Andrew D Cherniack

List of Publications by Year in Descending Order

149 papers	**71,654** citations	**80** h-index	**175** g-index
175 ext. papers	**93,486** ext. citations	**22.9** avg, IF	**9.25** L-index

#	Paper	IF	Citations
149	Microenvironment drives cell state, plasticity, and drug response in pancreatic cancer. *Cell*, **2021**, 184, 6119-6137.e26	56.2	13
148	Diminished Efficacy of Programmed Death-(Ligand)1 Inhibition in STK11- and KEAP1-Mutant Lung Adenocarcinoma Is Affected by KRAS Mutation Status. *Journal of Thoracic Oncology*, **2021**,	8.9	14
147	Quantification of aneuploidy in targeted sequencing data using ASCETS. *Bioinformatics*, **2021**, 37, 2461-2463	7.16	4
146	Extracellular Domain In-Frame Deletions Are Therapeutically Targetable Genomic Alterations That Function as Oncogenic Drivers in Cholangiocarcinoma. *Cancer Discovery*, **2021**, 11, 2488-2505	24.4	11
145	Activity of PD-1 blockade with Nivolumab among patients with recurrent atypical/anaplastic meningioma: Phase II trial results. *Neuro-Oncology*, **2021**,	1	7
144	DNMT3A mutation to identify a subset of non-small cell lung cancers with increased sensitivity to PD-(L)1 blockade.. *Journal of Clinical Oncology*, **2021**, 39, 9113-9113	2.2	1
143	Clinicopathologic, genomic, and tumor microenvironment correlates of aneuploidy and immunotherapy outcomes in NSCLC.. *Journal of Clinical Oncology*, **2021**, 39, 9119-9119	2.2	
142	Changes in PD-L1 tumor proportion score are associated with CD274 gene (encoding PD-L1) copy number variation in non-small cell lung cancer.. *Journal of Clinical Oncology*, **2021**, 39, 9029-9029	2.2	
141	Integrative modeling identifies genetic ancestry-associated molecular correlates in human cancer. *STAR Protocols*, **2021**, 2, 100483	1.4	0
140	Discovery and Features of an Alkylating Signature in Colorectal Cancer. *Cancer Discovery*, **2021**, 11, 2446-2455	24.4	7
139	Genomic Characterization of Metastatic Breast Cancer. *Clinical Cancer Research*, **2021**, 27, 1105-1118	12.9	11
138	Molecular Characterization and Therapeutic Targeting of Colorectal Cancers Harboring Receptor Tyrosine Kinase Fusions. *Clinical Cancer Research*, **2021**, 27, 1695-1705	12.9	9
137	Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway. *Cell Reports*, **2021**, 34, 108707	10.6	7
136	Structure of PDE3A-SLFN12 complex reveals requirements for activation of SLFN12 RNase. *Nature Communications*, **2021**, 12, 4375	17.4	7
135	SMARCA4 and Other SWItch/Sucrose NonFermentable Family Genomic Alterations in NSCLC: Clinicopathologic Characteristics and Outcomes to Immune Checkpoint Inhibition. *Journal of Thoracic Oncology*, **2021**, 16, 1176-1187	8.9	6
134	Analytical protocol to identify local ancestry-associated molecular features in cancer. *STAR Protocols*, **2021**, 2, 100766	1.4	0
133	A predominant enhancer co-amplified with the SOX2 oncogene is necessary and sufficient for its expression in squamous cancer. *Nature Communications*, **2021**, 12, 7139	17.4	3

