

Robert Baertsch

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

21,715
citations

218592

26
h-index

552653

26
g-index

33
all docs

33
docs citations

33
times ranked

29791
citing authors

#	ARTICLE	IF	CITATIONS
1	MEK-ERK signaling is a therapeutic target in metastatic castration resistant prostate cancer. Prostate Cancer and Prostatic Diseases, 2019, 22, 531-538.	2.0	66
2	Speciation network in Laurasiatheria: retrophylogenomic signals. Genome Research, 2017, 27, 997-1003.	2.4	38
3	TumorMap: Exploring the Molecular Similarities of Cancer Samples in an Interactive Portal. Cancer Research, 2017, 77, e111-e114.	0.4	59
4	N-Myc Drives Neuroendocrine Prostate Cancer Initiated from Human Prostate Epithelial Cells. Cancer Cell, 2016, 29, 536-547.	7.7	278
5	Genome sequence of the basal haplorrhine primate Tarsius syrichta reveals unusual insertions. Nature Communications, 2016, 7, 12997.	5.8	32
6	Pathway-Based Genomics Prediction using Generalized Elastic Net. PLoS Computational Biology, 2016, 12, e1004790.	1.5	84
7	A basal stem cell signature identifies aggressive prostate cancer phenotypes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6544-52.	3.3	168
8	Exploring Massive Incomplete Lineage Sorting in Arctoids (Laurasiatheria, Carnivora). Molecular Biology and Evolution, 2015, 32, msv188.	3.5	48
9	Abstract 731: Integrative genomic analysis to identify emergent enzalutamide resistance mechanisms in castration-resistant prostate cancer. , 2015, , .		1
10	Abstract A28: N-Myc drives small cell neuroendocrine cancer initiated from human prostate basal cells. , 2015, , .		0
11	Abstract B1-37: A signature catalog to classify tumor mixtures: application to recognition of metastatic disease in prostate cancer. , 2015, , .		0
12	Abstract 4177: Identification of pathways relevant for metastatic site prediction in prostate cancer. , 2014, , .		0
13	Abstract 60: The MedBook network for cancer precision medical care.. , 2013, , .		0
14	Identification of polo-like kinase 1 (PLK1) in aggressive prostate cancer by paradigm analysis.. Journal of Clinical Oncology, 2013, 31, 5006-5006.	0.8	0
15	The consensus coding sequence (CCDS) project: Identifying a common protein-coding gene set for the human and mouse genomes. Genome Research, 2009, 19, 1316-1323.	2.4	476
16	Mosaic retroposon insertion patterns in placental mammals. Genome Research, 2009, 19, 868-875.	2.4	79
17	Retrocopy contributions to the evolution of the human genome. BMC Genomics, 2008, 9, 466.	1.2	93
18	Using native and syntenically mapped cDNA alignments to improve <i>de novo</i> gene finding. Bioinformatics, 2008, 24, 637-644.	1.8	1,618

#	ARTICLE	IF	CITATIONS
19	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , 2007, 17, 1797-1808.	2.4	237
20	Pseudogenes in the ENCODE regions: Consensus annotation, analysis of transcription, and evolution. <i>Genome Research</i> , 2007, 17, 839-851.	2.4	191
21	A New Low-Cost Instream Antenna System for Tracking Passive Integrated Transponder (PIT)-Tagged Fish in Small Streams. <i>Transactions of the American Fisheries Society</i> , 2007, 136, 562-566.	0.6	39
22	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	6.0	1,283
23	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
24	Forces Shaping the Fastest Evolving Regions in the Human Genome. <i>PLoS Genetics</i> , 2006, 2, e168.	1.5	399
25	A Model for the Proteolipid Ring and Bafilomycin/Concanamycin-binding Site in the Vacuolar ATPase of <i>Neurospora crassa</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 31885-31893.	1.6	64
26	Forces Shaping the Fastest Evolving Regions in the Human Genome. <i>PLoS Genetics</i> , 2005, preprint, e168.	1.5	0
27	Aligning Multiple Genomic Sequences With the Threaded Blockset Aligner. <i>Genome Research</i> , 2004, 14, 708-715.	2.4	1,290
28	The Structure of a Rigorously Conserved RNA Element within the SARS Virus Genome. <i>PLoS Biology</i> , 2004, 3, e5.	2.6	137
29	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
30	Hotspots of mammalian chromosomal evolution. <i>Genome Biology</i> , 2004, 5, R23.	13.9	201
31	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
32	Human-Mouse Alignments with BLASTZ. <i>Genome Research</i> , 2003, 13, 103-107.	2.4	1,071
33	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319