## Nikolaus D Schultz

List of Publications by Year in descending order

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241 papers

141,538 citations

944 115 h-index 246 g-index

256 all docs

256 docs citations

256 times ranked

110902 citing authors

| #  | Article  | IF          | CITATIONS |
|----|--|-------------|-----------|
| 1  | Distinct Genomic Profiles are Associated With Conversion to Resection and Survival in Patients With Initially Unresectable Colorectal Liver Metastases Treated With Systemic and Hepatic Artery Chemotherapy. Annals of Surgery, 2022, 276, e474-e482. | 2.1         | 15        |
| 2  | Differences in Prostate Cancer Genomes by Self-reported Race: Contributions of Genetic Ancestry, Modifiable Cancer Risk Factors, and Clinical Factors. Clinical Cancer Research, 2022, 28, 318-326.  | 3.2         | 28        |
| 3  | Association of genomic profiles and survival in early onset and screeningâ€age colorectal cancer patients with liver metastases resected over 15 years. Journal of Surgical Oncology, 2022, 125, 880-888.  | 0.8         | 4         |
| 4  | Phase II Trial of Imatinib Plus Binimetinib in Patients With Treatment-Naive Advanced Gastrointestinal Stromal Tumor. Journal of Clinical Oncology, 2022, 40, 997-1008.  | 0.8         | 13        |
| 5  | Computational methods and translational applications for targeted nextâ€generation sequencing platforms. Genes Chromosomes and Cancer, 2022, 61, 322-331.  | 1.5         | 3         |
| 6  | Distinct Genomic Landscapes in Early-Onset and Late-Onset Endometrial Cancer. JCO Precision Oncology, 2022, 6, e2100401.   | 1.5         | 3         |
| 7  | Genome Nexus: A Comprehensive Resource for the Annotation and Interpretation of Genomic Variants in Cancer. JCO Clinical Cancer Informatics, 2022, 6, e2100144.  | 1.0         | 4         |
| 8  | Genomic characterization of metastatic patterns from prospective clinical sequencing of 25,000 patients. Cell, 2022, 185, 563-575.e11.   | 13.5        | 223       |
| 9  | Defining and Targeting Esophagogastric Cancer Genomic Subsets With Patient-Derived Xenografts. JCO Precision Oncology, 2022, 6, e2100242.  | 1.5         | 5         |
| 10 | MITI minimum information guidelines for highly multiplexed tissue images. Nature Methods, 2022, 19, 262-267.   | 9.0         | 37        |
| 11 | Genomic and Metabolic Hallmarks of SDH- and FH-deficient Renal Cell Carcinomas. European Urology<br>Focus, 2022, 8, 1278-1288.   | 1.6         | 11        |
| 12 | Clinical sequencing of soft tissue and bone sarcomas delineates diverse genomic landscapes and potential therapeutic targets. Nature Communications, 2022, 13, .   | <b>5.</b> 8 | 63        |
| 13 | The Impact of PIK3R1 Mutations and Insulin–PI3K–Glycolytic Pathway Regulation in Prostate Cancer.<br>Clinical Cancer Research, 2022, 28, 3603-3617.  | 3.2         | 7         |
| 14 | AACR Project GENIE: 100,000 Cases and Beyond. Cancer Discovery, 2022, 12, 2044-2057.   | 7.7         | 27        |
| 15 | Primary Tumor Location and Outcomes After Cytoreductive Surgery and Intraperitoneal<br>Chemotherapy for Peritoneal Metastases of Colorectal Origin. Annals of Surgical Oncology, 2021, 28,<br>1109-1117.   | 0.7         | 5         |
| 16 | Prospective pan-cancer germline testing using MSK-IMPACT informs clinical translation in 751 patients with pediatric solid tumors. Nature Cancer, 2021, 2, 357-365.  | 5.7         | 74        |
| 17 | A Genomic-Pathologic Annotated Risk Model to Predict Recurrence in Early-Stage Lung<br>Adenocarcinoma. JAMA Surgery, 2021, 156, e205601.   | 2.2         | 52        |
| 18 | OncoTree: A Cancer Classification System for Precision Oncology. JCO Clinical Cancer Informatics, 2021, 5, 221-230.  | 1.0         | 51        |

