

Gad Getz

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2843248/publications.pdf>

Version: 2024-02-01

370
papers

236,845
citations

³⁶
191
h-index

⁹⁵
356
g-index

413
all docs

413
docs citations

413
times ranked

191462
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Integrative genomics viewer. Nature Biotechnology, 2011, 29, 24-26. | 17.5 | 11,708 |
| 2 | Analysis of protein-coding genetic variation in 60,706 humans. Nature, 2016, 536, 285-291. | 27.8 | 9,051 |
| 3 | MicroRNA expression profiles classify human cancers. Nature, 2005, 435, 834-838. | 27.8 | 8,931 |
| 4 | The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585. | 21.4 | 6,815 |
| 5 | The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. Nature, 2012, 483, 603-607. | 27.8 | 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. | 16.8 | 6,138 |
| 7 | Inferring tumour purity and stromal and immune cell admixture from expression data. Nature Communications, 2013, 4, 2612. | 12.8 | 5,788 |
| 8 | Mutational heterogeneity in cancer and the search for new cancer-associated genes. Nature, 2013, 499, 214-218. | 27.8 | 4,761 |
| 9 | The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660. | 12.6 | 4,659 |
| 10 | Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074. | 27.0 | 4,139 |
| 11 | The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477. | 28.9 | 3,979 |
| 12 | Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. Nature Biotechnology, 2013, 31, 213-219. | 17.5 | 3,934 |
| 13 | The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14. | 14.3 | 3,706 |
| 14 | Age-Related Clonal Hematopoiesis Associated with Adverse Outcomes. New England Journal of Medicine, 2014, 371, 2488-2498. | 27.0 | 3,474 |
| 15 | The landscape of somatic copy-number alteration across human cancers. Nature, 2010, 463, 899-905. | 27.8 | 3,331 |
| 16 | Molecular and Genetic Properties of Tumors Associated with Local Immune Cytolytic Activity. Cell, 2015, 160, 48-61. | 28.9 | 2,948 |
| 17 | Somatic mutations affect key pathways in lung adenocarcinoma. Nature, 2008, 455, 1069-1075. | 27.8 | 2,694 |
| 18 | Discovery and saturation analysis of cancer genes across 21 tumour types. Nature, 2014, 505, 495-501. | 27.8 | 2,586 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498. | 27.0 | 2,582 |
| 20 | Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696. | 28.9 | 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. | 8.8 | 2,546 |
| 22 | The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025. | 28.9 | 2,435 |
| 23 | Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690. | 28.9 | 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. | 28.9 | 2,277 |
| 25 | A Landscape of Driver Mutations in Melanoma. <i>Cell</i> , 2012, 150, 251-263. | 28.9 | 2,247 |
| 26 | The Mutational Landscape of Head and Neck Squamous Cell Carcinoma. <i>Science</i> , 2011, 333, 1157-1160. | 12.6 | 2,225 |
| 27 | Next-generation characterization of the Cancer Cell Line Encyclopedia. <i>Nature</i> , 2019, 569, 503-508. | 27.8 | 2,149 |
| 28 | International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998. | 27.8 | 2,114 |
| 29 | An immunogenic personal neoantigen vaccine for patients with melanoma. <i>Nature</i> , 2017, 547, 217-221. | 27.8 | 2,112 |
| 30 | Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10. | 28.9 | 2,111 |
| 31 | The repertoire of mutational signatures in human cancer. <i>Nature</i> , 2020, 578, 94-101. | 27.8 | 2,104 |
| 32 | Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23. | 28.9 | 1,794 |
| 33 | Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25. | 28.9 | 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. | 28.9 | 1,718 |
| 35 | Absolute quantification of somatic DNA alterations in human cancer. <i>Nature Biotechnology</i> , 2012, 30, 413-421. | 17.5 | 1,710 |
| 36 | Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. <i>Cell</i> , 2015, 161, 933-945. | 28.9 | 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. | 28.9 | 1,695 |
| 38 | Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18. | 28.9 | 1,670 |
| 39 | Pan-cancer patterns of somatic copy number alteration. Nature Genetics, 2013, 45, 1134-1140. | 21.4 | 1,616 |
| 40 | Mapping the Hallmarks of Lung Adenocarcinoma with Massively Parallel Sequencing. Cell, 2012, 150, 1107-1120. | 28.9 | 1,591 |
| 41 | Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519. | 28.9 | 1,485 |
| 42 | Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13. | 16.8 | 1,428 |
| 43 | Integrative genomic analyses identify MITF as a lineage survival oncogene amplified in malignant melanoma. Nature, 2005, 436, 117-122. | 27.8 | 1,329 |
