

Gad Getz

List of Publications by Year in Descending Order

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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.

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	Single-cell profiling of tumour evolution in multiple myeloma - opportunities for precision medicine.. <i>Nature Reviews Clinical Oncology</i> , 2022 ,	19.4	10
382	Genomic predictors of response to PD-1 inhibition in children with germline DNA replication repair deficiency.. <i>Nature Medicine</i> , 2022 ,	50.5	2
381	Combined tumor and immune signals from genomes or transcriptomes predict outcomes of checkpoint inhibition in melanoma.. <i>Cell Reports Medicine</i> , 2022 , 3, 100500	18	2
380	CAR T cell killing requires the IFN β pathway in solid but not liquid tumours.. <i>Nature</i> , 2022 ,	50.4	9
379	Single-nucleus cross-tissue molecular reference maps toward understanding disease gene function.. <i>Science</i> , 2022 , 376, eabl4290	33.3	9
378	DNA Polymerase and Mismatch Repair Exert Distinct Microsatellite Instability Signatures in Normal and Malignant Human Cells. <i>Cancer Discovery</i> , 2021 , 11, 1176-1191	24.4	19
377	221 CRISPR screen identifies loss of IFN β signaling and downstream adhesion as a resistance mechanism to CAR T-cell cytotoxicity in solid but not liquid tumors 2021 , 9, A234-A234		
376	Single Cell Characterization of Myeloma and Its Precursor Conditions Reveals Transcriptional Signatures of Early Tumorigenesis. <i>Blood</i> , 2021 , 138, 2219-2219	2.2	
375	High Prevalence of Monoclonal Gammopathy in a Population at Risk: The First Results of the Promise Study. <i>Blood</i> , 2021 , 138, 152-152	2.2	0
374	Paralog knockout profiling identifies DUSP4 and DUSP6 as a digenic dependence in MAPK pathway-driven cancers. <i>Nature Genetics</i> , 2021 , 53, 1664-1672	36.3	6
373	Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. <i>Nature Biotechnology</i> , 2021 ,	44.5	13
372	Single-cell RNA sequencing: one step closer to the clinic. <i>Nature Medicine</i> , 2021 , 27, 375-376	50.5	5
371	RNA-SeQC 2: Efficient RNA-seq quality control and quantification for large cohorts. <i>Bioinformatics</i> , 2021 ,	7.2	4
370	Activation of the MAPK pathway mediates resistance to PI3K inhibitors in chronic lymphocytic leukemia. <i>Blood</i> , 2021 , 138, 44-56	2.2	7
369	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021 , 39, 509-528	24.3	71
368	Lack of transgenerational effects of ionizing radiation exposure from the Chernobyl accident. <i>Science</i> , 2021 , 372, 725-729	33.3	18
367	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. <i>Science</i> , 2021 , 372,	33.3	18