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|----|---|-----|-----------|
| 19 | Exploring the clinical significance of serous tubal intraepithelial carcinoma associated with advanced high-grade serous ovarian cancer: A Memorial Sloan Kettering Team Ovary Study. Gynecologic Oncology, 2021, 160, 696-703. | 0.6 | 2         |
| 20 | Next-Generation Sequencing of 487 Esophageal Adenocarcinomas Reveals Independently Prognostic Genomic Driver Alterations and Pathways. Clinical Cancer Research, 2021, 27, 3491-3498.   | 3.2 | 8         |
| 21 | The genomic landscape of carcinomas with mucinous differentiation. Scientific Reports, 2021, 11, 9478.  | 1.6 | 9         |
| 22 | A pan-cancer survey of cell line tumor similarity by feature-weighted molecular profiles. Cell Reports Methods, 2021, 1, 100039.  | 1.4 | 8         |
| 23 | CD38 in Advanced Prostate Cancers. European Urology, 2021, 79, 736-746.   | 0.9 | 21        |
| 24 | Prevalence of Germline Alterations on Targeted Tumor-Normal Sequencing of Esophagogastric Cancer. JAMA Network Open, 2021, 4, e2114753.   | 2.8 | 15        |
| 25 | Prevalence and Landscape of Actionable Genomic Alterations in Renal Cell Carcinoma. Clinical Cancer Research, 2021, 27, 5595-5606.  | 3.2 | 12        |
| 26 | Correlation Between Surrogate End Points and Overall Survival in a Multi-institutional Clinicogenomic Cohort of Patients With Non–Small Cell Lung or Colorectal Cancer. JAMA Network Open, 2021, 4, e2117547.                   | 2.8 | 20        |
| 27 | A Comprehensive Comparison of Early-Onset and Average-Onset Colorectal Cancers. Journal of the National Cancer Institute, 2021, 113, 1683-1692.   | 3.0 | 66        |
| 28 | Therapeutic Implications of Germline Testing in Patients With Advanced Cancers. Journal of Clinical Oncology, 2021, 39, 2698-2709.  | 0.8 | 83        |
| 29 | Genetic Determinants of Outcome in Intrahepatic Cholangiocarcinoma. Hepatology, 2021, 74, 1429-1444.  | 3.6 | 73        |
| 30 | Patterns of Metastatic Disease in Patients with Cancer Derived from Natural Language Processing of Structured CT Radiology Reports over a 10-year Period. Radiology, 2021, 301, 115-122.  | 3.6 | 19        |
| 31 | Therapeutic Implications of Detecting MAPK-Activating Alterations in Cutaneous and Unknown Primary Melanomas. Clinical Cancer Research, 2021, 27, 2226-2235.  | 3.2 | 25        |
| 32 | The context-specific role of germline pathogenicity in tumorigenesis. Nature Genetics, 2021, 53, 1577-1585.   | 9.4 | 44        |
| 33 | Molecular and phenotypic profiling of colorectal cancer patients in West Africa reveals biological insights. Nature Communications, 2021, 12, 6821.   | 5.8 | 15        |
| 34 | Development of Genome-Derived Tumor Type Prediction to Inform Clinical Cancer Care. JAMA Oncology, 2020, 6, 84.   | 3.4 | 66        |
| 35 | Assessment of Hepatic Arterial Infusion of Floxuridine in Combination With Systemic Gemcitabine and Oxaliplatin in Patients With Unresectable Intrahepatic Cholangiocarcinoma. JAMA Oncology, 2020, 6, 60.                      | 3.4 | 112       |
| 36 | Dickkopf-1 Can Lead to Immune Evasion in Metastatic Castration-Resistant Prostate Cancer. JCO Precision Oncology, 2020, 4, 1167-1179.   | 1.5 | 28        |

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|----|--|--------------|-----------|
| 37 | Accelerating precision medicine in metastatic prostate cancer. Nature Cancer, 2020, 1, 1041-1053.  | 5 <b>.</b> 7 | 45        |
| 38 | Specific Mutations in APC, but Not Alterations in DNA Damage Response, Associate With Outcomes of Patients With Metastatic Colorectal Cancer. Gastroenterology, 2020, 159, 1975-1978.e4.                                 | 0.6          | 26        |
| 39 | The Underlying Tumor Genomics of Predominant Histologic Subtypes in Lung Adenocarcinoma. Journal of Thoracic Oncology, 2020, 15, 1844-1856.  | 0.5          | 83        |
| 40 | Linked Entity Attribute Pair (LEAP): A Harmonization Framework for Data Pooling. JCO Clinical Cancer Informatics, 2020, 4, 691-699.  | 1.0          | 2         |
| 41 | First-line pembrolizumab and trastuzumab in HER2-positive oesophageal, gastric, or gastro-oesophageal junction cancer: an open-label, single-arm, phase 2 trial. Lancet Oncology, The, 2020, 21, 821-831.                | 5.1          | 243       |
| 42 | Oncogenic Genomic Alterations, Clinical Phenotypes, and Outcomes in Metastatic Castration-Sensitive Prostate Cancer. Clinical Cancer Research, 2020, 26, 3230-3238.  | 3.2          | 112       |
| 43 | Ribonucleotide reductase small subunit M2 is a master driver of aggressive prostate cancer.<br>Molecular Oncology, 2020, 14, 1881-1897.  | 2.1          | 22        |
| 44 | Phase and context shape the function of composite oncogenic mutations. Nature, 2020, 582, 100-103.   | 13.7         | 31        |
| 45 | Recent Advances in Systems and Network Medicine: Meeting Report from the First International Conference in Systems and Network Medicine. Systems Medicine (New Rochelle, N Y ), 2020, 3, 22-35.                          | 1.4          | 7         |
| 46 | Mismatch Repair–Deficient Rectal Cancer and Resistance to Neoadjuvant Chemotherapy. Clinical Cancer Research, 2020, 26, 3271-3279.   | 3.2          | 118       |
| 47 | A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer.<br>Nature Genetics, 2020, 52, 448-457.  | 9.4          | 104       |
| 48 | Systemic Chemotherapy for Metastatic Colitis-Associated Cancer Has a Worse Outcome Than Sporadic Colorectal Cancer: Matched Case Cohort Analysis. Clinical Colorectal Cancer, 2020, 19, e151-e156.                       | 1.0          | 11        |
| 49 | Regorafenib in Combination with Firstâ€Line Chemotherapy for Metastatic Esophagogastric Cancer.<br>Oncologist, 2020, 25, e68-e74.  | 1.9          | 10        |
| 50 | Characteristics and Outcome of <i>AKT1</i> E17K-Mutant Breast Cancer Defined through AACR Project GENIE, a Clinicogenomic Registry. Cancer Discovery, 2020, 10, 526-535.   | 7.7          | 36        |
| 51 | Coaltered <i>Ras/B-raf</i> and <i>TP53</i> Is Associated with Extremes of Survivorship and Distinct Patterns of Metastasis in Patients with Metastatic Colorectal Cancer. Clinical Cancer Research, 2020, 26, 1077-1085. | 3.2          | 62        |
| 52 | Pan-cancer Analysis of CDK12 Alterations Identifies a Subset of Prostate Cancers with Distinct Genomic and Clinical Characteristics. European Urology, 2020, 78, 671-679.  | 0.9          | 72        |
| 53 | Platinum-Based Chemotherapy in Metastatic Prostate Cancer With DNA Repair Gene Alterations. JCO Precision Oncology, 2020, 4, 355-366.  | 1.5          | 93        |
| 54 | Genomic Methods Identify Homologous Recombination Deficiency in Pancreas Adenocarcinoma and Optimize Treatment Selection. Clinical Cancer Research, 2020, 26, 3239-3247.   | 3.2          | 135       |