132	Impact of DNA Damage Response and Repair (DDR) Gene Mutations on Efficacy of PD-(L)1 Immune Checkpoint Inhibition in Non-Small Cell Lung Cancer. *Clinical Cancer Research*, **2020**, 26, 4135-4142	12.9	41
131	Ancestry-specific predisposing germline variants in cancer. *Genome Medicine*, **2020**, 12, 51	14.4	12
130	Loss of heterozygosity of essential genes represents a widespread class of potential cancer vulnerabilities. *Nature Communications*, **2020**, 11, 2517	17.4	21
129	Clinicopathological and genomic correlates of programmed cell death ligand 1 (PD-L1) expression in nonsquamous non-small-cell lung cancer. *Annals of Oncology*, **2020**, 31, 807-814	10.3	34
128	Interplay of somatic alterations and immune infiltration modulates response to PD-1 blockade in advanced clear cell renal cell carcinoma. *Nature Medicine*, **2020**, 26, 909-918	50.5	155
127	Mechanistic insights into cancer cell killing through interaction of phosphodiesterase 3A and schlafen family member 12. *Journal of Biological Chemistry*, **2020**, 295, 3431-3446	5.4	6
126	Molecular Mechanisms of Acquired Resistance to MET Tyrosine Kinase Inhibitors in Patients with MET Exon 14-Mutant NSCLC. *Clinical Cancer Research*, **2020**, 26, 2615-2625	12.9	60
125	Pan-cancer analysis of whole genomes. *Nature*, **2020**, 578, 82-93	50.4	840
124	Mammalian SWI/SNF Complex Genomic Alterations and Immune Checkpoint Blockade in Solid Tumors. *Cancer Immunology Research*, **2020**, 8, 1075-1084	12.5	21
123	Effect of STK11 mutations on efficacy of PD-1 inhibition in non-small cell lung cancer (NSCLC) and dependence on KRAS mutation status.. *Journal of Clinical Oncology*, **2020**, 38, e15113-e15113	2.2	5
122	Characterizing the landscape of genomic variants in high-risk pediatric osteosarcoma.. *Journal of Clinical Oncology*, **2020**, 38, 11530-11530	2.2	
121	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. *Cancer Cell*, **2020**, 37, 639-654.e6	24.3	56
120	Near haploidization is a genomic hallmark which defines a molecular subgroup of giant cell glioblastoma. *Neuro-Oncology Advances*, **2020**, 2, vdaa155	0.9	2
119	Synthetic Lethal Interaction between the ESCRT Paralog Enzymes VPS4A and VPS4B in Cancers Harboring Loss of Chromosome 18q or 16q. *Cell Reports*, **2020**, 33, 108493	10.6	7
118	Mechanisms and therapeutic implications of hypermutation in gliomas. *Nature*, **2020**, 580, 517-523	50.4	172
117	Integrated Genomic and Functional microRNA Analysis Identifies miR-30-5p as a Tumor Suppressor and Potential Therapeutic Nanomedicine in Head and Neck Cancer. *Clinical Cancer Research*, **2019**, 25, 2860-2873	12.9	41
116	Next-generation characterization of the Cancer Cell Line Encyclopedia. *Nature*, **2019**, 569, 503-508	50.4	962
115	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons Data. *Cell Systems*, **2019**, 9, 24-34.e10	10.6	64

114	Pooled Genomic Screens Identify Anti-apoptotic Genes as Targetable Mediators of Chemotherapy Resistance in Ovarian Cancer. *Molecular Cancer Research*, **2019**, 17, 2281-2293	6.6	15
113	Genomic landscape of de novo stage IV breast cancer.. *Journal of Clinical Oncology*, **2019**, 37, 1022-1022	2.2	3
112	Changes in tumor mutational burden in serially biopsied non-small cell lung cancer.. *Journal of Clinical Oncology*, **2019**, 37, e14286-e14286	2.2	1
111	Genomic and immune profiling of pre-invasive lung adenocarcinoma. *Nature Communications*, **2019**, 10, 5472	17.4	56
110	Amplification Associates with Aggressive Phenotype but Not Markers of AKT-MTOR Signaling in Endometrial Carcinoma. *Clinical Cancer Research*, **2019**, 25, 334-345	12.9	9
109	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. *Cell*, **2018**, 173, 400-416.e11	56.2	1072
108	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
107	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. *Cell*, **2018**, 173, 291-304.e6	56.2	888
106	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. *Cell*, **2018**, 173, 386-399.e10	56.2	133
105	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. *Cell*, **2018**, 173, 305-320.e10	56.2	166
104	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. *Cell*, **2018**, 173, 338-354.e15	56.2	560
103	Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*, **2018**, 173, 321-337.e10	56.2	1124
102	Pathogenic Germline Variants in 10,389 Adult Cancers. *Cell*, **2018**, 173, 355-370.e14	56.2	342
101	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. *Cell Reports*, **2018**, 23, 282-296.e4	10.6	188
100	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. *Cell Reports*, **2018**, 23, 227-238.e3	10.6	235
99	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. *Cell Reports*, **2018**, 23, 194-212.e6	10.6	146
98	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. *Cell Reports*, **2018**, 23, 297-312.e12	10.6	147
97	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. *Cell Reports*, **2018**, 23, 313-326.e5	10.6	295

