

Hannah Carter

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.

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	The Unfolded Protein Response at the Tumor-Immune Interface.. <i>Frontiers in Immunology</i> , 2022 , 13, 8231857	15.7	1
73	EPEN-18. Oncogenic 3D genome conformations identify novel therapeutic targets in ependymoma. <i>Neuro-Oncology</i> , 2022 , 24, i42-i42	1	
72	The unfolded protein response links tumor aneuploidy to local immune dysregulation. <i>EMBO Reports</i> , 2021 , 22, e52509	6.5	5
71	Intratumoral bacteria generate a new class of therapeutically relevant tumor antigens in melanoma. <i>Cancer Cell</i> , 2021 , 39, 601-603	24.3	3
70	A phenotypically supervised single-cell analysis protocol to study within-cell-type heterogeneity of cultured mammalian cells. <i>STAR Protocols</i> , 2021 , 2, 100561	1.4	
69	Neoantigen Controversies. <i>Annual Review of Biomedical Data Science</i> , 2021 , 4, 227-253	5.6	2
68	Phenotypically supervised single-cell sequencing parses within-cell-type heterogeneity. <i>iScience</i> , 2021 , 24, 101991	6.1	3
67	Activation of NF- κ B and p300/CBP potentiates cancer chemoimmunotherapy through induction of MHC-I antigen presentation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	5
66	In silico analysis suggests less effective MHC-II presentation of SARS-CoV-2 RBM peptides: Implication for neutralizing antibody responses. <i>PLoS ONE</i> , 2021 , 16, e0246731	3.7	3
65	Germline and Somatic Genetic Variants in the p53 Pathway Interact to Affect Cancer Risk, Progression, and Drug Response. <i>Cancer Research</i> , 2021 , 81, 1667-1680	10.1	7
64	The Cancer Epitope Database and Analysis Resource: A Blueprint for the Establishment of a New Bioinformatics Resource for Use by the Cancer Immunology Community. <i>Frontiers in Immunology</i> , 2021 , 12, 735609	8.4	2
63	Predicting functional consequences of mutations using molecular interaction network features. <i>Human Genetics</i> , 2021 , 1	6.3	2
62	Non-cancer-related pathogenic germline variants and expression consequences in ten-thousand cancer genomes. <i>Genome Medicine</i> , 2021 , 13, 147	14.4	0
61	Genomic and evolutionary classification of lung cancer in never smokers. <i>Nature Genetics</i> , 2021 , 53, 1348-1359	36.59	14
60	Targeted Coronary Artery Calcium Screening in High-Risk Younger Individuals Using Consumer Genetic Screening Results. <i>JACC: Cardiovascular Imaging</i> , 2021 , 14, 1398-1406	8.4	9
59	MHC-I genotype and tumor mutational burden predict response to immunotherapy. <i>Genome Medicine</i> , 2020 , 12, 45	14.4	32
58	IRE1 α and IGF signaling predict resistance to an endoplasmic reticulum stress-inducing drug in glioblastoma cells. <i>Scientific Reports</i> , 2020 , 10, 8348	4.9	9