| 44 | Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. Nature Genetics, 2012, 44, 685-689. | 21.4 | 1,300 |
| 45 | Initial genome sequencing and analysis of multiple myeloma. Nature, 2011, 471, 467-472. | 27.8 | 1,288 |
| 46 | BRAF mutation predicts sensitivity to MEK inhibition. Nature, 2006, 439, 358-362. | 27.8 | 1,264 |
| 47 | Defining T Cell States Associated with Response to Checkpoint Immunotherapy in Melanoma. Cell, 2018, 175, 998-1013.e20. | 28.9 | 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. | 30.7 | 1,224 |
| 49 | Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. Cell, 2013, 152, 714-726. | 28.9 | 1,202 |
| 50 | Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. Nature Genetics, 2012, 44, 1104-1110. | 21.4 | 1,186 |
| 51 | The human transcriptome across tissues and individuals. Science, 2015, 348, 660-665. | 12.6 | 1,127 |
| 52 | The genomic complexity of primary human prostate cancer. Nature, 2011, 470, 214-220. | 27.8 | 1,107 |
| 53 | Sequence analysis of mutations and translocations across breast cancer subtypes. Nature, 2012, 486, 405-409. | 27.8 | 1,107 |
| 54 | Punctuated Evolution of Prostate Cancer Genomes. Cell, 2013, 153, 666-677. | 28.9 | 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. | 21.4 | 1,023 |
| 56 | <i>CD3B1</i> and Other Novel Cancer Genes in Chronic Lymphocytic Leukemia. <i>New England Journal of Medicine</i> , 2011, 365, 2497-2506. | 27.0 | 1,021 |
| 57 | Characterizing the cancer genome in lung adenocarcinoma. <i>Nature</i> , 2007, 450, 893-898. | 27.8 | 1,020 |
| 58 | Advances in understanding cancer genomes through second-generation sequencing. <i>Nature Reviews Genetics</i> , 2010, 11, 685-696. | 16.3 | 1,014 |
| 59 | The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , 2013, 45, 279-284. | 21.4 | 990 |
| 60 | Neoantigen vaccine generates intratumoral T cell responses in phase Ib glioblastoma trial. <i>Nature</i> , 2019, 565, 234-239. | 27.8 | 956 |
| 61 | Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016, 48, 607-616. | 21.4 | 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. | 7.1 | 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. | 9.4 | 919 |
| 64 | Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. <i>Nature</i> , 2016, 539, 309-313. | 27.8 | 875 |
| 65 | Toil enables reproducible, open source, big biomedical data analyses. <i>Nature Biotechnology</i> , 2017, 35, 314-316. | 17.5 | 873 |
| 66 | Mutations driving CLL and their evolution in progression and relapse. <i>Nature</i> , 2015, 526, 525-530. | 27.8 | 868 |
| 67 | SOX2 is an amplified lineage-survival oncogene in lung and esophageal squamous cell carcinomas. <i>Nature Genetics</i> , 2009, 41, 1238-1242. | 21.4 | 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. | 7.1 | 853 |
| 69 | Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. <i>Cancer Cell</i> , 2014, 25, 91-101. | 16.8 | 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. | 21.4 | 830 |
| 71 | Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. <i>Cancer Discovery</i> , 2015, 5, 1164-1177. | 9.4 | 821 |
| 72 | Ex vivo culture of circulating breast tumor cells for individualized testing of drug susceptibility. <i>Science</i> , 2014, 345, 216-220. | 12.6 | 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. | 6.4 | 801 |
| 74 | The Genetic Landscape of Clinical Resistance to RAF Inhibition in Metastatic Melanoma. Cancer Discovery, 2014, 4, 94-109. | 9.4 | 782 |
| 75 | Tumor cells can follow distinct evolutionary paths to become resistant to epidermal growth factor receptor inhibition. Nature Medicine, 2016, 22, 262-269. | 30.7 | 768 |
| 76 | Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3. | 16.8 | 750 |
| 77 | RNA-SeQC: RNA-seq metrics for quality control and process optimization. Bioinformatics, 2012, 28, 1530-1532. | 4.1 | 746 |
| 78 | Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. Science, 2017, 355, . | 12.6 | 743 |
| 79 | Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28. | 28.9 | 738 |
| 80 | Landscape of genomic alterations in cervical carcinomas. Nature, 2014, 506, 371-375. | 27.8 | 708 |
| 81 | The evolutionary history of 2,658 cancers. Nature, 2020, 578, 122-128. | 27.8 | 690 |
| 82 | Resistance to checkpoint blockade therapy through inactivation of antigen presentation. Nature Communications, 2017, 8, 1136. | 12.8 | 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. | 7.1 | 685 |
| 84 | Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7. | 6.4 | 683 |
