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 g-index
65 all docs	65 docs citations	65 times ranked	48634 citing authors

#	Article	IF	Citations
1	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
2	GISTIC2.0 facilitates sensitive and confident localization of the targets of focal somatic copy-number alteration in human cancers. Genome Biology, 2011, 12, R41.	8.8	2,546
3	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
4	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	28.9	1,794
5	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
6	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
7	Pan-cancer patterns of somatic copy number alteration. Nature Genetics, 2013, 45, 1134-1140.	21.4	1,616
8	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	16.8	1,428
9	Sequence analysis of mutations and translocations across breast cancer subtypes. Nature, 2012, 486, 405-409.	27.8	1,107
10	Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. Cancer Cell, 2014, 25, 91-101.	16.8	847
11	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
12	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
13	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. Nature, 2012, 488, 49-56.	27.8	761
14	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
15	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
16	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. Nature Genetics, 2013, 45, 478-486.	21.4	671
17	Î²-Catenin-Driven Cancers Require a YAP1 Transcriptional Complex for Survival and Tumorigenesis. Cell, 2012, 151, 1457-1473.	28.9	647
18	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	16.8	642

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19	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	16.8	532
20	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	16.8	482
21	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	16.8	478
22	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	21.4	431
23	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	27.8	424
24	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	16.8	396
25	Genetic and Functional Studies Implicate HIF1Î± as a 14q Kidney Cancer Suppressor Gene. Cancer Discovery, 2011, 1, 222-235.	9.4	347
26	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5.	6.4	329
27	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	16.8	309
28	Tumor-suppressor genes that escape from X-inactivation contribute to cancer sex bias. Nature Genetics, 2017, 49, 10-16.	21.4	307
29	BET Bromodomain Inhibition of MYC-Amplified Medulloblastoma. Clinical Cancer Research, 2014, 20, 912-925.	7.0	296
30	SvABA: genome-wide detection of structural variants and indels by local assembly. Genome Research, 2018, 28, 581-591.	5.5	288
31	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	6.2	284
32	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	16.8	270
33	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	6.4	245
34	Gastrointestinal Adenocarcinomas of the Esophagus, Stomach, and Colon Exhibit Distinct Patterns of Genome Instability and Oncogenesis. Cancer Research, 2012, 72, 4383-4393.	0.9	242
35	MYB-QKI rearrangements in angiocentric glioma drive tumorigenicity through a tripartite mechanism. Nature Genetics, 2016, 48, 273-282.	21.4	214
36	Cancer Vulnerabilities Unveiled by Genomic Loss. Cell, 2012, 150, 842-854.	28.9	209

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37	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	6.4	204
38	Targeting wild-type KRAS-amplified gastroesophageal cancer through combined MEK and SHP2 inhibition. Nature Medicine, 2018, 24, 968-977.	30.7	196
39	Genomic analysis of diffuse pediatric low-grade gliomas identifies recurrent oncogenic truncating rearrangements in the transcription factor MYBL1. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8188-8193.	7.1	188
40	Pan-cancer genetic analysis identifies PARK2 as a master regulator of G1/S cyclins. Nature Genetics, 2014, 46, 588-594.	21.4	144
41	Genomic evolution and chemoresistance in germ-cell tumours. Nature, 2016, 540, 114-118.	27.8	139
42	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î² Superfamily. Cell Systems, 2018, 7, 422-437.e7.	6.2	134
43	Genomic landscape of high-grade meningiomas. Npj Genomic Medicine, 2017, 2, .	3.8	130
44	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	6.4	119
45	ATARiS: Computational quantification of gene suppression phenotypes from multisample RNAi screens. Genome Research, 2013, 23, 665-678.	5.5	110
46	Exome sequencing of lymphomas from three dog breeds reveals somatic mutation patterns reflecting genetic background. Genome Research, 2015, 25, 1634-1645.	5.5	96
47	Landscape of Genomic Alterations in Pituitary Adenomas. Clinical Cancer Research, 2017, 23, 1841-1851.	7.0	94
48	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. Gastroenterology, 2017, 153, 536-549.e26.	1.3	90
49	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	6.4	83
50	Systematic Interrogation of 3q26 Identifies TLOC1 and SKIL as Cancer Drivers. Cancer Discovery, 2013, 3, 1044-1057.	9.4	71
51	Integrated Genomic Analysis of the 8q24 Amplification in Endometrial Cancers Identifies ATAD2 as Essential to MYC-Dependent Cancers. PLoS ONE, 2013, 8, e54873.	2.5	70
52	MECP2 Is a Frequently Amplified Oncogene with a Novel Epigenetic Mechanism That Mimics the Role of Activated RAS in Malignancy. Cancer Discovery, 2016, 6, 45-58.	9.4	57
53	Clinical targeted exome-based sequencing in combination with genome-wide copy number profiling: precision medicine analysis of 203 pediatric brain tumors. Neuro-Oncology, 2017, 19, now294.	1.2	54
54	Clinical implementation of integrated whole-genome copy number and mutation profiling for glioblastoma. Neuro-Oncology, 2015, 17, 1344-1355.	1.2	40

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55	Expression profiles of 151 pediatric low-grade gliomas reveal molecular differences associated with location and histological subtype. Neuro-Oncology, 2015, 17, 1486-1496.	1.2	39
56	Somatic copy number alterations in gastric adenocarcinomas among Asian and Western patients. PLoS ONE, 2017, 12, e0176045.	2.5	28
57	Pan-Cancer Analysis Links PARK2 to BCL-XL-Dependent Control of Apoptosis. Neoplasia, 2017, 19, 75-83.	5.3	27
58	Recurrent hormone-binding domain truncated ESR1 amplifications in primary endometrial cancers suggest their implication in hormone independent growth. Scientific Reports, 2016, 6, 25521.	3.3	13