Peggy J Farnham

List of Publications by Year
in descending order

54 papers	17,205 citations	100601 38 h-index	190340 53 g-index
56 all docs	56 docs citations	56 times ranked	37932 citing authors

#	Article	IF	Citations
1	FOXC1 Binds Enhancers and Promotes Cisplatin Resistance in Bladder Cancer. Cancers, 2022, 14, 1717.	1.7	5
2	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
3	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	13.7	1,252
4	TENET 2.0: Identification of key transcriptional regulators and enhancers in lung adenocarcinoma. PLoS Genetics, 2020, 16, e1009023.	1.5	20
5	Characterization of the ZFX family of transcription factors that bind downstream of the start site of CpG island promoters. Nucleic Acids Research, 2020, 48, 5986-6000.	6.5	20
6	Genome-wide analysis of HOXC4 and HOXC6 regulated genes and binding sites in prostate cancer cells. PLoS ONE, 2020, 15, e0228590.	1.1	8
7	The prostate cancer risk variant rs55958994 regulates multiple gene expression through extreme long-range chromatin interaction to control tumor progression. Science Advances, 2019, 5, eaaw6710.	4.7	35
8	A high-resolution 3D epigenomic map reveals insights into the creation of the prostate cancer transcriptome. Nature Communications, 2019, 10, 4154.	5.8	87
9	Ezh2-dCas9 and KRAB-dCas9 enable engineering of epigenetic memory in a context-dependent manner. Epigenetics and Chromatin, 2019, 12, 26.	1.8	101
10	The Enigmatic HOX Genes: Can We Crack Their Code?. Cancers, 2019, 11, 323.	1.7	40
11	Threeâ€dimensional analysis reveals altered chromatin interaction by enhancer inhibitors harbors TCF7L2â€regulated cancer gene signature. Journal of Cellular Biochemistry, 2019, 120, 3056-3070.	1.2	9
12	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. Genome Research, 2018, 28, 310-320.	2.4	56
13	Defining Regulatory Elements in the Human Genome Using Nucleosome Occupancy and Methylome Sequencing (NOMe-Seq). Methods in Molecular Biology, 2018, 1766, 209-229.	0.4	12
14	Using 3D epigenomic maps of primary olfactory neuronal cells from living individuals to understand gene regulation. Science Advances, 2018, 4, eaav8550.	4.7	43
15	Transcriptome and epigenome landscape of human cortical development modeled in organoids. Science, 2018, 362, .	6.0	220
16	CRISPR-mediated deletion of prostate cancer risk-associated CTCF loop anchors identifies repressive chromatin loops. Genome Biology, 2018, 19, 160.	3.8	60
17	A Prostate Cancer Risk Element Functions as a Repressive Loop that Regulates HOXA13. Cell Reports, 2017, 21, 1411-1417.	2.9	68
18	dCas9-based epigenome editing suggests acquisition of histone methylation is not sufficient for target gene repression. Nucleic Acids Research, 2017, 45, 9901-9916.	6.5	160

