Hannah Carter

List of Publications by Citations

74 papers	3,872 citations	26 h-index	62 g-index
95 ext. papers	5,168 ext. citations	12.7 avg, IF	5.43 L-index

#	Paper	IF	Citations
74	Network-based stratification of tumor mutations. *Nature Methods*, **2013**, 10, 1108-15	21.6	546
73	Circulating tumour DNA methylation markers for diagnosis and prognosis of hepatocellular carcinoma. *Nature Materials*, **2017**, 16, 1155-1161	27	387
72	Cancer-specific high-throughput annotation of somatic mutations: computational prediction of driver missense mutations. *Cancer Research*, **2009**, 69, 6660-7	10.1	344
71	Hybrid Periportal Hepatocytes Regenerate the Injured Liver without Giving Rise to Cancer. *Cell*, **2015**, 162, 766-79	56.2	311
70	Identifying Mendelian disease genes with the variant effect scoring tool. *BMC Genomics*, **2013**, 14 Suppl 3, S3	4.5	240
69	Evaluation and accurate diagnoses of pediatric diseases using artificial intelligence. *Nature Medicine* , **2019**, 25, 433-438	50.5	206
68	MHC-I Genotype Restricts the Oncogenic Mutational Landscape. *Cell*, **2017**, 171, 1272-1283.e15	56.2	180
67	Epigenetic aging signatures in mice livers are slowed by dwarfism, calorie restriction and rapamycin treatment. *Genome Biology*, **2017**, 18, 57	18.3	176
66	Multi-tiered genomic analysis of head and neck cancer ties TP53 mutation to 3p loss. *Nature Genetics*, **2014**, 46, 939-43	36.3	101
65	CRAVAT: cancer-related analysis of variants toolkit. *Bioinformatics*, **2013**, 29, 647-8	7.2	98
64	Evolutionary Pressure against MHC Class II Binding Cancer Mutations. *Cell*, **2018**, 175, 416-428.e13	56.2	98
63	Genotype to phenotype via network analysis. *Current Opinion in Genetics and Development*, **2013**, 23, 611-21	4.9	88
62	CHASM and SNVBox: toolkit for detecting biologically important single nucleotide mutations in cancer. *Bioinformatics*, **2011**, 27, 2147-8	7.2	86
61	EPEN-04. ONCOGENIC 3D TUMOR GENOME ORGANIZATION IDENTIFIES NEW THERAPEUTIC TARGETS IN EPENDYMOMA. *Neuro-Oncology*, **2020**, 22, iii308-iii308	1	78
60	Interaction Landscape of Inherited Polymorphisms with Somatic Events in Cancer. *Cancer Discovery*, **2017**, 7, 410-423	24.4	77
59	3D collagen architecture induces a conserved migratory and transcriptional response linked to vasculogenic mimicry. *Nature Communications*, **2017**, 8, 1651	17.4	76
58	A global transcriptional network connecting noncoding mutations to changes in tumor gene expression. *Nature Genetics*, **2018**, 50, 613-620	36.3	74

57	Prioritization of driver mutations in pancreatic cancer using cancer-specific high-throughput annotation of somatic mutations (CHASM). *Cancer Biology and Therapy*, **2010**, 10, 582-7	4.6	70
56	Exploring the landscape of focal amplifications in cancer using AmpliconArchitect. *Nature Communications*, **2019**, 10, 392	17.4	59
55	Structure-Based Analysis Reveals Cancer Missense Mutations Target Protein Interaction Interfaces. *PLoS ONE*, **2016**, 11, e0152929	3.7	56
54	The Emerging Potential for Network Analysis to Inform Precision Cancer Medicine. *Journal of Molecular Biology*, **2018**, 430, 2875-2899	6.5	50
53	Integrative genomic analysis of mouse and human hepatocellular carcinoma. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E9879-E9888	11.5	40
52	Strength of immune selection in tumors varies with sex and age. *Nature Communications*, **2020**, 11, 4128	17.4	33
51	MHC-I genotype and tumor mutational burden predict response to immunotherapy. *Genome Medicine*, **2020**, 12, 45	14.4	32
50	Elevated neoantigen levels in tumors with somatic mutations in the HLA-A, HLA-B, HLA-C and B2M genes. *BMC Medical Genomics*, **2019**, 12, 107	3.7	28
49	Challenges in identifying cancer genes by analysis of exome sequencing data. *Nature Communications*, **2016**, 7, 12096	17.4	27
48	GPCRs show widespread differential mRNA expression and frequent mutation and copy number variation in solid tumors. *PLoS Biology*, **2019**, 17, e3000434	9.7	26
47	Immune DNA signature of T-cell infiltration in breast tumor exomes. *Scientific Reports*, **2016**, 6, 30064	4.9	24
46	Integrating molecular networks with genetic variant interpretation for precision medicine. *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*, **2019**, 11, e1443	6.6	23
45	Pan-cancer analysis reveals technical artifacts in TCGA germline variant calls. *BMC Genomics*, **2017**, 18, 458	4.5	21
44	Cell Adhesiveness Serves as a Biophysical Marker for Metastatic Potential. *Cancer Research*, **2020**, 80, 901-911	10.1	17
43	Using a genetic risk score to calculate the optimal age for an individual to undergo coronary artery calcium screening. *Journal of Cardiovascular Computed Tomography*, **2019**, 13, 203-210	2.8	14
42	Genomic and evolutionary classification of lung cancer in never smokers. *Nature Genetics*, **2021**, 53, 1348-1359	31.6	14
41	IRE1α regulates macrophage polarization, PD-L1 expression, and tumor survival. *PLoS Biology*, **2020**, 18, e3000687	9.7	11
40	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. *Human Mutation*, **2017**, 38, 1266-1276	4.7	9

