Matthew L Freedman

List of Publications by Citations

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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	3,666	27	60
papers	citations	h-index	g-index
73	4,849	14.9	4.41
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
67	Assessing the impact of population stratification on genetic association studies. *Nature Genetics*, **2004**, 36, 388-93	36.3	623
66	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, 14068-73	11.5	517
65	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. *Nature Genetics*, **2014**, 46, 1103-9	36.3	331
64	Principles for the post-GWAS functional characterization of cancer risk loci. *Nature Genetics*, **2011**, 43, 513-8	36.3	326
63	Modulation of long noncoding RNAs by risk SNPs underlying genetic predispositions to prostate cancer. *Nature Genetics*, **2016**, 48, 1142-50	36.3	158
62	The association between germline BRCA2 variants and sensitivity to platinum-based chemotherapy among men with metastatic prostate cancer. *Cancer*, **2017**, 123, 3532-3539	6.4	147
61	A Somatically Acquired Enhancer of the Androgen Receptor Is a Noncoding Driver in Advanced Prostate Cancer. *Cell*, **2018**, 174, 422-432.e13	56.2	129
60	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, 1052-67	24.4	104
59	A large multiethnic genome-wide association study of prostate cancer identifies novel risk variants and substantial ethnic differences. *Cancer Discovery*, **2015**, 5, 878-91	24.4	94
58	Implementation of Germline Testing for Prostate Cancer: Philadelphia Prostate Cancer Consensus Conference 2019. *Journal of Clinical Oncology*, **2020**, 38, 2798-2811	2.2	80
57	Detection of renal cell carcinoma using plasma and urine cell-free DNA methylomes. *Nature Medicine*, **2020**, 26, 1041-1043	50.5	72
56	Association of prostate cancer risk variants with gene expression in normal and tumor tissue. *Cancer Epidemiology Biomarkers and Prevention*, **2015**, 24, 255-60	4	69
55	CAUSEL: an epigenome- and genome-editing pipeline for establishing function of noncoding GWAS variants. *Nature Medicine*, **2015**, 21, 1357-63	50.5	65
54	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	11	65
53	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. *Nature Genetics*, **2020**, 52, 790-799	36.3	62
52	Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. *Human Molecular Genetics*, **2014**, 23, 5294-302	5.6	61
51	Inference of transcriptional regulation in cancers. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 7731-6	11.5	59

50	Enhancer Architecture and Essential Core Regulatory Circuitry of Chronic Lymphocytic Leukemia. *Cancer Cell*, **2018**, 34, 982-995.e7	24.3	58
49	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. *Nature Communications*, **2016**, 7, 12675	17.4	53
48	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	12.9	49
47	Inhibition of hypoxia-inducible factor-2α in renal cell carcinoma with belzutifan: a phase 1 trial and biomarker analysis. *Nature Medicine*, **2021**, 27, 802-805	50.5	48
46	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. *Nature Communications*, **2015**, 6, 8234	17.4	40
45	Super-Enhancer-Associated LncRNA UCA1 Interacts Directly with AMOT to Activate YAP Target Genes in Epithelial Ovarian Cancer. *IScience*, **2019**, 17, 242-255	6.1	38
44	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	15.4	37
43	CDK7 Inhibition Suppresses Castration-Resistant Prostate Cancer through MED1 Inactivation. *Cancer Discovery*, **2019**, 9, 1538-1555	24.4	35
42	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	36.3	33
41	Epigenetic remodeling regulates transcriptional changes between ovarian cancer and benign precursors. *JCI Insight*, **2016**, 1,	9.9	28
40	Integrative molecular characterization of sarcomatoid and rhabdoid renal cell carcinoma. *Nature Communications*, **2021**, 12, 808	17.4	26
39	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. *Nature Medicine*, **2019**, 25, 1615-1626	50.5	25
38	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, 1574-84	4	24
37	Detection of Molecular Signatures of Homologous Recombination Deficiency in Prostate Cancer with or without BRCA1/2 Mutations. *Clinical Cancer Research*, **2020**, 26, 2673-2680	12.9	22
36	Mammalian SWI/SNF Complex Genomic Alterations and Immune Checkpoint Blockade in Solid Tumors. *Cancer Immunology Research*, **2020**, 8, 1075-1084	12.5	21
35	Common variants at the CHEK2 gene locus and risk of epithelial ovarian cancer. *Carcinogenesis*, **2015**, 36, 1341-53	4.6	20
34	A Study of High-Grade Serous Ovarian Cancer Origins Implicates the SOX18 Transcription Factor in Tumor Development. *Cell Reports*, **2019**, 29, 3726-3735.e4	10.6	19
33	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. *British Journal of Cancer*, **2017**, 116, 524-535	8.7	18

