

W James Kent

List of Publications by Year in descending order

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Version: 2024-02-01

75
papers

81,225
citations

23500

58
h-index

79541

73
g-index

77
all docs

77
docs citations

77
times ranked

86322
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
2	The Human Genome Browser at UCSC. <i>Genome Research</i> , 2002, 12, 996-1006.	2.4	8,776
3	<tt>BLAT</tt>â€™The <tt>BLAST</tt>-Like Alignment Tool. <i>Genome Research</i> , 2002, 12, 656-664.	2.4	7,227
4	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,819
5	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
6	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. <i>Genome Research</i> , 2005, 15, 1034-1050.	2.4	3,517
7	The UCSC Table Browser data retrieval tool. <i>Nucleic Acids Research</i> , 2004, 32, 493D-496.	6.5	2,074
8	Galaxy: A platform for interactive large-scale genome analysis. <i>Genome Research</i> , 2005, 15, 1451-1455.	2.4	1,795
9	Ultraconserved Elements in the Human Genome. <i>Science</i> , 2004, 304, 1321-1325.	6.0	1,496
10	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
11	Aligning Multiple Genomic Sequences With the Threaded Blockset Aligner. <i>Genome Research</i> , 2004, 14, 708-715.	2.4	1,290
12	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	6.0	1,283
13	Assessing computational tools for the discovery of transcription factor binding sites. <i>Nature Biotechnology</i> , 2005, 23, 137-144.	9.4	1,121
14	Human-Mouse Alignments with BLASTZ. <i>Genome Research</i> , 2003, 13, 103-107.	2.4	1,071
15	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	13.7	1,016
16	The UCSC Genome Browser database: update 2011. <i>Nucleic Acids Research</i> , 2011, 39, D876-D882.	6.5	958
17	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	6.0	912
18	The UCSC Genome Browser database: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D670-D681.	6.5	891

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19	Toil enables reproducible, open source, big biomedical data analyses. <i>Nature Biotechnology</i> , 2017, 35, 314-316.	9.4	873
20	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
21	The UCSC genome browser and associated tools. <i>Briefings in Bioinformatics</i> , 2013, 14, 144-161.	3.2	736
22	The UCSC Genome Browser database: extensions and updates 2013. <i>Nucleic Acids Research</i> , 2012, 41, D64-D69.	6.5	732
23	The UCSC Genome Browser database: 2019 update. <i>Nucleic Acids Research</i> , 2019, 47, D853-D858.	6.5	699
24	ENCODE Data in the UCSC Genome Browser: year 5 update. <i>Nucleic Acids Research</i> , 2012, 41, D56-D63.	6.5	698
25	The UCSC Genome Browser database: 2014 update. <i>Nucleic Acids Research</i> , 2014, 42, D764-D770.	6.5	619
26	Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007, 450, 219-232.	13.7	573
27	The UCSC Genome Browser database: update 2010. <i>Nucleic Acids Research</i> , 2010, 38, D613-D619.	6.5	537
28	The UCSC Genome Browser database: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D762-D769.	6.5	476
29	The UCSC Known Genes. <i>Bioinformatics</i> , 2006, 22, 1036-1046.	1.8	462
30	A distal enhancer and an ultraconserved exon are derived from a novel retroposon. <i>Nature</i> , 2006, 441, 87-90.	13.7	452
31	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012, 13, 418.	13.9	410
32	The UCSC Genome Browser database: 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, D717-D725.	6.5	376
33	Track data hubs enable visualization of user-defined genome-wide annotations on the UCSC Genome Browser. <i>Bioinformatics</i> , 2014, 30, 1003-1005.	1.8	375
34	The UCSC Genome Browser database: 2021 update. <i>Nucleic Acids Research</i> , 2021, 49, D1046-D1057.	6.5	354
35	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D626-D634.	6.5	308
36	The Human Epigenome Browser at Washington University. <i>Nature Methods</i> , 2011, 8, 989-990.	9.0	302

