Matthew L Freedman

List of Publications by Year
in descending order

70 papers	5,748 citations	126907 33 h-index	114465 63 g-index
73 all docs	73 docs citations	73 times ranked	11501 citing authors

#	Article	IF	Citations
1	Assessing the impact of population stratification on genetic association studies. Nature Genetics, 2004, 36, 388-393.	21.4	734
2	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
3	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	21.4	408
4	Principles for the post-GWAS functional characterization of cancer risk loci. Nature Genetics, 2011, 43, 513-518.	21.4	392
5	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
6	The association between germline <scp>BRCA2</scp> variants and sensitivity to platinumâ€based chemotherapy among men with metastatic prostate cancer. Cancer, 2017, 123, 3532-3539.	4.1	217
7	Modulation of long noncoding RNAs by risk SNPs underlying genetic predispositions to prostate cancer. Nature Genetics, 2016, 48, 1142-1150.	21.4	196
8	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. Nature Genetics, 2020, 52, 790-799.	21.4	174
9	Implementation of Germline Testing for Prostate Cancer: Philadelphia Prostate Cancer Consensus Conference 2019. Journal of Clinical Oncology, 2020, 38, 2798-2811.	1.6	170
10	Detection of renal cell carcinoma using plasma and urine cell-free DNA methylomes. Nature Medicine, 2020, 26, 1041-1043.	30.7	161
11	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
12	Inhibition of hypoxia-inducible factor-2Î± in renal cell carcinoma with belzutifan: a phase 1 trial and biomarker analysis. Nature Medicine, 2021, 27, 802-805.	30.7	151
13	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
14	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
15	Enhancer Architecture and Essential Core Regulatory Circuitry of Chronic Lymphocytic Leukemia. Cancer Cell, 2018, 34, 982-995.e7.	16.8	101
16	Association of Prostate Cancer Risk Variants with Gene Expression in Normal and Tumor Tissue. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 255-260.	2.5	97
17	A Novel Mechanism Driving Poor-Prognosis Prostate Cancer: Overexpression of the DNA Repair Gene, Ribonucleotide Reductase Small Subunit M2 (RRM2). Clinical Cancer Research, 2019, 25, 4480-4492.	7.0	96
18	CAUSEL: an epigenome- and genome-editing pipeline for establishing function of noncoding GWAS variants. Nature Medicine, 2015, 21, 1357-1363.	30.7	90

#	Article	IF	Citations
19	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
20	CDK7 Inhibition Suppresses Castration-Resistant Prostate Cancer through MED1 Inactivation. Cancer Discovery, 2019, 9, 1538-1555.	9.4	88
21	Inference of transcriptional regulation in cancers. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7731-7736.	7.1	84
22	Integrative molecular characterization of sarcomatoid and rhabdoid renal cell carcinoma. Nature Communications, 2021, 12, 808.	12.8	84
23	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
24	Systematic Evaluation of Genetic Variation at the Androgen Receptor Locus and Risk of Prostate Cancer in a Multiethnic Cohort Study. American Journal of Human Genetics, 2005, 76, 82-90.	6.2	72
25	Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. Human Molecular Genetics, 2014, 23, 5294-5302.	2.9	71
26	Reprogramming of the FOXA1 cistrome in treatment-emergent neuroendocrine prostate cancer. Nature Communications, 2021, 12, 1979.	12.8	70
27	Detection of Molecular Signatures of Homologous Recombination Deficiency in Prostate Cancer with or without BRCA1/2 Mutations. Clinical Cancer Research, 2020, 26, 2673-2680.	7.0	64
28	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	12.8	63
29	Super-Enhancer-Associated LncRNA UCA1 Interacts Directly with AMOT to Activate YAP Target Genes in Epithelial Ovarian Cancer. IScience, 2019, 17, 242-255.	4.1	60
30	Non-coding somatic mutations converge on the PAX8 pathway in ovarian cancer. Nature Communications, 2020, 11, 2020.	12.8	52
31	Mammalian SWI/SNF Complex Genomic Alterations and Immune Checkpoint Blockade in Solid Tumors. Cancer Immunology Research, 2020, 8, 1075-1084.	3.4	47
32	Androgen receptor and MYC equilibration centralizes on developmental super-enhancer. Nature Communications, 2021, 12, 7308.	12.8	46
33	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. Nature Medicine, 2019, 25, 1615-1626.	30.7	45
34	Epigenetic remodeling regulates transcriptional changes between ovarian cancer and benign precursors. JCI Insight, 2016, 1, .	5.0	42
35	A Study of High-Grade Serous Ovarian Cancer Origins Implicates the SOX18 Transcription Factor in Tumor Development. Cell Reports, 2019, 29, 3726-3735.e4.	6.4	39
36	HOXB13 suppresses de novo lipogenesis through HDAC3-mediated epigenetic reprogramming in prostate cancer. Nature Genetics, 2022, 54, 670-683.	21.4	39

