Gad Getz

List of Publications by Year in descending order

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370 papers	236,845 citations	47 191 h-index	112 356 g-index
413 all docs	413 docs citations	413 times ranked	207149 citing authors

#	Article	IF	Citations
1	Integrative genomics viewer. Nature Biotechnology, 2011, 29, 24-26.	9.4	11,708
2	Analysis of protein-coding genetic variation in 60,706 humans. Nature, 2016, 536, 285-291.	13.7	9,051
3	MicroRNA expression profiles classify human cancers. Nature, 2005, 435, 834-838.	13.7	8,931
4	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	9.4	6,815
5	The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. Nature, 2012, 483, 603-607.	13.7	6,473
6	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. Cancer Cell, 2010, 17, 98-110.	7.7	6,138
7	Inferring tumour purity and stromal and immune cell admixture from expression data. Nature Communications, 2013, 4, 2612.	5.8	5,788
8	Mutational heterogeneity in cancer and the search for new cancer-associated genes. Nature, 2013, 499, 214-218.	13.7	4,761
9	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	6.0	4,659
10	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	13.9	4,139
11	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	13.5	3,979
12	Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. Nature Biotechnology, 2013, 31, 213-219.	9.4	3,934
13	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
14	Age-Related Clonal Hematopoiesis Associated with Adverse Outcomes. New England Journal of Medicine, 2014, 371, 2488-2498.	13.9	3,474
15	The landscape of somatic copy-number alteration across human cancers. Nature, 2010, 463, 899-905.	13.7	3,331
16	Molecular and Genetic Properties of Tumors Associated with Local Immune Cytolytic Activity. Cell, 2015, 160, 48-61.	13.5	2,948
17	Somatic mutations affect key pathways in lung adenocarcinoma. Nature, 2008, 455, 1069-1075.	13.7	2,694
18	Discovery and saturation analysis of cancer genes across 21 tumour types. Nature, 2014, 505, 495-501.	13.7	2,586

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19	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
20	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	13.5	2,562
21	GISTIC2.0 facilitates sensitive and confident localization of the targets of focal somatic copy-number alteration in human cancers. Genome Biology, 2011, 12, R41.	3.8	2,546
22	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	13.5	2,435
23	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	13.5	2,318
24	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	13.5	2,277
25	A Landscape of Driver Mutations in Melanoma. Cell, 2012, 150, 251-263.	13.5	2,247
26	The Mutational Landscape of Head and Neck Squamous Cell Carcinoma. Science, 2011, 333, 1157-1160.	6.0	2,225
27	Next-generation characterization of the Cancer Cell Line Encyclopedia. Nature, 2019, 569, 503-508.	13.7	2,149
28	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
29	An immunogenic personal neoantigen vaccine for patients with melanoma. Nature, 2017, 547, 217-221.	13.7	2,112
30	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
31	The repertoire of mutational signatures in human cancer. Nature, 2020, 578, 94-101.	13.7	2,104
32	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
33	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	13.5	1,742
34	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
35	Absolute quantification of somatic DNA alterations in human cancer. Nature Biotechnology, 2012, 30, 413-421.	9.4	1,710
36	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. Cell, 2015, 161, 933-945.	13.5	1,710

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37	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	13.5	1,695
38	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
39	Pan-cancer patterns of somatic copy number alteration. Nature Genetics, 2013, 45, 1134-1140.	9.4	1,616
40	Mapping the Hallmarks of Lung Adenocarcinoma with Massively Parallel Sequencing. Cell, 2012, 150, 1107-1120.	13.5	1,591
41	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	13.5	1,485
42	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	7.7	1,428
43	Integrative genomic analyses identify MITF as a lineage survival oncogene amplified in malignant melanoma. Nature, 2005, 436, 117-122.	13.7	1,329
44	Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. Nature Genetics, 2012, 44, 685-689.	9.4	1,300
45	Initial genome sequencing and analysis of multiple myeloma. Nature, 2011, 471, 467-472.	13.7	1,288
46	BRAF mutation predicts sensitivity to MEK inhibition. Nature, 2006, 439, 358-362.	13.7	1,264
47	Defining T Cell States Associated with Response to Checkpoint Immunotherapy in Melanoma. Cell, 2018, 175, 998-1013.e20.	13.5	1,260
48	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. Nature Medicine, 2018, 24, 679-690.	15.2	1,224
49	Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. Cell, 2013, 152, 714-726.	13.5	1,202
50	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. Nature Genetics, 2012, 44, 1104-1110.	9.4	1,186
51	The human transcriptome across tissues and individuals. Science, 2015, 348, 660-665.	6.0	1,127
52	The genomic complexity of primary human prostate cancer. Nature, 2011, 470, 214-220.	13.7	1,107
53	Sequence analysis of mutations and translocations across breast cancer subtypes. Nature, 2012, 486, 405-409.	13.7	1,107
54	Punctuated Evolution of Prostate Cancer Genomes. Cell, 2013, 153, 666-677.	13.5	1,107

