Gad Getz

List of Publications by Citations

383 papers	162,874 citations	169 h-index	403 g-index
413 ext. papers	207,778 ext. citations	24.1 avg, IF	7.67 L-index

#	Paper	IF	Citations
383	MicroRNA expression profiles classify human cancers. *Nature*, **2005**, 435, 834-8	50.4	7870
382	Integrative genomics viewer. *Nature Biotechnology*, **2011**, 29, 24-6	44.5	7463
381	Analysis of protein-coding genetic variation in 60,706 humans. *Nature*, **2016**, 536, 285-91	50.4	6940
380	Integrated genomic analysis identifies clinically relevant subtypes of glioblastoma characterized by abnormalities in PDGFRA, IDH1, EGFR, and NF1. *Cancer Cell*, **2010**, 17, 98-110	24.3	4782
379	The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. *Nature*, **2012**, 483, 603-7	50.4	4648
378	The Genotype-Tissue Expression (GTEx) project. *Nature Genetics*, **2013**, 45, 580-5	36.3	4179
377	Mutational heterogeneity in cancer and the search for new cancer-associated genes. *Nature*, **2013**, 499, 214-218	50.4	3616
376	Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. *Science*, **2015**, 348, 648-60	33.3	3242
375	Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. *New England Journal of Medicine*, **2013**, 368, 2059-74	59.2	3137
374	The somatic genomic landscape of glioblastoma. *Cell*, **2013**, 155, 462-77	56.2	2900
373	Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. *Nature Biotechnology*, **2013**, 31, 213-9	44.5	2830
372	The landscape of somatic copy-number alteration across human cancers. *Nature*, **2010**, 463, 899-905	50.4	2590
371	Inferring tumour purity and stromal and immune cell admixture from expression data. *Nature Communications*, **2013**, 4, 2612	17.4	2572
370	Age-related clonal hematopoiesis associated with adverse outcomes. *New England Journal of Medicine*, **2014**, 371, 2488-98	59.2	2314
369	Somatic mutations affect key pathways in lung adenocarcinoma. *Nature*, **2008**, 455, 1069-75	50.4	2280
368	Discovery and saturation analysis of cancer genes across 21 tumour types. *Nature*, **2014**, 505, 495-501	50.4	1990
367	The mutational landscape of head and neck squamous cell carcinoma. *Science*, **2011**, 333, 1157-60	33.3	1836

366	Molecular and genetic properties of tumors associated with local immune cytolytic activity. *Cell*, **2015**, 160, 48-61	56.2	1834
365	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. *New England Journal of Medicine*, **2015**, 372, 2481-98	59.2	1828
364	Genomic Classification of Cutaneous Melanoma. *Cell*, **2015**, 161, 1681-96	56.2	1807
363	A landscape of driver mutations in melanoma. *Cell*, **2012**, 150, 251-63	56.2	1799
362	The Immune Landscape of Cancer. *Immunity*, **2018**, 48, 812-830.e14	32.3	1754
361	The Molecular Taxonomy of Primary Prostate Cancer. *Cell*, **2015**, 163, 1011-25	56.2	1713
360	Integrated genomic characterization of papillary thyroid carcinoma. *Cell*, **2014**, 159, 676-90	56.2	1660
359	GISTIC2.0 facilitates sensitive and confident localization of the targets of focal somatic copy-number alteration in human cancers. *Genome Biology*, **2011**, 12, R41	18.3	1614
358	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613
357	An immunogenic personal neoantigen vaccine for patients with melanoma. *Nature*, **2017**, 547, 217-221	50.4	1375
356	Mapping the hallmarks of lung adenocarcinoma with massively parallel sequencing. *Cell*, **2012**, 150, 1107-20	56.2	1304
355	Absolute quantification of somatic DNA alterations in human cancer. *Nature Biotechnology*, **2012**, 30, 413-21	44.5	1229
354	Prospective derivation of a living organoid biobank of colorectal cancer patients. *Cell*, **2015**, 161, 933-45	56.2	1215
353	Pan-cancer patterns of somatic copy number alteration. *Nature Genetics*, **2013**, 45, 1134-40	36.3	1198
352	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. *Cell*, **2016**, 164, 550-63	56.2	1140
351	BRAF mutation predicts sensitivity to MEK inhibition. *Nature*, **2006**, 439, 358-62	50.4	1137
350	Integrative genomic analyses identify MITF as a lineage survival oncogene amplified in malignant melanoma. *Nature*, **2005**, 436, 117-22	50.4	1127
349	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. *Cell*, **2017**, 169, 1327-1341.e23	56.2	1125

