

David Haussler

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	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,	11.5	15
95	The Human Pangenome Project: a global resource to map genomic diversity.. <i>Nature</i> , 2022 , 604, 437-446	50.4	7
94	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes.. <i>Science</i> , 2021 , 374, abg8871	33.3	11
93	Picoscope: low-cost system for simultaneous longitudinal biological imaging. <i>Communications Biology</i> , 2021 , 4, 1261	6.7	2
92	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. <i>Cell Genomics</i> , 2021 , 1, 100029-100029		20
91	The UCSC Genome Browser database: 2022 update. <i>Nucleic Acids Research</i> , 2021 ,	20.1	15
90	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	9.7	1
89	The case for using mapped exonic non-duplicate reads when reporting RNA-sequencing depth: examples from pediatric cancer datasets. <i>GigaScience</i> , 2021 , 10,	7.6	1
88	A new SARS-CoV-2 lineage that shares mutations with known Variants of Concern is rejected by automated sequence repository quality control 2021 ,		1
87	A daily-updated database and tools for comprehensive SARS-CoV-2 mutation-annotated trees 2021 ,		4
86	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737-746	46.4	161
85	Cancer microenvironment and genomics: evolution in process. <i>Clinical and Experimental Metastasis</i> , 2021 , 1	4.7	2
84	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	36.3	58
83	The UCSC Genome Browser database: 2021 update. <i>Nucleic Acids Research</i> , 2021 , 49, D1046-D1057	20.1	106
82	Low cost cloud based remote microscopy for biological sciences. <i>Internet of Things (Netherlands)</i> , 2021 , 100454	6.9	2
81	A Daily-Updated Database and Tools for Comprehensive SARS-CoV-2 Mutation-Annotated Trees. <i>Molecular Biology and Evolution</i> , 2021 , 38, 5819-5824	8.3	12
80	Identification of a differentiation stall in epithelial mesenchymal transition in histone H3-mutant diffuse midline glioma. <i>GigaScience</i> , 2020 , 9,	7.6	1

79	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. <i>Nature Biotechnology</i> , 2020 , 38, 1044-1053	44.5	143
78	Neuromorphic Closed-Loop Control of a Flexible Modular Robot by a Simulated Spiking Central Pattern Generator 2020 ,		3
77	A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , 2020 , 11, 3400	17.4	7
76	Stability of SARS-CoV-2 phylogenies. <i>PLoS Genetics</i> , 2020 , 16, e1009175	6	43
75	Spiking neural state machine for gait frequency entrainment in a flexible modular robot. <i>PLoS ONE</i> , 2020 , 15, e0240267	3.7	2
74	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	7.6	12
73	Visualizing and interpreting cancer genomics data via the Xena platform. <i>Nature Biotechnology</i> , 2020 , 38, 675-678	44.5	676
72	ProTECT-Prediction of T-Cell Epitopes for Cancer Therapy. <i>Frontiers in Immunology</i> , 2020 , 11, 483296	8.4	5
71	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. <i>Nature</i> , 2020 , 587, 246-251	50.4	53
70	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020 , 587, 252-257	50.4	89
69	The UCSC SARS-CoV-2 Genome Browser. <i>Nature Genetics</i> , 2020 , 52, 991-998	36.3	44
68	Hydra: A mixture modeling framework for subtyping pediatric cancer cohorts using multimodal gene expression signatures. <i>PLoS Computational Biology</i> , 2020 , 16, e1007753	5	1
67	Hydra: A mixture modeling framework for subtyping pediatric cancer cohorts using multimodal gene expression signatures 2020 , 16, e1007753		
66	Hydra: A mixture modeling framework for subtyping pediatric cancer cohorts using multimodal gene expression signatures 2020 , 16, e1007753		
65	Hydra: A mixture modeling framework for subtyping pediatric cancer cohorts using multimodal gene expression signatures 2020 , 16, e1007753		
64	Spiking neural state machine for gait frequency entrainment in a flexible modular robot 2020 , 15, e0240267		
63	Spiking neural state machine for gait frequency entrainment in a flexible modular robot 2020 , 15, e0240267		
62	Spiking neural state machine for gait frequency entrainment in a flexible modular robot 2020 , 15, e0240267		