96	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. *Cell Reports*, **2018**, 23, 181-193.e7	10.6	366
95	The Immune Landscape of Cancer. *Immunity*, **2018**, 48, 812-830.e14	32.3	1754
94	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 172-180.e3	10.6	66
93	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. *Cell Reports*, **2018**, 23, 213-226.e3	10.6	56
92	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 239-254.e6	10.6	405
91	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. *Cell Reports*, **2018**, 23, 255-269.e4	10.6	112
90	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. *Cell Reports*, **2018**, 23, 270-281.e3	10.6	121
89	The Integrated Genomic Landscape of Thymic Epithelial Tumors. *Cancer Cell*, **2018**, 33, 244-258.e10	24.3	150
88	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. *Cell Systems*, **2018**, 6, 271-281.e7	10.6	320
87	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. *Cell Systems*, **2018**, 6, 282-300.e2	10.6	159
86	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	24.3	275
85	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. *Cancer Cell*, **2018**, 33, 676-689.e3	24.3	377
84	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. *Cancer Cell*, **2018**, 33, 721-735.e8	24.3	228
83	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. *Cancer Cell*, **2018**, 33, 690-705.e9	24.3	277
82	Somatic Superenhancer Duplications and Hotspot Mutations Lead to Oncogenic Activation of the KLF5 Transcription Factor. *Cancer Discovery*, **2018**, 8, 108-125	24.4	67
81	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. *Cancer Cell*, **2018**, 34, 211-224.e6	24.3	327
80	Integrated Molecular Characterization of Testicular Germ Cell Tumors. *Cell Reports*, **2018**, 23, 3392-3406	10.6	200
79	Abstract 3287: An integrated TCGA pan-cancer clinical data resource to drive high quality survival outcome analytics **2018**,		27

78	Abstract 3302: The molecular landscape of oncogenic signaling pathways in The Cancer Genome Atlas **2018**,		5
77	Identification of ADAR1 adenosine deaminase dependency in a subset of cancer cells. *Nature Communications*, **2018**, 9, 5450	17.4	83
76	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-ꞵ Superfamily. *Cell Systems*, **2018**, 7, 422-437.e7	10.6	85
75	BRCA1 ensures genome integrity by eliminating estrogen-induced pathological topoisomerase II-DNA complexes. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E10642-E10651	11.5	47
74	The chromatin accessibility landscape of primary human cancers. *Science*, **2018**, 362,	33.3	392
73	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. *Cancer Discovery*, **2018**, 8, 1548-1565	24.4	258
72	Targetable vulnerabilities in T- and NK-cell lymphomas identified through preclinical models. *Nature Communications*, **2018**, 9, 2024	17.4	54
71	Genome-scale analysis identifies paralog lethality as a vulnerability of chromosome 1p loss in cancer. *Nature Genetics*, **2018**, 50, 937-943	36.3	35
70	Integrated genomic and molecular characterization of cervical cancer. *Nature*, **2017**, 543, 378-384	50.4	755
69	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. *Cancer Cell*, **2017**, 31, 181-193	24.3	350
68	Comparison of Breast Cancer Molecular Features and Survival by African and European Ancestry in The Cancer Genome Atlas. *JAMA Oncology*, **2017**, 3, 1654-1662	13.4	146
67	RPC4046, A Novel Anti-interleukin-13 Antibody, Blocks IL-13 Binding to IL-13 ꞷ1 and ꞷ2 Receptors: A Randomized, Double-Blind, Placebo-Controlled, Dose-Escalation First-in-Human Study. *Advances in Therapy*, **2017**, 34, 1364-1381	4.1	19
66	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. *Cell*, **2017**, 169, 1327-1341.e23	56.2	1125
65	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	13.3	63
64	Integrated Molecular Characterization of Uterine Carcinosarcoma. *Cancer Cell*, **2017**, 31, 411-423	24.3	210
63	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. *Cell Reports*, **2017**, 18, 2780-2794	10.6	247
62	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. *Cell*, **2017**, 171, 540-556.e25	56.2	961
61	Genomic Activation of Reveals a Candidate Therapeutic Axis in Bladder Cancer. *Cancer Research*, **2017**, 77, 6987-6998	10.1	34