39	IRE1α and IGF signaling predict resistance to an endoplasmic reticulum stress-inducing drug in glioblastoma cells. *Scientific Reports*, **2020**, 10, 8348	4.9	9
38	Glioblastomas located in proximity to the subventricular zone (SVZ) exhibited enrichment of gene expression profiles associated with the cancer stem cell state. *Journal of Neuro-Oncology*, **2020**, 148, 455-462	4.8	9
37	Extracellular vesicles produced in B cells deliver tumor suppressor miR-335 to breast cancer cells disrupting oncogenic programming in vitro and in vivo. *Scientific Reports*, **2018**, 8, 17581	4.9	9
36	Targeted Coronary Artery Calcium Screening in High-Risk Younger Individuals Using Consumer Genetic Screening Results. *JACC: Cardiovascular Imaging*, **2021**, 14, 1398-1406	8.4	9
35	Predicting the functional consequences of somatic missense mutations found in tumors. *Methods in Molecular Biology*, **2014**, 1101, 135-59	1.4	8
34	Telomerase and CD4 T Cell Immunity in Cancer. *Cancers*, **2020**, 12,	6.6	8
33	Potential global impact of the N501Y mutation on MHC-II presentation and immune escape		7
32	Germline and Somatic Genetic Variants in the p53 Pathway Interact to Affect Cancer Risk, Progression, and Drug Response. *Cancer Research*, **2021**, 81, 1667-1680	10.1	7
31	Identifying mutation specific cancer pathways using a structurally resolved protein interaction network. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2015**, 84-95	1.3	6
30	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGI-5. *Human Mutation*, **2019**, 40, 1474-1485	4.7	5
29	The unfolded protein response links tumor aneuploidy to local immune dysregulation. *EMBO Reports*, **2021**, 22, e52509	6.5	5
28	Activation of NF-κB and p300/CBP potentiates cancer chemoimmunotherapy through induction of MHC-I antigen presentation. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	5
27	A common polymorphism in the retinoic acid pathway modifies adrenocortical carcinoma age-dependent incidence. *British Journal of Cancer*, **2020**, 122, 1231-1241	8.7	4
26	Exome-wide analysis of bi-allelic alterations identifies a Lynch phenotype in The Cancer Genome Atlas. *Genome Medicine*, **2018**, 10, 69	14.4	4
25	Mutation hotspots may not be drug targets. *Science*, **2019**, 364, 1228-1229	33.3	3
24	Intratumoral bacteria generate a new class of therapeutically relevant tumor antigens in melanoma. *Cancer Cell*, **2021**, 39, 601-603	24.3	3
23	Identifying Driver Interfaces Enriched for Somatic Missense Mutations in Tumors. *Methods in Molecular Biology*, **2019**, 1907, 51-72	1.4	3
22	Phenotypically supervised single-cell sequencing parses within-cell-type heterogeneity. *IScience*, **2021**, 24, 101991	6.1	3

21	In silico analysis suggests less effective MHC-II presentation of SARS-CoV-2 RBM peptides: Implication for neutralizing antibody responses. *PLoS ONE*, **2021**, 16, e0246731	3.7	3
20	Common genetic variation in the germline influences where and how tumors develop. *Molecular and Cellular Oncology*, **2017**, 4, e1302905	1.2	2
19	MHC-I genotype drives early immune selection of oncogenic mutations. *Molecular and Cellular Oncology*, **2018**, 5, e1409863	1.2	2
18	Germline and somatic genetic variants in the p53 pathway interact to affect cancer risk, progression and drug response		2
17	Loss of RNA-Binding Protein RBMS1 Promotes a Metastatic Transcriptional Program in Colorectal Cancer. *Cancer Discovery*, **2020**, 10, 1261-1262	24.4	2
16	Neoantigen Controversies. *Annual Review of Biomedical Data Science*, **2021**, 4, 227-253	5.6	2
15	The Cancer Epitope Database and Analysis Resource: A Blueprint for the Establishment of a New Bioinformatics Resource for Use by the Cancer Immunology Community. *Frontiers in Immunology*, **2021**, 12, 735609	8.4	2
14	Predicting functional consequences of mutations using molecular interaction network features. *Human Genetics*, **2021**, 1	6.3	2
13	Rare variant phasing using paired tumor:normal sequence data. *BMC Bioinformatics*, **2019**, 20, 265	3.6	1
12	The unfolded protein response links tumor aneuploidy to local immune dysregulation		1
11	Increasing metadata coverage of SRA BioSample entries using deep learning based Named Entity Recognition		1
10	Predicting functional consequences of mutations using molecular interaction network features		1
9	The Unfolded Protein Response at the Tumor-Immune Interface.. *Frontiers in Immunology*, **2022**, 13, 823857	8.4	1
8	Non-cancer-related pathogenic germline variants and expression consequences in ten-thousand cancer genomes. *Genome Medicine*, **2021**, 13, 147	14.4	0
7	Mutagenic exposures shape immunotherapy responses.. *Nature Cancer*, **2020**, 1, 1132-1133	15.4	
6	A phenotypically supervised single-cell analysis protocol to study within-cell-type heterogeneity of cultured mammalian cells. *STAR Protocols*, **2021**, 2, 100561	1.4	
5	IRE1 regulates macrophage polarization, PD-L1 expression, and tumor survival **2020**, 18, e3000687		
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3 IRE1α regulates macrophage polarization, PD-L1 expression, and tumor survival **2020**, 18, e3000687

2 IRE1α regulates macrophage polarization, PD-L1 expression, and tumor survival **2020**, 18, e3000687

1 EPEN-18. Oncogenic 3D genome conformations identify novel therapeutic targets in ependymoma. *Neuro-Oncology*, **2022**, 24, i42-i42 1