61	Spiking neural state machine for gait frequency entrainment in a flexible modular robot 2020 , 15, e0240267		
60	Barriers to accessing public cancer genomic data. <i>Scientific Data</i> , 2019 , 6, 98	8.2	13
59	Federated discovery and sharing of genomic data using Beacons. <i>Nature Biotechnology</i> , 2019 , 37, 220-224	44.5	42
58	Establishing Cerebral Organoids as Models of Human-Specific Brain Evolution. <i>Cell</i> , 2019 , 176, 743-756.e37	37.2	217
57	Comparative Tumor RNA Sequencing Analysis for Difficult-to-Treat Pediatric and Young Adult Patients With Cancer. <i>JAMA Network Open</i> , 2019 , 2, e1913968	10.4	22
56	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. <i>Cell Reports</i> , 2019 , 29, 1675-1689.e9	10.6	51
55	The UCSC Genome Browser database: 2019 update. <i>Nucleic Acids Research</i> , 2019 , 47, D853-D858	20.1	456
54	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	8	28
53	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	11.5	334
52	A Recurrent Mutation in Anaplastic Lymphoma Kinase with Distinct Neoepitope Conformations. <i>Frontiers in Immunology</i> , 2018 , 9, 99	8.4	16
51	High-resolution comparative analysis of great ape genomes. <i>Science</i> , 2018 , 360,	33.3	178
50	Comparative Annotation Toolkit (CAT)-simultaneous clade and personal genome annotation. <i>Genome Research</i> , 2018 , 28, 1029-1038	9.7	33
49	Combining accurate tumor genome simulation with crowdsourcing to benchmark somatic structural variant detection. <i>Genome Biology</i> , 2018 , 19, 188	18.3	29
48	BRCA Challenge: BRCA Exchange as a global resource for variants in BRCA1 and BRCA2. <i>PLoS Genetics</i> , 2018 , 14, e1007752	6	90
47	Human-Specific NOTCH2NL Genes Affect Notch Signaling and Cortical Neurogenesis. <i>Cell</i> , 2018 , 173, 1356-1369.e22	56.2	217
46	Toil enables reproducible, open source, big biomedical data analyses. <i>Nature Biotechnology</i> , 2017 , 35, 314-316	44.5	387
45	TumorMap: Exploring the Molecular Similarities of Cancer Samples in an Interactive Portal. <i>Cancer Research</i> , 2017 , 77, e1111-e1114	10.1	43
44	Representing and decomposing genomic structural variants as balanced integer flows on sequence graphs. <i>BMC Bioinformatics</i> , 2016 , 17, 400	3.6	6

