

Peggy J Farnham

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

17,205
citations

87888

38
h-index

168389

53
g-index

56
all docs

56
docs citations

56
times ranked

33989
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | FOXC1 Binds Enhancers and Promotes Cisplatin Resistance in Bladder Cancer. <i>Cancers</i> , 2022, 14, 1717. | 3.7 | 5 |
| 2 | Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698. | 27.8 | 123 |
| 3 | Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710. | 27.8 | 1,252 |
| 4 | TENET 2.0: Identification of key transcriptional regulators and enhancers in lung adenocarcinoma. <i>PLoS Genetics</i> , 2020, 16, e1009023. | 3.5 | 20 |
| 5 | 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. | 14.5 | 20 |
| 6 | Genome-wide analysis of HOXC4 and HOXC6 regulated genes and binding sites in prostate cancer cells. <i>PLoS ONE</i> , 2020, 15, e0228590. | 2.5 | 8 |
| 7 | 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. | 10.3 | 35 |
| 8 | A high-resolution 3D epigenomic map reveals insights into the creation of the prostate cancer transcriptome. <i>Nature Communications</i> , 2019, 10, 4154. | 12.8 | 87 |
| 9 | Ezh2-dCas9 and KRAB-dCas9 enable engineering of epigenetic memory in a context-dependent manner. <i>Epigenetics and Chromatin</i> , 2019, 12, 26. | 3.9 | 101 |
| 10 | The Enigmatic HOX Genes: Can We Crack Their Code?. <i>Cancers</i> , 2019, 11, 323. | 3.7 | 40 |
| 11 | 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. | 2.6 | 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. <i>Genome Research</i> , 2018, 28, 310-320. | 5.5 | 56 |
| 13 | 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. | 0.9 | 12 |
| 14 | Using 3D epigenomic maps of primary olfactory neuronal cells from living individuals to understand gene regulation. <i>Science Advances</i> , 2018, 4, eaav8550. | 10.3 | 43 |
| 15 | Transcriptome and epigenome landscape of human cortical development modeled in organoids. <i>Science</i> , 2018, 362, . | 12.6 | 220 |
| 16 | CRISPR-mediated deletion of prostate cancer risk-associated CTCF loop anchors identifies repressive chromatin loops. <i>Genome Biology</i> , 2018, 19, 160. | 8.8 | 60 |
| 17 | A Prostate Cancer Risk Element Functions as a Repressive Loop that Regulates HOXA13. <i>Cell Reports</i> , 2017, 21, 1411-1417. | 6.4 | 68 |
| 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. | 14.5 | 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. <i>Epigenetics and Chromatin</i> , 2016, 9, 50. | 3.9 | 53 |
| 20 | 4C-seq revealed long-range interactions of a functional enhancer at the 8q24 prostate cancer risk locus. <i>Scientific Reports</i> , 2016, 6, 22462. | 3.3 | 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. <i>Nucleic Acids Research</i> , 2016, 44, 4123-4133. | 14.5 | 32 |
| 22 | Inferring regulatory element landscapes and transcription factor networks from cancer methylomes. <i>Genome Biology</i> , 2015, 16, 105. | 9.6 | 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. <i>Epigenetics and Chromatin</i> , 2015, 8, 57. | 3.9 | 277 |
| 24 | Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015, 6, 6363. | 12.8 | 91 |
| 25 | Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330. | 27.8 | 5,653 |
| 26 | Epigenetic and transcriptional determinants of the human breast. <i>Nature Communications</i> , 2015, 6, 6351. | 12.8 | 56 |
| 27 | The role of DNA methylation in directing the functional organization of the cancer epigenome. <i>Genome Research</i> , 2015, 25, 467-477. | 5.5 | 90 |
| 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. | 5.2 | 80 |
| 29 | The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712. | 14.8 | 371 |
| 30 | Global loss of DNA methylation uncovers intronic enhancers in genes showing expression changes. <i>Genome Biology</i> , 2014, 15, 469. | 8.8 | 139 |
| 31 | Comprehensive Functional Annotation of 77 Prostate Cancer Risk Loci. <i>PLoS Genetics</i> , 2014, 10, e1004102. | 3.5 | 167 |
| 32 | Regulatory network decoded from epigenomes of surface ectoderm-derived cell types. <i>Nature Communications</i> , 2014, 5, 5442. | 12.8 | 25 |
| 33 | Analysis of an artificial zinc finger epigenetic modulator: widespread binding but limited regulation. <i>Nucleic Acids Research</i> , 2014, 42, 10856-10868. | 14.5 | 56 |
| 34 | Functional annotation of colon cancer risk SNPs. <i>Nature Communications</i> , 2014, 5, 5114. | 12.8 | 98 |
| 35 | Cross-talk between Site-specific Transcription Factors and DNA Methylation States. <i>Journal of Biological Chemistry</i> , 2013, 288, 34287-34294. | 3.4 | 172 |
| 36 | ZBTB33 binds unmethylated regions of the genome associated with actively expressed genes. <i>Epigenetics and Chromatin</i> , 2013, 6, 13. | 3.9 | 61 |

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|----|---|------|-----------|
| 37 | DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. <i>Nature Genetics</i> , 2013, 45, 836-841. | 21.4 | 207 |
| 38 | 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. | 5.5 | 162 |
| 39 | Uncovering Transcription Factor Modules Using One- and Three-dimensional Analyses. <i>Journal of Biological Chemistry</i> , 2012, 287, 30914-30921. | 3.4 | 7 |
| 40 | 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. | 9.6 | 109 |
| 41 | ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012, 22, 1813-1831. | 5.5 | 1,708 |
| 42 | 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. | 3.4 | 12 |
| 43 | Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012, 489, 91-100. | 27.8 | 1,384 |
| 44 | Using genomic technologies to investigate transcriptional regulation in normal and cancer cells. <i>FASEB Journal</i> , 2012, 26, 460.1. | 0.5 | 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. <i>Journal of Biological Chemistry</i> , 2011, 286, 11985-11996. | 3.4 | 45 |
| 46 | Using ChIP-Seq Technology to Generate High-Resolution Profiles of Histone Modifications. <i>Methods in Molecular Biology</i> , 2011, 791, 265-286. | 0.9 | 119 |
| 47 | Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , 2010, 28, 1097-1105. | 17.5 | 647 |
| 48 | The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010, 28, 1045-1048. | 17.5 | 1,705 |
| 49 | Using ChIP-seq Technology to Identify Targets of Zinc Finger Transcription Factors. <i>Methods in Molecular Biology</i> , 2010, 649, 437-455. | 0.9 | 57 |
| 50 | Insights from genomic profiling of transcription factors. <i>Nature Reviews Genetics</i> , 2009, 10, 605-616. | 16.3 | 473 |
| 51 | Discovering Hematopoietic Mechanisms through Genome-wide Analysis of GATA Factor Chromatin Occupancy. <i>Molecular Cell</i> , 2009, 36, 667-681. | 9.7 | 314 |
| 52 | 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. | 5.5 | 190 |
| 53 | The role of E2F in the mammalian cell cycle. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 1993, 1155, 125-131. | 7.4 | 74 |
| 54 | The Human Epigenome Browser at Washington University. , 0, . | | 1 |