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55	An APOBEC cytidine deaminase mutagenesis pattern is widespread in human cancers. Nature Genetics, 2013, 45, 970-976.	9.4	1,023
56	SF3B1and Other Novel Cancer Genes in Chronic Lymphocytic Leukemia. New England Journal of Medicine, 2011, 365, 2497-2506.	13.9	1,021
57	Characterizing the cancer genome in lung adenocarcinoma. Nature, 2007, 450, 893-898.	13.7	1,020
58	Advances in understanding cancer genomes through second-generation sequencing. Nature Reviews Genetics, 2010, 11, 685-696.	7.7	1,014
59	The genetic landscape of high-risk neuroblastoma. Nature Genetics, 2013, 45, 279-284.	9.4	990
60	Neoantigen vaccine generates intratumoral T cell responses in phase Ib glioblastoma trial. Nature, 2019, 565, 234-239.	13.7	956
61	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. Nature Genetics, 2016, 48, 607-616.	9.4	933
62	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, 20007-20012.	3.3	927
63	Molecular Mechanisms of Resistance to First- and Second-Generation ALK Inhibitors inALK-Rearranged Lung Cancer. Cancer Discovery, 2016, 6, 1118-1133.	7.7	919
64	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. Nature, 2016, 539, 309-313.	13.7	875
65	Toil enables reproducible, open source, big biomedical data analyses. Nature Biotechnology, 2017, 35, 314-316.	9.4	873
66	Mutations driving CLL and their evolution in progression and relapse. Nature, 2015, 526, 525-530.	13.7	868
67	SOX2 is an amplified lineage-survival oncogene in lung and esophageal squamous cell carcinomas. Nature Genetics, 2009, 41, 1238-1242.	9.4	862
68	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, 3879-3884.	3.3	853
69	Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. Cancer Cell, 2014, 25, 91-101.	7.7	847
70	Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. Nature Genetics, 2015, 47, 106-114.	9.4	830
71	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. Cancer Discovery, 2015, 5, 1164-1177.	7.7	821
72	Ex vivo culture of circulating breast tumor cells for individualized testing of drug susceptibility. Science, 2014, 345, 216-220.	6.0	808

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73	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
74	The Genetic Landscape of Clinical Resistance to RAF Inhibition in Metastatic Melanoma. Cancer Discovery, 2014, 4, 94-109.	7.7	782
75	Tumor cells can follow distinct evolutionary paths to become resistant to epidermal growth factor receptor inhibition. Nature Medicine, 2016, 22, 262-269.	15.2	768
76	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750
77	RNA-SeQC: RNA-seq metrics for quality control and process optimization. Bioinformatics, 2012, 28, 1530-1532.	1.8	746
78	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. Science, 2017, 355, .	6.0	743
79	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	13.5	738
80	Landscape of genomic alterations in cervical carcinomas. Nature, 2014, 506, 371-375.	13.7	708
81	The evolutionary history of 2,658 cancers. Nature, 2020, 578, 122-128.	13.7	690
82	Resistance to checkpoint blockade therapy through inactivation of antigen presentation. Nature Communications, 2017, 8, 1136.	5.8	686
83	Coupled two-way clustering analysis of gene microarray data. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 12079-12084.	3.3	685
84	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
85	Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. Nature, 2012, 488, 106-110.	13.7	675
86	Melanoma genome sequencing reveals frequent PREX2 mutations. Nature, 2012, 485, 502-506.	13.7	671
87	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. Nature Genetics, 2013, 45, 478-486.	9.4	671
88	Genomic Correlates of Immune-Cell Infiltrates in Colorectal Carcinoma. Cell Reports, 2016, 15, 857-865.	2.9	671
89	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	7.7	665
90	Genetic and transcriptional evolution alters cancer cell line drug response. Nature, 2018, 560, 325-330.	13.7	662

