

# Gad Getz

## List of Publications by Year in descending order

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Version: 2024-02-01

370  
papers

236,845  
citations

36

191  
h-index

94

356  
g-index

413  
all docs

413  
docs citations

413  
times ranked

191462  
citing authors

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

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|----|--|------|-----------|
| 19 | Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.                                 | 13.9 | 2,582     |
| 20 | Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 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. <i>Genome Biology</i> , 2011, 12, R41. | 3.8  | 2,546     |
| 22 | The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.   | 13.5 | 2,435     |
| 23 | Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.  | 13.5 | 2,318     |
| 24 | An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.                               | 13.5 | 2,277     |
| 25 | A Landscape of Driver Mutations in Melanoma. <i>Cell</i> , 2012, 150, 251-263.   | 13.5 | 2,247     |
| 26 | The Mutational Landscape of Head and Neck Squamous Cell Carcinoma. <i>Science</i> , 2011, 333, 1157-1160.  | 6.0  | 2,225     |
| 27 | Next-generation characterization of the Cancer Cell Line Encyclopedia. <i>Nature</i> , 2019, 569, 503-508.   | 13.7 | 2,149     |
| 28 | International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.   | 13.7 | 2,114     |
| 29 | An immunogenic personal neoantigen vaccine for patients with melanoma. <i>Nature</i> , 2017, 547, 217-221.   | 13.7 | 2,112     |
| 30 | Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.   | 13.5 | 2,111     |
| 31 | The repertoire of mutational signatures in human cancer. <i>Nature</i> , 2020, 578, 94-101.  | 13.7 | 2,104     |
| 32 | Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.  | 13.5 | 1,794     |
| 33 | Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 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. <i>Cell</i> , 2018, 173, 291-304.e6.                               | 13.5 | 1,718     |
| 35 | Absolute quantification of somatic DNA alterations in human cancer. <i>Nature Biotechnology</i> , 2012, 30, 413-421.   | 9.4  | 1,710     |
| 36 | Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. <i>Cell</i> , 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. <i>Cell</i> , 2016, 164, 550-563.                       | 13.5 | 1,695     |
| 38 | Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.   | 13.5 | 1,670     |
| 39 | Pan-cancer patterns of somatic copy number alteration. <i>Nature Genetics</i> , 2013, 45, 1134-1140.   | 9.4  | 1,616     |
| 40 | Mapping the Hallmarks of Lung Adenocarcinoma with Massively Parallel Sequencing. <i>Cell</i> , 2012, 150, 1107-1120.   | 13.5 | 1,591     |
| 41 | Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.   | 13.5 | 1,485     |
| 42 | Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.   | 7.7  | 1,428     |
| 43 | Integrative genomic analyses identify MITF as a lineage survival oncogene amplified in malignant melanoma. <i>Nature</i> , 2005, 436, 117-122.                   | 13.7 | 1,329     |
| 44 | Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. <i>Nature Genetics</i> , 2012, 44, 685-689.                            | 9.4  | 1,300     |
| 45 | Initial genome sequencing and analysis of multiple myeloma. <i>Nature</i> , 2011, 471, 467-472.  | 13.7 | 1,288     |
| 46 | BRAF mutation predicts sensitivity to MEK inhibition. <i>Nature</i> , 2006, 439, 358-362.  | 13.7 | 1,264     |
| 47 | Defining T Cell States Associated with Response to Checkpoint Immunotherapy in Melanoma. <i>Cell</i> , 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. <i>Nature Medicine</i> , 2018, 24, 679-690. | 15.2 | 1,224     |
| 49 | Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. <i>Cell</i> , 2013, 152, 714-726.   | 13.5 | 1,202     |
| 50 | Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. <i>Nature Genetics</i> , 2012, 44, 1104-1110.                       | 9.4  | 1,186     |
| 51 | The human transcriptome across tissues and individuals. <i>Science</i> , 2015, 348, 660-665.   | 6.0  | 1,127     |
| 52 | The genomic complexity of primary human prostate cancer. <i>Nature</i> , 2011, 470, 214-220.   | 13.7 | 1,107     |
| 53 | Sequence analysis of mutations and translocations across breast cancer subtypes. <i>Nature</i> , 2012, 486, 405-409.   | 13.7 | 1,107     |
| 54 | Punctuated Evolution of Prostate Cancer Genomes. <i>Cell</i> , 2013, 153, 666-677.   | 13.5 | 1,107     |