| 85 | Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. Nature, 2012, 488, 106-110. | 27.8 | 675 |
| 86 | Melanoma genome sequencing reveals frequent PREX2 mutations. Nature, 2012, 485, 502-506. | 27.8 | 671 |
| 87 | Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. Nature Genetics, 2013, 45, 478-486. | 21.4 | 671 |
| 88 | Genomic Correlates of Immune-Cell Infiltrates in Colorectal Carcinoma. Cell Reports, 2016, 15, 857-865. | 6.4 | 671 |
| 89 | The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330. | 16.8 | 665 |
| 90 | Genetic and transcriptional evolution alters cancer cell line drug response. Nature, 2018, 560, 325-330. | 27.8 | 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. | 21.4 | 642 |
| 92 | Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15. | 16.8 | 642 |
| 93 | Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14. | 28.9 | 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. | 6.2 | 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. | 9.4 | 596 |
| 96 | Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. <i>Nature Communications</i> , 2017, 8, 1324. | 12.8 | 584 |
| 97 | Comprehensive analysis of cancer-associated somatic mutations in class I HLA genes. <i>Nature Biotechnology</i> , 2015, 33, 1152-1158. | 17.5 | 573 |
| 98 | Genomic sequencing of meningiomas identifies oncogenic SMO and AKT1 mutations. <i>Nature Genetics</i> , 2013, 45, 285-289. | 21.4 | 532 |
| 99 | Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193. | 16.8 | 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. | 7.0 | 525 |
| 101 | The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5. | 6.4 | 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. | 30.7 | 508 |
| 103 | Somatic <i>ERCC2</i> Mutations Correlate with Cisplatin Sensitivity in Muscle-Invasive Urothelial Carcinoma. <i>Cancer Discovery</i> , 2014, 4, 1140-1153. | 9.4 | 506 |
| 104 | RB loss in resistant EGFR mutant lung adenocarcinomas that transform to small-cell lung cancer. <i>Nature Communications</i> , 2015, 6, 6377. | 12.8 | 498 |
| 105 | Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. <i>Nature Biotechnology</i> , 2014, 32, 479-484. | 17.5 | 495 |
| 106 | TET2 mutations predict response to hypomethylating agents in myelodysplastic syndrome patients. <i>Blood</i> , 2014, 124, 2705-2712. | 1.4 | 486 |
| 107 | Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736. | 16.8 | 482 |
| 108 | A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9. | 16.8 | 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. | 19.0 | 462 |
| 110 | Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018, 360, 331-335. | 12.6 | 461 |
| 111 | Oncotator: Cancer Variant Annotation Tool. <i>Human Mutation</i> , 2015, 36, E2423-E2429. | 2.5 | 448 |
| 112 | Genomic correlates of response to immune checkpoint blockade in microsatellite-stable solid tumors. <i>Nature Genetics</i> , 2018, 50, 1271-1281. | 21.4 | 438 |
| 113 | Comprehensive identification of mutational cancer driver genes across 12 tumor types. <i>Scientific Reports</i> , 2013, 3, 2650. | 3.3 | 437 |
| 114 | Resensitization to Crizotinib by the Lorlatinib<i>ALK</i>Resistance Mutation L1198F. <i>New England Journal of Medicine</i> , 2016, 374, 54-61. | 27.0 | 433 |
| 115 | Targetable genetic features of primary testicular and primary central nervous system lymphomas. <i>Blood</i> , 2016, 127, 869-881. | 1.4 | 429 |
| 116 | A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. <i>Nature Genetics</i> , 2017, 49, 1476-1486. | 21.4 | 427 |
| 117 | Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. <i>Nature</i> , 2020, 578, 102-111. | 27.8 | 424 |
| 118 | MAP Kinase Pathway Alterations in <i>BRAF</i>-Mutant Melanoma Patients with Acquired Resistance to Combined RAF/MEK Inhibition. <i>Cancer Discovery</i> , 2014, 4, 61-68. | 9.4 | 419 |
| 119 | The Genomic Landscape of Pediatric Ewing Sarcoma. <i>Cancer Discovery</i> , 2014, 4, 1326-1341. | 9.4 | 415 |
| 120 | Genomic complexity of multiple myeloma and its clinical implications. <i>Nature Reviews Clinical Oncology</i> , 2017, 14, 100-113. | 27.6 | 413 |
| 121 | Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35. | 28.9 | 410 |
| 122 | Exome sequencing identifies BRAF mutations in papillary craniopharyngiomas. <i>Nature Genetics</i> , 2014, 46, 161-165. | 21.4 | 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. | 14.5 | 407 |
| 124 | Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3. | 6.4 | 407 |
| 125 | Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8. | 16.8 | 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. | 21.4 | 389 |