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91	Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy. Nature Genetics, 2010, 42, 715-721.	9.4	642
92	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	7.7	642
93	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	13.5	620
94	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	2.9	605
95	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, 216-231.	7.7	596
96	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. Nature Communications, 2017, 8, 1324.	5.8	584
97	Comprehensive analysis of cancer-associated somatic mutations in class I HLA genes. Nature Biotechnology, 2015, 33, 1152-1158.	9.4	573
98	Genomic sequencing of meningiomas identifies oncogenic SMO and AKT1 mutations. Nature Genetics, 2013, 45, 285-289.	9.4	532
99	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	7.7	532
100	Integrative and Comparative Genomic Analysis of HPV-Positive and HPV-Negative Head and Neck Squamous Cell Carcinomas. Clinical Cancer Research, 2015, 21, 632-641.	3.2	525
101	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	2.9	523
102	Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. Nature Medicine, 2014, 20, 682-688.	15.2	508
103	Somatic ERCC2 Mutations Correlate with Cisplatin Sensitivity in Muscle-Invasive Urothelial Carcinoma. Cancer Discovery, 2014, 4, 1140-1153.	7.7	506
104	RB loss in resistant EGFR mutant lung adenocarcinomas that transform to small-cell lung cancer. Nature Communications, 2015, 6, 6377.	5.8	498
105	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. Nature Biotechnology, 2014, 32, 479-484.	9.4	495
106	TET2 mutations predict response to hypomethylating agents in myelodysplastic syndrome patients. Blood, 2014, 124, 2705-2712.	0.6	486
107	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	7.7	482
108	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	7.7	478

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109	High-resolution mapping of copy-number alterations with massively parallel sequencing. Nature Methods, 2009, 6, 99-103.	9.0	462
110	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. Science, 2018, 360, 331-335.	6.0	461
111	Oncotator: Cancer Variant Annotation Tool. Human Mutation, 2015, 36, E2423-E2429.	1.1	448
112	Genomic correlates of response to immune checkpoint blockade in microsatellite-stable solid tumors. Nature Genetics, 2018, 50, 1271-1281.	9.4	438
113	Comprehensive identification of mutational cancer driver genes across 12 tumor types. Scientific Reports, 2013, 3, 2650.	1.6	437
114	Resensitization to Crizotinib by the LorlatinibALKResistance Mutation L1198F. New England Journal of Medicine, 2016, 374, 54-61.	13.9	433
115	Targetable genetic features of primary testicular and primary central nervous system lymphomas. Blood, 2016, 127, 869-881.	0.6	429
116	A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. Nature Genetics, 2017, 49, 1476-1486.	9.4	427
117	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
118	MAP Kinase Pathway Alterations in BRAF-Mutant Melanoma Patients with Acquired Resistance to Combined RAF/MEK Inhibition. Cancer Discovery, 2014, 4, 61-68.	7.7	419
119	The Genomic Landscape of Pediatric Ewing Sarcoma. Cancer Discovery, 2014, 4, 1326-1341.	7.7	415
120	Genomic complexity of multiple myeloma and its clinical implications. Nature Reviews Clinical Oncology, 2017, 14, 100-113.	12.5	413
121	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. Cell, 2020, 182, 200-225.e35.	13.5	410
122	Exome sequencing identifies BRAF mutations in papillary craniopharyngiomas. Nature Genetics, 2014, 46, 161-165.	9.4	408
123	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-e67.	6.5	407
124	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	2.9	407
125	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	7.7	396
126	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. Nature Genetics, 2018, 50, 956-967.	9.4	389

