

Peggy J Farnham

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

17,205
citations

87723

38
h-index

168136

53
g-index

56
all docs

56
docs citations

56
times ranked

33989
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	13.7	5,653
2	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012, 22, 1813-1831.	2.4	1,708
3	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010, 28, 1045-1048.	9.4	1,705
4	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012, 489, 91-100.	13.7	1,384
5	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
6	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , 2010, 28, 1097-1105.	9.4	647
7	Insights from genomic profiling of transcription factors. <i>Nature Reviews Genetics</i> , 2009, 10, 605-616.	7.7	473
8	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712.	7.1	371
9	Discovering Hematopoietic Mechanisms through Genome-wide Analysis of GATA Factor Chromatin Occupancy. <i>Molecular Cell</i> , 2009, 36, 667-681.	4.5	314
10	Making sense of GWAS: using epigenomics and genome engineering to understand the functional relevance of SNPs in non-coding regions of the human genome. <i>Epigenetics and Chromatin</i> , 2015, 8, 57.	1.8	277
11	Transcriptome and epigenome landscape of human cortical development modeled in organoids. <i>Science</i> , 2018, 362, .	6.0	220
12	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. <i>Nature Genetics</i> , 2013, 45, 836-841.	9.4	207
13	A comprehensive ChIP&chip analysis of E2F1, E2F4, and E2F6 in normal and tumor cells reveals interchangeable roles of E2F family members. <i>Genome Research</i> , 2007, 17, 1550-1561.	2.4	190
14	Inferring regulatory element landscapes and transcription factor networks from cancer methylomes. <i>Genome Biology</i> , 2015, 16, 105.	13.9	178
15	Cross-talk between Site-specific Transcription Factors and DNA Methylation States. <i>Journal of Biological Chemistry</i> , 2013, 288, 34287-34294.	1.6	172
16	Comprehensive Functional Annotation of 77 Prostate Cancer Risk Loci. <i>PLoS Genetics</i> , 2014, 10, e1004102.	1.5	167
17	Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. <i>Genome Research</i> , 2013, 23, 1522-1540.	2.4	162
18	dCas9-based epigenome editing suggests acquisition of histone methylation is not sufficient for target gene repression. <i>Nucleic Acids Research</i> , 2017, 45, 9901-9916.	6.5	160

#	ARTICLE	IF	CITATIONS
19	Global loss of DNA methylation uncovers intronic enhancers in genes showing expression changes. <i>Genome Biology</i> , 2014, 15, 469.	3.8	139
20	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
21	Using ChIP-Seq Technology to Generate High-Resolution Profiles of Histone Modifications. <i>Methods in Molecular Biology</i> , 2011, 791, 265-286.	0.4	119
22	Cell type-specific binding patterns reveal that TCF7L2 can be tethered to the genome by association with GATA3. <i>Genome Biology</i> , 2012, 13, R52.	13.9	109
23	Ezh2-dCas9 and KRAB-dCas9 enable engineering of epigenetic memory in a context-dependent manner. <i>Epigenetics and Chromatin</i> , 2019, 12, 26.	1.8	101
24	Functional annotation of colon cancer risk SNPs. <i>Nature Communications</i> , 2014, 5, 5114.	5.8	98
25	Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015, 6, 6363.	5.8	91
26	The role of DNA methylation in directing the functional organization of the cancer epigenome. <i>Genome Research</i> , 2015, 25, 467-477.	2.4	90
27	A high-resolution 3D epigenomic map reveals insights into the creation of the prostate cancer transcriptome. <i>Nature Communications</i> , 2019, 10, 4154.	5.8	87
28	Demystifying the secret mission of enhancers: linking distal regulatory elements to target genes. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2015, 50, 550-573.	2.3	80
29	The role of E2F in the mammalian cell cycle. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 1993, 1155, 125-131.	3.3	74
30	A Prostate Cancer Risk Element Functions as a Repressive Loop that Regulates HOXA13. <i>Cell Reports</i> , 2017, 21, 1411-1417.	2.9	68
31	ZBTB33 binds unmethylated regions of the genome associated with actively expressed genes. <i>Epigenetics and Chromatin</i> , 2013, 6, 13.	1.8	61
32	CRISPR-mediated deletion of prostate cancer risk-associated CTCF loop anchors identifies repressive chromatin loops. <i>Genome Biology</i> , 2018, 19, 160.	3.8	60
33	Using ChIP-seq Technology to Identify Targets of Zinc Finger Transcription Factors. <i>Methods in Molecular Biology</i> , 2010, 649, 437-455.	0.4	57
34	Analysis of an artificial zinc finger epigenetic modulator: widespread binding but limited regulation. <i>Nucleic Acids Research</i> , 2014, 42, 10856-10868.	6.5	56
35	Epigenetic and transcriptional determinants of the human breast. <i>Nature Communications</i> , 2015, 6, 6351.	5.8	56
36	ZFX acts as a transcriptional activator in multiple types of human tumors by binding downstream from transcription start sites at the majority of CpG island promoters. <i>Genome Research</i> , 2018, 28, 310-320.	2.4	56