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19	Identification of activated enhancers and linked transcription factors in breast, prostate, and kidney tumors by tracing enhancer networks using epigenetic traits. Epigenetics and Chromatin, 2016, 9, 50.	1.8	53
20	4C-seq revealed long-range interactions of a functional enhancer at the 8q24 prostate cancer risk locus. Scientific Reports, 2016, 6, 22462.	1.6	30
21	Effects on the transcriptome upon deletion of a distal element cannot be predicted by the size of the H3K27Ac peak in human cells. Nucleic Acids Research, 2016, 44, 4123-4133.	6.5	32
22	Inferring regulatory element landscapes and transcription factor networks from cancer methylomes. Genome Biology, 2015, 16, 105.	13.9	178
23	Making sense of GWAS: using epigenomics and genome engineering to understand the functional relevance of SNPs in non-coding regions of the human genome. Epigenetics and Chromatin, 2015, 8, 57.	1.8	277
24	Intermediate DNA methylation is a conserved signature of genome regulation. Nature Communications, 2015, 6, 6363.	5.8	91
25	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
26	Epigenetic and transcriptional determinants of the human breast. Nature Communications, 2015, 6, 6351.	5.8	56
27	The role of DNA methylation in directing the functional organization of the cancer epigenome. Genome Research, 2015, 25, 467-477.	2.4	90
28	Demystifying the secret mission of enhancers: linking distal regulatory elements to target genes. Critical Reviews in Biochemistry and Molecular Biology, 2015, 50, 550-573.	2.3	80
29	The PsychENCODE project. Nature Neuroscience, 2015, 18, 1707-1712.	7.1	371
30	Global loss of DNA methylation uncovers intronic enhancers in genes showing expression changes. Genome Biology, 2014, 15, 469.	3.8	139
31	Comprehensive Functional Annotation of 77 Prostate Cancer Risk Loci. PLoS Genetics, 2014, 10, e1004102.	1.5	167
32	Regulatory network decoded from epigenomes of surface ectoderm-derived cell types. Nature Communications, 2014, 5, 5442.	5.8	25
33	Analysis of an artificial zinc finger epigenetic modulator: widespread binding but limited regulation. Nucleic Acids Research, 2014, 42, 10856-10868.	6.5	56
34	Functional annotation of colon cancer risk SNPs. Nature Communications, 2014, 5, 5114.	5.8	98
35	Cross-talk between Site-specific Transcription Factors and DNA Methylation States. Journal of Biological Chemistry, 2013, 288, 34287-34294.	1.6	172
36	ZBTB33 binds unmethylated regions of the genome associated with actively expressed genes. Epigenetics and Chromatin, 2013, 6, 13.	1.8	61

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37	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. Nature Genetics, 2013, 45, 836-841.	9.4	207
38	Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. Genome Research, 2013, 23, 1522-1540.	2.4	162
39	Uncovering Transcription Factor Modules Using One- and Three-dimensional Analyses. Journal of Biological Chemistry, 2012, 287, 30914-30921.	1.6	7
40	Cell type-specific binding patterns reveal that TCF7L2 can be tethered to the genome by association with GATA3. Genome Biology, 2012, 13, R52.	13.9	109
41	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome Research, 2012, 22, 1813-1831.	2.4	1,708
42	Thematic Minireview Series on Results from the ENCODE Project: Integrative Global Analyses of Regulatory Regions in the Human Genome. Journal of Biological Chemistry, 2012, 287, 30885-30887.	1.6	12
43	Architecture of the human regulatory network derived from ENCODE data. Nature, 2012, 489, 91-100.	13.7	1,384
44	Using genomic technologies to investigate transcriptional regulation in normal and cancer cells. FASEB Journal, 2012, 26, 460.1.	0.2	0
45	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. Journal of Biological Chemistry, 2011, 286, 11985-11996.	1.6	45
46	Using ChIP-Seq Technology to Generate High-Resolution Profiles of Histone Modifications. Methods in Molecular Biology, 2011, 791, 265-286.	0.4	119
47	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. Nature Biotechnology, 2010, 28, 1097-1105.	9.4	647
48	The NIH Roadmap Epigenomics Mapping Consortium. Nature Biotechnology, 2010, 28, 1045-1048.	9.4	1,705
49	Using ChIP-seq Technology to Identify Targets of Zinc Finger Transcription Factors. Methods in Molecular Biology, 2010, 649, 437-455.	0.4	57
50	Insights from genomic profiling of transcription factors. Nature Reviews Genetics, 2009, 10, 605-616.	7.7	473
51	Discovering Hematopoietic Mechanisms through Genome-wide Analysis of GATA Factor Chromatin Occupancy. Molecular Cell, 2009, 36, 667-681.	4.5	314
52	A comprehensive ChIPâ€"chip analysis of E2F1, E2F4, and E2F6 in normal and tumor cells reveals interchangeable roles of E2F family members. Genome Research, 2007, 17, 1550-1561.	2.4	190
53	The role of E2F in the mammalian cell cycle. Biochimica Et Biophysica Acta: Reviews on Cancer, 1993, 1155, 125-131.	3.3	74
54	The Human Epigenome Browser at Washington University. , 0, .		1