

Scott L Carter

List of Publications by Year in descending order

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Version: 2024-02-01

71
papers

42,350
citations

31902

53
h-index

85405

71
g-index

73
all docs

73
docs citations

73
times ranked

59027
citing authors

#	ARTICLE	IF	CITATIONS
1	CNGPLD: case-“control copy-number analysis using Gaussian process latent difference. <i>Bioinformatics</i> , 2022, , .	1.8	0
2	Microenvironmental Landscape of Human Melanoma Brain Metastases in Response to Immune Checkpoint Inhibition. <i>Cancer Immunology Research</i> , 2022, 10, 996-1012.	1.6	18
3	Distinct genetic pathways define pre-malignant versus compensatory clonal hematopoiesis in Shwachman-Diamond syndrome. <i>Nature Communications</i> , 2021, 12, 1334.	5.8	103
4	Palbociclib demonstrates intracranial activity in progressive brain metastases harboring cyclin-dependent kinase pathway alterations. <i>Nature Cancer</i> , 2021, 2, 498-502.	5.7	26
5	Detection of Leptomeningeal Disease Using Cell-Free DNA From Cerebrospinal Fluid. <i>JAMA Network Open</i> , 2021, 4, e2120040.	2.8	27
6	Phase II study of ipilimumab and nivolumab in leptomeningeal carcinomatosis. <i>Nature Communications</i> , 2021, 12, 5954.	5.8	35
7	Genomic and transcriptomic correlates of immunotherapy response within the tumor microenvironment of leptomeningeal metastases. <i>Nature Communications</i> , 2021, 12, 5955.	5.8	25
8	Inactivation of <i>Fbxw7</i> Impairs dsRNA Sensing and Confers Resistance to PD-1 Blockade. <i>Cancer Discovery</i> , 2020, 10, 1296-1311.	7.7	49
9	Single-arm, open-label phase 2 trial of pembrolizumab in patients with leptomeningeal carcinomatosis. <i>Nature Medicine</i> , 2020, 26, 1280-1284.	15.2	83
10	Temozolomide in secondary prevention of HER2-positive breast cancer brain metastases. <i>Future Oncology</i> , 2020, 16, 899-909.	1.1	22
11	Genomic characterization of human brain metastases identifies drivers of metastatic lung adenocarcinoma. <i>Nature Genetics</i> , 2020, 52, 371-377.	9.4	177
12	Integrative Molecular Characterization of Resistance to Neoadjuvant Chemoradiation in Rectal Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 5561-5571.	3.2	64
13	Targeting the PI3K/Akt/mTOR pathway with the pan-Akt inhibitor GDC-0068 in PIK3CA-mutant breast cancer brain metastases. <i>Neuro-Oncology</i> , 2019, 21, 1401-1411.	0.6	70
14	The Dual PI3K/mTOR Pathway Inhibitor GDC-0084 Achieves Antitumor Activity in <i>PIK3CA</i> -Mutant Breast Cancer Brain Metastases. <i>Clinical Cancer Research</i> , 2019, 25, 3374-3383.	3.2	57
15	MYD88 L265P mutation and CDKN2A loss are early mutational events in primary central nervous system diffuse large B-cell lymphomas. <i>Blood Advances</i> , 2019, 3, 375-383.	2.5	77
16	Detection of Mutations in Barrett’s Esophagus Before Progression to High-Grade Dysplasia or Adenocarcinoma. <i>Gastroenterology</i> , 2018, 155, 156-167.	0.6	110
17	DMD genomic deletions characterize a subset of progressive/higher-grade meningiomas with poor outcome. <i>Acta Neuropathologica</i> , 2018, 136, 779-792.	3.9	66
18	Real-time Genomic Characterization of Advanced Pancreatic Cancer to Enable Precision Medicine. <i>Cancer Discovery</i> , 2018, 8, 1096-1111.	7.7	256

