

Andreas Heger

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

27,222
citations

94381

37
h-index

168321

53
g-index

57
all docs

57
docs citations

57
times ranked

44812
citing authors

#	ARTICLE	IF	CITATIONS
1	Pfam: the protein families database. <i>Nucleic Acids Research</i> , 2014, 42, D222-D230.	6.5	5,425
2	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2012, 40, D290-D301.	6.5	3,306
3	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2010, 38, D211-D222.	6.5	2,693
4	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005, 438, 803-819.	13.7	2,215
5	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
6	Mouse genomic variation and its effect on phenotypes and gene regulation. <i>Nature</i> , 2011, 477, 289-294.	13.7	1,461
7	UMI-tools: modeling sequencing errors in Unique Molecular Identifiers to improve quantification accuracy. <i>Genome Research</i> , 2017, 27, 491-499.	2.4	1,316
8	Sequencing depth and coverage: key considerations in genomic analyses. <i>Nature Reviews Genetics</i> , 2014, 15, 121-132.	7.7	1,116
9	The genome of a songbird. <i>Nature</i> , 2010, 464, 757-762.	13.7	770
10	A ChIP-seq defined genome-wide map of vitamin D receptor binding: Associations with disease and evolution. <i>Genome Research</i> , 2010, 20, 1352-1360.	2.4	737
11	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012, 483, 169-175.	13.7	663
12	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	13.7	661
13	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008, 453, 175-183.	13.7	657
14	The genome of the green anole lizard and a comparative analysis with birds and mammals. <i>Nature</i> , 2011, 477, 587-591.	13.7	575
15	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	13.7	541
16	Population and single-cell genomics reveal the <i>Aire</i> dependency, relief from Polycomb silencing, and distribution of self-antigen expression in thymic epithelia. <i>Genome Research</i> , 2014, 24, 1918-1931.	2.4	308
17	Rapid automatic detection and alignment of repeats in protein sequences. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 224-237.	1.5	296
18	Targeting Polycomb to Pericentric Heterochromatin in Embryonic Stem Cells Reveals a Role for H2AK119u1 in PRC2 Recruitment. <i>Cell Reports</i> , 2014, 7, 1456-1470.	2.9	283

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19	Long non-coding RNAs and enhancer RNAs regulate the lipopolysaccharide-induced inflammatory response in human monocytes. <i>Nature Communications</i> , 2014, 5, 3979.	5.8	281
20	GAT: a simulation framework for testing the association of genomic intervals. <i>Bioinformatics</i> , 2013, 29, 2046-2048.	1.8	221
21	Epigenetic conservation at gene regulatory elements revealed by non-methylated DNA profiling in seven vertebrates. <i>ELife</i> , 2013, 2, e00348.	2.8	192
22	Next-generation Sequencing of Advanced Prostate Cancer Treated with Androgen-deprivation Therapy. <i>European Urology</i> , 2014, 66, 32-39.	0.9	139
23	Evolutionary rate analyses of orthologs and paralogs from 12 <i>Drosophila</i> genomes. <i>Genome Research</i> , 2007, 17, 1837-1849.	2.4	131
24	Uncertainty in homology inferences: Assessing and improving genomic sequence alignment. <i>Genome Research</i> , 2008, 18, 298-309.	2.4	128
25	Molecular evolution of genes in avian genomes. <i>Genome Biology</i> , 2010, 11, R68.	13.9	125
26	Exhaustive Enumeration of Protein Domain Families. <i>Journal of Molecular Biology</i> , 2003, 328, 749-767.	2.0	118
27	Long noncoding RNAs in B-cell development and activation. <i>Blood</i> , 2016, 128, e10-e19.	0.6	115
28	An analysis of the gene complement of a marsupial, <i>Monodelphis domestica</i> : Evolution of lineage-specific genes and giant chromosomes. <i>Genome Research</i> , 2007, 17, 969-981.	2.4	66
29	CGAT: computational genomics analysis toolkit. <i>Bioinformatics</i> , 2014, 30, 1290-1291.	1.8	65
30	Transcriptomic profiling of purified patient-derived dopamine neurons identifies convergent perturbations and therapeutics for Parkinson's disease. <i>Human Molecular Genetics</i> , 2017, 26, ddw412.	1.4	62
31	Evidence for conserved post-transcriptional roles of unitary pseudogenes and for frequent bifunctionality of mRNAs. <i>Genome Biology</i> , 2012, 13, R102.	13.9	61
32	Identification of a candidate prognostic gene signature by transcriptome analysis of matched pre- and post-treatment prostatic biopsies from patients with advanced prostate cancer. <i>BMC Cancer</i> , 2014, 14, 977.	1.1	49
33	Towards a covering set of protein family profiles. <i>Progress in Biophysics and Molecular Biology</i> , 2000, 73, 321-337.	1.4	46
34	Sensitive pattern discovery with 'fuzzy' alignments of distantly related proteins. <i>Bioinformatics</i> , 2003, 19, i130-i137.	1.8	41
35	Rapid bursts of androgen-binding protein (Abp) gene duplication occurred independently in diverse mammals. <i>BMC Evolutionary Biology</i> , 2008, 8, 46.	3.2	41
36	Defining the microbial transcriptional response to colitis through integrated host and microbiome profiling. <i>ISME Journal</i> , 2016, 10, 2389-2404.	4.4	40

