Eve Shinbrot

List of Publications by Year
in descending order

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52 papers	26,458 citations	57631 44 h-index	205818 48 g-index
56 all docs	56 docs citations	56 times ranked	37146 citing authors

#	Article	IF	Citations
1	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. Nature Communications, 2020, 11, 3644.	5.8	55
2	An enhanced genetic model of colorectal cancer progression history. Genome Biology, 2019, 20, 168.	3.8	34
3	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. Cancer Discovery, 2018, 8, 730-749.	7.7	367
4	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
5	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	13.5	1,718
6	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	13.5	228
7	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
8	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	13.5	1,417
9	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
10	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	13.5	620
11	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	2.9	333
12	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	2.9	407
13	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	2.9	245
14	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	2.9	205
15	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	2.9	523
16	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	2.9	683
17	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
18	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	2.9	119

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19	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	2.9	83
20	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
21	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	2.9	204
22	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	2.9	177
23	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	2.9	605
24	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	2.9	284
25	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9.	7.7	400
26	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750
27	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	7.7	396
28	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	7.7	478
29	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-β Superfamily. Cell Systems, 2018, 7, 422-437.e7.	2.9	134
30	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5.	2.9	329
31	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	7.7	623
32	Abstract 5506: NOTCH1 activation in head and neck squamous cell carcinoma leads to growth inhibition, changes in gene expression associated with early differentiation, and acquisition of stem cell-like properties. , 2018, , .		0
33	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
34	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	2.9	416
35	Comprehensive analysis of tumor NGS data to demonstrate pathways pointing to therapeutic targeting options.. Journal of Clinical Oncology, 2017, 35, e23153-e23153.	0.8	0
36	Tumor profiling from whole-genome and whole transcriptome sequencing to uncover gene fusions and structural variations in clinically relevant cancer genes.. Journal of Clinical Oncology, 2017, 35, e23118-e23118.	0.8	0

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37	Abstract 1286: Targeted deep sequencing of colorectal tumor tissues to study associations of tumor subtypes with germline genetic, lifestyle, and environmental risk factors. , 2017, , .		0
38	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. Cell Reports, 2016, 14, 2476-2489.	2.9	298
39	Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. Cell, 2016, 164, 538-549.	13.5	363
40	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. Cell Reports, 2016, 14, 907-919.	2.9	107
41	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	13.9	1,040
42	Abstract 5221: Linking the molecular profile of colorectal tumors to germline genetic and environmental risk factors. , 2016, , .		0
43	Abstract 136: Refining the molecular profile of colorectal tumors to expand prevention and treatment opportunities. , 2016, , .		0
44	Mutational Landscape of Aggressive Cutaneous Squamous Cell Carcinoma. Clinical Cancer Research, 2014, 20, 6582-6592.	3.2	493
45	Effects of <scp>TP53</scp> mutational status on gene expression patterns across 10 human cancer types. Journal of Pathology, 2014, 232, 522-533.	2.1	65
46	Trans-ancestry mutational landscape of hepatocellular carcinoma genomes. Nature Genetics, 2014, 46, 1267-1273.	9.4	655
47	Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. Genome Research, 2014, 24, 1740-1750.	2.4	244
48	Abstract 2211: Viral subtypes in hepatocellular carcinoma are associated with different mechanisms of WNT/CTNNB1 alteration. , 2014, , .		0
49	MLH1â€silenced and nonâ€silenced subgroups of hypermutated colorectal carcinomas have distinct mutational landscapes. Journal of Pathology, 2013, 229, 99-110.	2.1	67
50	Use of fusions to green fluorescent protein in the detection of apoptosis. Methods in Enzymology, 2000, 327, 513-IN8.	0.4	5
51	Morphological Detection of Plasma Membrane Changes During Apoptosis Using Enhanced Green Fluorescent Protein. BioTechniques, 1999, 26, 1064-1068.	0.8	3
52	Isolation and characterization of the platelet-derived growth factor beta receptor promoter. Developmental Dynamics, 1997, 208, 211-219.	0.8	5