60	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. *Cancer Cell*, **2017**, 32, 204-220.e15	24.3	391
59	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. *Cancer Cell*, **2017**, 32, 185-203.e13	24.3	896
58	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. *Cell*, **2017**, 171, 950-965.e28	56.2	451
57	The genomic landscape of tuberous sclerosis complex. *Nature Communications*, **2017**, 8, 15816	17.4	104
56	Comprehensive molecular characterization and analysis of muscle-invasive urothelial carcinomas.. *Journal of Clinical Oncology*, **2017**, 35, 4500-4500	2.2	4
55	Recurrent hormone-binding domain truncated ESR1 amplifications in primary endometrial cancers suggest their implication in hormone independent growth. *Scientific Reports*, **2016**, 6, 25521	4.9	11
54	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. *Nature Genetics*, **2016**, 48, 848-55	36.3	135
53	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. *Cancer Discovery*, **2016**, 6, 914-29	24.4	343
52	Identification of focally amplified lineage-specific super-enhancers in human epithelial cancers. *Nature Genetics*, **2016**, 48, 176-82	36.3	210
51	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. *Cell*, **2016**, 164, 550-63	56.2	1140
50	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. *New England Journal of Medicine*, **2016**, 374, 135-45	59.2	753
49	Comprehensive characterization of 412 muscle invasive urothelial carcinomas: Final analysis of The Cancer Genome Atlas (TCGA) project.. *Journal of Clinical Oncology*, **2016**, 34, 405-405	2.2	1
48	DNA defects, epigenetics, and gene expression in cancer-adjacent breast: a study from The Cancer Genome Atlas. *Npj Breast Cancer*, **2016**, 2, 16007	7.8	25
47	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Cancer Cell*, **2016**, 29, 723-736	24.3	324
46	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. *Nature Genetics*, **2016**, 48, 607-16	36.3	613
45	Genomic Classification of Cutaneous Melanoma. *Cell*, **2015**, 161, 1681-96	56.2	1807
44	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. *New England Journal of Medicine*, **2015**, 372, 2481-98	59.2	1828
43	The Molecular Taxonomy of Primary Prostate Cancer. *Cell*, **2015**, 163, 1011-25	56.2	1713

42	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. *Cell*, **2015**, 163, 506-19	56.2	1055
41	Rapid Intraoperative Molecular Characterization of Glioma. *JAMA Oncology*, **2015**, 1, 662-7	13.4	53
40	Comprehensive genomic characterization of head and neck squamous cell carcinomas. *Nature*, **2015**, 517, 576-82	50.4	2332
39	Abstract S2-04: Comprehensive molecular characterization of invasive lobular breast tumors **2015**,		7
38	Precision medicine approach in kidney cancer: A pan renal cell carcinoma (RCC) study across three cancer genome atlas (TCGA) datasets for clinically relevant target identification.. *Journal of Clinical Oncology*, **2015**, 33, 4564-4564	2.2	1
37	Molecular profiling of endometrial carcinoma precursor, primary and metastatic lesions suggests different targets for treatment in obese compared to non-obese patients. *Oncotarget*, **2015**, 6, 1327-39	3.3	42
36	Distinct MET alterations to induce a common phenotype and to define a MET-driven subset of papillary RCC: Results from the Cancer Genome Atlas (TCGA) Kidney Renal Papillary (KIRP) Working Group.. *Journal of Clinical Oncology*, **2015**, 33, 4521-4521	2.2	1
35	Abstract 2969: Progress in The Cancer Genome Atlas bladder cancer project **2015**,		2
34	Comprehensive molecular characterization of urothelial bladder carcinoma. *Nature*, **2014**, 507, 315-22	50.4	1963
33	Landscape of genomic alterations in cervical carcinomas. *Nature*, **2014**, 506, 371-5	50.4	541
32	Comprehensive molecular characterization of gastric adenocarcinoma. *Nature*, **2014**, 513, 202-9	50.4	3659
31	The somatic genomic landscape of chromophobe renal cell carcinoma. *Cancer Cell*, **2014**, 26, 319-330	24.3	521
30	Comprehensive molecular profiling of lung adenocarcinoma. *Nature*, **2014**, 511, 543-50	50.4	3310
29	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. *Cell*, **2014**, 158, 929-944	56.2	935
28	Endometrial Carcinoma Recurrence Score (ECARS) validates to identify aggressive disease and associates with markers of epithelial-mesenchymal transition and PI3K alterations. *Gynecologic Oncology*, **2014**, 134, 599-606	4.9	8
27	Genetic modifiers of EGFR dependence in non-small cell lung cancer. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 18661-6	11.5	37
26	Integrated genomic characterization of papillary thyroid carcinoma. *Cell*, **2014**, 159, 676-90	56.2	1660
25	Somatic genomic alterations in urothelial cancer: Results of the Cancer Genome Atlas (TCGA) bladder cancer (BC) analysis.. *Journal of Clinical Oncology*, **2014**, 32, 285-285	2.2	

