Matthew L Freedman

List of Publications by Year
in descending order

68	7,113	94433	102487
papers	citations	37 h-index	66 g-index

80	80	80	11482
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Detecting Neuroendocrine Prostate Cancer Through Tissue-Informed Cell-Free DNA Methylation Analysis. Clinical Cancer Research, 2022, 28, 928-938.	7.0	29
2	A multi-level investigation of the genetic relationship between endometriosis and ovarian cancer histotypes. Cell Reports Medicine, 2022, 3, 100542.	6.5	26
3	HOXB13 suppresses de novo lipogenesis through HDAC3-mediated epigenetic reprogramming in prostate cancer. Nature Genetics, 2022, 54, 670-683.	21.4	39
4	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
5	Androgen receptor reprogramming demarcates prognostic, context-dependent gene sets in primary and metastatic prostate cancer. Clinical Epigenetics, 2022, 14, 60.	4.1	8
6	CREB5 reprograms FOXA1 nuclear interactions to promote resistance to androgen receptor-targeting therapies. ELife, 2022, 11, .	6.0	10
7	MYC drives aggressive prostate cancer by disrupting transcriptional pause release at androgen receptor targets. Nature Communications, 2022, 13, 2559.	12.8	56
8	Response to supraphysiological testosterone is predicted by a distinct androgen receptor cistrome. JCI Insight, 2022, 7, .	5.0	9
9	Trans-ethnic variation in germline variants of patients with renal cell carcinoma. Cell Reports, 2021, 34, 108926.	6.4	16
10	EZH2 inhibition activates a dsRNAâ€“STINGâ€“interferon stress axis that potentiates response to PD-1 checkpoint blockade in prostate cancer. Nature Cancer, 2021, 2, 444-456.	13.2	118
11	Reprogramming of the FOXA1 cistrome in treatment-emergent neuroendocrine prostate cancer. Nature Communications, 2021, 12, 1979.	12.8	70
12	Epigenetic and transcriptional analysis reveals a core transcriptional program conserved in clonal prostate cancer metastases. Molecular Oncology, 2021, 15, 1942-1955.	4.6	10
13	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
14	Exonic variants undergoing allele-specific selection in cancers. BMC Medical Genomics, 2021, 14, 142.	1.5	0
15	A polymorphism in the promoter of FRAS1 is a candidate SNP associated with metastatic prostate cancer. Prostate, 2021, 81, 683-693.	2.3	5
16	Subtype heterogeneity and epigenetic convergence in neuroendocrine prostate cancer. Nature Communications, 2021, 12, 5775.	12.8	59
17	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
18	Predicting master transcription factors from pan-cancer expression data. Science Advances, 2021, 7, eabf6123.	10.3	30

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19	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
20	Androgen receptor and MYC equilibration centralizes on developmental super-enhancer. Nature Communications, 2021, 12, 7308.	12.8	46
21	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
22	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. Nature Genetics, 2020, 52, 790-799.	21.4	174
23	A rare variant of African ancestry activates 8q24 lncRNA hub by modulating cancer associated enhancer. Nature Communications, 2020, 11, 3598.	12.8	33
24	Detection of renal cell carcinoma using plasma and urine cell-free DNA methylomes. Nature Medicine, 2020, 26, 1041-1043.	30.7	161
25	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
26	Non-coding somatic mutations converge on the PAX8 pathway in ovarian cancer. Nature Communications, 2020, 11, 2020.	12.8	52
27	Evaluation of significant genome-wide association studies risk â€" SNPs in young breast cancer patients. PLoS ONE, 2019, 14, e0216997.	2.5	4
28	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
29	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
30	Enhancer Architecture and Essential Core Regulatory Circuitry of Chronic Lymphocytic Leukemia. Cancer Cell, 2018, 34, 982-995.e7.	16.8	101
31	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. Nature Communications, 2018, 9, 4079.	12.8	121
32	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
33	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	12.8	88
34	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. Nature Communications, 2017, 8, 15724.	12.8	106
35	Validation and genomic interrogation of the <scp>MET</scp> variant rs11762213 as a predictor of adverse outcomes in clear cell renal cell carcinoma. Cancer, 2016, 122, 402-410.	4.1	18
36	Pharmacogenomic Markers of Targeted Therapy Toxicity in Patients with Metastatic Renal Cell Carcinoma. European Urology Focus, 2016, 2, 633-639.	3.1	12

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37	Modulation of long noncoding RNAs by risk SNPs underlying genetic predispositions to prostate cancer. Nature Genetics, 2016, 48, 1142-1150.	21.4	196
38	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
39	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	12.8	50
40	Epigenetic remodeling regulates transcriptional changes between ovarian cancer and benign precursors. JCI Insight, 2016, 1, .	5.0	42
41	A novel genomic alteration of LSAMP associates with aggressive prostate cancer in African American men. EBioMedicine, 2015, 2, 1957-1964.	6.1	61
42	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	2.9	40
43	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
44	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
45	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	12.8	63
46	CAUSEL: an epigenome- and genome-editing pipeline for establishing function of noncoding GWAS variants. Nature Medicine, 2015, 21, 1357-1363.	30.7	90
47	The androgen receptor cistrome is extensively reprogrammed in human prostate tumorigenesis. Nature Genetics, 2015, 47, 1346-1351.	21.4	363
48	Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. Human Molecular Genetics, 2014, 23, 5294-5302.	2.9	71
49	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
50	Integrative eQTL-Based Analyses Reveal the Biology of Breast Cancer Risk Loci. Cell, 2013, 152, 633-641.	28.9	300
51	Clinical Uncertainty of Prostate Cancer Genetic Risk Panels. Science Translational Medicine, 2013, 5, 182ed6.	12.4	2
52	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
53	Association of Prostate Cancer Risk Loci with Disease Aggressiveness and Prostate Cancerâ€“Specific Mortality. Cancer Prevention Research, 2011, 4, 719-728.	1.5	48
54	Principles for the post-GWAS functional characterisation of risk loci. Nature Precedings, 2011, , .	0.1	0

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55	Principles for the post-GWAS functional characterization of cancer risk loci. Nature Genetics, 2011, 43, 513-518.	21.4	392
56	Genetics of Prostate Cancer Risk. Mount Sinai Journal of Medicine, 2010, 77, 643-654.	1.9	22
57	Principles for the post-GWAS functional characterisation of risk loci. Nature Precedings, 2010, , .	0.1	1
58	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
59	A systematic approach to understand the functional consequences of non-protein coding risk regions. Cell Cycle, 2010, 9, 256-259.	2.6	17
60	Chromosome 8q24-Associated Cancers and MYC. Genes and Cancer, 2010, 1, 555-559.	1.9	100
61	Functional Enhancers at the Gene-Poor 8q24 Cancer-Linked Locus. PLoS Genetics, 2009, 5, e1000597.	3.5	214
62	Evaluation of 8q24 and 17q Risk Loci and Prostate Cancer Mortality. Clinical Cancer Research, 2009, 15, 3223-3230.	7.0	46
63	Evaluation of the 8q24 Prostate Cancer Risk Locus and MYC Expression. Cancer Research, 2009, 69, 5568-5574.	0.9	110
64	The 8q24 cancer risk variant rs6983267 shows long-range interaction with MYC in colorectal cancer. Nature Genetics, 2009, 41, 882-884.	21.4	616
65	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
66	Multiple regions within 8q24 independently affect risk for prostate cancer. Nature Genetics, 2007, 39, 638-644.	21.4	621
67	Transferability of tag SNPs in genetic association studies in multiple populations. Nature Genetics, 2006, 38, 1298-1303.	21.4	224
68	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