366	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021 , 184, 2239-2254.e39	56.2	57
365	Inflammatory stromal cells in the myeloma microenvironment. <i>Nature Immunology</i> , 2021 , 22, 677-678	19.1	0
364	PANOPLY: a cloud-based platform for automated and reproducible proteogenomic data analysis. <i>Nature Methods</i> , 2021 , 18, 580-582	21.6	3
363	Longitudinal Single-Cell Dynamics of Chromatin Accessibility and Mitochondrial Mutations in Chronic Lymphocytic Leukemia Mirror Disease History. <i>Cancer Discovery</i> , 2021 ,	24.4	5
362	is mutated in clonal hematopoiesis and myelodysplastic syndromes and impacts RNA splicing. <i>Blood Cancer Discovery</i> , 2021 , 2, 500-517	7	0
361	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. <i>Nature Biotechnology</i> , 2021 , 39, 451-461	44.5	59
360	Subependymal giant cell astrocytomas are characterized by mTORC1 hyperactivation, a very low somatic mutation rate, and a unique gene expression profile. <i>Modern Pathology</i> , 2021 , 34, 264-279	9.8	1
359	The Lipogenic Regulator SREBP2 Induces Transferrin in Circulating Melanoma Cells and Suppresses Ferroptosis. <i>Cancer Discovery</i> , 2021 , 11, 678-695	24.4	31
358	Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021 , 34, 108707	10.6	7
357	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021 , 39, 361-379.e16	24.3	50
356	Multifunctional barcoding with ClonMapper enables high-resolution study of clonal dynamics during tumor evolution and treatment.. <i>Nature Cancer</i> , 2021 , 2, 758-772	15.4	8
355	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021 , 184, 4348-4371.e40	56.2	15
354	Parallel Genomic Alterations of Antigen and Payload Targets Mediate Polyclonal Acquired Clinical Resistance to Sacituzumab Govitecan in Triple-Negative Breast Cancer. <i>Cancer Discovery</i> , 2021 , 11, 2436-2445	24.4	8
353	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021 , 184, 5031-5052.e26	56.2	26
352	Molecular features of exceptional response to neoadjuvant anti-androgen therapy in high-risk localized prostate cancer. <i>Cell Reports</i> , 2021 , 36, 109665	10.6	4
351	Clonal hematopoiesis is associated with adverse outcomes in multiple myeloma patients undergoing transplant. <i>Nature Communications</i> , 2020 , 11, 2996	17.4	34
350	Identification of Somatic Acquired Mutations by cfDNA Analysis in Patients with Metastatic Breast Cancer. <i>Clinical Cancer Research</i> , 2020 , 26, 4852-4862	12.9	7
349	Sensitive Detection of Minimal Residual Disease in Patients Treated for Early-Stage Breast Cancer. <i>Clinical Cancer Research</i> , 2020 , 26, 2556-2564	12.9	32

348	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020 , 182, 200-225.e35	56.2	139
347	Predicting and affecting response to cancer therapy based on pathway-level biomarkers. <i>Nature Communications</i> , 2020 , 11, 3296	17.4	24
346	Passenger Mutations in More Than 2,500 Cancer Genomes: Overall Molecular Functional Impact and Consequences. <i>Cell</i> , 2020 , 180, 915-927.e16	56.2	38
345	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020 , 180, 729-748.e26	56.2	122
344	A deep learning system accurately classifies primary and metastatic cancers using passenger mutation patterns. <i>Nature Communications</i> , 2020 , 11, 728	17.4	60
343	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020 , 11, 729	17.4	38
342	The evolutionary history of 2,658 cancers. <i>Nature</i> , 2020 , 578, 122-128	50.4	307
341	The repertoire of mutational signatures in human cancer. <i>Nature</i> , 2020 , 578, 94-101	50.4	849
340	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020 , 578, 102-111	50.4	220
339	Single-cell RNA sequencing reveals compromised immune microenvironment in precursor stages of multiple myeloma. <i>Nature Cancer</i> , 2020 , 1, 493-506	15.4	73
338	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020 , 181, 236-249	56.2	140
337	Genetic Determinants and Evolutionary History of Richter's Syndrome. <i>Blood</i> , 2020 , 136, 47-48	2.2	3
336	The CLL-1100 Project: Towards Complete Genomic Characterization and Improved Prognostics for CLL. <i>Blood</i> , 2020 , 136, 3-4	2.2	2
335	Genomic Profiling of Smoldering Multiple Myeloma Identifies Patients at a High Risk of Disease Progression. <i>Journal of Clinical Oncology</i> , 2020 , 38, 2380-2389	2.2	46
334	Butler enables rapid cloud-based analysis of thousands of human genomes. <i>Nature Biotechnology</i> , 2020 , 38, 288-292	44.5	9
333	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020 , 183, 1436-1456.e31	56.2	71
332	Genomic Predictors of Good Outcome, Recurrence, or Progression in High-Grade T1 Non-Muscle-Invasive Bladder Cancer. <i>Cancer Research</i> , 2020 , 80, 4476-4486	10.1	20
331	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020 , 11, 4748	17.4	10