348	Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*, **2018**, 173, 321-337.e10	56.2	1124
347	Initial genome sequencing and analysis of multiple myeloma. *Nature*, **2011**, 471, 467-72	50.4	1117
346	Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. *Nature Genetics*, **2012**, 44, 685-9	36.3	1079
345	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. *Cell*, **2018**, 173, 400-416.e11	56.2	1072
344	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. *Cell*, **2015**, 163, 506-19	56.2	1055
343	Evolution and impact of subclonal mutations in chronic lymphocytic leukemia. *Cell*, **2013**, 152, 714-26	56.2	1006
342	The genomic complexity of primary human prostate cancer. *Nature*, **2011**, 470, 214-20	50.4	984
341	Next-generation characterization of the Cancer Cell Line Encyclopedia. *Nature*, **2019**, 569, 503-508	50.4	962
340	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. *Cell*, **2017**, 171, 540-556.e25	56.2	961
339	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. *Nature Genetics*, **2012**, 44, 1104-10	36.3	919
338	Characterizing the cancer genome in lung adenocarcinoma. *Nature*, **2007**, 450, 893-8	50.4	900
337	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. *Cancer Cell*, **2017**, 32, 185-203.e13	24.9	896
336	Sequence analysis of mutations and translocations across breast cancer subtypes. *Nature*, **2012**, 486, 405-9	50.4	895
335	Advances in understanding cancer genomes through second-generation sequencing. *Nature Reviews Genetics*, **2010**, 11, 685-96	30.1	890
334	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
333	SF3B1 and other novel cancer genes in chronic lymphocytic leukemia. *New England Journal of Medicine*, **2011**, 365, 2497-506	59.2	875
332	Punctuated evolution of prostate cancer genomes. *Cell*, **2013**, 153, 666-77	56.2	862
331	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854

330	The repertoire of mutational signatures in human cancer. *Nature*, **2020**, 578, 94-101	50.4	849
329	Human genomics. The human transcriptome across tissues and individuals. *Science*, **2015**, 348, 660-5	33.3	833
328	Assessing the significance of chromosomal aberrations in cancer: methodology and application to glioma. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 20007-12	11.5	812
327	An APOBEC cytidine deaminase mutagenesis pattern is widespread in human cancers. *Nature Genetics*, **2013**, 45, 970-6	36.3	774
326	Discovery and prioritization of somatic mutations in diffuse large B-cell lymphoma (DLBCL) by whole-exome sequencing. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 3879-84	11.5	735
325	SOX2 is an amplified lineage-survival oncogene in lung and esophageal squamous cell carcinomas. *Nature Genetics*, **2009**, 41, 1238-42	36.3	733
324	The genetic landscape of high-risk neuroblastoma. *Nature Genetics*, **2013**, 45, 279-84	36.3	717
323	Cancer therapy. Ex vivo culture of circulating breast tumor cells for individualized testing of drug susceptibility. *Science*, **2014**, 345, 216-20	33.3	670
322	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. *Nature Medicine*, **2018**, 24, 679-690	50.5	659
321	Mutations driving CLL and their evolution in progression and relapse. *Nature*, **2015**, 526, 525-30	50.4	658
320	Widespread genetic heterogeneity in multiple myeloma: implications for targeted therapy. *Cancer Cell*, **2014**, 25, 91-101	24.3	657
319	Molecular Mechanisms of Resistance to First- and Second-Generation ALK Inhibitors in ALK-Rearranged Lung Cancer. *Cancer Discovery*, **2016**, 6, 1118-1133	24.4	648
318	Defining T Cell States Associated with Response to Checkpoint Immunotherapy in Melanoma. *Cell*, **2018**, 175, 998-1013.e20	56.2	631
317	The genetic landscape of clinical resistance to RAF inhibition in metastatic melanoma. *Cancer Discovery*, **2014**, 4, 94-109	24.4	626
316	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. *Nature Genetics*, **2016**, 48, 607-16	36.3	613
315	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. *Cancer Discovery*, **2015**, 5, 1164-1177	24.4	581
314	Neoantigen vaccine generates intratumoral T cell responses in phase Ib glioblastoma trial. *Nature*, **2019**, 565, 234-239	50.4	569
313	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. *Nature*, **2016**, 539, 309-313	50.4	561

