Andreas Heger

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1302395/publications.pdf

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52	27,222	94381 37	168321 53
papers	citations	h-index	g-index
57	57	57	44812
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Response to Vitamin D Supplementation in the Setting of a Randomized, Placebo-Controlled Trial. EBioMedicine, 2018, 31, 133-142.	2.7	29
2	The Light Chain IgLV3-21 Defines a New Poor Prognostic Subgroup in Chronic Lymphocytic Leukemia: Results of a Multicenter Study. Clinical Cancer Research, 2018, 24, 5048-5057.	3.2	38
3	Investigation into the role of the germline epigenome in the transmission of glucocorticoid-programmed effects across generations. Genome Biology, 2018, 19, 50.	3.8	20
4	Transcriptomic profiling of purified patient-derived dopamine neurons identifies convergent perturbations and therapeutics for Parkinsonâ€™s disease. Human Molecular Genetics, 2017, 26, ddw412.	1.4	62
5	UMI-tools: modeling sequencing errors in Unique Molecular Identifiers to improve quantification accuracy. Genome Research, 2017, 27, 491-499.	2.4	1,316
6	11Î²-hydroxysteroid dehydrogenase-1 deficiency alters the gut microbiome response to Western diet. Journal of Endocrinology, 2017, 232, 273-283.	1.2	11
7	Familial childhood-onset progressive cerebellar syndrome associated with the <i>ATP1A3</i> mutation. Neurology: Genetics, 2017, 3, e145.	0.9	15
8	Long noncoding RNAs in B-cell development and activation. Blood, 2016, 128, e10-e19.	0.6	115
9	Defining the microbial transcriptional response to colitis through integrated host and microbiome profiling. ISME Journal, 2016, 10, 2389-2404.	4.4	40
10	CGAT: a model for immersive personalized training in computational genomics. Briefings in Functional Genomics, 2015, 15, 32-7.	1.3	4
11	Population and single-cell genomics reveal the <i>Aire</i> dependency, relief from Polycomb silencing, and distribution of self-antigen expression in thymic epithelia. Genome Research, 2014, 24, 1918-1931.	2.4	308
12	CGAT: computational genomics analysis toolkit. Bioinformatics, 2014, 30, 1290-1291.	1.8	65
13	Identification of a candidate prognostic gene signature by transcriptome analysis of matched pre- and post-treatment prostatic biopsies from patients with advanced prostate cancer. BMC Cancer, 2014, 14, 977.	1.1	49
14	Pfam: the protein families database. Nucleic Acids Research, 2014, 42, D222-D230.	6.5	5,425
15	Sequencing depth and coverage: key considerations in genomic analyses. Nature Reviews Genetics, 2014, 15, 121-132.	7.7	1,116
16	Next-generation Sequencing of Advanced Prostate Cancer Treated with Androgen-deprivation Therapy. European Urology, 2014, 66, 32-39.	0.9	139
17	Long non-coding RNAs and enhancer RNAs regulate the lipopolysaccharide-induced inflammatory response in human monocytes. Nature Communications, 2014, 5, 3979.	5.8	281
18	Targeting Polycomb to Pericentric Heterochromatin in Embryonic Stem Cells Reveals a Role for H2AK119u1 in PRC2 Recruitment. Cell Reports, 2014, 7, 1456-1470.	2.9	283