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19	Germline and somatic BAP1 mutations in high-grade rhabdoid meningiomas. <i>Neuro-Oncology</i> , 2017, 19, now235.	0.6	99
20	Loss of PTEN Is Associated with Resistance to Anti-PD-1 Checkpoint Blockade Therapy in Metastatic Uterine Leiomyosarcoma. <i>Immunity</i> , 2017, 46, 197-204.	6.6	400
21	Genomic Heterogeneity and Exceptional Response to Dual Pathway Inhibition in Anaplastic Thyroid Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 2367-2373.	3.2	24
22	Landscape of Genomic Alterations in Pituitary Adenomas. <i>Clinical Cancer Research</i> , 2017, 23, 1841-1851.	3.2	94
23	Genomic Evolution after Chemoradiotherapy in Anal Squamous Cell Carcinoma. <i>Clinical Cancer Research</i> , 2017, 23, 3214-3222.	3.2	44
24	Genomic Resistance Patterns to Second-Generation Androgen Blockade in Paired Tumor Biopsies of Metastatic Castration-Resistant Prostate Cancer. <i>JCO Precision Oncology</i> , 2017, 1, 1-11.	1.5	13
25	Systematic genomic and translational efficiency studies of uveal melanoma. <i>PLoS ONE</i> , 2017, 12, e0178189.	1.1	34
26	Genomic evolution and chemoresistance in germ-cell tumours. <i>Nature</i> , 2016, 540, 114-118.	13.7	139
27	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	7.7	482
28	Brain Metastasis: Clinical Implications of Branched Evolution. <i>Trends in Cancer</i> , 2016, 2, 332-337.	3.8	16
29	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. <i>Nature Genetics</i> , 2016, 48, 848-855.	9.4	174
30	A comparative assessment of clinical whole exome and transcriptome profiling across sequencing centers: implications for precision cancer medicine. <i>Oncotarget</i> , 2016, 7, 52888-52899.	0.8	18
31	Long-term Benefit of PD-L1 Blockade in Lung Cancer Associated with <i>JAK3</i> Activation. <i>Cancer Immunology Research</i> , 2015, 3, 855-863.	1.6	60
32	Paired exome analysis of Barrett's esophagus and adenocarcinoma. <i>Nature Genetics</i> , 2015, 47, 1047-1055.	9.4	310
33	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	13.9	2,582
34	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. <i>Cell</i> , 2015, 161, 933-945.	13.5	1,710
35	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. <i>Cancer Discovery</i> , 2015, 5, 1164-1177.	7.7	821
36	Mutations driving CLL and their evolution in progression and relapse. <i>Nature</i> , 2015, 526, 525-530.	13.7	868

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37	Genomic Correlate of Exceptional Erlotinib Response in Head and Neck Squamous Cell Carcinoma. <i>JAMA Oncology</i> , 2015, 1, 238.	3.4	44
38	Complementary genomic approaches highlight the PI3K/mTOR pathway as a common vulnerability in osteosarcoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5564-73.	3.3	355
39	The Genetic Landscape of Clinical Resistance to RAF Inhibition in Metastatic Melanoma. <i>Cancer Discovery</i> , 2014, 4, 94-109.	7.7	782
40	The Genomic Landscape of Pediatric Ewing Sarcoma. <i>Cancer Discovery</i> , 2014, 4, 1326-1341.	7.7	415
41	MAP Kinase Pathway Alterations in <i>BRAF</i> -Mutant Melanoma Patients with Acquired Resistance to Combined RAF/MEK Inhibition. <i>Cancer Discovery</i> , 2014, 4, 61-68.	7.7	419
42	Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. <i>Cancer Cell</i> , 2014, 25, 91-101.	7.7	847
43	Genetic and Clonal Dissection of Murine Small Cell Lung Carcinoma Progression by Genome Sequencing. <i>Cell</i> , 2014, 156, 1298-1311.	13.5	241
44	Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. <i>Nature Medicine</i> , 2014, 20, 682-688.	15.2	508
45	Landscape of genomic alterations in cervical carcinomas. <i>Nature</i> , 2014, 506, 371-375.	13.7	708
46	Response and Acquired Resistance to Everolimus in Anaplastic Thyroid Cancer. <i>New England Journal of Medicine</i> , 2014, 371, 1426-1433.	13.9	290
47	An APOBEC cytidine deaminase mutagenesis pattern is widespread in human cancers. <i>Nature Genetics</i> , 2013, 45, 970-976.	9.4	1,023
48	A Tumor Suppressor Complex with GAP Activity for the Rag GTPases That Signal Amino Acid Sufficiency to mTORC1. <i>Science</i> , 2013, 340, 1100-1106.	6.0	863
49	Pan-cancer patterns of somatic copy number alteration. <i>Nature Genetics</i> , 2013, 45, 1134-1140.	9.4	1,616
50	Somatic mutation of CDKN1B in small intestine neuroendocrine tumors. <i>Nature Genetics</i> , 2013, 45, 1483-1486.	9.4	275
51	Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. <i>Cell</i> , 2013, 152, 714-726.	13.5	1,202
52	Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. <i>Nature Biotechnology</i> , 2013, 31, 213-219.	9.4	3,934
53	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. <i>Nature Genetics</i> , 2013, 45, 478-486.	9.4	671
54	Punctuated Evolution of Prostate Cancer Genomes. <i>Cell</i> , 2013, 153, 666-677.	13.5	1,107