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37	Identification of activated enhancers and linked transcription factors in breast, prostate, and kidney tumors by tracing enhancer networks using epigenetic traits. <i>Epigenetics and Chromatin</i> , 2016, 9, 50.	1.8	53
38	Genome-wide Analysis of Transcription Factor E2F1 Mutant Proteins Reveals That N- and C-terminal Protein Interaction Domains Do Not Participate in Targeting E2F1 to the Human Genome. <i>Journal of Biological Chemistry</i> , 2011, 286, 11985-11996.	1.6	45
39	Using 3D epigenomic maps of primary olfactory neuronal cells from living individuals to understand gene regulation. <i>Science Advances</i> , 2018, 4, eaav8550.	4.7	43
40	The Enigmatic HOX Genes: Can We Crack Their Code?. <i>Cancers</i> , 2019, 11, 323.	1.7	40
41	The prostate cancer risk variant rs55958994 regulates multiple gene expression through extreme long-range chromatin interaction to control tumor progression. <i>Science Advances</i> , 2019, 5, eaaw6710.	4.7	35
42	Effects on the transcriptome upon deletion of a distal element cannot be predicted by the size of the H3K27Ac peak in human cells. <i>Nucleic Acids Research</i> , 2016, 44, 4123-4133.	6.5	32
43	4C-seq revealed long-range interactions of a functional enhancer at the 8q24 prostate cancer risk locus. <i>Scientific Reports</i> , 2016, 6, 22462.	1.6	30
44	Regulatory network decoded from epigenomes of surface ectoderm-derived cell types. <i>Nature Communications</i> , 2014, 5, 5442.	5.8	25
45	TENET 2.0: Identification of key transcriptional regulators and enhancers in lung adenocarcinoma. <i>PLoS Genetics</i> , 2020, 16, e1009023.	1.5	20
46	Characterization of the ZFX family of transcription factors that bind downstream of the start site of CpG island promoters. <i>Nucleic Acids Research</i> , 2020, 48, 5986-6000.	6.5	20
47	Thematic Minireview Series on Results from the ENCODE Project: Integrative Global Analyses of Regulatory Regions in the Human Genome. <i>Journal of Biological Chemistry</i> , 2012, 287, 30885-30887.	1.6	12
48	Defining Regulatory Elements in the Human Genome Using Nucleosome Occupancy and Methylome Sequencing (NOME-Seq). <i>Methods in Molecular Biology</i> , 2018, 1766, 209-229.	0.4	12
49	Three-dimensional analysis reveals altered chromatin interaction by enhancer inhibitors harbors TCF7L2-regulated cancer gene signature. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 3056-3070.	1.2	9
50	Genome-wide analysis of HOXC4 and HOXC6 regulated genes and binding sites in prostate cancer cells. <i>PLoS ONE</i> , 2020, 15, e0228590.	1.1	8
51	Uncovering Transcription Factor Modules Using One- and Three-dimensional Analyses. <i>Journal of Biological Chemistry</i> , 2012, 287, 30914-30921.	1.6	7
52	FOXC1 Binds Enhancers and Promotes Cisplatin Resistance in Bladder Cancer. <i>Cancers</i> , 2022, 14, 1717.	1.7	5
53	The Human Epigenome Browser at Washington University. , 0, .		1
54	Using genomic technologies to investigate transcriptional regulation in normal and cancer cells. <i>FASEB Journal</i> , 2012, 26, 460.1.	0.2	0