312	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. *Nature Genetics*, **2013**, 45, 478-86	36.3	558
311	Melanoma genome sequencing reveals frequent PREX2 mutations. *Nature*, **2012**, 485, 502-6	50.4	555
310	Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. *Nature*, **2012**, 488, 106-10	50.4	552
309	Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. *Nature Genetics*, **2015**, 47, 106-14	36.3	547
308	Landscape of genomic alterations in cervical carcinomas. *Nature*, **2014**, 506, 371-5	50.4	541
307	RNA-SeQC: RNA-seq metrics for quality control and process optimization. *Bioinformatics*, **2012**, 28, 1530-2	7.2	538
306	Tumor cells can follow distinct evolutionary paths to become resistant to epidermal growth factor receptor inhibition. *Nature Medicine*, **2016**, 22, 262-9	50.5	533
305	Coupled two-way clustering analysis of gene microarray data. *Proceedings of the National Academy of Sciences of the United States of America*, **2000**, 97, 12079-84	11.5	528
304	The somatic genomic landscape of chromophobe renal cell carcinoma. *Cancer Cell*, **2014**, 26, 319-330	24.3	521
303	Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy. *Nature Genetics*, **2010**, 42, 715-21	36.3	521
302	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. *Science*, **2017**, 355,	33.3	455
301	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. *Cell*, **2017**, 171, 950-965.e28	56.2	451
300	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. *Nature Biotechnology*, **2014**, 32, 479-84	44.5	434
299	Genomic Correlates of Immune-Cell Infiltrates in Colorectal Carcinoma. *Cell Reports*, **2016**, 15, 857-865	10.6	422
298	Comprehensive genomic analysis of rhabdomyosarcoma reveals a landscape of alterations affecting a common genetic axis in fusion-positive and fusion-negative tumors. *Cancer Discovery*, **2014**, 4, 216-31	24.4	417
297	High-resolution mapping of copy-number alterations with massively parallel sequencing. *Nature Methods*, **2009**, 6, 99-103	21.6	417
296	TET2 mutations predict response to hypomethylating agents in myelodysplastic syndrome patients. *Blood*, **2014**, 124, 2705-12	2.2	411
295	Resistance to checkpoint blockade therapy through inactivation of antigen presentation. *Nature Communications*, **2017**, 8, 1136	17.4	409

294	Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. *Nature Medicine*, **2014**, 20, 682-8	50.5	406
293	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 239-254.e6	10.6	405
292	Integrative and comparative genomic analysis of HPV-positive and HPV-negative head and neck squamous cell carcinomas. *Clinical Cancer Research*, **2015**, 21, 632-41	12.9	398
291	Genomic sequencing of meningiomas identifies oncogenic SMO and AKT1 mutations. *Nature Genetics*, **2013**, 45, 285-9	36.3	397
290	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. *Cancer Cell*, **2017**, 32, 204-220.e15	24.3	391
289	Toil enables reproducible, open source, big biomedical data analyses. *Nature Biotechnology*, **2017**, 35, 314-316	44.5	387
288	Genetic and transcriptional evolution alters cancer cell line drug response. *Nature*, **2018**, 560, 325-330	50.4	379
287	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. *Cancer Cell*, **2018**, 33, 676-689.e3	24.3	377
286	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
285	Somatic ERCC2 mutations correlate with cisplatin sensitivity in muscle-invasive urothelial carcinoma. *Cancer Discovery*, **2014**, 4, 1140-53	24.4	361
284	Comprehensive analysis of cancer-associated somatic mutations in class I HLA genes. *Nature Biotechnology*, **2015**, 33, 1152-8	44.5	359
283	RB loss in resistant EGFR mutant lung adenocarcinomas that transform to small-cell lung cancer. *Nature Communications*, **2015**, 6, 6377	17.4	358
282	MAP kinase pathway alterations in BRAF-mutant melanoma patients with acquired resistance to combined RAF/MEK inhibition. *Cancer Discovery*, **2014**, 4, 61-8	24.4	351
281	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. *Cancer Cell*, **2017**, 31, 181-193	24.3	350
280	Comprehensive identification of mutational cancer driver genes across 12 tumor types. *Scientific Reports*, **2013**, 3, 2650	4.9	350
279	Pathogenic Germline Variants in 10,389 Adult Cancers. *Cell*, **2018**, 173, 355-370.e14	56.2	342
278	Resensitization to Crizotinib by the Lorlatinib ALK Resistance Mutation L1198F. *New England Journal of Medicine*, **2016**, 374, 54-61	59.2	334
277	Oncotator: cancer variant annotation tool. *Human Mutation*, **2015**, 36, E2423-9	4.7	332