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|----|--|------|-----------|
| 55 | Tumor Mutation Burden and Efficacy of EGFR-Tyrosine Kinase Inhibitors in Patients with <i>EGFR</i> -Mutant Lung Cancers. Clinical Cancer Research, 2019, 25, 1063-1069.  | 3.2  | 257       |
| 56 | Phase II study of trastuzumab with modified docetaxel, cisplatin, and 5 fluorouracil in metastatic HER2-positive gastric cancer. Gastric Cancer, 2019, 22, 355-362.  | 2.7  | 11        |
| 57 | Cancer-associated mutations in DICER1 RNase Illa and Illb domains exert similar effects on miRNA biogenesis. Nature Communications, 2019, 10, 3682.  | 5.8  | 48        |
| 58 | Clinical and Molecular Predictors of Response to Immune Checkpoint Inhibitors in Patients with Advanced Esophagogastric Cancer. Clinical Cancer Research, 2019, 25, 6160-6169.                                 | 3.2  | 73        |
| 59 | Tumour lineage shapes BRCA-mediated phenotypes. Nature, 2019, 571, 576-579.  | 13.7 | 295       |
| 60 | Integration and Analysis of CPTAC Proteomics Data in the Context of Cancer Genomics in the cBioPortal. Molecular and Cellular Proteomics, 2019, 18, 1893-1898.   | 2.5  | 106       |
| 61 | Genomic stratification beyond Ras/Bâ€Raf in colorectal liver metastasis patients treated with hepatic arterial infusion. Cancer Medicine, 2019, 8, 6538-6548.  | 1.3  | 8         |
| 62 | Analysis of Tumor Genomic Pathway Alterations Using Broad-Panel Next-Generation Sequencing in Surgically Resected Lung Adenocarcinoma. Clinical Cancer Research, 2019, 25, 7475-7484.                          | 3.2  | 30        |
| 63 | Genomic correlates of clinical outcome in advanced prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11428-11436.                                   | 3.3  | 839       |
| 64 | The expanding landscape of â€~oncohistone' mutations in human cancers. Nature, 2019, 567, 473-478.   | 13.7 | 271       |
| 65 | Efficacy of Combined VEGFR1-3, PDGF $\hat{I}^2$ , and FGFR1-3 Blockade Using Nintedanib for Esophagogastric Cancer. Clinical Cancer Research, 2019, 25, 3811-3817.   | 3.2  | 10        |
| 66 | Real-World Outcomes of an Automated Physician Support System for Genome-Driven Oncology. JCO Precision Oncology, 2019, 3, 1-13.  | 1.5  | 6         |
| 67 | Harmonization of Tumor Mutational Burden Quantification and Association With Response to Immune Checkpoint Blockade in Non–Small-Cell Lung Cancer. JCO Precision Oncology, 2019, 3, 1-12.                      | 1.5  | 58        |
| 68 | Analysis of the Prevalence of Microsatellite Instability in Prostate Cancer and Response to Immune Checkpoint Blockade. JAMA Oncology, 2019, 5, 471.   | 3.4  | 426       |
| 69 | <i>EGFR</i> and <i>MET</i> Amplifications Determine Response to HER2 Inhibition in <i>ERBB2</i> Amplified Esophagogastric Cancer. Cancer Discovery, 2019, 9, 199-209.  | 7.7  | 115       |
| 70 | Genetic and Epigenetic Determinants of Aggressiveness in Cribriform Carcinoma of the Prostate. Molecular Cancer Research, 2019, 17, 446-456.   | 1.5  | 44        |
| 71 | Prospective Genotyping of Hepatocellular Carcinoma: Clinical Implications of Next-Generation Sequencing for Matching Patients to Targeted and Immune Therapies. Clinical Cancer Research, 2019, 25, 2116-2126. | 3.2  | 390       |
| 72 | FOLFCIS Treatment and Genomic Correlates of Response in Advanced Anal Squamous Cell Cancer. Clinical Colorectal Cancer, 2019, 18, e39-e52.   | 1.0  | 21        |