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24	A Tumor suppressor complex with GAP activity for the Rag GTPases that signal amino acid sufficiency to mTORC1. *Science*, **2013**, 340, 1100-6	33.3	637
23	Pan-cancer patterns of somatic copy number alteration. *Nature Genetics*, **2013**, 45, 1134-40	36.3	1198
22	Activation of the PD-1 pathway contributes to immune escape in EGFR-driven lung tumors. *Cancer Discovery*, **2013**, 3, 1355-63	24.4	831
21	Integrated genomic characterization of endometrial carcinoma. *Nature*, **2013**, 497, 67-73	50.4	2800
20	Comprehensive molecular characterization of clear cell renal cell carcinoma. *Nature*, **2013**, 499, 43-9	50.4	2184
19	Comprehensive molecular characterization of human colon and rectal cancer. *Nature*, **2012**, 487, 330-7	50.4	5640
18	Comprehensive molecular portraits of human breast tumours. *Nature*, **2012**, 490, 61-70	50.4	8025
17	Comprehensive genomic characterization of squamous cell lung cancers. *Nature*, **2012**, 489, 519-25	50.4	2820
16	Functional comparison of recombinant acidic mammalian chitinase with enzyme from murine bronchoalveolar lavage. *Protein Expression and Purification*, **2011**, 75, 55-62	2	8
15	Glioblastoma-derived epidermal growth factor receptor carboxyl-terminal deletion mutants are transforming and are sensitive to EGFR-directed therapies. *Cancer Research*, **2011**, 71, 7587-96	10.1	62
14	Loss of the retinoblastoma binding protein 2 (RBP2) histone demethylase suppresses tumorigenesis in mice lacking Rb1 or Men1. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 13379-86	11.5	121
13	Suppression of oxidative metabolism and mitochondrial biogenesis by the transcriptional corepressor RIP140 in mouse adipocytes. *Journal of Clinical Investigation*, **2006**, 116, 125-36	15.9	176
12	G(alpha)11 signaling through ARF6 regulates F-actin mobilization and GLUT4 glucose transporter translocation to the plasma membrane. *Molecular and Cellular Biology*, **2001**, 21, 5262-75	4.8	57
11	Function of the Neurospora crassa mitochondrial tyrosyl-tRNA synthetase in RNA splicing. Role of the idiosyncratic N-terminal extension and different modes of interaction with different group I introns. *Journal of Molecular Biology*, **2001**, 307, 75-92	6.5	38
10	The protein-tyrosine kinase fer associates with signaling complexes containing insulin receptor substrate-1 and phosphatidylinositol 3-kinase. *Journal of Biological Chemistry*, **2000**, 275, 38995-9000	5.4	16
9	Role of the Raf/mitogen-activated protein kinase pathway in p21ras desensitization. *Journal of Biological Chemistry*, **1996**, 271, 16674-7	5.4	17
8	Disassembly of Son-of-sevenless Proteins from Grb2 during p21 Desensitization by Insulin. *Journal of Biological Chemistry*, **1995**, 270, 1485-1488	5.4	75
7	Divergent mechanisms for homologous desensitization of p21ras by insulin and growth factors. *Journal of Biological Chemistry*, **1995**, 270, 23421-8	5.4	33

6	Binding of the Ras activator son of sevenless to insulin receptor substrate-1 signaling complexes. *Science*, **1993**, 260, 1950-2	33.3	283
5	Function of Neurospora mitochondrial tyrosyl-tRNA synthetase in RNA splicing requires an idiosyncratic domain not found in other synthetases. *Cell*, **1990**, 62, 745-55	56.2	73
4	Effects of verapamil on histamine-and carbachol-induced contraction of pulmonary tissues in vitro. *Chest*, **1984**, 86, 762-6	5.3	16
3	The tumor microenvironment drives transcriptional phenotypes and their plasticity in metastatic pancreatic cancer		5
2	Loss of heterozygosity of essential genes represents a widespread class of potential cancer vulnerabilities		1
1	The Tangent copy-number inference pipeline for cancer genome analyses		3