# Matthew L Freedman

List of Publications by Year
in descending order

| 68 papers | 7,113 citations | 37 h-index | 66 g-index |
|---|---|---|---|
| 80 all docs | 80 docs citations | 80 times ranked | 11482 citing authors |

94433

102487

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 1 | Multiple regions within 8q24 independently affect risk for prostate cancer. Nature Genetics, 2007, 39, 638-644. | 21.4 | 621 |
| 2 | The 8q24 cancer risk variant rs6983267 shows long-range interaction with MYC in colorectal cancer. Nature Genetics, 2009, 41, 882-884. | 21.4 | 616 |
| 3 | Admixture mapping identifies 8q24 as a prostate cancer risk locus in African-American men. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14068-14073. | 7.1 | 575 |
| 4 | Principles for the post-GWAS functional characterization of cancer risk loci. Nature Genetics, 2011, 43, 513-518. | 21.4 | 392 |
| 5 | The androgen receptor cistrome is extensively reprogrammed in human prostate tumorigenesis. Nature Genetics, 2015, 47, 1346-1351. | 21.4 | 363 |
| 6 | 8q24 prostate, breast, and colon cancer risk loci show tissue-specific long-range interaction with *MYC*. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9742-9746. | 7.1 | 353 |
| 7 | Integrative eQTL-Based Analyses Reveal the Biology of Breast Cancer Risk Loci. Cell, 2013, 152, 633-641. | 28.9 | 300 |
| 8 | A Somatically Acquired Enhancer of the Androgen Receptor Is a Noncoding Driver in Advanced Prostate Cancer. Cell, 2018, 174, 422-432.e13. | 28.9 | 234 |
| 9 | Transferability of tag SNPs in genetic association studies in multiple populations. Nature Genetics, 2006, 38, 1298-1303. | 21.4 | 224 |
| 10 | Functional Enhancers at the Gene-Poor 8q24 Cancer-Linked Locus. PLoS Genetics, 2009, 5, e1000597. | 3.5 | 214 |
| 11 | Modulation of long noncoding RNAs by risk SNPs underlying genetic predispositions to prostate cancer. Nature Genetics, 2016, 48, 1142-1150. | 21.4 | 196 |
| 12 | Prostate cancer reactivates developmental epigenomic programs during metastatic progression. Nature Genetics, 2020, 52, 790-799. | 21.4 | 174 |
| 13 | Detection of renal cell carcinoma using plasma and urine cell-free DNA methylomes. Nature Medicine, 2020, 26, 1041-1043. | 30.7 | 161 |
| 14 | Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067. | 9.4 | 157 |
| 15 | A Common 8q24 Variant in Prostate and Breast Cancer from a Large Nested Case-Control Study. Cancer Research, 2007, 67, 2951-2956. | 0.9 | 136 |
| 16 | Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. Nature Communications, 2018, 9, 4079. | 12.8 | 121 |
| 17 | EZH2 inhibition activates a dsRNA–STING–interferon stress axis that potentiates response to PD-1 checkpoint blockade in prostate cancer. Nature Cancer, 2021, 2, 444-456. | 13.2 | 118 |
| 18 | A Large Multiethnic Genome-Wide Association Study of Prostate Cancer Identifies Novel Risk Variants and Substantial Ethnic Differences. Cancer Discovery, 2015, 5, 878-891. | 9.4 | 111 |