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|----|--|------|-----------|
| 55 | An APOBEC cytidine deaminase mutagenesis pattern is widespread in human cancers. <i>Nature Genetics</i> , 2013, 45, 970-976.   | 9.4  | 1,023     |
| 56 | <i>MYD88</i> and Other Novel Cancer Genes in Chronic Lymphocytic Leukemia. <i>New England Journal of Medicine</i> , 2011, 365, 2497-2506.  | 13.9 | 1,021     |
| 57 | Characterizing the cancer genome in lung adenocarcinoma. <i>Nature</i> , 2007, 450, 893-898.   | 13.7 | 1,020     |
| 58 | Advances in understanding cancer genomes through second-generation sequencing. <i>Nature Reviews Genetics</i> , 2010, 11, 685-696.   | 7.7  | 1,014     |
| 59 | The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , 2013, 45, 279-284.  | 9.4  | 990       |
| 60 | Neoantigen vaccine generates intratumoral T cell responses in phase Ib glioblastoma trial. <i>Nature</i> , 2019, 565, 234-239.   | 13.7 | 956       |
| 61 | Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016, 48, 607-616.  | 9.4  | 933       |
| 62 | Assessing the significance of chromosomal aberrations in cancer: Methodology and application to glioma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 20007-20012.             | 3.3  | 927       |
| 63 | Molecular Mechanisms of Resistance to First- and Second-Generation ALK Inhibitors in <i>ALK</i> -Rearranged Lung Cancer. <i>Cancer Discovery</i> , 2016, 6, 1118-1133.   | 7.7  | 919       |
| 64 | Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. <i>Nature</i> , 2016, 539, 309-313.   | 13.7 | 875       |
| 65 | Toil enables reproducible, open source, big biomedical data analyses. <i>Nature Biotechnology</i> , 2017, 35, 314-316.   | 9.4  | 873       |
| 66 | Mutations driving CLL and their evolution in progression and relapse. <i>Nature</i> , 2015, 526, 525-530.  | 13.7 | 868       |
| 67 | SOX2 is an amplified lineage-survival oncogene in lung and esophageal squamous cell carcinomas. <i>Nature Genetics</i> , 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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3879-3884. | 3.3  | 853       |
| 69 | Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. <i>Cancer Cell</i> , 2014, 25, 91-101.  | 7.7  | 847       |
| 70 | Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. <i>Nature Genetics</i> , 2015, 47, 106-114.   | 9.4  | 830       |
| 71 | Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. <i>Cancer Discovery</i> , 2015, 5, 1164-1177.   | 7.7  | 821       |
| 72 | Ex vivo culture of circulating breast tumor cells for individualized testing of drug susceptibility. <i>Science</i> , 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. <i>Nature Genetics</i> , 2010, 42, 715-721.   | 9.4  | 642       |
| 92  | Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.   | 7.7  | 642       |
| 93  | Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.  | 13.5 | 620       |
| 94  | Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 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. <i>Cancer Discovery</i> , 2014, 4, 216-231. | 7.7  | 596       |
| 96  | Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. <i>Nature Communications</i> , 2017, 8, 1324.  | 5.8  | 584       |
| 97  | Comprehensive analysis of cancer-associated somatic mutations in class I HLA genes. <i>Nature Biotechnology</i> , 2015, 33, 1152-1158.   | 9.4  | 573       |
| 98  | Genomic sequencing of meningiomas identifies oncogenic SMO and AKT1 mutations. <i>Nature Genetics</i> , 2013, 45, 285-289.   | 9.4  | 532       |
| 99  | Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 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. <i>Clinical Cancer Research</i> , 2015, 21, 632-641.                                       | 3.2  | 525       |
| 101 | The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 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. <i>Nature Medicine</i> , 2014, 20, 682-688.                            | 15.2 | 508       |
| 103 | Somatic <i>ERCC2</i> Mutations Correlate with Cisplatin Sensitivity in Muscle-Invasive Urothelial Carcinoma. <i>Cancer Discovery</i> , 2014, 4, 1140-1153.   | 7.7  | 506       |
| 104 | RB loss in resistant EGFR mutant lung adenocarcinomas that transform to small-cell lung cancer. <i>Nature Communications</i> , 2015, 6, 6377.  | 5.8  | 498       |
| 105 | Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. <i>Nature Biotechnology</i> , 2014, 32, 479-484.  | 9.4  | 495       |
| 106 | TET2 mutations predict response to hypomethylating agents in myelodysplastic syndrome patients. <i>Blood</i> , 2014, 124, 2705-2712.   | 0.6  | 486       |
| 107 | Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.  | 7.7  | 482       |
| 108 | A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.   | 7.7  | 478       |