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|----|--|------|-----------|
| 73 | Genomic Differences Between "Primary―and "Secondary―Muscle-invasive Bladder Cancer as a Basis for Disparate Outcomes to Cisplatin-based Neoadjuvant Chemotherapy. European Urology, 2019, 75, 231-239. | 0.9  | 104       |
| 74 | Data Portals and Analysis. , 2019, , 169-196.  |      | 1         |
| 75 | Genetic hallmarks of recurrent/metastatic adenoid cystic carcinoma. Journal of Clinical Investigation, 2019, 129, 4276-4289.   | 3.9  | 134       |
| 76 | Abnormal oxidative metabolism in a quiet genomic background underlies clear cell papillary renal cell carcinoma. ELife, 2019, 8, .   | 2.8  | 31        |
| 77 | Annotation of Somatic Genomic Variants in Hematologic Diseases Using OncoKB, a Precision Oncology Knowledgebase. Blood, 2019, 134, 2148-2148.  | 0.6  | 3         |
| 78 | The SS18-SSX Oncoprotein Hijacks KDM2B-PRC1.1 to Drive Synovial Sarcoma. Cancer Cell, 2018, 33, 527-541.e8.  | 7.7  | 99        |
| 79 | Unifying cancer and normal RNA sequencing data from different sources. Scientific Data, 2018, 5, 180061.   | 2.4  | 152       |
| 80 | 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     |
| 81 | Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.   | 13.5 | 1,670     |
| 82 | 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     |
| 83 | A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.   | 13.5 | 228       |
| 84 | Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.   | 13.5 | 272       |
| 85 | Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.   | 13.5 | 1,417     |
| 86 | Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.   | 13.5 | 2,111     |
| 87 | Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.  | 13.5 | 620       |
| 88 | 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       |
| 89 | Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.   | 2.9  | 407       |
| 90 | The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.  | 2.9  | 523       |

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|-----|---|-----|-----------|
| 91  | 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       |
| 92  | The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.  | 6.6 | 3,706     |
| 93  | Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.  | 2.9 | 119       |
| 94  | Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.   | 2.9 | 801       |
| 95  | G2S: a web-service for annotating genomic variants on 3D protein structures. Bioinformatics, 2018, 34, 1949-1950.   | 1.8 | 10        |
| 96  | Accelerating Discovery of Functional Mutant Alleles in Cancer. Cancer Discovery, 2018, 8, 174-183.  | 7.7 | 275       |
| 97  | Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. Cancer Cell, 2018, 33, 125-136.e3.   | 7.7 | 589       |
| 98  | Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.  | 2.9 | 284       |
| 99  | IncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic IncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9.  | 7.7 | 400       |
| 100 | Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.  | 7.7 | 750       |
| 101 | Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.  | 7.7 | 396       |
| 102 | A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.  | 7.7 | 478       |
| 103 | The long tail of oncogenic drivers in prostate cancer. Nature Genetics, 2018, 50, 645-651.  | 9.4 | 601       |
| 104 | Systematic Functional Annotation of Somatic Mutations in Cancer. Cancer Cell, 2018, 33, 450-462.e10.  | 7.7 | 213       |
| 105 | Small-Cell Carcinomas of the Bladder and Lung Are Characterized by a Convergent but Distinct Pathogenesis. Clinical Cancer Research, 2018, 24, 1965-1973.   | 3.2 | 85        |
| 106 | Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. Cancer Discovery, 2018, 8, 49-58.   | 7.7 | 275       |
| 107 | American Association for Cancer Research Project Genomics Evidence Neoplasia Information Exchange: From Inception to First Data Release and Beyond—Lessons Learned and Member Institutions' Perspectives. JCO Clinical Cancer Informatics, 2018, 2, 1-14.                         | 1.0 | 33        |
| 108 | Molecular Determinants of Response to Antiâ€"Programmed Cell Death (PD)-1 and Antiâ€"Programmed Death-Ligand 1 (PD-L1) Blockade in Patients With Nonâ€"Small-Cell Lung Cancer Profiled With Targeted Next-Generation Sequencing. Journal of Clinical Oncology, 2018, 36, 633-641. | 0.8 | 1,109     |

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|-----|---|------|-----------|
| 109 | Immunogenomic analyses associate immunological alterations with mismatch repair defects in prostate cancer. Journal of Clinical Investigation, 2018, 128, 4441-4453.                                  | 3.9  | 155       |
| 110 | Loss of the FAT1 Tumor Suppressor Promotes Resistance to CDK4/6 Inhibitors via the Hippo Pathway. Cancer Cell, 2018, 34, 893-905.e8.  | 7.7  | 307       |
| 111 | A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î <sup>2</sup> Superfamily. Cell Systems, 2018, 7, 422-437.e7.                                  | 2.9  | 134       |
| 112 | The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. Cancer Cell, 2018, 34, 427-438.e6.  | 7.7  | 633       |
| 113 | Comprehensive Molecular Profiling of Intrahepatic and Extrahepatic Cholangiocarcinomas: Potential Targets for Intervention. Clinical Cancer Research, 2018, 24, 4154-4161.                            | 3.2  | 348       |
| 114 | KMT2C mediates the estrogen dependence of breast cancer through regulation of ERÎ $\pm$ enhancer function. Oncogene, 2018, 37, 4692-4710.   | 2.6  | 102       |
| 115 | Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.  | 7.7  | 623       |
| 116 | Genome doubling shapes the evolution and prognosis of advanced cancers. Nature Genetics, 2018, 50, 1189-1195.   | 9.4  | 411       |
| 117 | Rates of TP53 Mutation are Significantly Elevated in African American Patients with Gastric Cancer.<br>Annals of Surgical Oncology, 2018, 25, 2027-2033.  | 0.7  | 19        |
| 118 | <i>KMT2C</i> Mutations in Diffuse-Type Gastric Adenocarcinoma Promote Epithelial-to-Mesenchymal Transition. Clinical Cancer Research, 2018, 24, 6556-6569.  | 3.2  | 70        |
| 119 | Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.  | 2.9  | 324       |
| 120 | Tumor copy number alteration burden is a pan-cancer prognostic factor associated with recurrence and death. ELife, 2018, 7, .   | 2.8  | 217       |
| 121 | 3D clusters of somatic mutations in cancer reveal numerous rare mutations as functional targets.<br>Genome Medicine, 2017, 9, 4.  | 3.6  | 170       |
| 122 | ARF Confers a Context-Dependent Response to Chemotherapy in Muscle-Invasive Bladder Cancer. Cancer Research, 2017, 77, 1035-1046.   | 0.4  | 15        |
| 123 | Recurrent patterns of DNA copy number alterations in tumors reflect metabolic selection pressures. Molecular Systems Biology, 2017, 13, 914.  | 3.2  | 73        |
| 124 | Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. Nature Medicine, 2017, 23, 703-713.   | 15,2 | 2,473     |
| 125 | Multicenter phase II study of temozolomide and myeloablative chemotherapy with autologous stem cell transplant for newly diagnosed anaplastic oligodendroglioma. Neuro-Oncology, 2017, 19, 1380-1390. | 0.6  | 35        |
| 126 | Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.   | 13.5 | 1,794     |