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19	Insights into the evolution of Darwinâ€™s finches from comparative analysis of the Geospiza magnirostris genome sequence. BMC Genomics, 2013, 14, 95.	1.2	38
20	GAT: a simulation framework for testing the association of genomic intervals. Bioinformatics, 2013, 29, 2046-2048.	1.8	221
21	Epigenetic conservation at gene regulatory elements revealed by non-methylated DNA profiling in seven vertebrates. ELife, 2013, 2, e00348.	2.8	192
22	The Pfam protein families database. Nucleic Acids Research, 2012, 40, D290-D301.	6.5	3,306
23	Evidence for conserved post-transcriptional roles of unitary pseudogenes and for frequent bifunctionality of mRNAs. Genome Biology, 2012, 13, R102.	13.9	61
24	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	13.7	663
25	The genome of the green anole lizard and a comparative analysis with birds and mammals. Nature, 2011, 477, 587-591.	13.7	575
26	Mouse genomic variation and its effect on phenotypes and gene regulation. Nature, 2011, 477, 289-294.	13.7	1,461
27	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	13.7	541
28	Transcriptomic analysis supports similar functional roles for the two thymuses of the tammar wallaby. BMC Genomics, 2011, 12, 420.	1.2	21
29	The genome of a songbird. Nature, 2010, 464, 757-762.	13.7	770
30	A ChIP-seq defined genome-wide map of vitamin D receptor binding: Associations with disease and evolution. Genome Research, 2010, 20, 1352-1360.	2.4	737
31	Accelerated Evolution of PAK3- and PIM1-like Kinase Gene Families in the Zebra Finch, Taeniopygia guttata. Molecular Biology and Evolution, 2010, 27, 1923-1934.	3.5	12
32	Molecular evolution of genes in avian genomes. Genome Biology, 2010, 11, R68.	13.9	125
33	The Pfam protein families database. Nucleic Acids Research, 2010, 38, D211-D222.	6.5	2,693
34	Accurate Estimation of Gene Evolutionary Rates Using XRATE, with an Application to Transmembrane Proteins. Molecular Biology and Evolution, 2009, 26, 1715-1721.	3.5	9
35	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	13.7	657
36	Rapid bursts of androgen-binding protein (Abp) gene duplication occurred independently in diverse mammals. BMC Evolutionary Biology, 2008, 8, 46.	3.2	41

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37	Uncertainty in homology inferences: Assessing and improving genomic sequence alignment. Genome Research, 2008, 18, 298-309.	2.4	128
38	PairsDB atlas of protein sequence space. Nucleic Acids Research, 2008, 36, D276-D280.	6.5	13
39	OPTIC: orthologous and paralogous transcripts in clades. Nucleic Acids Research, 2007, 36, D267-D270.	6.5	23
40	The global trace graph, a novel paradigm for searching protein sequence databases. Bioinformatics, 2007, 23, 2361-2367.	1.8	20
41	Variable Strength of Translational Selection Among 12 Drosophila Species. Genetics, 2007, 177, 1337-1348.	1.2	37
42	An analysis of the gene complement of a marsupial, Monodelphis domestica: Evolution of lineage-specific genes and giant chromosomes. Genome Research, 2007, 17, 969-981.	2.4	66
43	Evolutionary rate analyses of orthologs and paralogs from 12 <i>Drosophila</i> genomes. Genome Research, 2007, 17, 1837-1849.	2.4	131
44	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	13.7	661
45	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	13.7	1,886
46	Genome sequence, comparative analysis and haplotype structure of the domestic dog. Nature, 2005, 438, 803-819.	13.7	2,215
47	ADDA: a domain database with global coverage of the protein universe. Nucleic Acids Research, 2004, 33, D188-D191.	6.5	39
48	Accurate Detection of Very Sparse Sequence Motifs. Journal of Computational Biology, 2004, 11, 843-857.	0.8	18
49	Exhaustive Enumeration of Protein Domain Families. Journal of Molecular Biology, 2003, 328, 749-767.	2.0	118
50	Sensitive pattern discovery with 'fuzzy' alignments of distantly related proteins. Bioinformatics, 2003, 19, i130-i137.	1.8	41
51	Rapid automatic detection and alignment of repeats in protein sequences. Proteins: Structure, Function and Bioinformatics, 2000, 41, 224-237.	1.5	296
52	Towards a covering set of protein family profiles. Progress in Biophysics and Molecular Biology, 2000, 73, 321-337.	1.4	46