32	Non-coding somatic mutations converge on the PAX8 pathway in ovarian cancer. *Nature Communications*, **2020**, 11, 2020	17.4	17
31	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. *Gynecologic Oncology*, **2019**, 153, 343-355	4.9	16
30	Exome sequencing reveals recurrent germ line variants in patients with familial Waldenström macroglobulinemia. *Blood*, **2016**, 127, 2598-606	2.2	16
29	A rare variant of African ancestry activates 8q24 lncRNA hub by modulating cancer associated enhancer. *Nature Communications*, **2020**, 11, 3598	17.4	11
28	Reprogramming of the FOXA1 cistrome in treatment-emergent neuroendocrine prostate cancer. *Nature Communications*, **2021**, 12, 1979	17.4	11
27	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	11	5
26	A multi-level investigation of the genetic relationship between endometriosis and ovarian cancer histotypes.. *Cell Reports Medicine*, **2022**, 3, 100542	18	5
25	Androgen receptor and MYC equilibration centralizes on developmental super-enhancer.. *Nature Communications*, **2021**, 12, 7308	17.4	4
24	Allele-Specific QTL Fine Mapping with PLASMA. *American Journal of Human Genetics*, **2020**, 106, 170-187	11	3
23	Trans-ethnic variation in germline variants of patients with renal cell carcinoma. *Cell Reports*, **2021**, 34, 108926	10.6	3
22	Sensitive detection of renal cell carcinoma using plasma and urine cell-free DNA methylomes.. *Journal of Clinical Oncology*, **2020**, 38, 728-728	2.2	2
21	Predicting master transcription factors from pan-cancer expression data. *Science Advances*, **2021**, 7, eabf6123	14.3	2
20	H3K27ac HiChIP in prostate cell lines identifies risk genes for prostate cancer susceptibility. *American Journal of Human Genetics*, **2021**, 108, 2284-2300	11	2
19	Detecting neuroendocrine prostate cancer through tissue-informed cell-free DNA methylation analysis.. *Clinical Cancer Research*, **2021**,	12.9	1
18	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	2.2	1
17	Epigenetic and transcriptional analysis reveals a core transcriptional program conserved in clonal prostate cancer metastases. *Molecular Oncology*, **2021**, 15, 1942-1955	7.9	1
16	Outcomes of older men receiving docetaxel for metastatic hormone-sensitive prostate cancer. *Prostate Cancer and Prostatic Diseases*, **2021**, 24, 1181-1188	6.2	1
15	Dana-Farber Cancer Institute/Mass General Brigham Fellowship Response to the COVID-19 Pandemic. *JCO Oncology Practice*, **2021**, 17, 541-545	2.3	1

List of Publications

14	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	3.6	1
13	ASCL1 activates neuronal stem cell-like lineage programming through remodeling of the chromatin landscape in prostate cancer.. *Nature Communications*, **2022**, 13, 2282	17.4	1
12	Androgen receptor reprogramming demarcates prognostic, context-dependent gene sets in primary and metastatic prostate cancer.. *Clinical Epigenetics*, **2022**, 14, 60	7.7	1
11	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	2.2	0
10	A genome-scale CRISPR screen reveals PRMT1 as a critical regulator of androgen receptor signaling in prostate cancer.. *Cell Reports*, **2022**, 38, 110417	10.6	0
9	Prevalence of pathogenic germline risk variants (PVs) in 1,829 renal cell carcinoma (RCC) patients (pts).. *Journal of Clinical Oncology*, **2020**, 38, 659-659	2.2	
8	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	11	
7	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	2.2	
6	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	2.2	
5	Detection of urothelial carcinoma using plasma cell-free methylated DNA.. *Journal of Clinical Oncology*, **2020**, 38, 5046-5046	2.2	
4	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	2.2	
3	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	2.2	
2	Megaloblastic Anemia and Mitochondriopathy Caused by a Homozygous Mutation in Sideroflexin-4.. *Blood*, **2012**, 120, 79-79	2.2	
1	Genetic ancestry and clinical outcomes to immune checkpoint inhibitors among seven common cancers.. *Journal of Clinical Oncology*, **2021**, 39, 10536-10536	2.2	