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|-----|---|------|-----------|
| 109 | High-resolution mapping of copy-number alterations with massively parallel sequencing. <i>Nature Methods</i> , 2009, 6, 99-103.   | 9.0  | 462       |
| 110 | Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018, 360, 331-335.   | 6.0  | 461       |
| 111 | Oncotator: Cancer Variant Annotation Tool. <i>Human Mutation</i> , 2015, 36, E2423-E2429.   | 1.1  | 448       |
| 112 | Genomic correlates of response to immune checkpoint blockade in microsatellite-stable solid tumors. <i>Nature Genetics</i> , 2018, 50, 1271-1281.   | 9.4  | 438       |
| 113 | Comprehensive identification of mutational cancer driver genes across 12 tumor types. <i>Scientific Reports</i> , 2013, 3, 2650.  | 1.6  | 437       |
| 114 | Resensitization to Crizotinib by the Lorlatinib-Resistant ALK Mutation L1198F. <i>New England Journal of Medicine</i> , 2016, 374, 54-61.   | 13.9 | 433       |
| 115 | Targetable genetic features of primary testicular and primary central nervous system lymphomas. <i>Blood</i> , 2016, 127, 869-881.  | 0.6  | 429       |
| 116 | A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. <i>Nature Genetics</i> , 2017, 49, 1476-1486.   | 9.4  | 427       |
| 117 | Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 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. <i>Cancer Discovery</i> , 2014, 4, 61-68.  | 7.7  | 419       |
| 119 | The Genomic Landscape of Pediatric Ewing Sarcoma. <i>Cancer Discovery</i> , 2014, 4, 1326-1341.   | 7.7  | 415       |
| 120 | Genomic complexity of multiple myeloma and its clinical implications. <i>Nature Reviews Clinical Oncology</i> , 2017, 14, 100-113.  | 12.5 | 413       |
| 121 | Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.  | 13.5 | 410       |
| 122 | Exome sequencing identifies BRAF mutations in papillary craniopharyngiomas. <i>Nature Genetics</i> , 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. <i>Nucleic Acids Research</i> , 2013, 41, e67-e67. | 6.5  | 407       |
| 124 | Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.  | 2.9  | 407       |
| 125 | Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 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. <i>Nature Genetics</i> , 2018, 50, 956-967.  | 9.4  | 389       |