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|---|---------|-----|-----------|
| 19 | Evaluation of the 8q24 Prostate Cancer Risk Locus and *MYC* Expression. Cancer Research, 2009, 69, 5568-5574. | 0.9 | 110 |
| 20 | Genome-wide association study identifies multiple risk loci for renal cell carcinoma. Nature Communications, 2017, 8, 15724. | 12.8 | 106 |
| 21 | Genetic and functional analyses implicate the *NUDT11* , *HNF1B* , and *SLC22A3* genes in prostate cancer pathogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11252-11257. | 7.1 | 102 |
| 22 | Enhancer Architecture and Essential Core Regulatory Circuitry of Chronic Lymphocytic Leukemia. Cancer Cell, 2018, 34, 982-995.e7. | 16.8 | 101 |
| 23 | Chromosome 8q24-Associated Cancers and MYC. Genes and Cancer, 2010, 1, 555-559. | 1.9 | 100 |
| 24 | CAUSEL: an epigenome- and genome-editing pipeline for establishing function of noncoding GWAS variants. Nature Medicine, 2015, 21, 1357-1363. | 30.7 | 90 |
| 25 | A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. Nature Genetics, 2019, 51, 815-823. | 21.4 | 89 |
| 26 | Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256. | 12.8 | 88 |
| 27 | Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. Human Molecular Genetics, 2014, 23, 5294-5302. | 2.9 | 71 |
| 28 | Reprogramming of the FOXA1 cistrome in treatment-emergent neuroendocrine prostate cancer. Nature Communications, 2021, 12, 1979. | 12.8 | 70 |
| 29 | Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234. | 12.8 | 63 |
| 30 | A novel genomic alteration of LSAMP associates with aggressive prostate cancer in African American men. EBioMedicine, 2015, 2, 1957-1964. | 6.1 | 61 |
| 31 | Subtype heterogeneity and epigenetic convergence in neuroendocrine prostate cancer. Nature Communications, 2021, 12, 5775. | 12.8 | 59 |
| 32 | MYC drives aggressive prostate cancer by disrupting transcriptional pause release at androgen receptor targets. Nature Communications, 2022, 13, 2559. | 12.8 | 56 |
| 33 | Non-coding somatic mutations converge on the PAX8 pathway in ovarian cancer. Nature Communications, 2020, 11, 2020. | 12.8 | 52 |
| 34 | Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. Human Molecular Genetics, 2015, 24, 5603-5618. | 2.9 | 50 |
| 35 | Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979. | 12.8 | 50 |
| 36 | Association of Prostate Cancer Risk Loci with Disease Aggressiveness and Prostate Cancer–Specific Mortality. Cancer Prevention Research, 2011, 4, 719-728. | 1.5 | 48 |

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|---|---------|-----|-----------|
| 37 | Evaluation of 8q24 and 17q Risk Loci and Prostate Cancer Mortality. Clinical Cancer Research, 2009, 15, 3223-3230. | 7.0 | 46 |
| 38 | Androgen receptor and MYC equilibration centralizes on developmental super-enhancer. Nature Communications, 2021, 12, 7308. | 12.8 | 46 |
| 39 | Identification of Novel Susceptibility Loci and Genes for Prostate Cancer Risk: A Transcriptome-Wide Association Study in Over 140,000 European Descendants. Cancer Research, 2019, 79, 3192-3204. | 0.9 | 43 |
| 40 | Epigenetic remodeling regulates transcriptional changes between ovarian cancer and benign precursors. JCI Insight, 2016, 1, . | 5.0 | 42 |
| 41 | Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607. | 2.9 | 40 |
| 42 | Plasma cell-free DNA variant analysis compared with methylated DNA analysis in renal cell carcinoma. Genetics in Medicine, 2020, 22, 1366-1373. | 2.4 | 40 |
| 43 | HOXB13 suppresses de novo lipogenesis through HDAC3-mediated epigenetic reprogramming in prostate cancer. Nature Genetics, 2022, 54, 670-683. | 21.4 | 39 |
| 44 | ASCL1 activates neuronal stem cell-like lineage programming through remodeling of the chromatin landscape in prostate cancer. Nature Communications, 2022, 13, 2282. | 12.8 | 34 |
| 45 | A rare variant of African ancestry activates 8q24 lncRNA hub by modulating cancer associated enhancer. Nature Communications, 2020, 11, 3598. | 12.8 | 33 |
| 46 | Clinical Utility of Cell-free and Circulating Tumor DNA in Kidney and Bladder Cancer: A Critical Review of Current Literature. European Urology Oncology, 2021, 4, 893-903. | 5.4 | 31 |
| 47 | H3K27ac HiChIP in prostate cell lines identifies risk genes for prostate cancer susceptibility. American Journal of Human Genetics, 2021, 108, 2284-2300. | 6.2 | 31 |
| 48 | Predicting master transcription factors from pan-cancer expression data. Science Advances, 2021, 7, eabf6123. | 10.3 | 30 |
| 49 | Detecting Neuroendocrine Prostate Cancer Through Tissue-Informed Cell-Free DNA Methylation Analysis. Clinical Cancer Research, 2022, 28, 928-938. | 7.0 | 29 |
| 50 | A multi-level investigation of the genetic relationship between endometriosis and ovarian cancer histotypes. Cell Reports Medicine, 2022, 3, 100542. | 6.5 | 26 |
| 51 | Genetics of Prostate Cancer Risk. Mount Sinai Journal of Medicine, 2010, 77, 643-654. | 1.9 | 22 |
| 52 | Validation and genomic interrogation of the <scp><i>MET</i></scp> variant rs11762213 as a predictor of adverse outcomes in clear cell renal cell carcinoma. Cancer, 2016, 122, 402-410. | 4.1 | 18 |
| 53 | A systematic approach to understand the functional consequences of non-protein coding risk regions. Cell Cycle, 2010, 9, 256-259. | 2.6 | 17 |
| 54 | Trans-ethnic variation in germline variants of patients with renal cell carcinoma. Cell Reports, 2021, 34, 108926. | 6.4 | 16 |

