

Steven E Schumacher

List of Publications by Year in descending order

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58
papers

32,723
citations

34105

52
h-index

133252

59
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65
all docs

65
docs citations

65
times ranked

48634
citing authors

#	ARTICLE	IF	CITATIONS
1	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	27.8	424
2	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020, 52, 331-341.	21.4	431
3	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	28.9	1,670
4	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018, 173, 291-304.e6.	28.9	1,718
5	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	28.9	2,111
6	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018, 23, 194-212.e6.	6.4	245
7	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	14.3	3,706
8	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	6.4	119
9	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	6.4	83
10	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	6.4	801
11	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018, 23, 255-269.e4.	6.4	204
12	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018, 33, 244-258.e10.	16.8	270
13	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018, 6, 282-300.e2.	6.2	284
14	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	16.8	750
15	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	16.8	396
16	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	16.8	478
17	SvABA: genome-wide detection of structural variants and indels by local assembly. <i>Genome Research</i> , 2018, 28, 581-591.	5.5	288
18	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018, 7, 422-437.e7.	6.2	134

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19	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018, 25, 1304-1317.e5.	6.4	329
20	Targeting wild-type KRAS-amplified gastroesophageal cancer through combined MEK and SHP2 inhibition. <i>Nature Medicine</i> , 2018, 24, 968-977.	30.7	196
21	Clinical targeted exome-based sequencing in combination with genome-wide copy number profiling: precision medicine analysis of 203 pediatric brain tumors. <i>Neuro-Oncology</i> , 2017, 19, now294.	1.2	54
22	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.	16.8	532
23	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	28.9	1,794
24	Sporadic Early-Onset Diffuse Gastric Cancers Have High Frequency of Somatic CDH1 Alterations, but Low Frequency of Somatic RHOA Mutations Compared With Late-Onset Cancers. <i>Gastroenterology</i> , 2017, 153, 536-549.e26.	1.3	90
25	Genomic landscape of high-grade meningiomas. <i>Npj Genomic Medicine</i> , 2017, 2, .	3.8	130
26	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	16.8	309
27	Pan-Cancer Analysis Links PARK2 to BCL-XL-Dependent Control of Apoptosis. <i>Neoplasia</i> , 2017, 19, 75-83.	5.3	27
28	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	27.8	787
29	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	16.8	642
30	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	16.8	1,428
31	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	28.9	738
32	Landscape of Genomic Alterations in Pituitary Adenomas. <i>Clinical Cancer Research</i> , 2017, 23, 1841-1851.	7.0	94
33	Tumor-suppressor genes that escape from X-inactivation contribute to cancer sex bias. <i>Nature Genetics</i> , 2017, 49, 10-16.	21.4	307
34	Somatic copy number alterations in gastric adenocarcinomas among Asian and Western patients. <i>PLoS ONE</i> , 2017, 12, e0176045.	2.5	28
35	Genomic evolution and chemoresistance in germ-cell tumours. <i>Nature</i> , 2016, 540, 114-118.	27.8	139
36	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	16.8	482

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37	Recurrent hormone-binding domain truncated ESR1 amplifications in primary endometrial cancers suggest their implication in hormone independent growth. <i>Scientific Reports</i> , 2016, 6, 25521.	3.3	13
38	MYB-QKI rearrangements in angiocentric glioma drive tumorigenicity through a tripartite mechanism. <i>Nature Genetics</i> , 2016, 48, 273-282.	21.4	214
39	<i>MECP2</i> Is a Frequently Amplified Oncogene with a Novel Epigenetic Mechanism That Mimics the Role of Activated RAS in Malignancy. <i>Cancer Discovery</i> , 2016, 6, 45-58.	9.4	57
40	Expression profiles of 151 pediatric low-grade gliomas reveal molecular differences associated with location and histological subtype. <i>Neuro-Oncology</i> , 2015, 17, 1486-1496.	1.2	39
41	Clinical implementation of integrated whole-genome copy number and mutation profiling for glioblastoma. <i>Neuro-Oncology</i> , 2015, 17, 1344-1355.	1.2	40
42	Exome sequencing of lymphomas from three dog breeds reveals somatic mutation patterns reflecting genetic background. <i>Genome Research</i> , 2015, 25, 1634-1645.	5.5	96
43	Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. <i>Cancer Cell</i> , 2014, 25, 91-101.	16.8	847
44	Pan-cancer genetic analysis identifies <i>PARK2</i> as a master regulator of G1/S cyclins. <i>Nature Genetics</i> , 2014, 46, 588-594.	21.4	144
45	BET Bromodomain Inhibition of <i>MYC</i> -Amplified Medulloblastoma. <i>Clinical Cancer Research</i> , 2014, 20, 912-925.	7.0	296
46	Pan-cancer patterns of somatic copy number alteration. <i>Nature Genetics</i> , 2013, 45, 1134-1140.	21.4	1,616
47	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. <i>Nature Genetics</i> , 2013, 45, 478-486.	21.4	671
48	Systematic Interrogation of 3q26 Identifies <i>TLOC1</i> and <i>SKIL</i> as Cancer Drivers. <i>Cancer Discovery</i> , 2013, 3, 1044-1057.	9.4	71
49	ATARiS: Computational quantification of gene suppression phenotypes from multisample RNAi screens. <i>Genome Research</i> , 2013, 23, 665-678.	5.5	110
50	Genomic analysis of diffuse pediatric low-grade gliomas identifies recurrent oncogenic truncating rearrangements in the transcription factor <i>MYBL1</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8188-8193.	7.1	188
51	Integrated Genomic Analysis of the 8q24 Amplification in Endometrial Cancers Identifies <i>ATAD2</i> as Essential to <i>MYC</i> -Dependent Cancers. <i>PLoS ONE</i> , 2013, 8, e54873.	2.5	70
52	Gastrointestinal Adenocarcinomas of the Esophagus, Stomach, and Colon Exhibit Distinct Patterns of Genome Instability and Oncogenesis. <i>Cancer Research</i> , 2012, 72, 4383-4393.	0.9	242
53	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , 2012, 488, 49-56.	27.8	761
54	β -Catenin-Driven Cancers Require a YAP1 Transcriptional Complex for Survival and Tumorigenesis. <i>Cell</i> , 2012, 151, 1457-1473.	28.9	647

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55	Cancer Vulnerabilities Unveiled by Genomic Loss. <i>Cell</i> , 2012, 150, 842-854.	28.9	209
56	Sequence analysis of mutations and translocations across breast cancer subtypes. <i>Nature</i> , 2012, 486, 405-409.	27.8	1,107
57	GISTIC2.0 facilitates sensitive and confident localization of the targets of focal somatic copy-number alteration in human cancers. <i>Genome Biology</i> , 2011, 12, R41.	8.8	2,546
58	Genetic and Functional Studies Implicate <i>HIF1</i> as a 14q Kidney Cancer Suppressor Gene. <i>Cancer Discovery</i> , 2011, 1, 222-235.	9.4	347