

# Matthew L Freedman

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

67

papers

3,666

citations

27

h-index

60

g-index

73

ext. papers

4,849

ext. citations

14.9

avg, IF

4.41

L-index

#	Paper	IF	Citations
67	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> , <b>2022</b> , 6, e2100448	3.6	1
66	A genome-scale CRISPR screen reveals PRMT1 as a critical regulator of androgen receptor signaling in prostate cancer.. <i>Cell Reports</i> , <b>2022</b> , 38, 110417	10.6	0
65	A multi-level investigation of the genetic relationship between endometriosis and ovarian cancer histotypes.. <i>Cell Reports Medicine</i> , <b>2022</b> , 3, 100542	18	5
64	ASCL1 activates neuronal stem cell-like lineage programming through remodeling of the chromatin landscape in prostate cancer.. <i>Nature Communications</i> , <b>2022</b> , 13, 2282	17.4	1
63	Androgen receptor reprogramming demarcates prognostic, context-dependent gene sets in primary and metastatic prostate cancer.. <i>Clinical Epigenetics</i> , <b>2022</b> , 14, 60	7.7	1
62	Androgen receptor and MYC equilibration centralizes on developmental super-enhancer.. <i>Nature Communications</i> , <b>2021</b> , 12, 7308	17.4	4
61	Detecting neuroendocrine prostate cancer through tissue-informed cell-free DNA methylation analysis.. <i>Clinical Cancer Research</i> , <b>2021</b> ,	12.9	1
60	Predicting master transcription factors from pan-cancer expression data. <i>Science Advances</i> , <b>2021</b> , 7, eabf6133	13	2
59	H3K27ac HiChIP in prostate cell lines identifies risk genes for prostate cancer susceptibility. <i>American Journal of Human Genetics</i> , <b>2021</b> , 108, 2284-2300	11	2
58	Allele-specific epigenetic activity in prostate cancer and normal prostate tissue implicates prostate cancer risk mechanisms. <i>American Journal of Human Genetics</i> , <b>2021</b> , 108, 2071-2085	11	
57	EZH2 inhibition activates a dsRNA-STING-interferon stress axis that potentiates response to PD-1 checkpoint blockade in prostate cancer. <i>Nature Cancer</i> , <b>2021</b> , 2, 444-456	15.4	37
56	Reprogramming of the FOXA1 cistrome in treatment-emergent neuroendocrine prostate cancer. <i>Nature Communications</i> , <b>2021</b> , 12, 1979	17.4	11
55	Epigenetic and transcriptional analysis reveals a core transcriptional program conserved in clonal prostate cancer metastases. <i>Molecular Oncology</i> , <b>2021</b> , 15, 1942-1955	7.9	1
54	Inhibition of hypoxia-inducible factor-2 $\beta$ in renal cell carcinoma with belzutifan: a phase 1 trial and biomarker analysis. <i>Nature Medicine</i> , <b>2021</b> , 27, 802-805	50.5	48
53	Outcomes of older men receiving docetaxel for metastatic hormone-sensitive prostate cancer. <i>Prostate Cancer and Prostatic Diseases</i> , <b>2021</b> , 24, 1181-1188	6.2	1
52	Genetic ancestry and clinical outcomes to immune checkpoint inhibitors among seven common cancers.. <i>Journal of Clinical Oncology</i> , <b>2021</b> , 39, 10536-10536	2.2	
51	Integrative molecular characterization of sarcomatoid and rhabdoid renal cell carcinoma. <i>Nature Communications</i> , <b>2021</b> , 12, 808	17.4	26

50	Trans-ethnic variation in germline variants of patients with renal cell carcinoma. <i>Cell Reports</i> , <b>2021</b> , 34, 108926	10.6	3
49	Dana-Farber Cancer Institute/Mass General Brigham Fellowship Response to the COVID-19 Pandemic. <i>JCO Oncology Practice</i> , <b>2021</b> , 17, 541-545	2.3	1
48	Detection of renal cell carcinoma using plasma and urine cell-free DNA methylomes. <i>Nature Medicine</i> , <b>2020</b> , 26, 1041-1043	50.5	72
47	Implementation of Germline Testing for Prostate Cancer: Philadelphia Prostate Cancer Consensus Conference 2019. <i>Journal of Clinical Oncology</i> , <b>2020</b> , 38, 2798-2811	2.2	80
46	Detection of Molecular Signatures of Homologous Recombination Deficiency in Prostate Cancer with or without BRCA1/2 Mutations. <i>Clinical Cancer Research</i> , <b>2020</b> , 26, 2673-2680	12.9	22
45	Allele-Specific QTL Fine Mapping with PLASMA. <i>American Journal of Human Genetics</i> , <b>2020</b> , 106, 170-187 <sup>11</sup>		3
44	Mammalian SWI/SNF Complex Genomic Alterations and Immune Checkpoint Blockade in Solid Tumors. <i>Cancer Immunology Research</i> , <b>2020</b> , 8, 1075-1084	12.5	21
43	Non-coding somatic mutations converge on the PAX8 pathway in ovarian cancer. <i>Nature Communications</i> , <b>2020</b> , 11, 2020	17.4	17
42	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> , <b>2020</b> , 38, 43-43	2.2	1
41	Sensitive detection of renal cell carcinoma using plasma and urine cell-free DNA methylomes.. <i>Journal of Clinical Oncology</i> , <b>2020</b> , 38, 728-728	2.2	2
40	Prevalence of pathogenic germline risk variants (PVs) in 1,829 renal cell carcinoma (RCC) patients (pts).. <i>Journal of Clinical Oncology</i> , <b>2020</b> , 38, 659-659	2.2	
39	Detection of urothelial carcinoma using plasma cell-free methylated DNA.. <i>Journal of Clinical Oncology</i> , <b>2020</b> , 38, 5046-5046	2.2	
38	Ovarian Cancer Risk Variants Are Enriched in Histotype-Specific Enhancers and Disrupt Transcription Factor Binding Sites. <i>American Journal of Human Genetics</i> , <b>2020</b> , 107, 622-635	11	5
37	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. <i>Nature Genetics</i> , <b>2020</b> , 52, 790-799	36.3	62
36	A rare variant of African ancestry activates 8q24 lncRNA hub by modulating cancer associated enhancer. <i>Nature Communications</i> , <b>2020</b> , 11, 3598	17.4	11
35	CDK7 Inhibition Suppresses Castration-Resistant Prostate Cancer through MED1 Inactivation. <i>Cancer Discovery</i> , <b>2019</b> , 9, 1538-1555	24.4	35
34	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. <i>Nature Medicine</i> , <b>2019</b> , 25, 1615-1626	50.5	25
33	A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. <i>Nature Genetics</i> , <b>2019</b> , 51, 815-823	36.3	33

