# Victor E Velculescu

## List of Publications by Year in descending order



| | | | |
|---|---|---|---|
| 223 papers | 95,235 citations | 1377 111 h-index | 3844 184 g-index |
| 232 all docs | 232 docs citations | 232 times ranked | 94503 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Automated next-generation profiling of genomic alterations in human cancers. Nature Communications, 2022, 13, . | 5.8 | 8 |
| 2 | Peripheral blood immune cell dynamics reflect antitumor immune responses and predict clinical response to immunotherapy. , 2022, 10, e004688. | | 34 |
| 3 | Abstract 536: Prognostic value of post-surgery liquid biopsy cell-free circulating tumor DNA in stage III colon cancer patients - PLCRC-PROVENC3 study. Cancer Research, 2022, 82, 536-536. | 0.4 | 0 |
| 4 | Cell-free DNA (cfDNA) fragmentomes predict tumor burden in metastatic colorectal cancer (mCRC).. Journal of Clinical Oncology, 2022, 40, 3541-3541. | 0.8 | 0 |
| 5 | DELFI-L101: Development of a blood-based assay that evaluates cell-free DNA fragmentation patterns to detect lung cancer.. Journal of Clinical Oncology, 2022, 40, TPS3164-TPS3164. | 0.8 | 1 |
| 6 | Natural Language Processing Approaches for Retrieval of Clinically Relevant Genomic Information in Cancer. Studies in Health Technology and Informatics, 2022, , . | 0.2 | 0 |
| 7 | Reply to: Limitations of molecular testing in combination with computerized tomographic for lung cancer screening. Nature Communications, 2022, 13, . | 5.8 | 0 |
| 8 | Modeling cell-free DNA fragment size densities for non-invasive detection of cancer.. Journal of Clinical Oncology, 2021, 39, 3058-3058. | 0.8 | 0 |
| 9 | Immunogenomic features of pathologic response to neoadjuvant immune checkpoint blockade in esophageal cancer.. Journal of Clinical Oncology, 2021, 39, 4042-4042. | 0.8 | 0 |
| 10 | Abstract 1617: Sex-specific genomic determinants of response to immunotherapy. , 2021, , . | | 0 |
| 11 | Abstract 540: Molecular response evaluation of patients with metastatic colorectal cancer using circulating tumor DNA. , 2021, , . | | 0 |
| 12 | Transcriptional programs of neoantigen-specific TIL in anti-PD-1-treated lung cancers. Nature, 2021, 596, 126-132. | 13.7 | 234 |
| 13 | Abstract 570: Detecting cancer using genome-wide cfDNA nucleosomal fragmentation in a prospective multi cancer cohort. , 2021, , . | | 0 |
| 14 | Detection and characterization of lung cancer using cell-free DNA fragmentomes. Nature Communications, 2021, 12, 5060. | 5.8 | 161 |
| 15 | Durvalumab with platinum-pemetrexed for unresectable pleural mesothelioma: survival, genomic and immunologic analyses from the phase 2 PrE0505 trial. Nature Medicine, 2021, 27, 1910-1920. | 15.2 | 62 |
| 16 | KRAS A146 Mutations Are Associated With Distinct Clinical Behavior in Patients With Colorectal Liver Metastases. JCO Precision Oncology, 2021, 5, 1758-1767. | 1.5 | 9 |
| 17 | Multimodal genomic features predict outcome of immune checkpoint blockade in non-small-cell lung cancer. Nature Cancer, 2020, 1, 99-111. | 5.7 | 141 |