57	IRE1 β regulates macrophage polarization, PD-L1 expression, and tumor survival. <i>PLoS Biology</i> , 2020 , 18, e3000687	9.7	11
56	Glioblastomas located in proximity to the subventricular zone (SVZ) exhibited enrichment of gene expression profiles associated with the cancer stem cell state. <i>Journal of Neuro-Oncology</i> , 2020 , 148, 455-462	4.8	9
55	A common polymorphism in the retinoic acid pathway modifies adrenocortical carcinoma age-dependent incidence. <i>British Journal of Cancer</i> , 2020 , 122, 1231-1241	8.7	4
54	Cell Adhesiveness Serves as a Biophysical Marker for Metastatic Potential. <i>Cancer Research</i> , 2020 , 80, 901-911	10.1	17
53	EPEN-04. ONCOGENIC 3D TUMOR GENOME ORGANIZATION IDENTIFIES NEW THERAPEUTIC TARGETS IN EPENDYMOMA. <i>Neuro-Oncology</i> , 2020 , 22, iii308-iii308	1	78
52	Telomerase and CD4 T Cell Immunity in Cancer. <i>Cancers</i> , 2020 , 12,	6.6	8
51	Loss of RNA-Binding Protein RBMS1 Promotes a Metastatic Transcriptional Program in Colorectal Cancer. <i>Cancer Discovery</i> , 2020 , 10, 1261-1262	24.4	2
50	Strength of immune selection in tumors varies with sex and age. <i>Nature Communications</i> , 2020 , 11, 4128	17.4	33
49	Mutagenic exposures shape immunotherapy responses.. <i>Nature Cancer</i> , 2020 , 1, 1132-1133	15.4	
48	IRE1 β regulates macrophage polarization, PD-L1 expression, and tumor survival 2020 , 18, e3000687		
47	IRE1 β regulates macrophage polarization, PD-L1 expression, and tumor survival 2020 , 18, e3000687		
46	IRE1 β regulates macrophage polarization, PD-L1 expression, and tumor survival 2020 , 18, e3000687		
45	IRE1 β regulates macrophage polarization, PD-L1 expression, and tumor survival 2020 , 18, e3000687		
44	Exploring the landscape of focal amplifications in cancer using AmpliconArchitect. <i>Nature Communications</i> , 2019 , 10, 392	17.4	59
43	Rare variant phasing using paired tumor:normal sequence data. <i>BMC Bioinformatics</i> , 2019 , 20, 265	3.6	1
42	Using a genetic risk score to calculate the optimal age for an individual to undergo coronary artery calcium screening. <i>Journal of Cardiovascular Computed Tomography</i> , 2019 , 13, 203-210	2.8	14
41	Evaluation and accurate diagnoses of pediatric diseases using artificial intelligence. <i>Nature Medicine</i> , 2019 , 25, 433-438	50.5	206
40	Elevated neoantigen levels in tumors with somatic mutations in the HLA-A, HLA-B, HLA-C and B2M genes. <i>BMC Medical Genomics</i> , 2019 , 12, 107	3.7	28

39	Mutation hotspots may not be drug targets. <i>Science</i> , 2019 , 364, 1228-1229	33.3	3
38	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGI-5. <i>Human Mutation</i> , 2019 , 40, 1474-1485	4.7	5
37	GPCRs show widespread differential mRNA expression and frequent mutation and copy number variation in solid tumors. <i>PLoS Biology</i> , 2019 , 17, e3000434	9.7	26
36	Identifying Driver Interfaces Enriched for Somatic Missense Mutations in Tumors. <i>Methods in Molecular Biology</i> , 2019 , 1907, 51-72	1.4	3
35	Integrating molecular networks with genetic variant interpretation for precision medicine. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2019 , 11, e1443	6.6	23
34	MHC-I genotype drives early immune selection of oncogenic mutations. <i>Molecular and Cellular Oncology</i> , 2018 , 5, e1409863	1.2	2
33	A global transcriptional network connecting noncoding mutations to changes in tumor gene expression. <i>Nature Genetics</i> , 2018 , 50, 613-620	36.3	74
32	The Emerging Potential for Network Analysis to Inform Precision Cancer Medicine. <i>Journal of Molecular Biology</i> , 2018 , 430, 2875-2899	6.5	50
31	Extracellular vesicles produced in B cells deliver tumor suppressor miR-335 to breast cancer cells disrupting oncogenic programming in vitro and in vivo. <i>Scientific Reports</i> , 2018 , 8, 17581	4.9	9
30	Integrative genomic analysis of mouse and human hepatocellular carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E9879-E9888	11.5	40
29	Exome-wide analysis of bi-allelic alterations identifies a Lynch phenotype in The Cancer Genome Atlas. <i>Genome Medicine</i> , 2018 , 10, 69	14.4	4
28	Evolutionary Pressure against MHC Class II Binding Cancer Mutations. <i>Cell</i> , 2018 , 175, 416-428.e13	56.2	98
27	Interaction Landscape of Inherited Polymorphisms with Somatic Events in Cancer. <i>Cancer Discovery</i> , 2017 , 7, 410-423	24.4	77
26	Epigenetic aging signatures in mice livers are slowed by dwarfism, calorie restriction and rapamycin treatment. <i>Genome Biology</i> , 2017 , 18, 57	18.3	176
25	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. <i>Human Mutation</i> , 2017 , 38, 1266-1276	4.7	9
24	Common genetic variation in the germline influences where and how tumors develop. <i>Molecular and Cellular Oncology</i> , 2017 , 4, e1302905	1.2	2
23	MHC-I Genotype Restricts the Oncogenic Mutational Landscape. <i>Cell</i> , 2017 , 171, 1272-1283.e15	56.2	180
22	Circulating tumour DNA methylation markers for diagnosis and prognosis of hepatocellular carcinoma. <i>Nature Materials</i> , 2017 , 16, 1155-1161	27	387