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|-----|--|------|-----------|
| 127 | Ibrutinib Unmasks Critical Role of Bruton Tyrosine Kinase in Primary CNS Lymphoma. Cancer Discovery, 2017, 7, 1018-1029.   | 7.7  | 302       |
| 128 | ERF mutations reveal a balance of ETS factors controlling prostate oncogenesis. Nature, 2017, 546, 671-675.  | 13.7 | 70        |
| 129 | PathwayMapper: a collaborative visual web editor for cancer pathways and genomic data. Bioinformatics, 2017, 33, 2238-2240.  | 1.8  | 50        |
| 130 | Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. Cancer Discovery, 2017, 7, 596-609.                              | 7.7  | 490       |
| 131 | Morphological characterization of colorectal cancers in The Cancer Genome Atlas reveals distinct morphology–molecular associations: clinical and biological implications. Modern Pathology, 2017, 30, 599-609.   | 2.9  | 74        |
| 132 | Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.  | 13.5 | 1,742     |
| 133 | The RNA-editing enzyme ADAR promotes lung adenocarcinoma migration and invasion by stabilizing <code><i>FAK</i>.</code> Science Signaling, 2017, 10, .   | 1.6  | 52        |
| 134 | Conditional Selection of Genomic Alterations Dictates Cancer Evolution and Oncogenic Dependencies. Cancer Cell, 2017, 32, 155-168.e6.  | 7.7  | 93        |
| 135 | Real-Time Genomic Profiling of Pancreatic Ductal Adenocarcinoma: Potential Actionability and Correlation with Clinical Phenotype. Clinical Cancer Research, 2017, 23, 6094-6100.                                 | 3.2  | 161       |
| 136 | Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.   | 13.5 | 738       |
| 137 | Next-generation Sequencing of Nonmuscle Invasive Bladder Cancer Reveals Potential Biomarkers and Rational Therapeutic Targets. European Urology, 2017, 72, 952-959.  | 0.9  | 263       |
| 138 | Prospective Genomic Profiling of Prostate Cancer Across Disease States Reveals Germline and Somatic Alterations That May Affect Clinical Decision Making. JCO Precision Oncology, 2017, 2017, 1-16.              | 1.5  | 286       |
| 139 | OncoKB: A Precision Oncology Knowledge Base. JCO Precision Oncology, 2017, 2017, 1-16.   | 1.5  | 1,266     |
| 140 | Mitochondrial respiratory gene expression is suppressed in many cancers. ELife, 2017, 6, .   | 2.8  | 102       |
| 141 | A Multi-Method Approach for Proteomic Network Inference in 11 Human Cancers. PLoS Computational Biology, 2016, 12, e1004765.   | 1.5  | 32        |
| 142 | Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. New England Journal of Medicine, 2016, 375, 443-453.   | 13.9 | 1,205     |
| 143 | The metabolic co-regulator PGC1α suppresses prostate cancer metastasis. Nature Cell Biology, 2016, 18, 645-656.  | 4.6  | 176       |
| 144 | Genomic Alterations Observed in Colitis-Associated Cancers Are Distinct From Those Found in Sporadic Colorectal Cancers and Vary by Type of Inflammatory Bowel Disease. Gastroenterology, 2016, 151, 278-287.e6. | 0.6  | 147       |