32	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> , <b>2019</b> , 25, 4480-4492	12.9	49
31	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. <i>Gynecologic Oncology</i> , <b>2019</b> , 153, 343-355	4.9	16
30	Super-Enhancer-Associated LncRNA UCA1 Interacts Directly with AMOT to Activate YAP Target Genes in Epithelial Ovarian Cancer. <i>iScience</i> , <b>2019</b> , 17, 242-255	6.1	38
29	Cell-free DNA analysis in renal cell carcinoma: Comparison with tumor sequencing and correlation with response to therapy.. <i>Journal of Clinical Oncology</i> , <b>2019</b> , 37, 655-655	2.2	
28	Circulating cell-free methylated DNA (cfmeDNA) to predict postoperative recurrence in patients with muscle-invasive bladder cancer (MIBC).. <i>Journal of Clinical Oncology</i> , <b>2019</b> , 37, 454-454	2.2	
27	A Study of High-Grade Serous Ovarian Cancer Origins Implicates the SOX18 Transcription Factor in Tumor Development. <i>Cell Reports</i> , <b>2019</b> , 29, 3726-3735.e4	10.6	19
26	A Somatically Acquired Enhancer of the Androgen Receptor Is a Noncoding Driver in Advanced Prostate Cancer. <i>Cell</i> , <b>2018</b> , 174, 422-432.e13	56.2	129
25	Enhancer Architecture and Essential Core Regulatory Circuitry of Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , <b>2018</b> , 34, 982-995.e7	24.3	58
24	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. <i>British Journal of Cancer</i> , <b>2017</b> , 116, 524-535	8.7	18
23	The association between germline BRCA2 variants and sensitivity to platinum-based chemotherapy among men with metastatic prostate cancer. <i>Cancer</i> , <b>2017</b> , 123, 3532-3539	6.4	147
22	Modulation of long noncoding RNAs by risk SNPs underlying genetic predispositions to prostate cancer. <i>Nature Genetics</i> , <b>2016</b> , 48, 1142-50	36.3	158
21	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> , <b>2016</b> , 6, 1052-67	24.4	104
20	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , <b>2016</b> , 7, 12675	17.4	53
19	Epigenetic remodeling regulates transcriptional changes between ovarian cancer and benign precursors. <i>JCI Insight</i> , <b>2016</b> , 1,	9.9	28
18	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> , <b>2016</b> , 34, 1540-1540	2.2	0
17	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> , <b>2016</b> , 34, 4541-4541	2.2	
16	Exome sequencing reveals recurrent germ line variants in patients with familial Waldenström macroglobulinemia. <i>Blood</i> , <b>2016</b> , 127, 2598-606	2.2	16
15	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> , <b>2015</b> , 24, 1574-84	4	24

14	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. <i>Nature Communications</i> , <b>2015</b> , 6, 8234	17.4	40
13	Common variants at the CHEK2 gene locus and risk of epithelial ovarian cancer. <i>Carcinogenesis</i> , <b>2015</b> , 36, 1341-53	4.6	20
12	CAUSEL: an epigenome- and genome-editing pipeline for establishing function of noncoding GWAS variants. <i>Nature Medicine</i> , <b>2015</b> , 21, 1357-63	50.5	65
11	Association of prostate cancer risk variants with gene expression in normal and tumor tissue. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2015</b> , 24, 255-60	4	69
10	Inference of transcriptional regulation in cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 7731-6	11.5	59
9	A large multiethnic genome-wide association study of prostate cancer identifies novel risk variants and substantial ethnic differences. <i>Cancer Discovery</i> , <b>2015</b> , 5, 878-91	24.4	94
8	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , <b>2014</b> , 46, 1103-9	36.3	331
7	Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 5294-302	5.6	61
6	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> , <b>2012</b> , 30, 4543-4543	2.2	
5	Megaloblastic Anemia and Mitochondriopathy Caused by a Homozygous Mutation in Sideroflexin-4.. <i>Blood</i> , <b>2012</b> , 120, 79-79	2.2	
4	Principles for the post-GWAS functional characterization of cancer risk loci. <i>Nature Genetics</i> , <b>2011</b> , 43, 513-8	36.3	326
3	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> , <b>2006</b> , 103, 14068-73	11.5	517
2	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> , <b>2005</b> , 76, 82-90	11	65
1	Assessing the impact of population stratification on genetic association studies. <i>Nature Genetics</i> , <b>2004</b> , 36, 388-93	36.3	623