, e0240267	3.7	2
17	Picroscope: low-cost system for simultaneous longitudinal biological imaging. *Communications Biology*, **2021**, 4, 1261	6.7	2
16	Cancer microenvironment and genomics: evolution in process. *Clinical and Experimental Metastasis*, **2021**, 1	4.7	2
15	Low cost cloud based remote microscopy for biological sciences. *Internet of Things (Netherlands)*, **2021**, 100454	6.9	2
14	Identification of a differentiation stall in epithelial mesenchymal transition in histone H3-mutant diffuse midline glioma. *GigaScience*, **2020**, 9,	7.6	1
13	Detecting the Coevolution in and among Protein Domains. *PLoS Computational Biology*, **2005**, preprint, e211	5	1
12	Positive selection in noncoding genomic regions of vocal learning birds is associated with genes implicated in vocal learning and speech functions in humans. *Genome Research*, **2021**, 31, 2035-2049	9.7	1
11	The Human Epigenome Browser at Washington University		1
10	The case for using mapped exonic non-duplicate reads when reporting RNA-sequencing depth: examples from pediatric cancer datasets. *GigaScience*, **2021**, 10,	7.6	1
9	A new SARS-CoV-2 lineage that shares mutations with known Variants of Concern is rejected by automated sequence repository quality control **2021**,		1
8	Hydra: A mixture modeling framework for subtyping pediatric cancer cohorts using multimodal gene expression signatures. *PLoS Computational Biology*, **2020**, 16, e1007753	5	1

LIST OF PUBLICATIONS

7   Hydra: A mixture modeling framework for subtyping pediatric cancer cohorts using multimodal gene expression signatures **2020**, 16, e1007753

6   Hydra: A mixture modeling framework for subtyping pediatric cancer cohorts using multimodal gene expression signatures **2020**, 16, e1007753

5   Hydra: A mixture modeling framework for subtyping pediatric cancer cohorts using multimodal gene expression signatures **2020**, 16, e1007753

4   Spiking neural state machine for gait frequency entrainment in a flexible modular robot **2020**, 15, e0240267

3   Spiking neural state machine for gait frequency entrainment in a flexible modular robot **2020**, 15, e0240267

2   Spiking neural state machine for gait frequency entrainment in a flexible modular robot **2020**, 15, e0240267

1   Spiking neural state machine for gait frequency entrainment in a flexible modular robot **2020**, 15, e0240267