330	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020 , 11, 4330	17.4	23
329	Distinct evolutionary paths in chronic lymphocytic leukemia during resistance to the graft-versus-leukemia effect. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	7
328	Cell type-specific genetic regulation of gene expression across human tissues. <i>Science</i> , 2020 , 369,	33.3	68
327	Liquid versus tissue biopsy for detecting acquired resistance and tumor heterogeneity in gastrointestinal cancers. <i>Nature Medicine</i> , 2019 , 25, 1415-1421	50.5	161
326	Mitochondrial Reprogramming Underlies Resistance to BCL-2 Inhibition in Lymphoid Malignancies. <i>Cancer Cell</i> , 2019 , 36, 369-384.e13	24.3	107
325	Passenger Hotspot Mutations in Cancer. <i>Cancer Cell</i> , 2019 , 36, 288-301.e14	24.3	38
324	A Murine Model of Chronic Lymphocytic Leukemia Based on B Cell-Restricted Expression of Sf3b1 Mutation and Atm Deletion. <i>Cancer Cell</i> , 2019 , 35, 283-296.e5	24.3	37
323	RNA sequence analysis reveals macroscopic somatic clonal expansion across normal tissues. <i>Science</i> , 2019 , 364,	33.3	226
322	The Genomic and Immune Landscapes of Lethal Metastatic Breast Cancer. <i>Cell Reports</i> , 2019 , 27, 2690-2708.e108	27.8	108
321	Growth dynamics in naturally progressing chronic lymphocytic leukaemia. <i>Nature</i> , 2019 , 570, 474-479	50.4	47
320	Genomic Evolutionary Patterns of Leiomyosarcoma and Liposarcoma. <i>Clinical Cancer Research</i> , 2019 , 25, 5135-5142	12.9	11
319	Next-generation characterization of the Cancer Cell Line Encyclopedia. <i>Nature</i> , 2019 , 569, 503-508	50.4	962
318	TAS-120 Overcomes Resistance to ATP-Competitive FGFR Inhibitors in Patients with FGFR2 Fusion-Positive Intrahepatic Cholangiocarcinoma. <i>Cancer Discovery</i> , 2019 , 9, 1064-1079	24.4	154
317	Analyzing Frequently Mutated Genes and the Association With Tumor Mutation Load. <i>JAMA Oncology</i> , 2019 , 5, 577	13.4	4
316	Control of tumor-associated macrophages and T cells in glioblastoma via AHR and CD39. <i>Nature Neuroscience</i> , 2019 , 22, 729-740	25.5	166
315	WRN helicase is a synthetic lethal target in microsatellite unstable cancers. <i>Nature</i> , 2019 , 568, 551-556	50.4	137
314	A (fire)cloud-based DNA methylation data preprocessing and quality control platform. <i>BMC Bioinformatics</i> , 2019 , 20, 160	3.6	4
313	Mutations in RABL3 alter KRAS prenylation and are associated with hereditary pancreatic cancer. <i>Nature Genetics</i> , 2019 , 51, 1308-1314	36.3	31

312	PD-1 blockade in subprimed CD8 cells induces dysfunctional PD-1CD38 cells and anti-PD-1 resistance. <i>Nature Immunology</i> , 2019 , 20, 1231-1243	19.1	132
311	Comparative Genomic Analyses Defines Shared and Unique Features of cHL and PMBL and New Mechanisms of Sensitivity to PD-1 Blockade. <i>Blood</i> , 2019 , 134, 1493-1493	2.2	
310	Genomic analyses of PMBL reveal new drivers and mechanisms of sensitivity to PD-1 blockade. <i>Blood</i> , 2019 , 134, 2369-2382	2.2	32
309	Genomic analyses of flow-sorted Hodgkin Reed-Sternberg cells reveal complementary mechanisms of immune evasion. <i>Blood Advances</i> , 2019 , 3, 4065-4080	7.8	38
308	Scaling computational genomics to millions of individuals with GPUs. <i>Genome Biology</i> , 2019 , 20, 228	18.3	20
307	Neoantigen vaccine generates intratumoral T cell responses in phase Ib glioblastoma trial. <i>Nature</i> , 2019 , 565, 234-239	50.4	569
306	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018 , 360, 331-335	33.3	255
305	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018 , 173, 400-416.e11	56.2	1072
304	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
303	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018 , 173, 291-304.e6	56.2	888
302	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
301	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
300	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018 , 173, 355-370.e14	56.2	342
299	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018 , 23, 282-296.e4	10.6	188
298	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018 , 23, 227-238.e3	10.6	235
297	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018 , 23, 313-326.e5	10.6	295
296	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018 , 23, 181-193.e7	10.6	366
295	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754