276	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Cancer Cell*, **2016**, 29, 723-736	24.3	324
275	Systematic investigation of genetic vulnerabilities across cancer cell lines reveals lineage-specific dependencies in ovarian cancer. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 12372-7	11.5	321
274	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. *Cell Systems*, **2018**, 6, 271-281.e7	10.6	320
273	Exome sequencing identifies BRAF mutations in papillary craniopharyngiomas. *Nature Genetics*, **2014**, 46, 161-5	36.3	320
272	Targetable genetic features of primary testicular and primary central nervous system lymphomas. *Blood*, **2016**, 127, 869-81	2.2	317
271	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. *Nature Communications*, **2017**, 8, 1324	17.4	314
270	The evolutionary history of 2,658 cancers. *Nature*, **2020**, 578, 122-128	50.4	307
269	The genomic landscape of pediatric Ewing sarcoma. *Cancer Discovery*, **2014**, 4, 1326-41	24.4	302
268	Discovery and characterization of artifactual mutations in deep coverage targeted capture sequencing data due to oxidative DNA damage during sample preparation. *Nucleic Acids Research*, **2013**, 41, e67	20.1	301
267	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. *Cell Reports*, **2018**, 23, 313-326.e5	10.6	295
266	Somatic mutations predict poor outcome in patients with myelodysplastic syndrome after hematopoietic stem-cell transplantation. *Journal of Clinical Oncology*, **2014**, 32, 2691-8	2.2	295
265	RNF43 is frequently mutated in colorectal and endometrial cancers. *Nature Genetics*, **2014**, 46, 1264-6	36.3	287
264	A remarkably simple genome underlies highly malignant pediatric rhabdoid cancers. *Journal of Clinical Investigation*, **2012**, 122, 2983-8	15.9	286
263	DNA microarrays identification of primary and secondary target genes regulated by p53. *Oncogene*, **2001**, 20, 2225-34	9.2	282
262	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. *Cancer Cell*, **2018** , 33, 690-705.e9	24.3	277
261	Mutations in isocitrate dehydrogenase 1 and 2 occur frequently in intrahepatic cholangiocarcinomas and share hypermethylation targets with glioblastomas. *Oncogene*, **2013**, 32, 3091-100	9.2	277
260	Complementary genomic approaches highlight the PI3K/mTOR pathway as a common vulnerability in osteosarcoma. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, E5564-73	11.5	275
259	Genomic complexity of multiple myeloma and its clinical implications. *Nature Reviews Clinical Oncology*, **2017**, 14, 100-113	19.4	267

258	Polyclonal Secondary Mutations Drive Acquired Resistance to FGFR Inhibition in Patients with FGFR2 Fusion-Positive Cholangiocarcinoma. *Cancer Discovery*, **2017**, 7, 252-263	24.4	262
257	Making sense of cancer genomic data. *Genes and Development*, **2011**, 25, 534-55	12.6	260
256	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. *Science*, **2018**, 360, 331-335	33.3	255
255	A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. *Nature Genetics*, **2017**, 49, 1476-1486	36.3	255
254	Genomic correlates of response to immune checkpoint blockade in microsatellite-stable solid tumors. *Nature Genetics*, **2018**, 50, 1271-1281	36.3	249
253	Systematic identification of personal tumor-specific neoantigens in chronic lymphocytic leukemia. *Blood*, **2014**, 124, 453-62	2.2	249
252	Modeling genomic diversity and tumor dependency in malignant melanoma. *Cancer Research*, **2008**, 68, 664-73	10.1	248
251	Integrated genomic profiling of endometrial carcinoma associates aggressive tumors with indicators of PI3 kinase activation. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 4834-9	11.5	244
250	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion. *Nature Genetics*, **2011**, 43, 964-968	36.3	242
249	Epidermal growth factor receptor activation in glioblastoma through novel missense mutations in the extracellular domain. *PLoS Medicine*, **2006**, 3, e485	11.6	242
248	Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. *Genome Research*, **2015**, 25, 316-27	9.7	240
247	Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. *Cell*, **2016**, 164, 538-49	56.2	239
246	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. *Nature Genetics*, **2018**, 50, 956-967	36.3	239
245	An APOBEC3A hypermutation signature is distinguishable from the signature of background mutagenesis by APOBEC3B in human cancers. *Nature Genetics*, **2015**, 47, 1067-72	36.3	238
244	Somatic ERCC2 mutations are associated with a distinct genomic signature in urothelial tumors. *Nature Genetics*, **2016**, 48, 600-606	36.3	238
243	Response and acquired resistance to everolimus in anaplastic thyroid cancer. *New England Journal of Medicine*, **2014**, 371, 1426-33	59.2	237
242	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. *Cell Reports*, **2018**, 23, 227-238.e3	10.6	235
241	Paired exome analysis of Barrett's esophagus and adenocarcinoma. *Nature Genetics*, **2015**, 47, 1047-55	36.3	232