21	3D collagen architecture induces a conserved migratory and transcriptional response linked to vasculogenic mimicry. <i>Nature Communications</i> , 2017 , 8, 1651	17.4	76
20	Pan-cancer analysis reveals technical artifacts in TCGA germline variant calls. <i>BMC Genomics</i> , 2017 , 18, 458	4.5	21
19	Challenges in identifying cancer genes by analysis of exome sequencing data. <i>Nature Communications</i> , 2016 , 7, 12096	17.4	27
18	Structure-Based Analysis Reveals Cancer Missense Mutations Target Protein Interaction Interfaces. <i>PLoS ONE</i> , 2016 , 11, e0152929	3.7	56
17	Immune DNA signature of T-cell infiltration in breast tumor exomes. <i>Scientific Reports</i> , 2016 , 6, 30064	4.9	24
16	Hybrid Periportal Hepatocytes Regenerate the Injured Liver without Giving Rise to Cancer. <i>Cell</i> , 2015 , 162, 766-79	56.2	311
15	Identifying mutation specific cancer pathways using a structurally resolved protein interaction network. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2015 , 84-95	1.3	6
14	Multi-tiered genomic analysis of head and neck cancer ties TP53 mutation to 3p loss. <i>Nature Genetics</i> , 2014 , 46, 939-43	36.3	101
13	Predicting the functional consequences of somatic missense mutations found in tumors. <i>Methods in Molecular Biology</i> , 2014 , 1101, 135-59	1.4	8
12	Identifying Mendelian disease genes with the variant effect scoring tool. <i>BMC Genomics</i> , 2013 , 14 Suppl 3, S3	4.5	240
11	Network-based stratification of tumor mutations. <i>Nature Methods</i> , 2013 , 10, 1108-15	21.6	546
10	Genotype to phenotype via network analysis. <i>Current Opinion in Genetics and Development</i> , 2013 , 23, 611-21	4.9	88
9	CRAVAT: cancer-related analysis of variants toolkit. <i>Bioinformatics</i> , 2013 , 29, 647-8	7.2	98
8	CHASM and SNVBox: toolkit for detecting biologically important single nucleotide mutations in cancer. <i>Bioinformatics</i> , 2011 , 27, 2147-8	7.2	86
7	Prioritization of driver mutations in pancreatic cancer using cancer-specific high-throughput annotation of somatic mutations (CHASM). <i>Cancer Biology and Therapy</i> , 2010 , 10, 582-7	4.6	70
6	Cancer-specific high-throughput annotation of somatic mutations: computational prediction of driver missense mutations. <i>Cancer Research</i> , 2009 , 69, 6660-7	10.1	344
5	The unfolded protein response links tumor aneuploidy to local immune dysregulation		1
4	Increasing metadata coverage of SRA BioSample entries using deep learning based Named Entity Recognition		1

3	Germline and somatic genetic variants in the p53 pathway interact to affect cancer risk, progression and drug response	2
2	Predicting functional consequences of mutations using molecular interaction network features	1
1	Potential global impact of the N501Y mutation on MHC-II presentation and immune escape	7