294	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 239-254.e6	10.6	405
293	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018 , 23, 270-281.e3	10.6	121
292	Genomic characterization of biliary tract cancers identifies driver genes and predisposing mutations. <i>Journal of Hepatology</i> , 2018 , 68, 959-969	13.4	149
291	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018 , 33, 244-258.e10	24.3	150
290	Distinct mutational signatures characterize concurrent loss of polymerase proofreading and mismatch repair. <i>Nature Communications</i> , 2018 , 9, 1746	17.4	95
289	Whole-exome sequencing of cell-free DNA and circulating tumor cells in multiple myeloma. <i>Nature Communications</i> , 2018 , 9, 1691	17.4	103
288	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. <i>Nature Medicine</i> , 2018 , 24, 679-690	50.5	659
287	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018 , 6, 271-281.e7	10.6	320
286	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	24.3	377
285	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228
284	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018 , 33, 690-705.e9	24.3	277
283	SvABA: genome-wide detection of structural variants and indels by local assembly. <i>Genome Research</i> , 2018 , 28, 581-591	9.7	149
282	Widespread Chromosomal Losses and Mitochondrial DNA Alterations as Genetic Drivers in Hcthle Cell Carcinoma. <i>Cancer Cell</i> , 2018 , 34, 242-255.e5	24.3	93
281	Genomic correlates of response to immune checkpoint blockade in microsatellite-stable solid tumors. <i>Nature Genetics</i> , 2018 , 50, 1271-1281	36.3	249
280	Genetic and transcriptional evolution alters cancer cell line drug response. <i>Nature</i> , 2018 , 560, 325-330	50.4	379
279	Real-time Genomic Characterization of Advanced Pancreatic Cancer to Enable Precision Medicine. <i>Cancer Discovery</i> , 2018 , 8, 1096-1111	24.4	156
278	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018 , 23, 3392-3406.e10	10.6	200
277	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. <i>Cell</i> , 2018 , 174, 433-447.e19	56.2	155

276	Tumor fraction in cell-free DNA as a biomarker in prostate cancer. <i>JCI Insight</i> , 2018 , 3,	9.9	49
275	Comprehensive Genomic Analysis of Primary Mediastinal B-Cell Lymphoma. <i>Blood</i> , 2018 , 132, 1564-1564.e2	2.2	4
274	Clonal and Single Cell Dynamics of Resistance to Graft-Versus-Leukemia (GvL) in Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2018 , 132, 820-820	2.2	
273	NetSig: network-based discovery from cancer genomes. <i>Nature Methods</i> , 2018 , 15, 61-66	21.6	61
272	Association of Cell-Free DNA Tumor Fraction and Somatic Copy Number Alterations With Survival in Metastatic Triple-Negative Breast Cancer. <i>Journal of Clinical Oncology</i> , 2018 , 36, 543-553	2.2	113
271	Quantification of somatic mutation flow across individual cell division events by lineage sequencing. <i>Genome Research</i> , 2018 , 28, 1901-1918	9.7	10
270	Comment on "DNA damage is a pervasive cause of sequencing errors, directly confounding variant identification". <i>Science</i> , 2018 , 361,	33.3	1
269	Type 2 diabetes genetic loci informed by multi-trait associations point to disease mechanisms and subtypes: A soft clustering analysis. <i>PLoS Medicine</i> , 2018 , 15, e1002654	11.6	180
268	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018 , 7, 422-437.e7	10.6	85
267	Defining T Cell States Associated with Response to Checkpoint Immunotherapy in Melanoma. <i>Cell</i> , 2018 , 175, 998-1013.e20	56.2	631
266	Mutational processes shape the landscape of TP53 mutations in human cancer. <i>Nature Genetics</i> , 2018 , 50, 1381-1387	36.3	165
265	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. <i>Nature Genetics</i> , 2018 , 50, 956-967	36.3	239
264	DeTiN: overcoming tumor-in-normal contamination. <i>Nature Methods</i> , 2018 , 15, 531-534	21.6	32
263	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017 , 31, 181-193	24.3	350
262	Toil enables reproducible, open source, big biomedical data analyses. <i>Nature Biotechnology</i> , 2017 , 35, 314-316	44.5	387
261	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
260	Modeling Genomic Instability and Selection Pressure in a Mouse Model of Melanoma. <i>Cell Reports</i> , 2017 , 19, 1304-1312	10.6	12
259	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. <i>Gastroenterology</i> , 2017 , 153, 536-549.e26	13.3	63

