

Emily C Hodges

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

6,551
citations

236925

25
h-index

330143

37
g-index

43
all docs

43
docs citations

43
times ranked

11343
citing authors

#	ARTICLE	IF	CITATIONS
1	Sorting of Small RNAs into Arabidopsis Argonaute Complexes Is Directed by the 5' Terminal Nucleotide. <i>Cell</i> , 2008, 133, 116-127.	28.9	1,196
2	Pseudogene-derived small interfering RNAs regulate gene expression in mouse oocytes. <i>Nature</i> , 2008, 453, 534-538.	27.8	960
3	Genome-wide in situ exon capture for selective resequencing. <i>Nature Genetics</i> , 2007, 39, 1522-1527.	21.4	635
4	Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007, 450, 219-232.	27.8	573
5	Sperm Methylation Profiles Reveal Features of Epigenetic Inheritance and Evolution in Primates. <i>Cell</i> , 2011, 146, 1029-1041.	28.9	368
6	Site identification in high-throughput RNA-protein interaction data. <i>Bioinformatics</i> , 2012, 28, 3013-3020.	4.1	272
7	Directional DNA Methylation Changes and Complex Intermediate States Accompany Lineage Specificity in the Adult Hematopoietic Compartment. <i>Molecular Cell</i> , 2011, 44, 17-28.	9.7	261
8	Targeted Investigation of the Neandertal Genome by Array-Based Sequence Capture. <i>Science</i> , 2010, 328, 723-725.	12.6	255
9	A single Hox locus in <i>Drosophila</i> produces functional microRNAs from opposite DNA strands. <i>Genes and Development</i> , 2008, 22, 8-13.	5.9	205
10	High definition profiling of mammalian DNA methylation by array capture and single molecule bisulfite sequencing. <i>Genome Research</i> , 2009, 19, 1593-1605.	5.5	198
11	Systematic discovery and characterization of fly microRNAs using 12 <i>Drosophila</i> genomes. <i>Genome Research</i> , 2007, 17, 1865-1879.	5.5	182
12	Exome sequencing and disease-network analysis of a single family implicate a mutation in <i>KIF1A</i> in hereditary spastic paraparesis. <i>Genome Research</i> , 2011, 21, 658-664.	5.5	172
13	Hybrid selection of discrete genomic intervals on custom-designed microarrays for massively parallel sequencing. <i>Nature Protocols</i> , 2009, 4, 960-974.	12.0	171
14	Updates to the RMAP short-read mapping software. <i>Bioinformatics</i> , 2009, 25, 2841-2842.	4.1	152
15	Two waves of de novo methylation during mouse germ cell development. <i>Genes and Development</i> , 2014, 28, 1544-1549.	5.9	123
16	Genomic landscape of human allele-specific DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7332-7337.	7.1	114
17	Evolutionary flux of canonical microRNAs and mirtrons in <i>Drosophila</i> . <i>Nature Genetics</i> , 2010, 42, 6-9.	21.4	105
18	An Epigenetic Memory of Pregnancy in the Mouse Mammary Gland. <i>Cell Reports</i> , 2015, 11, 1102-1109.	6.4	88

#	ARTICLE	IF	CITATIONS
19	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014, 24, R1035-R1037.	3.9	73
20	De novo DNA demethylation and noncoding transcription define active intergenic regulatory elements. <i>Genome Research</i> , 2013, 23, 1601-1614.	5.5	58
21	ATAC-Me Captures Prolonged DNA Methylation of Dynamic Chromatin Accessibility Loci during Cell Fate Transitions. <i>Molecular Cell</i> , 2020, 77, 1350-1364.e6.	9.7	47
22	Conservation of small RNA pathways in platypus. <i>Genome Research</i> , 2008, 18, 995-1004.	5.5	39
23	The evolutionary and phylogeographic history of woolly mammoths: a comprehensive mitogenomic analysis. <i>Scientific Reports</i> , 2017, 7, 44585.	3.3	39
24	Neurog3-Independent Methylation Is the Earliest Detectable Mark Distinguishing Pancreatic Progenitor Identity. <i>Developmental Cell</i> , 2019, 48, 49-63.e7.	7.0	36
25	Neanderthal introgression reintroduced functional ancestral alleles lost in Eurasian populations. <i>Nature Ecology and Evolution</i> , 2020, 4, 1332-1341.	7.8	33
26	A novel approach for evaluating the efficiency of siRNAs on protein levels in cultured cells. <i>Nucleic Acids Research</i> , 2004, 32, 17e-17.	14.5	30
27	Evolutionary expansion of DNA hypomethylation in the mammalian germline genome. <i>Genome Research</i> , 2018, 28, 145-158.	5.5	30
28	Accelerated Discovery of Novel Protein Function in Cultured Human Cells. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1319-1327.	3.8	24
29	Deacetylase activity of histone deacetylase 3 is required for productive <i>V</i> DJ recombination and B-cell development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8608-8613.	7.1	22
30	Targeted Enrichment of Specific Regions in the Human Genome by Array Hybridization. <i>Current Protocols in Human Genetics</i> , 2010, 66, Unit 18.3.	3.5	16
31	SLC5A3-Dependent Myo-inositol Auxotrophy in Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2022, 12, 450-467.	9.4	14
32	Transcriptional Silencing of <i>ALDH2</i> Confers a Dependency on Fanconi Anemia Proteins in Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2021, 11, 2300-2315.	9.4	13
33	Thorough validation of siRNA-induced cell death phenotypes defines new anti-apoptotic protein. <i>Nucleic Acids Research</i> , 2006, 34, e13-e13.	14.5	11
34	Dual detection of chromatin accessibility and DNA methylation using ATAC-Me. <i>Nature Protocols</i> , 2021, 16, 5377-5397.	12.0	10
35	Deep Sequencing of Target Linkage Assay-Identified Regions in Familial Breast Cancer: Methods, Analysis Pipeline and Troubleshooting. <i>PLoS ONE</i> , 2010, 5, e9976.	2.5	6
36	NovelFam3000 “Uncharacterized human protein domains conserved across model organisms. <i>BMC Genomics</i> , 2006, 7, 48.	2.8	5

#	ARTICLE	IF	CITATIONS
37	Sequencing in High Definition Drives a Changing Worldview of the Epigenome. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a033076.	6.2	1