240	Characterization of HPV and host genome interactions in primary head and neck cancers. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 15544-9	11.5	229
239	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. *Cancer Cell*, **2018**, 33, 721-735.e8	24.3	228
238	RNA sequence analysis reveals macroscopic somatic clonal expansion across normal tissues. *Science* , **2019**, 364,	33.3	226
237	Identification of driver genes in hepatocellular carcinoma by exome sequencing. *Hepatology*, **2013**, 58, 1693-702	11.2	223
236	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature*, **2020**, 578, 102-111	50.4	220
235	Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. *Nature Communications*, **2016**, 7, 11589	17.4	220
234	Somatic mutation of CDKN1B in small intestine neuroendocrine tumors. *Nature Genetics*, **2013**, 45, 1483-6	36.3	219
233	Integrated genome-wide DNA copy number and expression analysis identifies distinct mechanisms of primary chemoresistance in ovarian carcinomas. *Clinical Cancer Research*, **2009**, 15, 1417-27	12.9	217
232	Locally disordered methylation forms the basis of intratumor methylome variation in chronic lymphocytic leukemia. *Cancer Cell*, **2014**, 26, 813-825	24.3	216
231	Integrative analysis of the melanoma transcriptome. *Genome Research*, **2010**, 20, 413-27	9.7	216
230	PathSeq: software to identify or discover microbes by deep sequencing of human tissue. *Nature Biotechnology*, **2011**, 29, 393-6	44.5	213
229	Clinical Acquired Resistance to RAF Inhibitor Combinations in BRAF-Mutant Colorectal Cancer through MAPK Pathway Alterations. *Cancer Discovery*, **2015**, 5, 358-67	24.4	211
228	Integrated Molecular Characterization of Uterine Carcinosarcoma. *Cancer Cell*, **2017**, 31, 411-423	24.3	210
227	Functional analysis of receptor tyrosine kinase mutations in lung cancer identifies oncogenic extracellular domain mutations of ERBB2. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 14476-81	11.5	208
226	Assessing the clinical utility of cancer genomic and proteomic data across tumor types. *Nature Biotechnology*, **2014**, 32, 644-52	44.5	205
225	Predicting drug susceptibility of non-small cell lung cancers based on genetic lesions. *Journal of Clinical Investigation*, **2009**, 119, 1727-40	15.9	205
224	Identification of the JNK signaling pathway as a functional target of the tumor suppressor PTEN. *Cancer Cell*, **2007**, 11, 555-69	24.3	202
223	Temporal dissection of tumorigenesis in primary cancers. *Cancer Discovery*, **2011**, 1, 137-43	24.4	201

