W James Kent

List of Publications by Year in descending order

75 papers	81,225 citations	27035 58 h-index	90395 73 g-index
77 all docs	77 docs citations	77 times ranked	96145 citing authors

#	Article	IF	Citations
1	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	13.7	21,074
2	The Human Genome Browser at UCSC. Genome Research, 2002, 12, 996-1006.	2.4	8,776
3	<tt>BLAT</tt>â€"The <tt>BLAST</tt>-Like Alignment Tool. Genome Research, 2002, 12, 656-664.	2.4	7,227
4	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	13.7	6,319
5	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
6	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. Genome Research, 2005, 15, 1034-1050.	2.4	3,517
7	The UCSC Table Browser data retrieval tool. Nucleic Acids Research, 2004, 32, 493D-496.	6.5	2,074
8	Galaxy: A platform for interactive large-scale genome analysis. Genome Research, 2005, 15, 1451-1455.	2.4	1,795
9	Ultraconserved Elements in the Human Genome. Science, 2004, 304, 1321-1325.	6.0	1,496
10	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	13.7	1,444
11	Aligning Multiple Genomic Sequences With the Threaded Blockset Aligner. Genome Research, 2004, 14, 708-715.	2.4	1,290
12	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	6.0	1,283
13	Assessing computational tools for the discovery of transcription factor binding sites. Nature Biotechnology, 2005, 23, 137-144.	9.4	1,121
14	Human-Mouse Alignments with BLASTZ. Genome Research, 2003, 13, 103-107.	2.4	1,071
15	A high-resolution map of human evolutionary constraint using 29 mammals. Nature, 2011, 478, 476-482.	13.7	1,016
16	The UCSC Genome Browser database: update 2011. Nucleic Acids Research, 2011, 39, D876-D882.	6.5	958
17	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	6.0	912
18	The UCSC Genome Browser database: 2015 update. Nucleic Acids Research, 2015, 43, D670-D681.	6.5	891

#	Article	IF	Citations
19	Toil enables reproducible, open source, big biomedical data analyses. Nature Biotechnology, 2017, 35, 314-316.	9.4	873
20	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, 11484-11489.	3.3	792
21	The UCSC genome browser and associated tools. Briefings in Bioinformatics, 2013, 14, 144-161.	3.2	736
22	The UCSC Genome Browser database: extensions and updates 2013. Nucleic Acids Research, 2012, 41, D64-D69.	6.5	732
23	The UCSC Genome Browser database: 2019 update. Nucleic Acids Research, 2019, 47, D853-D858.	6.5	699
24	ENCODE Data in the UCSC Genome Browser: year 5 update. Nucleic Acids Research, 2012, 41, D56-D63.	6.5	698
25	The UCSC Genome Browser database: 2014 update. Nucleic Acids Research, 2014, 42, D764-D770.	6.5	619
26	Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures. Nature, 2007, 450, 219-232.	13.7	573
27	The UCSC Genome Browser database: update 2010. Nucleic Acids Research, 2010, 38, D613-D619.	6.5	537
28	The UCSC Genome Browser database: 2018 update. Nucleic Acids Research, 2018, 46, D762-D769.	6.5	476
29	The UCSC Known Genes. Bioinformatics, 2006, 22, 1036-1046.	1.8	462
30	A distal enhancer and an ultraconserved exon are derived from a novel retroposon. Nature, 2006, 441, 87-90.	13.7	452
31	An encyclopedia of mouse DNA elements (Mouse ENCODE). Genome Biology, 2012, 13, 418.	13.9	410
32	The UCSC Genome Browser database: 2016 update. Nucleic Acids Research, 2016, 44, D717-D725.	6.5	376
33	Track data hubs enable visualization of user-defined genome-wide annotations on the UCSC Genome Browser. Bioinformatics, 2014, 30, 1003-1005.	1.8	375
34	The UCSC Genome Browser database: 2021 update. Nucleic Acids Research, 2021, 49, D1046-D1057.	6.5	354
35	OUP accepted manuscript. Nucleic Acids Research, 2017, 45, D626-D634.	6.5	308
36	The Human Epigenome Browser at Washington University. Nature Methods, 2011, 8, 989-990.	9.0	302

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37	The UCSC Genome Browser database: extensions and updates 2011. Nucleic Acids Research, 2012, 40, D918-D923.	6.5	294
38	Over 20% of human transcripts might form sense-antisense pairs. Nucleic Acids Research, 2004, 32, 4812-4820.	6.5	287
39	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. Genome Research, 2003, 13, 13-26.	2.4	263
40	Reconstructing contiguous regions of an ancestral genome. Genome Research, 2006, 16, 1557-1565.	2.4	246
41	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	2.4	237
42	The DNA sequence of human chromosome 7. Nature, 2003, 424, 157-164.	13.7	236
43	ENCODE whole-genome data in the UCSC Genome Browser: update 2012. Nucleic Acids Research, 2012, 40, D912-D917.	6.5	220
44	ENCODE whole-genome data in the UCSC Genome Browser. Nucleic Acids Research, 2010, 38, D620-D625.	6.5	218
45	Centromere reference models for human chromosomes X and Y satellite arrays. Genome Research, 2014, 24, 697-707.	2.4	210
46	Hotspots of mammalian chromosomal evolution. Genome Biology, 2004, 5, R23.	13.9	201
47	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	2.4	184
48	The UCSC Genome Browser database: 2022 update. Nucleic Acids Research, 2022, 50, D1115-D1122.	6.5	175
49	The UCSC Cancer Genomics Browser. Nature Methods, 2009, 6, 239-240.	9.0	167
50	Environmentally Induced Foregut Remodeling by PHA-4/FoxA and DAF-12/NHR. Science, 2004, 305, 1743-1746.	6.0	164
51	ENCODE whole-genome data in the UCSC genome browser (2011 update). Nucleic Acids Research, 2011, 39, D871-D875.	6.5	164
52	The UCSC Genome Browser. Current Protocols in Bioinformatics, 2009, 28, Unit1.4.	25.8	149
53	UCSC Genome Browser enters 20th year. Nucleic Acids Research, 2020, 48, D756-D761.	6.5	138
54	Retrocopy contributions to the evolution of the human genome. BMC Genomics, 2008, 9, 466.	1.2	93

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

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73	Piloting the zebrafish genome browser. Developmental Dynamics, 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