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|-----|---|------|-----------|
| 145 | Comprehensive Molecular Characterization of Salivary Duct Carcinoma Reveals Actionable Targets and Similarity to Apocrine Breast Cancer. Clinical Cancer Research, 2016, 22, 4623-4633.                             | 3.2  | 153       |
| 146 | Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.   | 7.7  | 482       |
| 147 | Genetic Determinants of Cisplatin Resistance in Patients With Advanced Germ Cell Tumors. Journal of Clinical Oncology, 2016, 34, 4000-4007.   | 0.8  | 147       |
| 148 | Molecular analysis of aggressive renal cell carcinoma with unclassified histology reveals distinct subsets. Nature Communications, 2016, 7, 13131.  | 5.8  | 140       |
| 149 | MutationAligner: a resource of recurrent mutation hotspots in protein domains in cancer. Nucleic Acids Research, 2016, 44, D986-D991.   | 6.5  | 21        |
| 150 | rcellminer: exploring molecular profiles and drug response of the NCI-60 cell lines in R. Bioinformatics, 2016, 32, 1272-1274.  | 1.8  | 39        |
| 151 | Deletions linked to TP53 loss drive cancer through p53-independent mechanisms. Nature, 2016, 531, 471-475.  | 13.7 | 202       |
| 152 | Translational Bioinformatics and Clinical Research (Biomedical) Informatics. Clinics in Laboratory Medicine, 2016, 36, 153-181.   | 0.7  | 6         |
| 153 | Substantial interindividual and limited intraindividual genomic diversity among tumors from men with metastatic prostate cancer. Nature Medicine, 2016, 22, 369-378.  | 15.2 | 572       |
| 154 | Identifying recurrent mutations in cancer reveals widespread lineage diversity and mutational specificity. Nature Biotechnology, 2016, 34, 155-163.   | 9.4  | 634       |
| 155 | Chemotherapy Resistance in Diffuse-Type Gastric Adenocarcinoma Is Mediated by RhoA Activation in Cancer Stem-Like Cells. Clinical Cancer Research, 2016, 22, 971-983.   | 3.2  | 89        |
| 156 | Multiplexed immunofluorescence delineates proteomic cancer cell states associated with metabolism. JCI Insight, 2016, $1$ , .   | 2.3  | 41        |
| 157 | Genomic and transcriptomic hallmarks of poorly differentiated and anaplastic thyroid cancers. Journal of Clinical Investigation, 2016, 126, 1052-1066.  | 3.9  | 874       |
| 158 | Integrative Clinical Genomics of Advanced Prostate Cancer. Cell, 2015, 161, 1215-1228.  | 13.5 | 2,660     |
| 159 | Identification of low abundance microbiome in clinical samples using whole genome sequencing. Genome Biology, 2015, 16, 265.  | 3.8  | 90        |
| 160 | Genomic Predictors of Survival in Patients with High-grade Urothelial Carcinoma of the Bladder. European Urology, 2015, 67, 198-201.  | 0.9  | 122       |
| 161 | <i>PIK3CA</i> Mutations Are Associated With Decreased Benefit to Neoadjuvant Human Epidermal<br>Growth Factor Receptor 2–Targeted Therapies in Breast Cancer. Journal of Clinical Oncology, 2015, 33,<br>1334-1339. | 0.8  | 201       |
| 162 | Response to MET Inhibitors in Patients with Stage IV Lung Adenocarcinomas Harboring <i>MET</i> Mutations Causing Exon 14 Skipping. Cancer Discovery, 2015, 5, 842-849.  | 7.7  | 514       |

| #   | Article  | IF   | Citations |
|-----|--|------|-----------|
| 163 | Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.   | 13.9 | 2,582     |
| 164 | Translational Bioinformatics and Clinical Research (Biomedical) Informatics. Surgical Pathology Clinics, 2015, 8, 269-288.   | 0.7  | 5         |
| 165 | Systematic identification of cancer driving signaling pathways based on mutual exclusivity of genomic alterations. Genome Biology, 2015, 16, 45.   | 3.8  | 145       |
| 166 | Identifying Actionable Targets through Integrative Analyses of GEM Model and Human Prostate Cancer Genomic Profiling. Molecular Cancer Therapeutics, 2015, 14, 278-288.                        | 1.9  | 29        |
| 167 | Molecular Subtypes of Uterine Leiomyosarcoma and Correlation with Clinical Outcome. Neoplasia, 2015, 17, 183-189.  | 2.3  | 33        |
| 168 | Somatic <i>POLE</i> mutations cause an ultramutated giant cell high-grade glioma subtype with better prognosis. Neuro-Oncology, 2015, 17, 1356-1364.   | 0.6  | 94        |
| 169 | Clinical implementation of integrated whole-genome copy number and mutation profiling for glioblastoma. Neuro-Oncology, 2015, 17, 1344-1355.   | 0.6  | 40        |
| 170 | The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.   | 13.5 | 2,435     |
| 171 | Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. Cell Systems, 2015, 1, 197-209.   | 2.9  | 94        |
| 172 | Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.   | 13.5 | 1,485     |
| 173 | Genomic Characterization of Upper Tract Urothelial Carcinoma. European Urology, 2015, 68, 970-977.   | 0.9  | 202       |
| 174 | Expression of the Carboxy-Terminal Portion of MUC16/CA125 Induces Transformation and Tumor Invasion. PLoS ONE, 2015, 10, e0126633.   | 1.1  | 41        |
| 175 | Distinctive Genomic Alterations in Testicular Diffuse Large B Cell Lymphoma. Blood, 2015, 126, 3655-3655.  | 0.6  | 1         |
| 176 | Integrative genome-wide analysis of the determinants of RNA splicing in kidney renal clear cell carcinoma. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 44-55. | 0.7  | 5         |
| 177 | Prediction of individualized therapeutic vulnerabilities in cancer from genomic profiles.<br>Bioinformatics, 2014, 30, 2051-2059.  | 1.8  | 30        |
| 178 | Copy number alteration burden predicts prostate cancer relapse. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11139-11144.                       | 3.3  | 299       |
| 179 | The performance of BRCA1 immunohistochemistry for detecting germline, somatic, and epigenetic BRCA1 loss in high-grade serous ovarian cancer. Annals of Oncology, 2014, 25, 2372-2378.         | 0.6  | 31        |
| 180 | Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.  | 13.5 | 2,318     |

