

Andreas Heger

List of Publications by Citations

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Version: 2024-04-03

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

55 papers	21,382 citations	35 h-index	57 g-index
57 ext. papers	25,315 ext. citations	16.6 avg, IF	6.18 L-index

#	Paper	IF	Citations
55	Pfam: the protein families database. <i>Nucleic Acids Research</i> , 2014 , 42, D222-30	20.1	3975
54	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2012 , 40, D290-301	20.1	2844
53	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2010 , 38, D211-22	20.1	2467
52	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005 , 438, 803-19	50.4	1809
51	Evolution of genes and genomes on the Drosophila phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
50	Mouse genomic variation and its effect on phenotypes and gene regulation. <i>Nature</i> , 2011 , 477, 289-94	50.4	1087
49	Sequencing depth and coverage: key considerations in genomic analyses. <i>Nature Reviews Genetics</i> , 2014 , 15, 121-32	30.1	799
48	The genome of a songbird. <i>Nature</i> , 2010 , 464, 757-62	50.4	655
47	A ChIP-seq defined genome-wide map of vitamin D receptor binding: associations with disease and evolution. <i>Genome Research</i> , 2010 , 20, 1352-60	9.7	606
46	UMI-tools: modeling sequencing errors in Unique Molecular Identifiers to improve quantification accuracy. <i>Genome Research</i> , 2017 , 27, 491-499	9.7	585
45	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. <i>Nature</i> , 2007 , 447, 167-77	50.4	577
44	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008 , 453, 175-83	50.4	545
43	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012 , 483, 169-75	50.4	517
42	The genome of the green anole lizard and a comparative analysis with birds and mammals. <i>Nature</i> , 2011 , 477, 587-91	50.4	478
41	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011 , 469, 529-33	50.4	431
40	Rapid automatic detection and alignment of repeats in protein sequences. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 41, 224-37	4.2	235
39	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	10.6	233

38	Long non-coding RNAs and enhancer RNAs regulate the lipopolysaccharide-induced inflammatory response in human monocytes. <i>Nature Communications</i> , 2014 , 5, 3979	17.4	212
37	Population and single-cell genomics reveal the Aire dependency, relief from Polycomb silencing, and distribution of self-antigen expression in thymic epithelia. <i>Genome Research</i> , 2014 , 24, 1918-31	9.7	197
36	Epigenetic conservation at gene regulatory elements revealed by non-methylated DNA profiling in seven vertebrates. <i>ELife</i> , 2013 , 2, e00348	8.9	148
35	GAT: a simulation framework for testing the association of genomic intervals. <i>Bioinformatics</i> , 2013 , 29, 2046-8	7.2	136
34	Evolutionary rate analyses of orthologs and paralogs from 12 Drosophila genomes. <i>Genome Research</i> , 2007 , 17, 1837-49	9.7	110
33	Exhaustive enumeration of protein domain families. <i>Journal of Molecular Biology</i> , 2003 , 328, 749-67	6.5	107
32	Uncertainty in homology inferences: assessing and improving genomic sequence alignment. <i>Genome Research</i> , 2008 , 18, 298-309	9.7	100
31	Next-generation sequencing of advanced prostate cancer treated with androgen-deprivation therapy. <i>European Urology</i> , 2014 , 66, 32-9	10.2	99
30	Molecular evolution of genes in avian genomes. <i>Genome Biology</i> , 2010 , 11, R68	18.3	92
29	Long noncoding RNAs in B-cell development and activation. <i>Blood</i> , 2016 , 128, e10-9	2.2	79
28	Evidence for conserved post-transcriptional roles of unitary pseudogenes and for frequent bifunctionality of mRNAs. <i>Genome Biology</i> , 2012 , 13, R102	18.3	51
27	Transcriptomic profiling of purified patient-derived dopamine neurons identifies convergent perturbations and therapeutics for Parkinson's disease. <i>Human Molecular Genetics</i> , 2017 , 26, 552-566	5.6	47
26	CGAT: computational genomics analysis toolkit. <i>Bioinformatics</i> , 2014 , 30, 1290-1	7.2	44
25	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, 969-81	9.7	43
24	Rapid bursts of androgen-binding protein (Abp) gene duplication occurred independently in diverse mammals. <i>BMC Evolutionary Biology</i> , 2008 , 8, 46	3	38
23	Towards a covering set of protein family profiles. <i>Progress in Biophysics and Molecular Biology</i> , 2000 , 73, 321-37	4.7	38
22	Sensitive pattern discovery with fuzzy alignments of distantly related proteins. <i>Bioinformatics</i> , 2003 , 19 Suppl 1, i130-7	7.2	37
21	ADDA: a domain database with global coverage of the protein universe. <i>Nucleic Acids Research</i> , 2005 , 33, D188-91	20.1	36

20	Variable strength of translational selection among 12 <i>Drosophila</i> species. <i>Genetics</i> , 2007 , 177, 1337-48	4	34
19	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	4.5	33
18	Defining the microbial transcriptional response to colitis through integrated host and microbiome profiling. <i>ISME Journal</i> , 2016 , 10, 2389-404	11.9	31
17	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	4.8	28
16	OPTIC: orthologous and paralogous transcripts in clades. <i>Nucleic Acids Research</i> , 2008 , 36, D267-70	20.1	22
15	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	12.9	21
14	Genomic Response to Vitamin D Supplementation in the Setting of a Randomized, Placebo-Controlled Trial. <i>EBioMedicine</i> , 2018 , 31, 133-142	8.8	20
13	Transcriptomic analysis supports similar functional roles for the two thymuses of the tammar wallaby. <i>BMC Genomics</i> , 2011 , 12, 420	4.5	19
12	The global trace graph, a novel paradigm for searching protein sequence databases. <i>Bioinformatics</i> , 2007 , 23, 2361-7	7.2	19
11	Accurate detection of very sparse sequence motifs. <i>Journal of Computational Biology</i> , 2004 , 11, 843-57	1.7	15
10	UMI-tools: Modelling sequencing errors in Unique Molecular Identifiers to improve quantification accuracy		15
9	Investigation into the role of the germline epigenome in the transmission of glucocorticoid-programmed effects across generations. <i>Genome Biology</i> , 2018 , 19, 50	18.3	14
8	Familial childhood-onset progressive cerebellar syndrome associated with the mutation. <i>Neurology: Genetics</i> , 2017 , 3, e145	3.8	12
7	PairsDB atlas of protein sequence space. <i>Nucleic Acids Research</i> , 2008 , 36, D276-80	20.1	12
6	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, 1923-34	8.3	9
5	11 β -hydroxysteroid dehydrogenase-1 deficiency alters the gut microbiome response to Western diet. <i>Journal of Endocrinology</i> , 2017 , 232, 273-283	4.7	8
4	Accurate estimation of gene evolutionary rates using XRATE, with an application to transmembrane proteins. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1715-21	8.3	7
3	CGAT: a model for immersive personalized training in computational genomics. <i>Briefings in Functional Genomics</i> , 2016 , 15, 32-7	4.9	4

2	Automated Sequence-Based Approaches for Identifying Domain Families 2013 , 1-24	1
1	Effect of vitamin D supplementation on biomarkers of inflammation and immune function: functional genomics analysis of the BEST-D trial	1