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127	RNF43 is frequently mutated in colorectal and endometrial cancers. Nature Genetics, 2014, 46, 1264-1266.	9.4	388
128	Polyclonal Secondary FGFR2 Mutations Drive Acquired Resistance to FGFR Inhibition in Patients with FGFR2 Fusionâ€“Positive Cholangiocarcinoma. Cancer Discovery, 2017, 7, 252-263.	7.7	384
129	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, 12372-12377.	3.3	383
130	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.	3.9	373
131	RNA sequence analysis reveals macroscopic somatic clonal expansion across normal tissues. Science, 2019, 364, .	6.0	369
132	Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. Cell, 2016, 164, 538-549.	13.5	363
133	Somatic Mutations Predict Poor Outcome in Patients With Myelodysplastic Syndrome After Hematopoietic Stem-Cell Transplantation. Journal of Clinical Oncology, 2014, 32, 2691-2698.	0.8	359
134	Liquid versus tissue biopsy for detecting acquired resistance and tumor heterogeneity in gastrointestinal cancers. Nature Medicine, 2019, 25, 1415-1421.	15.2	359
135	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.	3.3	355
136	An APOBEC3A hypermutation signature is distinguishable from the signature of background mutagenesis by APOBEC3B in human cancers. Nature Genetics, 2015, 47, 1067-1072.	9.4	354
137	Somatic ERCC2 mutations are associated with a distinct genomic signature in urothelial tumors. Nature Genetics, 2016, 48, 600-606.	9.4	352
138	A remarkably simple genome underlies highly malignant pediatric rhabdoid cancers. Journal of Clinical Investigation, 2012, 122, 2983-2988.	3.9	347
139	Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. Genome Research, 2015, 25, 316-327.	2.4	343
140	Mutational processes shape the landscape of TP53 mutations in human cancer. Nature Genetics, 2018, 50, 1381-1387.	9.4	334
141	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	13.5	334
142	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
143	Control of tumor-associated macrophages and T cells in glioblastoma via AHR and CD39. Nature Neuroscience, 2019, 22, 729-740.	7.1	327
144	Proteogenomic and metabolomic characterization of human glioblastoma. Cancer Cell, 2021, 39, 509-528.e20.	7.7	327

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145	Mutations in isocitrate dehydrogenase 1 and 2 occur frequently in intrahepatic cholangiocarcinomas and share hypermethylation targets with glioblastomas. Oncogene, 2013, 32, 3091-3100.	2.6	324
146	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	2.9	324
147	Locally Disordered Methylation Forms the Basis of Intratumor Methylome Variation in Chronic Lymphocytic Leukemia. Cancer Cell, 2014, 26, 813-825.	7.7	323
148	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, 15544-15549.	3.3	317
149	Making sense of cancer genomic data. Genes and Development, 2011, 25, 534-555.	2.7	313
150	Paired exome analysis of Barrett's esophagus and adenocarcinoma. Nature Genetics, 2015, 47, 1047-1055.	9.4	310
151	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	7.7	309
152	DNA microarrays identification of primary and secondary target genes regulated by p53. Oncogene, 2001, 20, 2225-2234.	2.6	308
153	Tumor-suppressor genes that escape from X-inactivation contribute to cancer sex bias. Nature Genetics, 2017, 49, 10-16.	9.4	307
154	Epidermal Growth Factor Receptor Activation in Glioblastoma through Novel Missense Mutations in the Extracellular Domain. PLoS Medicine, 2006, 3, e485.	3.9	298
155	Proteogenomic Characterization of Endometrial Carcinoma. Cell, 2020, 180, 729-748.e26.	13.5	296
156	Response and Acquired Resistance to Everolimus in Anaplastic Thyroid Cancer. New England Journal of Medicine, 2014, 371, 1426-1433.	13.9	290
157	PathSeq: software to identify or discover microbes by deep sequencing of human tissue. Nature Biotechnology, 2011, 29, 393-396.	9.4	289
158	SvABA: genome-wide detection of structural variants and indels by local assembly. Genome Research, 2018, 28, 581-591.	2.4	288
159	Systematic identification of personal tumor-specific neoantigens in chronic lymphocytic leukemia. Blood, 2014, 124, 453-462.	0.6	286
160	Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. Nature Communications, 2016, 7, 11589.	5.8	285
161	Modeling Genomic Diversity and Tumor Dependency in Malignant Melanoma. Cancer Research, 2008, 68, 664-673.	0.4	275
162	Somatic mutation of CDKN1B in small intestine neuroendocrine tumors. Nature Genetics, 2013, 45, 1483-1486.	9.4	275