| #   | Article  | IF   | Citations |
|-----|--|------|-----------|
| 181 | Recurrent SMARCA4 mutations in small cell carcinoma of the ovary. Nature Genetics, 2014, 46, 424-426.  | 9.4  | 291       |
| 182 | Synthetic Lethality in ATM-Deficient <i>RAD50</i> -Mutant Tumors Underlies Outlier Response to Cancer Therapy. Cancer Discovery, 2014, 4, 1014-1021.   | 7.7  | 114       |
| 183 | Loss of NF1 in Cutaneous Melanoma Is Associated with RAS Activation and MEK Dependence. Cancer Research, 2014, 74, 2340-2350.  | 0.4  | 266       |
| 184 | Tumor Genetic Analyses of Patients with Metastatic Renal Cell Carcinoma and Extended Benefit from mTOR Inhibitor Therapy. Clinical Cancer Research, 2014, 20, 1955-1964.                                     | 3.2  | 208       |
| 185 | MLL3 Is a Haploinsufficient 7q Tumor Suppressor in Acute Myeloid Leukemia. Cancer Cell, 2014, 25, 652-665.   | 7.7  | 274       |
| 186 | Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. Genome Research, 2014, 24, 1740-1750.                                 | 2.4  | 244       |
| 187 | Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550.  | 13.7 | 4,572     |
| 188 | Loss of the tyrosine phosphatase PTPRD leads to aberrant STAT3 activation and promotes gliomagenesis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8149-8154. | 3.3  | 80        |
| 189 | Integrating biological pathways and genomic profiles with ChiBE 2. BMC Genomics, 2014, 15, 642.  | 1.2  | 24        |
| 190 | Genome-wide analysis of noncoding regulatory mutations in cancer. Nature Genetics, 2014, 46, 1160-1165.  | 9.4  | 469       |
| 191 | Collection, integration and analysis of cancer genomic profiles: from data to insight. Current Opinion in Genetics and Development, 2014, 24, 92-98.   | 1.5  | 22        |
| 192 | Analytic and Clinical Validation of a Prostate Cancer–Enhanced Messenger RNA Detection Assay in Whole Blood as a Prognostic Biomarker for Survival. European Urology, 2014, 65, 1191-1197.                   | 0.9  | 66        |
| 193 | BridgeDb app: unifying identifier mapping services for Cytoscape. F1000Research, 2014, 3, 148.   | 0.8  | 11        |
| 194 | Clinical multiplexed exome sequencing distinguishes adult oligodendroglial neoplasms from astrocytic and mixed lineage gliomas. Oncotarget, 2014, 5, 8083-8092.  | 0.8  | 55        |
| 195 | Evaluating cell lines as tumour models by comparison of genomic profiles. Nature Communications, 2013, 4, 2126.  | 5.8  | 1,108     |
| 196 | Analysis of microRNA-target interactions across diverse cancer types. Nature Structural and Molecular Biology, 2013, 20, 1325-1332.  | 3.6  | 184       |
| 197 | The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.   | 13.5 | 3,979     |
| 198 | The molecular diversity of Luminal A breast tumors. Breast Cancer Research and Treatment, 2013, 141, 409-420.  | 1.1  | 120       |

| #   | Article  | IF   | CITATIONS |
|-----|--|------|-----------|
| 199 | Prevalence and Co-Occurrence of Actionable Genomic Alterations in High-Grade Bladder Cancer. Journal of Clinical Oncology, 2013, 31, 3133-3140.  | 0.8  | 282       |
| 200 | The Cancer Genome Atlas Pan-Cancer analysis project. Nature Genetics, 2013, 45, 1113-1120.   | 9.4  | 6,265     |
| 201 | Emerging landscape of oncogenic signatures across human cancers. Nature Genetics, 2013, 45, 1127-1133.   | 9.4  | 1,190     |
| 202 | Pattern discovery and cancer gene identification in integrated cancer genomic data. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4245-4250.   | 3.3  | 361       |
| 203 | <i>MLH1</i> à€silenced and nonâ€silenced subgroups of hypermutated colorectal carcinomas have distinct mutational landscapes. Journal of Pathology, 2013, 229, 99-110.   | 2.1  | 67        |
| 204 | SQSTM1 Is a Pathogenic Target of 5q Copy Number Gains in Kidney Cancer. Cancer Cell, 2013, 24, 738-750.  | 7.7  | 135       |
| 205 | Using MEMo to Discover Mutual Exclusivity Modules in Cancer. Current Protocols in Bioinformatics, 2013, 41, Unit 8.17.   | 25.8 | 29        |
| 206 | Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.  | 13.7 | 4,075     |
| 207 | Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal. Science Signaling, 2013, 6, pl1.   | 1.6  | 11,344    |
| 208 | The mutational landscape of adenoid cystic carcinoma. Nature Genetics, 2013, 45, 791-798.  | 9.4  | 394       |
| 209 | An Epidemiologic and Genomic Investigation Into the Obesity Paradox in Renal Cell Carcinoma. Journal of the National Cancer Institute, 2013, 105, 1862-1870.   | 3.0  | 231       |
| 210 | Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.   | 13.7 | 2,839     |
| 211 | Cancer cells preferentially lose small chromosomes. International Journal of Cancer, 2013, 132, 2316-2326.   | 2.3  | 143       |
| 212 | Adverse Outcomes in Clear Cell Renal Cell Carcinoma with Mutations of 3p21 Epigenetic Regulators <i>BAP1</i> and <i>SETD2</i> : A Report by MSKCC and the KIRC TCGA Research Network. Clinical Cancer Research, 2013, 19, 3259-3267. | 3.2  | 301       |
| 213 | BRCA1 Immunohistochemistry in a Molecularly Characterized Cohort of Ovarian High-Grade Serous Carcinomas. American Journal of Surgical Pathology, 2013, 37, 138-146.   | 2.1  | 54        |
| 214 | Comprehensive Analysis of Long Non-Coding RNAs in Ovarian Cancer Reveals Global Patterns and Targeted DNA Amplification. PLoS ONE, 2013, 8, e80306.  | 1,1  | 90        |
| 215 | Distinct Patterns of Dysregulated Expression of Enzymes Involved in Androgen Synthesis and Metabolism in Metastatic Prostate Cancer Tumors. Cancer Research, 2012, 72, 6142-6152.  | 0.4  | 175       |
| 216 | Genomic Complexity and AKT Dependence in Serous Ovarian Cancer. Cancer Discovery, 2012, 2, 56-67.  | 7.7  | 109       |