| 18 | Integrative Tumor and Immune Cell Multi-omic Analyses Predict Response to Immune Checkpoint Blockade in Melanoma. Cell Reports Medicine, 2020, 1, 100139. | 3.3 | 45 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Combining PARP with ATR inhibition overcomes PARP inhibitor and platinum resistance in ovarian cancer models. Nature Communications, 2020, 11, 3726. | 5.8 | 169 |
| 20 | Inherited Rare, Deleterious Variants in ATM Increase Lung Adenocarcinoma Risk. Journal of Thoracic Oncology, 2020, 15, 1871-1879. | 0.5 | 24 |
| 21 | Conserved Interferon-Î³ Signaling Drives Clinical Response to Immune Checkpoint Blockade Therapy in Melanoma. Cancer Cell, 2020, 38, 500-515.e3. | 7.7 | 203 |
| 22 | Neoadjuvant nivolumab plus ipilimumab in resectable non-small cell lung cancer. , 2020, 8, e001282. | | 108 |
| 23 | Genomic characterization of malignant progression in neoplastic pancreatic cysts. Nature Communications, 2020, 11, 4085. | 5.8 | 77 |
| 24 | Diagnostic Strategies toward Clinical Implementation of Liquid Biopsy RAS/BRAF Circulating Tumor DNA Analyses in Patients with Metastatic Colorectal Cancer. Journal of Molecular Diagnostics, 2020, 22, 1430-1437. | 1.2 | 19 |
| 25 | High-Throughput Prediction of MHC Class I and II Neoantigens with MHCnuggets. Cancer Immunology Research, 2020, 8, 396-408. | 1.6 | 103 |
| 26 | White blood cell and cell-free DNA analyses for detection of residual disease in gastric cancer. Nature Communications, 2020, 11, 525. | 5.8 | 158 |
| 27 | Compartmental Analysis of T-cell Clonal Dynamics as a Function of Pathologic Response to Neoadjuvant PD-1 Blockade in Resectable Nonâ€“Small Cell Lung Cancer. Clinical Cancer Research, 2020, 26, 1327-1337. | 3.2 | 90 |
| 28 | Genomeâ€wide investigation of intragenic DNA methylation identifies ZMIZ1 gene as a prognostic marker in glioblastoma and multiple cancer types. International Journal of Cancer, 2019, 145, 3425-3435. | 2.3 | 16 |
| 29 | Phase I Study of Rapid Alternation of Sunitinib and Regorafenib for the Treatment of Tyrosine Kinase Inhibitor Refractory Gastrointestinal Stromal Tumors. Clinical Cancer Research, 2019, 25, 7287-7293. | 3.2 | 37 |
| 30 | Combined MEK and BCL-2/XL Inhibition Is Effective in High-Grade Serous Ovarian Cancer Patientâ€“Derived Xenograft Models and BIM Levels Are Predictive of Responsiveness. Molecular Cancer Therapeutics, 2019, 18, 642-655. | 1.9 | 39 |
| 31 | Genome-wide cell-free DNA fragmentation in patients with cancer. Nature, 2019, 570, 385-389. | 13.7 | 764 |
| 32 | Circulating Tumor DNA as a Clinical Test in Resected Pancreatic Cancer. Clinical Cancer Research, 2019, 25, 4973-4984. | 3.2 | 118 |
| 33 | Persistent mutant oncogene specific T cells in two patients benefitting from anti-PD-1. , 2019, 7, 40. | | 42 |
| 34 | Noninvasive Detection of Microsatellite Instability and High Tumor Mutation Burden in Cancer Patients Treated with PD-1 Blockade. Clinical Cancer Research, 2019, 25, 7024-7034. | 3.2 | 104 |
| 35 | Early Noninvasive Detection of Response to Targeted Therapy in Nonâ€“Small Cell Lung Cancer. Cancer Research, 2019, 79, 1204-1213. | 0.4 | 75 |
| 36 | Dynamics of Tumor and Immune Responses during Immune Checkpoint Blockade in Nonâ€“Small Cell Lung Cancer. Cancer Research, 2019, 79, 1214-1225. | 0.4 | 226 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | Neoadjuvant nivolumab plus concurrent chemoradiation in stage II/III esophageal/gastroesophageal junction cancer.. Journal of Clinical Oncology, 2019, 37, 142-142. | 0.8 | 21 |