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37	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
38	A rare variant of African ancestry activates 8q24 lncRNA hub by modulating cancer associated enhancer. Nature Communications, 2020, 11, 3598.	12.8	33
39	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
40	Predicting master transcription factors from pan-cancer expression data. Science Advances, 2021, 7, eabf6123.	10.3	30
41	Detecting Neuroendocrine Prostate Cancer Through Tissue-Informed Cell-Free DNA Methylation Analysis. Clinical Cancer Research, 2022, 28, 928-938.	7.0	29
42	Network-Based Integration of GWAS and Gene Expression Identifies a HOX-Centric Network Associated with Serous Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1574-1584.	2.5	28
43	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. Gynecologic Oncology, 2019, 153, 343-355.	1.4	28
44	A multi-level investigation of the genetic relationship between endometriosis and ovarian cancer histotypes. Cell Reports Medicine, 2022, 3, 100542.	6.5	26
45	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	2.8	24
46	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. British Journal of Cancer, 2017, 116, 524-535.	6.4	23
47	Exome sequencing reveals recurrent germ line variants in patients with familial WaldenstrÃ¶m macroglobulinemia. Blood, 2016, 127, 2598-2606.	1.4	22
48	A genome-scale CRISPR screen reveals PRMT1 as a critical regulator of androgen receptor signaling in prostate cancer. Cell Reports, 2022, 38, 110417.	6.4	17
49	Trans-ethnic variation in germline variants of patients with renal cell carcinoma. Cell Reports, 2021, 34, 108926.	6.4	16
50	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
51	Allele-Specific QTL Fine Mapping with PLASMA. American Journal of Human Genetics, 2020, 106, 170-187.	6.2	14
52	Epigenetic and transcriptional analysis reveals a core transcriptional program conserved in clonal prostate cancer metastases. Molecular Oncology, 2021, 15, 1942-1955.	4.6	10
53	CREB5 reprograms FOXA1 nuclear interactions to promote resistance to androgen receptor-targeting therapies. ELife, 2022, 11, .	6.0	10
54	Androgen receptor reprogramming demarcates prognostic, context-dependent gene sets in primary and metastatic prostate cancer. Clinical Epigenetics, 2022, 14, 60.	4.1	8

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55	Outcomes of older men receiving docetaxel for metastatic hormone-sensitive prostate cancer. Prostate Cancer and Prostatic Diseases, 2021, 24, 1181-1188.	3.9	7
56	Biomarker-Based Phase II Study of Sapanisertib (TAK-228): An mTORC1/2 Inhibitor in Patients With Refractory Metastatic Renal Cell Carcinoma. JCO Precision Oncology, 2022, 6, e2100448.	3.0	5
57	Dana-Farber Cancer Institute/Mass General Brigham Fellowship Response to the COVID-19 Pandemic. JCO Oncology Practice, 2021, 17, 541-545.	2.9	3
58	Genome-wide association study (GWAS) of response to androgen deprivation therapy (ADT) and survival in metastatic prostate cancer (PCa).. Journal of Clinical Oncology, 2016, 34, 1540-1540.	1.6	3
59	Response to olaparib or carboplatin in a real-world cohort of men with DNA damage repair (DDR) deficient metastatic castration-resistant prostate cancer (mCRPC).. Journal of Clinical Oncology, 2020, 38, 43-43.	1.6	3
60	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
61	Sensitive detection of renal cell carcinoma using plasma and urine cell-free DNA methylomes.. Journal of Clinical Oncology, 2020, 38, 728-728.	1.6	2
62	Genetic ancestry and clinical outcomes to immune checkpoint inhibitors among seven common cancers.. Journal of Clinical Oncology, 2021, 39, 10536-10536.	1.6	0
63	Association of inherited genetic variation with clinical outcome in patients with advanced renal cell carcinoma treated with mTOR inhibition.. Journal of Clinical Oncology, 2012, 30, 4543-4543.	1.6	0
64	Megaloblastic Anemia and Mitochondriopathy Caused by a Homozygous Mutation in Sideroflexin-4.. Blood, 2012, 120, 79-79.	1.4	0
65	Fixed tissue ChIP-seq (FiT-Seq) of archived FFPE clinical bladder cancer (BC) samples to reveal tumor-specific enhancer and super-enhancer profiles.. Journal of Clinical Oncology, 2016, 34, 4541-4541.	1.6	0
66	Cell-free DNA analysis in renal cell carcinoma: Comparison with tumor sequencing and correlation with response to therapy.. Journal of Clinical Oncology, 2019, 37, 655-655.	1.6	0
67	Circulating cell-free methylated DNA (cfmeDNA) to predict postoperative recurrence in patients with muscle-invasive bladder cancer (MIBC).. Journal of Clinical Oncology, 2019, 37, 454-454.	1.6	0
68	Detection of urothelial carcinoma using plasma cell-free methylated DNA.. Journal of Clinical Oncology, 2020, 38, 5046-5046.	1.6	0
69	Prevalence of pathogenic germline risk variants (PVs) in 1,829 renal cell carcinoma (RCC) patients (pts).. Journal of Clinical Oncology, 2020, 38, 659-659.	1.6	0
70	OUP accepted manuscript. Oncologist, 2022, , .	3.7	0