| #   | Article   | IF   | Citations |
|-----|---|------|-----------|
| 217 | Comparative analysis of SV40 17kT and LT function in vivo demonstrates that LTâ $\in$ <sup>M</sup> s C-terminus re-programs hepatic gene expression and is necessary for tumorigenesis in the liver. Oncogenesis, 2012, 1, e28-e28. | 2.1  | 13        |
| 218 | A cluster of cooperating tumor-suppressor gene candidates in chromosomal deletions. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8212-8217.  | 3.3  | 138       |
| 219 | Mutual exclusivity analysis identifies oncogenic network modules. Genome Research, 2012, 22, 398-406.   | 2.4  | 597       |
| 220 | The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. Cancer Discovery, 2012, 2, 401-404.  | 7.7  | 12,801    |
| 221 | 53BP1 Is a Haploinsufficient Tumor Suppressor and Protects Cells from Radiation Response in Glioma.<br>Cancer Research, 2012, 72, 5250-5260.  | 0.4  | 34        |
| 222 | Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.  | 13.7 | 10,282    |
| 223 | MEF Promotes Stemness in the Pathogenesis of Gliomas. Cell Stem Cell, 2012, 11, 836-844.  | 5.2  | 37        |
| 224 | Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.   | 13.7 | 3,483     |
| 225 | Integrated Analyses of microRNAs Demonstrate Their Widespread Influence on Gene Expression in High-Grade Serous Ovarian Carcinoma. PLoS ONE, 2012, 7, e34546.   | 1.1  | 104       |
| 226 | Integrative Subtype Discovery in Glioblastoma Using iCluster. PLoS ONE, 2012, 7, e35236.  | 1.1  | 196       |
| 227 | Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.   | 13.7 | 6,541     |
| 228 | Time to Recurrence and Survival in Serous Ovarian Tumors Predicted from Integrated Genomic Profiles. PLoS ONE, 2011, 6, e24709.   | 1.1  | 88        |
| 229 | Identification of PHLPP1 as a Tumor Suppressor Reveals the Role of Feedback Activation in PTEN-Mutant Prostate Cancer Progression. Cancer Cell, 2011, 20, 173-186.  | 7.7  | 158       |
| 230 | Frequent Alterations and Epigenetic Silencing of Differentiation Pathway Genes in Structurally Rearranged Liposarcomas. Cancer Discovery, 2011, 1, 587-597.   | 7.7  | 108       |
| 231 | Off-target effects dominate a large-scale RNAi screen for modulators of the TGF- $\hat{l}^2$ pathway and reveal microRNA regulation of TGFBR2. Silence: A Journal of RNA Regulation, 2011, 2, 3.                                    | 8.0  | 78        |
| 232 | 18F-Fluorodeoxy-glucose Positron Emission Tomography Marks MYC-Overexpressing Human Basal-Like Breast Cancers. Cancer Research, 2011, 71, 5164-5174.  | 0.4  | 113       |
| 233 | Pathway Commons, a web resource for biological pathway data. Nucleic Acids Research, 2011, 39, D685-D690.   | 6.5  | 980       |
| 234 | Integrative Genomic Profiling of Human Prostate Cancer. Cancer Cell, 2010, 18, 11-22.   | 7.7  | 3,151     |

| #   | Article   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 235 | Somatic mutations of the Parkinson's disease–associated gene PARK2 in glioblastoma and other human malignancies. Nature Genetics, 2010, 42, 77-82.  | 9.4 | 336       |
| 236 | Automated Network Analysis Identifies Core Pathways in Glioblastoma. PLoS ONE, 2010, 5, e8918.  | 1.1 | 318       |
| 237 | The tyrosine phosphatase PTPRD is a tumor suppressor that is frequently inactivated and mutated in glioblastoma and other human cancers. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 9435-9440. | 3.3 | 246       |
| 238 | Expression patterns of mitotic and meiotic cell cycle regulators in testicular cancer and development. International Journal of Cancer, 2005, 116, 207-217.   | 2.3 | 21        |
| 239 | Defining the spermatogonial stem cell. Developmental Biology, 2004, 269, 393-410.   | 0.9 | 126       |
| 240 | Spermatogonial Stem Cells in the Rat and Mouse., 2004,, 179-185.  |     | 1         |
| 241 | A multitude of genes expressed solely in meiotic or postmeiotic spermatogenic cells offers a myriad of contraceptive targets. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12201-12206.          | 3.3 | 514       |