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|-----|--|------|-----------|
| 127 | RNF43 is frequently mutated in colorectal and endometrial cancers. <i>Nature Genetics</i> , 2014, 46, 1264-1266. | 21.4 | 388 |
| 128 | Polyclonal Secondary <i>FGFR2</i> Mutations Drive Acquired Resistance to FGFR Inhibition in Patients with <i>FGFR2</i> Fusion-Positive Cholangiocarcinoma. <i>Cancer Discovery</i> , 2017, 7, 252-263. | 9.4 | 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. | 7.1 | 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. | 8.4 | 373 |
| 131 | RNA sequence analysis reveals macroscopic somatic clonal expansion across normal tissues. <i>Science</i> , 2019, 364, . | 12.6 | 369 |
| 132 | Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. <i>Cell</i> , 2016, 164, 538-549. | 28.9 | 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. | 1.6 | 359 |
| 134 | Liquid versus tissue biopsy for detecting acquired resistance and tumor heterogeneity in gastrointestinal cancers. <i>Nature Medicine</i> , 2019, 25, 1415-1421. | 30.7 | 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. | 7.1 | 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. | 21.4 | 354 |
| 137 | Somatic ERCC2 mutations are associated with a distinct genomic signature in urothelial tumors. <i>Nature Genetics</i> , 2016, 48, 600-606. | 21.4 | 352 |
| 138 | A remarkably simple genome underlies highly malignant pediatric rhabdoid cancers. <i>Journal of Clinical Investigation</i> , 2012, 122, 2983-2988. | 8.2 | 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. | 5.5 | 343 |
| 140 | Mutational processes shape the landscape of TP53 mutations in human cancer. <i>Nature Genetics</i> , 2018, 50, 1381-1387. | 21.4 | 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. | 28.9 | 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. | 6.4 | 333 |
| 143 | Control of tumor-associated macrophages and T cells in glioblastoma via AHR and CD39. <i>Nature Neuroscience</i> , 2019, 22, 729-740. | 14.8 | 327 |
| 144 | Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20. | 16.8 | 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. | 5.9 | 324 |
| 146 | Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406. | 6.4 | 324 |
| 147 | Locally Disordered Methylation Forms the Basis of Intratumor Methylome Variation in Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2014, 26, 813-825. | 16.8 | 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. | 7.1 | 317 |
| 149 | Making sense of cancer genomic data. <i>Genes and Development</i> , 2011, 25, 534-555. | 5.9 | 313 |
| 150 | Paired exome analysis of Barrett's esophagus and adenocarcinoma. <i>Nature Genetics</i> , 2015, 47, 1047-1055. | 21.4 | 310 |
| 151 | Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423. | 16.8 | 309 |
| 152 | DNA microarrays identification of primary and secondary target genes regulated by p53. <i>Oncogene</i> , 2001, 20, 2225-2234. | 5.9 | 308 |
| 153 | Tumor-suppressor genes that escape from X-inactivation contribute to cancer sex bias. <i>Nature Genetics</i> , 2017, 49, 10-16. | 21.4 | 307 |
| 154 | Epidermal Growth Factor Receptor Activation in Glioblastoma through Novel Missense Mutations in the Extracellular Domain. <i>PLoS Medicine</i> , 2006, 3, e485. | 8.4 | 298 |
| 155 | Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26. | 28.9 | 296 |
| 156 | Response and Acquired Resistance to Everolimus in Anaplastic Thyroid Cancer. <i>New England Journal of Medicine</i> , 2014, 371, 1426-1433. | 27.0 | 290 |
| 157 | PathSeq: software to identify or discover microbes by deep sequencing of human tissue. <i>Nature Biotechnology</i> , 2011, 29, 393-396. | 17.5 | 289 |
| 158 | SvABA: genome-wide detection of structural variants and indels by local assembly. <i>Genome Research</i> , 2018, 28, 581-591. | 5.5 | 288 |
| 159 | Systematic identification of personal tumor-specific neoantigens in chronic lymphocytic leukemia. <i>Blood</i> , 2014, 124, 453-462. | 1.4 | 286 |
| 160 | Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. <i>Nature Communications</i> , 2016, 7, 11589. | 12.8 | 285 |
| 161 | Modeling Genomic Diversity and Tumor Dependency in Malignant Melanoma. <i>Cancer Research</i> , 2008, 68, 664-673. | 0.9 | 275 |
| 162 | Somatic mutation of CDKN1B in small intestine neuroendocrine tumors. <i>Nature Genetics</i> , 2013, 45, 1483-1486. | 21.4 | 275 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 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. | 7.1 | 273 |
| 164 | Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. Cell, 2020, 183, 1436-1456.e31. | 28.9 | 273 |
| 165 | Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10. | 28.9 | 272 |
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