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37	The UCSC Genome Browser database: extensions and updates 2011. <i>Nucleic Acids Research</i> , 2012, 40, D918-D923.	6.5	294
38	Over 20% of human transcripts might form sense-antisense pairs. <i>Nucleic Acids Research</i> , 2004, 32, 4812-4820.	6.5	287
39	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. <i>Genome Research</i> , 2003, 13, 13-26.	2.4	263
40	Reconstructing contiguous regions of an ancestral genome. <i>Genome Research</i> , 2006, 16, 1557-1565.	2.4	246
41	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , 2007, 17, 1797-1808.	2.4	237
42	The DNA sequence of human chromosome 7. <i>Nature</i> , 2003, 424, 157-164.	13.7	236
43	ENCODE whole-genome data in the UCSC Genome Browser: update 2012. <i>Nucleic Acids Research</i> , 2012, 40, D912-D917.	6.5	220
44	ENCODE whole-genome data in the UCSC Genome Browser. <i>Nucleic Acids Research</i> , 2010, 38, D620-D625.	6.5	218
45	Centromere reference models for human chromosomes X and Y satellite arrays. <i>Genome Research</i> , 2014, 24, 697-707.	2.4	210
46	Hotspots of mammalian chromosomal evolution. <i>Genome Biology</i> , 2004, 5, R23.	13.9	201
47	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
48	The UCSC Genome Browser database: 2022 update. <i>Nucleic Acids Research</i> , 2022, 50, D1115-D1122.	6.5	175
49	The UCSC Cancer Genomics Browser. <i>Nature Methods</i> , 2009, 6, 239-240.	9.0	167
50	Environmentally Induced Foregut Remodeling by PHA-4/FoxA and DAF-12/NHR. <i>Science</i> , 2004, 305, 1743-1746.	6.0	164
51	ENCODE whole-genome data in the UCSC genome browser (2011 update). <i>Nucleic Acids Research</i> , 2011, 39, D871-D875.	6.5	164
52	The UCSC Genome Browser. <i>Current Protocols in Bioinformatics</i> , 2009, 28, Unit1.4.	25.8	149
53	UCSC Genome Browser enters 20th year. <i>Nucleic Acids Research</i> , 2020, 48, D756-D761.	6.5	138
54	Retrocopy contributions to the evolution of the human genome. <i>BMC Genomics</i> , 2008, 9, 466.	1.2	93

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55	The ENCODE Project at UC Santa Cruz. <i>Nucleic Acids Research</i> , 2007, 35, D663-D667.	6.5	92
56	The UCSC Genome Browser. <i>Current Protocols in Bioinformatics</i> , 2012, 40, Unit1.4.	25.8	86
57	The UCSC SARS-CoV-2 Genome Browser. <i>Nature Genetics</i> , 2020, 52, 991-998.	9.4	79
58	UCSC Data Integrator and Variant Annotation Integrator. <i>Bioinformatics</i> , 2016, 32, 1430-1432.	1.8	78
59	The UCSC cancer genomics browser: update 2011. <i>Nucleic Acids Research</i> , 2011, 39, D951-D959.	6.5	57
60	Computational screening of conserved genomic DNA in search of functional noncoding elements. <i>Nature Methods</i> , 2005, 2, 535-545.	9.0	52
61	Navigating protected genomics data with UCSC Genome Browser in a Box. <i>Bioinformatics</i> , 2015, 31, 764-766.	1.8	49
62	Building a Pan-Genome Reference for a Population. <i>Journal of Computational Biology</i> , 2015, 22, 387-401.	0.8	48
63	Ontology application and use at the ENCODE DCC. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	42
64	The UCSC Genome Browser. <i>Current Protocols in Bioinformatics</i> , 2007, 17, Unit 1.4.	25.8	41
65	The UCSC Genome Browser. <i>Current Protocols in Human Genetics</i> , 2011, 71, Unit18.6.	3.5	38
66	The UCSC repeat browser allows discovery and visualization of evolutionary conflict across repeat families. <i>Mobile DNA</i> , 2020, 11, 13.	1.3	31
67	The NIH BD2K center for big data in translational genomics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1143-1147.	2.2	30
68	Utilizing mapping targets of sequences underrepresented in the reference assembly to reduce false positive alignments. <i>Nucleic Acids Research</i> , 2015, 43, gkv671.	6.5	29
69	Comparative Genomic Analysis Using the UCSC Genome Browser. <i>Methods in Molecular Biology</i> , 2007, 395, 17-33.	0.4	23
70	Understanding genome browsing. <i>Nature Biotechnology</i> , 2009, 27, 153-155.	9.4	22
71	Variation resources at UC Santa Cruz. <i>Nucleic Acids Research</i> , 2007, 35, D716-D720.	6.5	19
72	The UCSC Ebola Genome Portal. <i>PLOS Currents</i> , 2014, 6, .	1.4	6

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73	Piloting the zebrafish genome browser. <i>Developmental Dynamics</i> , 2006, 235, 747-753.	0.8	5
74	The Human Epigenome Browser at Washington University. , 0, .		1
75	Databases and Genome Browsers. , 2010, , 905-921.		0