222	Integrated Molecular Characterization of Testicular Germ Cell Tumors. *Cell Reports*, **2018**, 23, 3392-3406	10.6	200
221	Recurrent and functional regulatory mutations in breast cancer. *Nature*, **2017**, 547, 55-60	50.4	192
220	Genetic and clonal dissection of murine small cell lung carcinoma progression by genome sequencing. *Cell*, **2014**, 156, 1298-1311	56.2	191
219	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
218	ContEst: estimating cross-contamination of human samples in next-generation sequencing data. *Bioinformatics*, **2011**, 27, 2601-2	7.2	181
217	Type 2 diabetes genetic loci informed by multi-trait associations point to disease mechanisms and subtypes: A soft clustering analysis. *PLoS Medicine*, **2018**, 15, e1002654	11.6	180
216	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. *Science*, **2015**, 348, 666-9	33.3	170
215	Classification of human astrocytic gliomas on the basis of gene expression: a correlated group of genes with angiogenic activity emerges as a strong predictor of subtypes. *Cancer Research*, **2003**, 63, 6613-25	10.1	168
214	Tumor-suppressor genes that escape from X-inactivation contribute to cancer sex bias. *Nature Genetics*, **2017**, 49, 10-16	36.3	167
213	Control of tumor-associated macrophages and T cells in glioblastoma via AHR and CD39. *Nature Neuroscience*, **2019**, 22, 729-740	25.5	166
212	The genomic landscape of juvenile myelomonocytic leukemia. *Nature Genetics*, **2015**, 47, 1326-1333	36.3	166
211	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. *Cell*, **2018**, 173, 305-320.e10	56.2	166
210	Mutational processes shape the landscape of TP53 mutations in human cancer. *Nature Genetics*, **2018**, 50, 1381-1387	36.3	165
209	High order chromatin architecture shapes the landscape of chromosomal alterations in cancer. *Nature Biotechnology*, **2011**, 29, 1109-13	44.5	162
208	Liquid versus tissue biopsy for detecting acquired resistance and tumor heterogeneity in gastrointestinal cancers. *Nature Medicine*, **2019**, 25, 1415-1421	50.5	161
207	Real-time Genomic Characterization of Advanced Pancreatic Cancer to Enable Precision Medicine. *Cancer Discovery*, **2018**, 8, 1096-1111	24.4	156
206	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, 8188-93	11.5	156
205	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. *Cell*, **2018**, 174, 433-447.e19	56.2	155

204	KDM4A lysine demethylase induces site-specific copy gain and rereplication of regions amplified in tumors. *Cell*, **2013**, 154, 541-55	56.2	155
203	TAS-120 Overcomes Resistance to ATP-Competitive FGFR Inhibitors in Patients with FGFR2 Fusion-Positive Intrahepatic Cholangiocarcinoma. *Cancer Discovery*, **2019**, 9, 1064-1079	24.4	154
202	The Integrated Genomic Landscape of Thymic Epithelial Tumors. *Cancer Cell*, **2018**, 33, 244-258.e10	24.3	150
201	Genomic characterization of biliary tract cancers identifies driver genes and predisposing mutations. *Journal of Hepatology*, **2018**, 68, 959-969	13.4	149
200	SvABA: genome-wide detection of structural variants and indels by local assembly. *Genome Research*, **2018**, 28, 581-591	9.7	149
199	Integrative analysis reveals an outcome-associated and targetable pattern of p53 and cell cycle deregulation in diffuse large B cell lymphoma. *Cancer Cell*, **2012**, 22, 359-72	24.3	148
198	Somatic retrotransposition in human cancer revealed by whole-genome and exome sequencing. *Genome Research*, **2014**, 24, 1053-63	9.7	147
197	Dramatic Response of BRAF V600E Mutant Papillary Craniopharyngioma to Targeted Therapy. *Journal of the National Cancer Institute*, **2016**, 108,	9.7	144
196	Comprehensive assessment of cancer missense mutation clustering in protein structures. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, E5486-95	11.5	142
195	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. *Cell*, **2020**, 181, 236-249	56.2	140
194	Integrative and comparative genomic analysis of lung squamous cell carcinomas in East Asian patients. *Journal of Clinical Oncology*, **2014**, 32, 121-8	2.2	140
193	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. *Cell*, **2020**, 182, 200-225.e35	56.2	139
192	Whole-genome sequencing reveals activation-induced cytidine deaminase signatures during indolent chronic lymphocytic leukaemia evolution. *Nature Communications*, **2015**, 6, 8866	17.4	139
191	WRN helicase is a synthetic lethal target in microsatellite unstable cancers. *Nature*, **2019**, 568, 551-556	50.4	137
190	Inhibitor-sensitive FGFR2 and FGFR3 mutations in lung squamous cell carcinoma. *Cancer Research*, **2013**, 73, 5195-205	10.1	136
189	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. *Nature Genetics*, **2016**, 48, 848-55	36.3	135
188	PD-1 blockade in subprimed CD8 cells induces dysfunctional PD-1CD38 cells and anti-PD-1 resistance. *Nature Immunology*, **2019**, 20, 1231-1243	19.1	132
187	High-resolution genomic and expression analyses of copy number alterations in breast tumors. *Genes Chromosomes and Cancer*, **2008**, 47, 530-42	5	123

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