| 38 | Early shifts in immune cell subsets to predict response to immune checkpoint blockade in non-small cell lung cancer (NSCLC).. Journal of Clinical Oncology, 2019, 37, 105-105. | 0.8 | 2 |
| 39 | Genome-wide cell-free DNA fragmentation profiling for early cancer detection.. Journal of Clinical Oncology, 2019, 37, 3018-3018. | 0.8 | 1 |
| 40 | Abstract 3977: Clinical validation of cell-free circulating tumor DNA to detect therapy resistance and disease progression in metastatic colorectal cancer patients. , 2019, , . | | 0 |
| 41 | Abstract 4041: Coupling neoantigen specific T cell clonotypes and their molecular phenotypes at the single cell level in resectable anti-PD-1 treated NSCLC. , 2019, , . | | 0 |
| 42 | Abstract 1065: Comprehensive molecular and experimental characterization of ovarian clear cell carcinoma cell lines forin vivodrug development. , 2019, , . | | 0 |
| 43 | Neoadjuvant PD-1 Blockade in Resectable Lung Cancer. New England Journal of Medicine, 2018, 378, 1976-1986. | 13.9 | 1,495 |
| 44 | American Association for Cancer Research Project Genomics Evidence Neoplasia Information Exchange: From Inception to First Data Release and Beyondâ€"Lessons Learned and Member Institutionsâ€™ Perspectives. JCO Clinical Cancer Informatics, 2018, 2, 1-14. | 1.0 | 33 |
| 45 | Ipilimumab plus nivolumab and DNA-repair defects in AR-V7-expressing metastatic prostate cancer. Oncotarget, 2018, 9, 28561-28571. | 0.8 | 129 |
| 46 | BRAF Mutations Occur Infrequently in Ovarian Cancer but Suggest Responsiveness to BRAF and MEK Inhibition. JCO Precision Oncology, 2018, 2, 1-6. | 1.5 | 6 |
| 47 | Integrated Genomic, Epigenomic, and Expression Analyses of Ovarian Cancer Cell Lines. Cell Reports, 2018, 25, 2617-2633. | 2.9 | 74 |
| 48 | A machine learning approach for somatic mutation discovery. Science Translational Medicine, 2018, 10, . | 5.8 | 80 |
| 49 | The Mutation-Associated Neoantigen Functional Expansion of Specific T Cells (MANAFEST) Assay: A Sensitive Platform for Monitoring Antitumor Immunity. Cancer Immunology Research, 2018, 6, 888-899. | 1.6 | 118 |
| 50 | Abstract CT079: Neoadjuvant PD-1 blockade in resectable lung cancer. Cancer Research, 2018, 78, CT079-CT079. | 0.4 | 4 |
| 51 | Phase Ib study of rapid alternation of sunitinib (SU) and regorafenib (RE) in patients (pts) with advanced gastrointestinal stromal tumor (GIST).. Journal of Clinical Oncology, 2018, 36, 11510-11510. | 0.8 | 1 |
| 52 | Circulating tumor DNA dynamics in resectable gastric cancer.. Journal of Clinical Oncology, 2018, 36, 4069-4069. | 0.8 | 2 |
| 53 | Immune checkpoint inhibition in elderly non-small cell lung cancer patients.. Journal of Clinical Oncology, 2018, 36, 137-137. | 0.8 | 1 |
| 54 | Pan-Cancer assessment of tumor mutational burden using a comprehensive genomic profiling assay.. Journal of Clinical Oncology, 2018, 36, 157-157. | 0.8 | 1 |

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|---|---|---|---|
| 55 | Induction nivolumab or nivolumab/ipilimumab prior to concurrent chemoradiation plus nivolumab in patients with operable stage II/III esophageal/gastroesophageal junction cancer.. Journal of Clinical Oncology, 2018, 36, TPS4140-TPS4140. | 0.8 | 0 |