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|-----|--|------|-----------|
| 127 | RNF43 is frequently mutated in colorectal and endometrial cancers. <i>Nature Genetics</i> , 2014, 46, 1264-1266.   | 9.4  | 388       |
| 128 | Polyclonal Secondary <i>FGFR2</i> Mutations Drive Acquired Resistance to FGFR Inhibition in Patients with FGFR2 Fusion-Positive Cholangiocarcinoma. <i>Cancer Discovery</i> , 2017, 7, 252-263.  | 7.7  | 384       |
| 129 | Systematic investigation of genetic vulnerabilities across cancer cell lines reveals lineage-specific dependencies in ovarian cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 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. <i>PLoS Medicine</i> , 2018, 15, e1002654.   | 3.9  | 373       |
| 131 | RNA sequence analysis reveals macroscopic somatic clonal expansion across normal tissues. <i>Science</i> , 2019, 364, .  | 6.0  | 369       |
| 132 | Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. <i>Cell</i> , 2016, 164, 538-549.  | 13.5 | 363       |
| 133 | Somatic Mutations Predict Poor Outcome in Patients With Myelodysplastic Syndrome After Hematopoietic Stem-Cell Transplantation. <i>Journal of Clinical Oncology</i> , 2014, 32, 2691-2698.   | 0.8  | 359       |
| 134 | Liquid versus tissue biopsy for detecting acquired resistance and tumor heterogeneity in gastrointestinal cancers. <i>Nature Medicine</i> , 2019, 25, 1415-1421.   | 15.2 | 359       |
| 135 | Complementary genomic approaches highlight the PI3K/mTOR pathway as a common vulnerability in osteosarcoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 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. <i>Nature Genetics</i> , 2015, 47, 1067-1072.  | 9.4  | 354       |
| 137 | Somatic ERCC2 mutations are associated with a distinct genomic signature in urothelial tumors. <i>Nature Genetics</i> , 2016, 48, 600-606.   | 9.4  | 352       |
| 138 | A remarkably simple genome underlies highly malignant pediatric rhabdoid cancers. <i>Journal of Clinical Investigation</i> , 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. <i>Genome Research</i> , 2015, 25, 316-327.  | 2.4  | 343       |
| 140 | Mutational processes shape the landscape of TP53 mutations in human cancer. <i>Nature Genetics</i> , 2018, 50, 1381-1387.  | 9.4  | 334       |
| 141 | The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249.   | 13.5 | 334       |
| 142 | Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018, 23, 282-296.e4.  | 2.9  | 333       |
| 143 | Control of tumor-associated macrophages and T cells in glioblastoma via AHR and CD39. <i>Nature Neuroscience</i> , 2019, 22, 729-740.  | 7.1  | 327       |
| 144 | Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 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. <i>Oncogene</i> , 2013, 32, 3091-3100.        | 2.6  | 324       |
| 146 | Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.  | 2.9  | 324       |
| 147 | Locally Disordered Methylation Forms the Basis of Intratumor Methylome Variation in Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2014, 26, 813-825.   | 7.7  | 323       |
| 148 | Characterization of HPV and host genome interactions in primary head and neck cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15544-15549. | 3.3  | 317       |
| 149 | Making sense of cancer genomic data. <i>Genes and Development</i> , 2011, 25, 534-555.  | 2.7  | 313       |
| 150 | Paired exome analysis of Barrett's esophagus and adenocarcinoma. <i>Nature Genetics</i> , 2015, 47, 1047-1055.  | 9.4  | 310       |
| 151 | Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.  | 7.7  | 309       |
| 152 | DNA microarrays identification of primary and secondary target genes regulated by p53. <i>Oncogene</i> , 2001, 20, 2225-2234.   | 2.6  | 308       |
| 153 | Tumor-suppressor genes that escape from X-inactivation contribute to cancer sex bias. <i>Nature Genetics</i> , 2017, 49, 10-16.   | 9.4  | 307       |
| 154 | Epidermal Growth Factor Receptor Activation in Glioblastoma through Novel Missense Mutations in the Extracellular Domain. <i>PLoS Medicine</i> , 2006, 3, e485.   | 3.9  | 298       |
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