

Matthew L Freedman

List of Publications by Year in descending order

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Version: 2024-02-01

70
papers

5,748
citations

145106

33
h-index

129628

63
g-index

73
all docs

73
docs citations

73
times ranked

12699
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessing the impact of population stratification on genetic association studies. <i>Nature Genetics</i> , 2004, 36, 388-393.	9.4	734
2	Admixture mapping identifies 8q24 as a prostate cancer risk locus in African-American men. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14068-14073.	3.3	575
3	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , 2014, 46, 1103-1109.	9.4	408
4	Principles for the post-GWAS functional characterization of cancer risk loci. <i>Nature Genetics</i> , 2011, 43, 513-518.	9.4	392
5	A Somatically Acquired Enhancer of the Androgen Receptor Is a Noncoding Driver in Advanced Prostate Cancer. <i>Cell</i> , 2018, 174, 422-432.e13.	13.5	234
6	The association between germline <i>BRCA2</i> variants and sensitivity to platinum-based chemotherapy among men with metastatic prostate cancer. <i>Cancer</i> , 2017, 123, 3532-3539.	2.0	217
7	Modulation of long noncoding RNAs by risk SNPs underlying genetic predispositions to prostate cancer. <i>Nature Genetics</i> , 2016, 48, 1142-1150.	9.4	196
8	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. <i>Nature Genetics</i> , 2020, 52, 790-799.	9.4	174
9	Implementation of Germline Testing for Prostate Cancer: Philadelphia Prostate Cancer Consensus Conference 2019. <i>Journal of Clinical Oncology</i> , 2020, 38, 2798-2811.	0.8	170
10	Detection of renal cell carcinoma using plasma and urine cell-free DNA methylomes. <i>Nature Medicine</i> , 2020, 26, 1041-1043.	15.2	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. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	7.7	157
12	Inhibition of hypoxia-inducible factor-2 α in renal cell carcinoma with belzutifan: a phase 1 trial and biomarker analysis. <i>Nature Medicine</i> , 2021, 27, 802-805.	15.2	151
13	EZH2 inhibition activates a dsRNA-“STING”-interferon stress axis that potentiates response to PD-1 checkpoint blockade in prostate cancer. <i>Nature Cancer</i> , 2021, 2, 444-456.	5.7	118
14	A Large Multiethnic Genome-Wide Association Study of Prostate Cancer Identifies Novel Risk Variants and Substantial Ethnic Differences. <i>Cancer Discovery</i> , 2015, 5, 878-891.	7.7	111
15	Enhancer Architecture and Essential Core Regulatory Circuitry of Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2018, 34, 982-995.e7.	7.7	101
16	Association of Prostate Cancer Risk Variants with Gene Expression in Normal and Tumor Tissue. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 255-260.	1.1	97
17	A Novel Mechanism Driving Poor-Prognosis Prostate Cancer: Overexpression of the DNA Repair Gene, Ribonucleotide Reductase Small Subunit M2 (RRM2). <i>Clinical Cancer Research</i> , 2019, 25, 4480-4492.	3.2	96
18	CAUSEL: an epigenome- and genome-editing pipeline for establishing function of noncoding GWAS variants. <i>Nature Medicine</i> , 2015, 21, 1357-1363.	15.2	90

