Andreas Heger

List of Publications by Year
in descending order

52 papers	27,222 citations	94433 37 h-index	168389 53 g-index
57 all docs	57 docs citations	57 times ranked	44812 citing authors

#	Article	IF	Citations
1	Pfam: the protein families database. Nucleic Acids Research, 2014, 42, D222-D230.	14.5	5,425
2	The Pfam protein families database. Nucleic Acids Research, 2012, 40, D290-D301.	14.5	3,306
3	The Pfam protein families database. Nucleic Acids Research, 2010, 38, D211-D222.	14.5	2,693
4	Genome sequence, comparative analysis and haplotype structure of the domestic dog. Nature, 2005, 438, 803-819.	27.8	2,215
5	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
6	Mouse genomic variation and its effect on phenotypes and gene regulation. Nature, 2011, 477, 289-294.	27.8	1,461
7	UMI-tools: modeling sequencing errors in Unique Molecular Identifiers to improve quantification accuracy. Genome Research, 2017, 27, 491-499.	5.5	1,316
8	Sequencing depth and coverage: key considerations in genomic analyses. Nature Reviews Genetics, 2014, 15, 121-132.	16.3	1,116
9	The genome of a songbird. Nature, 2010, 464, 757-762.	27.8	770
10	A ChIP-seq defined genome-wide map of vitamin D receptor binding: Associations with disease and evolution. Genome Research, 2010, 20, 1352-1360.	5.5	737
11	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	27.8	663
12	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	27.8	661
13	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	27.8	657
14	The genome of the green anole lizard and a comparative analysis with birds and mammals. Nature, 2011, 477, 587-591.	27.8	575
15	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	27.8	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. Genome Research, 2014, 24, 1918-1931.	5.5	308
17	Rapid automatic detection and alignment of repeats in protein sequences. Proteins: Structure, Function and Bioinformatics, 2000, 41, 224-237.	2.6	296
18	Targeting Polycomb to Pericentric Heterochromatin in Embryonic Stem Cells Reveals a Role for H2AK119u1 in PRC2 Recruitment. Cell Reports, 2014, 7, 1456-1470.	6.4	283

#	ARTICLE	IF	CITATIONS
19	Long non-coding RNAs and enhancer RNAs regulate the lipopolysaccharide-induced inflammatory response in human monocytes. Nature Communications, 2014, 5, 3979.	12.8	281
20	GAT: a simulation framework for testing the association of genomic intervals. Bioinformatics, 2013, 29, 2046-2048.	4.1	221
21	Epigenetic conservation at gene regulatory elements revealed by non-methylated DNA profiling in seven vertebrates. ELife, 2013, 2, e00348.	6.0	192
22	Next-generation Sequencing of Advanced Prostate Cancer Treated with Androgen-deprivation Therapy. European Urology, 2014, 66, 32-39.	1.9	139
23	Evolutionary rate analyses of orthologs and paralogs from 12 *Drosophila* genomes. Genome Research, 2007, 17, 1837-1849.	5.5	131
24	Uncertainty in homology inferences: Assessing and improving genomic sequence alignment. Genome Research, 2008, 18, 298-309.	5.5	128
25	Molecular evolution of genes in avian genomes. Genome Biology, 2010, 11, R68.	9.6	125
26	Exhaustive Enumeration of Protein Domain Families. Journal of Molecular Biology, 2003, 328, 749-767.	4.2	118
27	Long noncoding RNAs in B-cell development and activation. Blood, 2016, 128, e10-e19.	1.4	115
28	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.	5.5	66
29	CGAT: computational genomics analysis toolkit. Bioinformatics, 2014, 30, 1290-1291.	4.1	65
30	Transcriptomic profiling of purified patient-derived dopamine neurons identifies convergent perturbations and therapeutics for Parkinson's disease. Human Molecular Genetics, 2017, 26, ddw412.	2.9	62
31	Evidence for conserved post-transcriptional roles of unitary pseudogenes and for frequent bifunctionality of mRNAs. Genome Biology, 2012, 13, R102.	9.6	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. BMC Cancer, 2014, 14, 977.	2.6	49
33	Towards a covering set of protein family profiles. Progress in Biophysics and Molecular Biology, 2000, 73, 321-337.	2.9	46
34	Sensitive pattern discovery with 'fuzzy' alignments of distantly related proteins. Bioinformatics, 2003, 19, i130-i137.	4.1	41
35	Rapid bursts of androgen-binding protein (Abp) gene duplication occurred independently in diverse mammals. BMC Evolutionary Biology, 2008, 8, 46.	3.2	41
36	Defining the microbial transcriptional response to colitis through integrated host and microbiome profiling. ISME Journal, 2016, 10, 2389-2404.	9.8	40

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37	ADDA: a domain database with global coverage of the protein universe. Nucleic Acids Research, 2004, 33, D188-D191.	14.5	39
38	Insights into the evolution of Darwinâ€™s finches from comparative analysis of the Geospiza magnirostris genome sequence. BMC Genomics, 2013, 14, 95.	2.8	38
39	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.	7.0	38
40	Variable Strength of Translational Selection Among 12 Drosophila Species. Genetics, 2007, 177, 1337-1348.	2.9	37
41	Genomic Response to Vitamin D Supplementation in the Setting of a Randomized, Placebo-Controlled Trial. EBioMedicine, 2018, 31, 133-142.	6.1	29
42	OPTIC: orthologous and paralogous transcripts in clades. Nucleic Acids Research, 2007, 36, D267-D270.	14.5	23
43	Transcriptomic analysis supports similar functional roles for the two thymuses of the tammar wallaby. BMC Genomics, 2011, 12, 420.	2.8	21
44	The global trace graph, a novel paradigm for searching protein sequence databases. Bioinformatics, 2007, 23, 2361-2367.	4.1	20
45	Investigation into the role of the germline epigenome in the transmission of glucocorticoid-programmed effects across generations. Genome Biology, 2018, 19, 50.	8.8	20
46	Accurate Detection of Very Sparse Sequence Motifs. Journal of Computational Biology, 2004, 11, 843-857.	1.6	18
47	Familial childhood-onset progressive cerebellar syndrome associated with the *ATP1A3* mutation. Neurology: Genetics, 2017, 3, e145.	1.9	15
48	PairsDB atlas of protein sequence space. Nucleic Acids Research, 2008, 36, D276-D280.	14.5	13
49	Accelerated Evolution of PAK3- and PIM1-like Kinase Gene Families in the Zebra Finch, Taeniopygia guttata. Molecular Biology and Evolution, 2010, 27, 1923-1934.	8.9	12
50	11Î²-hydroxysteroid dehydrogenase-1 deficiency alters the gut microbiome response to Western diet. Journal of Endocrinology, 2017, 232, 273-283.	2.6	11
51	Accurate Estimation of Gene Evolutionary Rates Using XRATE, with an Application to Transmembrane Proteins. Molecular Biology and Evolution, 2009, 26, 1715-1721.	8.9	9
52	CGAT: a model for immersive personalized training in computational genomics. Briefings in Functional Genomics, 2015, 15, 32-7.	2.7	4