258	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. <i>Science</i> , 2017 , 355,	33.3	455
257	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017 , 31, 411-423	24.3	210
256	Polyclonal Secondary Mutations Drive Acquired Resistance to FGFR Inhibition in Patients with FGFR2 Fusion-Positive Cholangiocarcinoma. <i>Cancer Discovery</i> , 2017 , 7, 252-263	24.4	262
255	Resistance to checkpoint blockade therapy through inactivation of antigen presentation. <i>Nature Communications</i> , 2017 , 8, 1136	17.4	409
254	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017 , 171, 540-556.e25	37.5	961
253	A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. <i>Nature Genetics</i> , 2017 , 49, 1476-1486	36.3	255
252	Analysis of somatic microsatellite indels identifies driver events in human tumors. <i>Nature Biotechnology</i> , 2017 , 35, 951-959	44.5	72
251	Comparison of algorithms for the detection of cancer drivers at subgene resolution. <i>Nature Methods</i> , 2017 , 14, 782-788	21.6	51
250	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017 , 32, 204-220.e15	24.3	391
249	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017 , 32, 185-203.e13	31.9	966
248	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. <i>Nature Communications</i> , 2017 , 8, 1324	17.4	314
247	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28	56.2	451
246	An immunogenic personal neoantigen vaccine for patients with melanoma. <i>Nature</i> , 2017 , 547, 217-221	50.4	1375
245	Rare germline variants in ATM are associated with chronic lymphocytic leukemia. <i>Leukemia</i> , 2017 , 31, 2244-2247	10.7	9
244	Recurrent and functional regulatory mutations in breast cancer. <i>Nature</i> , 2017 , 547, 55-60	50.4	192
243	Genomic complexity of multiple myeloma and its clinical implications. <i>Nature Reviews Clinical Oncology</i> , 2017 , 14, 100-113	19.4	267
242	Survival of Del17p CLL Depends on Genomic Complexity and Somatic Mutation. <i>Clinical Cancer Research</i> , 2017 , 23, 735-745	12.9	62
241	Genomic Evolution after Chemoradiotherapy in Anal Squamous Cell Carcinoma. <i>Clinical Cancer Research</i> , 2017 , 23, 3214-3222	12.9	28