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19	A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. <i>Nature Genetics</i> , 2019, 51, 815-823.	9.4	89
20	CDK7 Inhibition Suppresses Castration-Resistant Prostate Cancer through MED1 Inactivation. <i>Cancer Discovery</i> , 2019, 9, 1538-1555.	7.7	88
21	Inference of transcriptional regulation in cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7731-7736.	3.3	84
22	Integrative molecular characterization of sarcomatoid and rhabdoid renal cell carcinoma. <i>Nature Communications</i> , 2021, 12, 808.	5.8	84
23	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	5.8	78
24	Systematic Evaluation of Genetic Variation at the Androgen Receptor Locus and Risk of Prostate Cancer in a Multiethnic Cohort Study. <i>American Journal of Human Genetics</i> , 2005, 76, 82-90.	2.6	72
25	Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. <i>Human Molecular Genetics</i> , 2014, 23, 5294-5302.	1.4	71
26	Reprogramming of the FOXA1 cistrome in treatment-emergent neuroendocrine prostate cancer. <i>Nature Communications</i> , 2021, 12, 1979.	5.8	70
27	Detection of Molecular Signatures of Homologous Recombination Deficiency in Prostate Cancer with or without BRCA1/2 Mutations. <i>Clinical Cancer Research</i> , 2020, 26, 2673-2680.	3.2	64
28	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. <i>Nature Communications</i> , 2015, 6, 8234.	5.8	63
29	Super-Enhancer-Associated LncRNA UCA1 Interacts Directly with AMOT to Activate YAP Target Genes in Epithelial Ovarian Cancer. <i>IScience</i> , 2019, 17, 242-255.	1.9	60
30	Non-coding somatic mutations converge on the PAX8 pathway in ovarian cancer. <i>Nature Communications</i> , 2020, 11, 2020.	5.8	52
31	Mammalian SWI/SNF Complex Genomic Alterations and Immune Checkpoint Blockade in Solid Tumors. <i>Cancer Immunology Research</i> , 2020, 8, 1075-1084.	1.6	47
32	Androgen receptor and MYC equilibration centralizes on developmental super-enhancer. <i>Nature Communications</i> , 2021, 12, 7308.	5.8	46
33	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. <i>Nature Medicine</i> , 2019, 25, 1615-1626.	15.2	45
34	Epigenetic remodeling regulates transcriptional changes between ovarian cancer and benign precursors. <i>JCI Insight</i> , 2016, 1, .	2.3	42
35	A Study of High-Grade Serous Ovarian Cancer Origins Implicates the SOX18 Transcription Factor in Tumor Development. <i>Cell Reports</i> , 2019, 29, 3726-3735.e4.	2.9	39
36	HOXB13 suppresses de novo lipogenesis through HDAC3-mediated epigenetic reprogramming in prostate cancer. <i>Nature Genetics</i> , 2022, 54, 670-683.	9.4	39

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37	ASCL1 activates neuronal stem cell-like lineage programming through remodeling of the chromatin landscape in prostate cancer. <i>Nature Communications</i> , 2022, 13, 2282.	5.8	34
38	A rare variant of African ancestry activates 8q24 lncRNA hub by modulating cancer associated enhancer. <i>Nature Communications</i> , 2020, 11, 3598.	5.8	33
39	H3K27ac HiChIP in prostate cell lines identifies risk genes for prostate cancer susceptibility. <i>American Journal of Human Genetics</i> , 2021, 108, 2284-2300.	2.6	31
40	Predicting master transcription factors from pan-cancer expression data. <i>Science Advances</i> , 2021, 7, eabf6123.	4.7	30
41	Detecting Neuroendocrine Prostate Cancer Through Tissue-Informed Cell-Free DNA Methylation Analysis. <i>Clinical Cancer Research</i> , 2022, 28, 928-938.	3.2	29
42	Network-Based Integration of GWAS and Gene Expression Identifies a HOX-Centric Network Associated with Serous Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1574-1584.	1.1	28
43	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. <i>Gynecologic Oncology</i> , 2019, 153, 343-355.	0.6	28
44	A multi-level investigation of the genetic relationship between endometriosis and ovarian cancer histotypes. <i>Cell Reports Medicine</i> , 2022, 3, 100542.	3.3	26
45	Common variants at the CHEK2 gene locus and risk of epithelial ovarian cancer. <i>Carcinogenesis</i> , 2015, 36, 1341-1353.	1.3	24
46	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. <i>British Journal of Cancer</i> , 2017, 116, 524-535.	2.9	23
47	Exome sequencing reveals recurrent germ line variants in patients with familial Waldenström macroglobulinemia. <i>Blood</i> , 2016, 127, 2598-2606.	0.6	22
48	A genome-scale CRISPR screen reveals PRMT1 as a critical regulator of androgen receptor signaling in prostate cancer. <i>Cell Reports</i> , 2022, 38, 110417.	2.9	17
49	Trans-ethnic variation in germline variants of patients with renal cell carcinoma. <i>Cell Reports</i> , 2021, 34, 108926.	2.9	16
50	Ovarian Cancer Risk Variants Are Enriched in Histotype-Specific Enhancers and Disrupt Transcription Factor Binding Sites. <i>American Journal of Human Genetics</i> , 2020, 107, 622-635.	2.6	14
51	Allele-Specific QTL Fine Mapping with PLASMA. <i>American Journal of Human Genetics</i> , 2020, 106, 170-187.	2.6	14
52	Epigenetic and transcriptional analysis reveals a core transcriptional program conserved in clonal prostate cancer metastases. <i>Molecular Oncology</i> , 2021, 15, 1942-1955.	2.1	10
53	CREB5 reprograms FOXA1 nuclear interactions to promote resistance to androgen receptor-targeting therapies. <i>ELife</i> , 2022, 11, .	2.8	10
54	Androgen receptor reprogramming demarcates prognostic, context-dependent gene sets in primary and metastatic prostate cancer. <i>Clinical Epigenetics</i> , 2022, 14, 60.	1.8	8