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| 55 | Ovarian Cancer Risk Variants Are Enriched in Histotype-Specific Enhancers and Disrupt Transcription Factor Binding Sites. American Journal of Human Genetics, 2020, 107, 622-635. | 6.2 | 14 |
| 56 | Pharmacogenomic Markers of Targeted Therapy Toxicity in Patients with Metastatic Renal Cell Carcinoma. European Urology Focus, 2016, 2, 633-639. | 3.1 | 12 |
| 57 | Epigenetic and transcriptional analysis reveals a core transcriptional program conserved in clonal prostate cancer metastases. Molecular Oncology, 2021, 15, 1942-1955. | 4.6 | 10 |
| 58 | CREB5 reprograms FOXA1 nuclear interactions to promote resistance to androgen receptor-targeting therapies. ELife, 2022, 11, . | 6.0 | 10 |
| 59 | Response to supraphysiological testosterone is predicted by a distinct androgen receptor cistrome. JCI Insight, 2022, 7, . | 5.0 | 9 |
| 60 | Androgen receptor reprogramming demarcates prognostic, context-dependent gene sets in primary and metastatic prostate cancer. Clinical Epigenetics, 2022, 14, 60. | 4.1 | 8 |
| 61 | A polymorphism in the promoter of FRAS1 is a candidate SNP associated with metastatic prostate cancer. Prostate, 2021, 81, 683-693. | 2.3 | 5 |
| 62 | Evaluation of significant genome-wide association studies risk â€" SNPs in young breast cancer patients. PLoS ONE, 2019, 14, e0216997. | 2.5 | 4 |
| 63 | Allele-specific epigenetic activity in prostate cancer and normal prostate tissue implicates prostate cancer risk mechanisms. American Journal of Human Genetics, 2021, 108, 2071-2085. | 6.2 | 3 |
| 64 | Clinical Uncertainty of Prostate Cancer Genetic Risk Panels. Science Translational Medicine, 2013, 5, 182ed6. | 12.4 | 2 |
| 65 | Principles for the post-GWAS functional characterisation of risk loci. Nature Precedings, 2010, , . | 0.1 | 1 |
| 66 | Validation and genomic interrogation of the MET variant rs11762213 as a predictor of adverse outcomes in clear cell renal cell carcinoma.. Journal of Clinical Oncology, 2014, 32, 395-395. | 1.6 | 1 |
| 67 | Principles for the post-GWAS functional characterisation of risk loci. Nature Precedings, 2011, , . | 0.1 | 0 |
| 68 | Exonic variants undergoing allele-specific selection in cancers. BMC Medical Genomics, 2021, 14, 142. | 1.5 | 0 |