240	Tumor-suppressor genes that escape from X-inactivation contribute to cancer sex bias. <i>Nature Genetics</i> , 2017 , 49, 10-16	36.3	167
239	Resolving the phylogenetic origin of glioblastoma via multifocal genomic analysis of pre-treatment and treatment-resistant autopsy specimens. <i>Npj Precision Oncology</i> , 2017 , 1, 33	9.8	17
238	The evolutionary landscape of chronic lymphocytic leukemia treated with ibrutinib targeted therapy. <i>Nature Communications</i> , 2017 , 8, 2185	17.4	99
237	Mutational patterns in chemotherapy resistant muscle-invasive bladder cancer. <i>Nature Communications</i> , 2017 , 8, 2193	17.4	62
236	Systematic genomic and translational efficiency studies of uveal melanoma. <i>PLoS ONE</i> , 2017 , 12, e0178189	18.9	21
235	Analysis of protein-coding genetic variation in 60,706 humans. <i>Nature</i> , 2016 , 536, 285-91	50.4	6940
234	Molecular Mechanisms of Resistance to First- and Second-Generation ALK Inhibitors in ALK-Rearranged Lung Cancer. <i>Cancer Discovery</i> , 2016 , 6, 1118-1133	24.4	648
233	Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. <i>Nature Communications</i> , 2016 , 7, 11589	17.4	220
232	Transcriptomic Characterization of SF3B1 Mutation Reveals Its Pleiotropic Effects in Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2016 , 30, 750-763	24.3	115
231	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. <i>Nature</i> , 2016 , 539, 309-313	50.4	561
230	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. <i>Nature Genetics</i> , 2016 , 48, 848-55	36.3	135
229	Regulation of Transient Site-specific Copy Gain by MicroRNA. <i>Journal of Biological Chemistry</i> , 2016 , 291, 4862-71	5.4	20
228	Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. <i>Cell</i> , 2016 , 164, 538-49	56.2	239
227	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016 , 164, 550-63	56.2	1140
226	Tumor cells can follow distinct evolutionary paths to become resistant to epidermal growth factor receptor inhibition. <i>Nature Medicine</i> , 2016 , 22, 262-9	50.5	533
225	Resensitization to Crizotinib by the Lorlatinib ALK Resistance Mutation L1198F. <i>New England Journal of Medicine</i> , 2016 , 374, 54-61	59.2	334
224	Dramatic Response of BRAF V600E Mutant Papillary Craniopharyngioma to Targeted Therapy. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	144
223	The Landscape of Dynamic Genetic Changes in Ibrutinib-Treated CLL. <i>Blood</i> , 2016 , 128, 188-188	2.2	3

222	Whole-Exome Sequencing and Targeted Deep Sequencing of cfDNA Enables a Comprehensive Mutational Profiling of Multiple Myeloma. <i>Blood</i> , 2016 , 128, 197-197	2.2	7
221	In Silico and Functional Characterization of TBL1XR1 as a Tumor Suppressor in Large B-Cell Lymphomas. <i>Blood</i> , 2016 , 128, 612-612	2.2	3
220	Whole Exome Sequencing and Targeted Sequencing Reveal the Heterogeneity of Genomic Evolution and Mutational Profile in Smoldering Multiple Myeloma. <i>Blood</i> , 2016 , 128, 237-237	2.2	
219	Whole Exome Sequencing Identifies TSC1/TSC2 Biallelic Loss as the Primary and Sufficient Driver Event for Renal Angiomyolipoma Development. <i>PLoS Genetics</i> , 2016 , 12, e1006242	6	62
218	Genomic evolution and chemoresistance in germ-cell tumours. <i>Nature</i> , 2016 , 540, 114-118	50.4	100
217	Phenotypic Characterization of a Comprehensive Set of MAPK1/ERK2 Missense Mutants. <i>Cell Reports</i> , 2016 , 17, 1171-1183	10.6	78
216	Genomic Correlates of Immune-Cell Infiltrates in Colorectal Carcinoma. <i>Cell Reports</i> , 2016 , 15, 857-865	10.6	422
215	Characterizing genomic alterations in cancer by complementary functional associations. <i>Nature Biotechnology</i> , 2016 , 34, 539-46	44.5	57
214	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016 , 29, 723-736	24.3	324
213	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016 , 48, 607-16	36.3	613
212	Systematic Functional Interrogation of Rare Cancer Variants Identifies Oncogenic Alleles. <i>Cancer Discovery</i> , 2016 , 6, 714-26	24.4	100
211	Somatic ERCC2 mutations are associated with a distinct genomic signature in urothelial tumors. <i>Nature Genetics</i> , 2016 , 48, 600-606	36.3	238
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32	Cluster analysis of human autoantibody reactivities in health and in type 1 diabetes mellitus: a bio-informatic approach to immune complexity. <i>Journal of Autoimmunity</i> , 2003 , 21, 65-75	15.5	42
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24	Framework for quality assessment of whole genome, cancer sequences	6
23	The evolutionary history of 2,658 cancers	28
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