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55	Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , 2013, 499, 214-218.	13.7	4,761
56	The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , 2013, 45, 279-284.	9.4	990
57	Somatic rearrangements across cancer reveal classes of samples with distinct patterns of DNA breakage and rearrangement-induced hypermutability. <i>Genome Research</i> , 2013, 23, 228-235.	2.4	124
58	Resistance to CDK2 Inhibitors Is Associated with Selection of Polyploid Cells in <i>CCNE1</i> -Amplified Ovarian Cancer. <i>Clinical Cancer Research</i> , 2013, 19, 5960-5971.	3.2	97
59	Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. <i>Nature</i> , 2012, 488, 106-110.	13.7	675
60	Melanoma genome sequencing reveals frequent <i>PREX2</i> mutations. <i>Nature</i> , 2012, 485, 502-506.	13.7	671
61	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. <i>Nature Genetics</i> , 2012, 44, 1104-1110.	9.4	1,186
62	Absolute quantification of somatic DNA alterations in human cancer. <i>Nature Biotechnology</i> , 2012, 30, 413-421.	9.4	1,710
63	Exome sequencing identifies recurrent <i>SPOP</i> , <i>FOXA1</i> and <i>MED12</i> mutations in prostate cancer. <i>Nature Genetics</i> , 2012, 44, 685-689.	9.4	1,300
64	Sequence analysis of mutations and translocations across breast cancer subtypes. <i>Nature</i> , 2012, 486, 405-409.	13.7	1,107
65	A remarkably simple genome underlies highly malignant pediatric rhabdoid cancers. <i>Journal of Clinical Investigation</i> , 2012, 122, 2983-2988.	3.9	347
66	The Mutational Landscape of Head and Neck Squamous Cell Carcinoma. <i>Science</i> , 2011, 333, 1157-1160.	6.0	2,225
67	The genomic complexity of primary human prostate cancer. <i>Nature</i> , 2011, 470, 214-220.	13.7	1,107
68	Stathmin is superior to AKT and phospho-AKT staining for the detection of phosphoinositide 3-kinase activation and aggressive endometrial cancer. <i>Histopathology</i> , 2010, 57, 641-646.	1.6	16
69	High-resolution mapping of copy-number alterations with massively parallel sequencing. <i>Nature Methods</i> , 2009, 6, 99-103.	9.0	462
70	A signature of chromosomal instability inferred from gene expression profiles predicts clinical outcome in multiple human cancers. <i>Nature Genetics</i> , 2006, 38, 1043-1048.	9.4	1,002
71	Redefinition of Affymetrix probe sets by sequence overlap with cDNA microarray probes reduces cross-platform inconsistencies in cancer-associated gene expression measurements. <i>BMC Bioinformatics</i> , 2005, 6, 107.	1.2	113