

Peggy J Farnham

List of Publications by Year in Descending Order

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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.

54
papers

11,919
citations

36
h-index

56
g-index

56
ext. papers

15,318
ext. citations

15.8
avg, IF

5.8
L-index

#	Paper	IF	Citations
54	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	20.1	6
53	Genome-wide analysis of HOXC4 and HOXC6 regulated genes and binding sites in prostate cancer cells. <i>PLoS ONE</i> , 2020 , 15, e0228590	3.7	4
52	Perspectives on ENCODE. <i>Nature</i> , 2020 , 583, 693-698	50.4	61
51	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020 , 583, 699-710	50.4	360
50	TENET 2.0: Identification of key transcriptional regulators and enhancers in lung adenocarcinoma. <i>PLoS Genetics</i> , 2020 , 16, e1009023	6	6
49	A high-resolution 3D epigenomic map reveals insights into the creation of the prostate cancer transcriptome. <i>Nature Communications</i> , 2019 , 10, 4154	17.4	36
48	Ezh2-dCas9 and KRAB-dCas9 enable engineering of epigenetic memory in a context-dependent manner. <i>Epigenetics and Chromatin</i> , 2019 , 12, 26	5.8	55
47	The Enigmatic HOX Genes: Can We Crack Their Code?. <i>Cancers</i> , 2019 , 11,	6.6	23
46	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	14.3	19
45	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	4.7	3
44	ZFX acts as a transcriptional activator in multiple types of human tumors by binding downstream of transcription start sites at the majority of CpG island promoters. <i>Genome Research</i> , 2018 ,	9.7	29
43	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	1.4	8
42	Using 3D epigenomic maps of primary olfactory neuronal cells from living individuals to understand gene regulation. <i>Science Advances</i> , 2018 , 4, eaav8550	14.3	24
41	Transcriptome and epigenome landscape of human cortical development modeled in organoids. <i>Science</i> , 2018 , 362,	33.3	142
40	CRISPR-mediated deletion of prostate cancer risk-associated CTCF loop anchors identifies repressive chromatin loops. <i>Genome Biology</i> , 2018 , 19, 160	18.3	36
39	A Prostate Cancer Risk Element Functions as a Repressive Loop that Regulates HOXA13. <i>Cell Reports</i> , 2017 , 21, 1411-1417	10.6	39
38	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	20.1	100

37	4C-seq revealed long-range interactions of a functional enhancer at the 8q24 prostate cancer risk locus. <i>Scientific Reports</i> , 2016 , 6, 22462	4.9	25
36	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, 4123-33	20.1	29
35	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	5.8	40
34	Epigenetic and transcriptional determinants of the human breast. <i>Nature Communications</i> , 2015 , 6, 6351	17.4	44
33	The role of DNA methylation in directing the functional organization of the cancer epigenome. <i>Genome Research</i> , 2015 , 25, 467-77	9.7	62
32	Demystifying the secret mission of enhancers: linking distal regulatory elements to target genes. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2015 , 50, 550-73	8.7	62
31	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015 , 18, 1707-12	25.5	226
30	Inferring regulatory element landscapes and transcription factor networks from cancer methylomes. <i>Genome Biology</i> , 2015 , 16, 105	18.3	123
29	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	5.8	187
28	Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015 , 6, 6363	17.4	67
27	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015 , 518, 317-30	50.4	3849
26	Functional annotation of colon cancer risk SNPs. <i>Nature Communications</i> , 2014 , 5, 5114	17.4	85
25	Global loss of DNA methylation uncovers intronic enhancers in genes showing expression changes. <i>Genome Biology</i> , 2014 , 15, 469	18.3	108
24	Comprehensive functional annotation of 77 prostate cancer risk loci. <i>PLoS Genetics</i> , 2014 , 10, e1004102	6	132
23	Regulatory network decoded from epigenomes of surface ectoderm-derived cell types. <i>Nature Communications</i> , 2014 , 5, 5442	17.4	22
22	Analysis of an artificial zinc finger epigenetic modulator: widespread binding but limited regulation. <i>Nucleic Acids Research</i> , 2014 , 42, 10856-68	20.1	50
21	Cross-talk between site-specific transcription factors and DNA methylation states. <i>Journal of Biological Chemistry</i> , 2013 , 288, 34287-94	5.4	136
20	ZBTB33 binds unmethylated regions of the genome associated with actively expressed genes. <i>Epigenetics and Chromatin</i> , 2013 , 6, 13	5.8	50

19	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. <i>Nature Genetics</i> , 2013 , 45, 836-41	36.3	154
18	Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. <i>Genome Research</i> , 2013 , 23, 1522-40	9.7	119
17	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	18.3	85
16	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012 , 22, 1813-31	9.7	1211
15	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, 30885-7	5.4	12
14	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012 , 489, 91-100	50.4	1104
13	Uncovering transcription factor modules using one- and three-dimensional analyses. <i>Journal of Biological Chemistry</i> , 2012 , 287, 30914-21	5.4	5
12	Using genomic technologies to investigate transcriptional regulation in normal and cancer cells. <i>FASEB Journal</i> , 2012 , 26, 460.1	0.9	
11	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, 11985-96	5.4	38
10	Using ChIP-seq technology to generate high-resolution profiles of histone modifications. <i>Methods in Molecular Biology</i> , 2011 , 791, 265-86	1.4	90
9	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , 2010 , 28, 1097-105	44.5	570
8	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010 , 28, 1045-8	44.5	1284
7	Using ChIP-seq technology to identify targets of zinc finger transcription factors. <i>Methods in Molecular Biology</i> , 2010 , 649, 437-55	1.4	45
6	Insights from genomic profiling of transcription factors. <i>Nature Reviews Genetics</i> , 2009 , 10, 605-16	30.1	427
5	Discovering hematopoietic mechanisms through genome-wide analysis of GATA factor chromatin occupancy. <i>Molecular Cell</i> , 2009 , 36, 667-81	17.6	276
4	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, 1550-61	9.7	164
3	The role of E2F in the mammalian cell cycle. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 1993 , 1155, 125-31	11.2	54
2	The Human Epigenome Browser at Washington University		1

- 1 Frequent lack of repressive capacity of promoter DNA methylation identified through genome-wide epigenomic manipulation