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55	Outcomes of older men receiving docetaxel for metastatic hormone-sensitive prostate cancer. <i>Prostate Cancer and Prostatic Diseases</i> , 2021, 24, 1181-1188.	2.0	7
56	Biomarker-Based Phase II Study of Sapanisertib (TAK-228): An mTORC1/2 Inhibitor in Patients With Refractory Metastatic Renal Cell Carcinoma. <i>JCO Precision Oncology</i> , 2022, 6, e2100448.	1.5	5
57	Dana-Farber Cancer Institute/Mass General Brigham Fellowship Response to the COVID-19 Pandemic. <i>JCO Oncology Practice</i> , 2021, 17, 541-545.	1.4	3
58	Genome-wide association study (GWAS) of response to androgen deprivation therapy (ADT) and survival in metastatic prostate cancer (PCa).. <i>Journal of Clinical Oncology</i> , 2016, 34, 1540-1540.	0.8	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).. <i>Journal of Clinical Oncology</i> , 2020, 38, 43-43.	0.8	3
60	Allele-specific epigenetic activity in prostate cancer and normal prostate tissue implicates prostate cancer risk mechanisms. <i>American Journal of Human Genetics</i> , 2021, 108, 2071-2085.	2.6	3
61	Sensitive detection of renal cell carcinoma using plasma and urine cell-free DNA methylomes.. <i>Journal of Clinical Oncology</i> , 2020, 38, 728-728.	0.8	2
62	Genetic ancestry and clinical outcomes to immune checkpoint inhibitors among seven common cancers.. <i>Journal of Clinical Oncology</i> , 2021, 39, 10536-10536.	0.8	0
63	Association of inherited genetic variation with clinical outcome in patients with advanced renal cell carcinoma treated with mTOR inhibition.. <i>Journal of Clinical Oncology</i> , 2012, 30, 4543-4543.	0.8	0
64	Megaloblastic Anemia and Mitochondriopathy Caused by a Homozygous Mutation in Sideroflexin-4.. <i>Blood</i> , 2012, 120, 79-79.	0.6	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.. <i>Journal of Clinical Oncology</i> , 2016, 34, 4541-4541.	0.8	0
66	Cell-free DNA analysis in renal cell carcinoma: Comparison with tumor sequencing and correlation with response to therapy.. <i>Journal of Clinical Oncology</i> , 2019, 37, 655-655.	0.8	0
67	Circulating cell-free methylated DNA (cfmeDNA) to predict postoperative recurrence in patients with muscle-invasive bladder cancer (MIBC).. <i>Journal of Clinical Oncology</i> , 2019, 37, 454-454.	0.8	0
68	Detection of urothelial carcinoma using plasma cell-free methylated DNA.. <i>Journal of Clinical Oncology</i> , 2020, 38, 5046-5046.	0.8	0
69	Prevalence of pathogenic germline risk variants (PVs) in 1,829 renal cell carcinoma (RCC) patients (pts).. <i>Journal of Clinical Oncology</i> , 2020, 38, 659-659.	0.8	0
70	OUP accepted manuscript. <i>Oncologist</i> , 2022, , .	1.9	0