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163	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, 4834-4839.	3.3	273
164	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. Cell, 2020, 183, 1436-1456.e31.	13.5	273
165	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
166	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion. Nature Genetics, 2011, 43, 964-968.	9.4	270
167	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	7.7	270
168	Recurrent and functional regulatory mutations in breast cancer. Nature, 2017, 547, 55-60.	13.7	269
169	Integrated Genome-Wide DNA Copy Number and Expression Analysis Identifies Distinct Mechanisms of Primary Chemoresistance in Ovarian Carcinomas. Clinical Cancer Research, 2009, 15, 1417-1427.	3.2	266
170	Clinical Acquired Resistance to RAF Inhibitor Combinations in BRAF-Mutant Colorectal Cancer through MAPK Pathway Alterations. Cancer Discovery, 2015, 5, 358-367.	7.7	265
171	Identification of driver genes in hepatocellular carcinoma by exome sequencing. Hepatology, 2013, 58, 1693-1702.	3.6	264
172	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	13.5	260
173	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. Cell, 2018, 174, 433-447.e19.	13.5	258
174	Assessing the clinical utility of cancer genomic and proteomic data across tumor types. Nature Biotechnology, 2014, 32, 644-652.	9.4	257
175	Real-time Genomic Characterization of Advanced Pancreatic Cancer to Enable Precision Medicine. Cancer Discovery, 2018, 8, 1096-1111.	7.7	256
176	Genomic characterization of biliary tract cancers identifies driver genes and predisposing mutations. Journal of Hepatology, 2018, 68, 959-969.	1.8	254
177	TAS-120 Overcomes Resistance to ATP-Competitive FGFR Inhibitors in Patients with FGFR2 Fusionâ€“Positive Intrahepatic Cholangiocarcinoma. Cancer Discovery, 2019, 9, 1064-1079.	7.7	254
178	WRN helicase is a synthetic lethal target in microsatellite unstable cancers. Nature, 2019, 568, 551-556.	13.7	253
179	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
180	Integrative analysis of the melanoma transcriptome. Genome Research, 2010, 20, 413-427.	2.4	248

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181	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, 14476-14481.	3.3	246
182	Genetic and Clonal Dissection of Murine Small Cell Lung Carcinoma Progression by Genome Sequencing. Cell, 2014, 156, 1298-1311.	13.5	241
183	Temporal Dissection of Tumorigenesis in Primary Cancers. Cancer Discovery, 2011, 1, 137-143.	7.7	240
184	Proteogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	13.5	236
185	ContEst: estimating cross-contamination of human samples in next-generation sequencing data. Bioinformatics, 2011, 27, 2601-2602.	1.8	235
186	The genomic landscape of juvenile myelomonocytic leukemia. Nature Genetics, 2015, 47, 1326-1333.	9.4	233
187	Predicting drug susceptibility of nonâ€“small cell lung cancers based on genetic lesions. Journal of Clinical Investigation, 2009, 119, 1727-1740.	3.9	230
188	Mitochondrial Reprogramming Underlies Resistance to BCL-2 Inhibition in Lymphoid Malignancies. Cancer Cell, 2019, 36, 369-384.e13.	7.7	224
189	Whole-genome sequencing reveals activation-induced cytidine deaminase signatures during indolent chronic lymphocytic leukaemia evolution. Nature Communications, 2015, 6, 8866.	5.8	223
190	PD-1 blockade in subprimed CD8 cells induces dysfunctional PD-1+CD38hi cells and anti-PD-1 resistance. Nature Immunology, 2019, 20, 1231-1243.	7.0	217
191	Identification of the JNK Signaling Pathway as a Functional Target of the Tumor Suppressor PTEN. Cancer Cell, 2007, 11, 555-569.	7.7	214
192	Cell typeâ€“specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	6.0	210
193	Single-cell RNA sequencing reveals compromised immune microenvironment in precursor stages of multiple myeloma. Nature Cancer, 2020, 1, 493-506.	5.7	209
194	High order chromatin architecture shapes the landscape of chromosomal alterations in cancer. Nature Biotechnology, 2011, 29, 1109-1113.	9.4	204
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