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37	ADDA: a domain database with global coverage of the protein universe. <i>Nucleic Acids Research</i> , 2004, 33, D188-D191.	6.5	39
38	Insights into the evolution of Darwin's finches from comparative analysis of the <i>Geospiza magnirostris</i> genome sequence. <i>BMC Genomics</i> , 2013, 14, 95.	1.2	38
39	The Light Chain IgLV3-21 Defines a New Poor Prognostic Subgroup in Chronic Lymphocytic Leukemia: Results of a Multicenter Study. <i>Clinical Cancer Research</i> , 2018, 24, 5048-5057.	3.2	38
40	Variable Strength of Translational Selection Among 12 <i>Drosophila</i> Species. <i>Genetics</i> , 2007, 177, 1337-1348.	1.2	37
41	Genomic Response to Vitamin D Supplementation in the Setting of a Randomized, Placebo-Controlled Trial. <i>EBioMedicine</i> , 2018, 31, 133-142.	2.7	29
42	OPTIC: orthologous and paralogous transcripts in clades. <i>Nucleic Acids Research</i> , 2007, 36, D267-D270.	6.5	23
43	Transcriptomic analysis supports similar functional roles for the two thymuses of the tammar wallaby. <i>BMC Genomics</i> , 2011, 12, 420.	1.2	21
44	The global trace graph, a novel paradigm for searching protein sequence databases. <i>Bioinformatics</i> , 2007, 23, 2361-2367.	1.8	20
45	Investigation into the role of the germline epigenome in the transmission of glucocorticoid-programmed effects across generations. <i>Genome Biology</i> , 2018, 19, 50.	3.8	20
46	Accurate Detection of Very Sparse Sequence Motifs. <i>Journal of Computational Biology</i> , 2004, 11, 843-857.	0.8	18
47	Familial childhood-onset progressive cerebellar syndrome associated with the <i>ATP1A3</i> mutation. <i>Neurology: Genetics</i> , 2017, 3, e145.	0.9	15
48	PairsDB atlas of protein sequence space. <i>Nucleic Acids Research</i> , 2008, 36, D276-D280.	6.5	13
49	Accelerated Evolution of PAK3- and PIM1-like Kinase Gene Families in the Zebra Finch, <i>Taeniopygia guttata</i> . <i>Molecular Biology and Evolution</i> , 2010, 27, 1923-1934.	3.5	12
50	11 β -hydroxysteroid dehydrogenase-1 deficiency alters the gut microbiome response to Western diet. <i>Journal of Endocrinology</i> , 2017, 232, 273-283.	1.2	11
51	Accurate Estimation of Gene Evolutionary Rates Using XRATE, with an Application to Transmembrane Proteins. <i>Molecular Biology and Evolution</i> , 2009, 26, 1715-1721.	3.5	9
52	CGAT: a model for immersive personalized training in computational genomics. <i>Briefings in Functional Genomics</i> , 2015, 15, 32-7.	1.3	4