

# Eve Shinbrot

## List of Publications by Citations

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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.

48  
papers

14,703  
citations

43  
h-index

56  
g-index

56  
ext. papers

21,454  
ext. citations

21.8  
avg, IF

4.15  
L-index

#	Paper	IF	Citations
48	The Immune Landscape of Cancer. <i>Immunity</i> , <b>2018</b> , 48, 812-830.e14	32.3	1754
47	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , <b>2017</b> , 169, 1327-1341.e23	56.2	1125
46	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , <b>2018</b> , 173, 321-337.e10	56.2	1124
45	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , <b>2018</b> , 173, 291-304.e6	56.2	888
44	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , <b>2018</b> , 173, 371-385.e18	56.2	854
43	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , <b>2016</b> , 374, 135-45	59.2	753
42	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , <b>2018</b> , 173, 338-354.e15	56.2	560
41	Trans-ancestry mutational landscape of hepatocellular carcinoma genomes. <i>Nature Genetics</i> , <b>2014</b> , 46, 1267-73	36.3	491
40	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , <b>2018</b> , 23, 239-254.e6	10.6	405
39	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , <b>2018</b> , 33, 676-689.e3	24.3	377
38	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , <b>2018</b> , 23, 181-193.e7	10.6	366
37	Mutational landscape of aggressive cutaneous squamous cell carcinoma. <i>Clinical Cancer Research</i> , <b>2014</b> , 20, 6582-92	12.9	362
36	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , <b>2018</b> , 173, 355-370.e14	56.2	342
35	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , <b>2018</b> , 34, 211-224.e6	24.3	327
34	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , <b>2018</b> , 6, 271-281.e7	10.6	320
33	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , <b>2018</b> , 23, 313-326.e5	10.6	295
32	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , <b>2018</b> , 33, 690-705.e9	24.3	277

31	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , <b>2018</b> , 33, 706-720.e9	24.3	275
30	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , <b>2017</b> , 18, 2780-2794	10.6	247
29	Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. <i>Cell</i> , <b>2016</b> , 164, 538-49	56.2	239
28	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. <i>Cancer Discovery</i> , <b>2018</b> , 8, 730-749	24.4	235
27	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , <b>2018</b> , 23, 227-238.e3	10.6	235
26	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , <b>2018</b> , 33, 721-735.e8	24.3	228
25	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. <i>Cell Reports</i> , <b>2016</b> , 14, 2476-89	10.6	228
24	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , <b>2018</b> , 23, 282-296.e4	10.6	188
23	Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. <i>Genome Research</i> , <b>2014</b> , 24, 1740-50	9.7	187
22	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , <b>2018</b> , 173, 305-320.e10	56.2	166
21	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , <b>2018</b> , 6, 282-300.e2	10.6	159
20	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , <b>2018</b> , 25, 1304-1317.e5	10.6	152
19	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , <b>2018</b> , 23, 297-312.e12	10.6	147
18	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , <b>2018</b> , 23, 194-212.e6	10.6	146
17	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , <b>2018</b> , 173, 386-399.e12	56.2	133
16	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , <b>2018</b> , 23, 270-281.e3	10.6	121
15	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , <b>2018</b> , 23, 255-269.e4	10.6	112
14	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- $\beta$ Superfamily. <i>Cell Systems</i> , <b>2018</b> , 7, 422-437.e7	10.6	85

13	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. <i>Cell Reports</i> , <b>2016</b> , 14, 907-919	10.6	75
12	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , <b>2018</b> , 23, 172-180.e3	10.6	66
11	MLH1-silenced and non-silenced subgroups of hypermutated colorectal carcinomas have distinct mutational landscapes. <i>Journal of Pathology</i> , <b>2013</b> , 229, 99-110	9.4	58
10	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , <b>2018</b> , 23, 213-226.e3	9.3	56
9	Effects of TP53 mutational status on gene expression patterns across 10 human cancer types. <i>Journal of Pathology</i> , <b>2014</b> , 232, 522-33	9.4	52
8	An enhanced genetic model of colorectal cancer progression history. <i>Genome Biology</i> , <b>2019</b> , 20, 168	18.3	21
7	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. <i>Nature Communications</i> , <b>2020</b> , 11, 3644	17.4	16
6	Mutation signatures reveal biological processes in human cancer		11
5	Use of fusions to green fluorescent protein in the detection of apoptosis. <i>Methods in Enzymology</i> , <b>2000</b> , 327, 513-22	1.7	5
4	Morphological detection of plasma membrane changes during apoptosis using enhanced green fluorescent protein. <i>BioTechniques</i> , <b>1999</b> , 26, 1064-6, 1068	2.5	3
3	Isolation and characterization of the platelet-derived growth factor beta receptor promoter. <i>Developmental Dynamics</i> , <b>1997</b> , 208, 211-9	2.9	2
2	Comprehensive analysis of tumor NGS data to demonstrate pathways pointing to therapeutic targeting options.. <i>Journal of Clinical Oncology</i> , <b>2017</b> , 35, e23153-e23153	2.2	
1	Tumor profiling from whole-genome and whole transcriptome sequencing to uncover gene fusions and structural variations in clinically relevant cancer genes.. <i>Journal of Clinical Oncology</i> , <b>2017</b> , 35, e23118-e23118	2.2	23118