43	The UCSC Genome Browser database: 2016 update. <i>Nucleic Acids Research</i> , 2016 , 44, D717-25	20.1	317
42	UCSC Data Integrator and Variant Annotation Integrator. <i>Bioinformatics</i> , 2016 , 32, 1430-2	7.2	38
41	Long-read sequence assembly of the gorilla genome. <i>Science</i> , 2016 , 352, aae0344	33.3	282
40	Chromosome-scale shotgun assembly using an in vitro method for long-range linkage. <i>Genome Research</i> , 2016 , 26, 342-50	9.7	415
39	The UCSC Cancer Genomics Browser: update 2015. <i>Nucleic Acids Research</i> , 2015 , 43, D812-7	20.1	223
38	The NIH BD2K center for big data in translational genomics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015 , 22, 1143-7	8.6	24
37	Feather development genes and associated regulatory innovation predate the origin of Dinosauria. <i>Molecular Biology and Evolution</i> , 2015 , 32, 23-8	8.3	42
36	The UCSC Genome Browser database: 2015 update. <i>Nucleic Acids Research</i> , 2015 , 43, D670-81	20.1	712
35	Combining tumor genome simulation with crowdsourcing to benchmark somatic single-nucleotide-variant detection. <i>Nature Methods</i> , 2015 , 12, 623-30	21.6	201
34	Navigating protected genomics data with UCSC Genome Browser in a Box. <i>Bioinformatics</i> , 2015 , 31, 764-6.2	6.2	33
33	Building a pan-genome reference for a population. <i>Journal of Computational Biology</i> , 2015 , 22, 387-401	1.7	41
32	Comparative assembly hubs: web-accessible browsers for comparative genomics. <i>Bioinformatics</i> , 2014 , 30, 3293-301	7.2	22
31	An evolutionary arms race between KRAB zinc-finger genes ZNF91/93 and SVA/L1 retrotransposons. <i>Nature</i> , 2014 , 516, 242-5	50.4	281
30	RADIA: RNA and DNA integrated analysis for somatic mutation detection. <i>PLoS ONE</i> , 2014 , 9, e111516	3.7	59
29	Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , 2014 , 24, 2077-89	9.7	74
28	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014 , 346, 1254449	33.3	231
27	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014 , 346, 1320-31	33.3	1182
26	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014 , 346, 1311-20	33.3	628

25	The birds of Genome10K. <i>GigaScience</i> , 2014 , 3, 32	7.6	6
24	The Cancer Genomics Hub (CGHub): overcoming cancer through the power of torrential data. <i>Database: the Journal of Biological Databases and Curation</i> , 2014 , 2014,	5	115
23	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013 , 2, 10	7.6	461
22	HAL: a hierarchical format for storing and analyzing multiple genome alignments. <i>Bioinformatics</i> , 2013 , 29, 1341-2	7.2	78
21	GENCODE: the reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , 2012 , 22, 1760-74	9.7	3142
20	Cactus graphs for genome comparisons. <i>Journal of Computational Biology</i> , 2011 , 18, 469-81	1.7	66
19	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011 , 469, 529-33	50.4	431
18	The Human Epigenome Browser at Washington University. <i>Nature Methods</i> , 2011 , 8, 989-90	21.6	240
17	Cactus: Algorithms for genome multiple sequence alignment. <i>Genome Research</i> , 2011 , 21, 1512-28	9.7	170
16	Using native and syntenically mapped cDNA alignments to improve de novo gene finding. <i>Bioinformatics</i> , 2008 , 24, 637-44	7.2	871
15	Comparative genomics search for losses of long-established genes on the human lineage. <i>PLoS Computational Biology</i> , 2007 , 3, e247	5	93
14	Detecting the Coevolution in and among Protein Domains. <i>PLoS Computational Biology</i> , 2005 , preprint, e211	5	1
13	Aligning multiple genomic sequences with the threaded blockset aligner. <i>Genome Research</i> , 2004 , 14, 708-15	9.7	1006
12	Human-mouse alignments with BLASTZ. <i>Genome Research</i> , 2003 , 13, 103-7	9.7	920
11	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, 11484-9	11.5	624
10	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002 , 420, 520-62	50.4	5376
9	The human genome browser at UCSC. <i>Genome Research</i> , 2002 , 12, 996-1006	9.7	5840
8	Rapid discrimination among individual DNA hairpin molecules at single-nucleotide resolution using an ion channel. <i>Nature Biotechnology</i> , 2001 , 19, 248-52	44.5	350

7	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001 , 409, 860-921	50.4	17366
6	The Human Epigenome Browser at Washington University		1
5	Comparative Annotation Toolkit (CAT) - simultaneous clade and personal genome annotation		7
4	Efficient de novo assembly of eleven human genomes using PromethION sequencing and a novel nanopore toolkit		29
3	Progressive alignment with Cactus: a multiple-genome aligner for the thousand-genome era		15
2	Pandemic-Scale Phylogenomics Reveals Elevated Recombination Rates in the SARS-CoV-2 Spike Region		16
1	Automated assembly of high-quality diploid human reference genomes		3