| 56 | Abstract 4596: Early noninvasive prediction of response to targeted therapy in non-small cell lung cancer. , 2018, , . | | 0 |
| 57 | Abstract 3271: A machine learning approach for somatic mutation discovery. , 2018, , . | | 0 |
| 58 | Abstract 3668: ctDNA and TCR dynamics predict response toimmune checkpoint blockade in non-small cell lung cancer. , 2018, , . | | 0 |
| 59 | Abstract LB-154: Pathologic features of response to neoadjuvant anti-PD-1 in resected non-small cell lung carcinoma (NSCLC): A proposal for quantitative immune-related pathologic response criteria (irPRC). , 2018, , . | | 0 |
| 60 | AACR Project GENIE: Powering Precision Medicine through an International Consortium. Cancer Discovery, 2017, 7, 818-831. | 7.7 | 1,235 |
| 61 | Precancer Atlas to Drive Precision Prevention Trials. Cancer Research, 2017, 77, 1510-1541. | 0.4 | 116 |
| 62 | Circulating Tumor DNA for Mutation Detection and Identification of Mechanisms of Resistance in Non-Small Cell Lung Cancer. Molecular Diagnosis and Therapy, 2017, 21, 375-384. | 1.6 | 12 |
| 63 | Evolution of Neoantigen Landscape during Immune Checkpoint Blockade in Nonâ€“Small Cell Lung Cancer. Cancer Discovery, 2017, 7, 264-276. | 7.7 | 706 |
| 64 | Cancer DNA in the Circulation. JAMA - Journal of the American Medical Association, 2017, 318, 1272. | 3.8 | 69 |
| 65 | High grade serous ovarian carcinomas originate in the fallopian tube. Nature Communications, 2017, 8, 1093. | 5.8 | 515 |
| 66 | Chronic Cigarette Smoke-Induced Epigenomic Changes Precede Sensitization of Bronchial Epithelial Cells to Single-Step Transformation by KRAS Mutations. Cancer Cell, 2017, 32, 360-376.e6. | 7.7 | 162 |
| 67 | Clinical study of genomic drivers in pancreatic ductal adenocarcinoma. British Journal of Cancer, 2017, 117, 572-582. | 2.9 | 26 |
| 68 | Direct detection of early-stage cancers using circulating tumor DNA. Science Translational Medicine, 2017, 9, . | 5.8 | 808 |
| 69 | Epigenetic Therapy Ties MYC Depletion to Reversing Immune Evasion and Treating Lung Cancer. Cell, 2017, 171, 1284-1300.e21. | 13.5 | 366 |
| 70 | The Effect of Preservative and Temperature on the Analysis of Circulating Tumor DNA. Clinical Cancer Research, 2017, 23, 2471-2477. | 3.2 | 154 |
| 71 | Establishment of Patient-Derived Tumor Xenograft Models of Epithelial Ovarian Cancer for Preclinical Evaluation of Novel Therapeutics. Clinical Cancer Research, 2017, 23, 1263-1273. | 3.2 | 95 |
| 72 | Abstract LB-102: Landscape analysis of the initial data release from AACR Project GENIE. , 2017, , . | | 1 |

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|---|---|---|---|
| 73 | Abstract NG01: Evolution of neoantigen landscape during immune checkpoint blockade in non-small cell lung cancer. , 2017, , . | | 23 |
| 74 | Neoadjuvant nivolumab in early-stage, resectable non-small cell lung cancers.. Journal of Clinical Oncology, 2017, 35, 8508-8508. | 0.8 | 25 |
| 75 | Abstract LB-246: Detection of circulating tumor DNA in early stage cancers. , 2017, , . | | 0 |
| 76 | Abstract 4954: Clinical validation of a cell-free DNA liquid biopsy approach for noninvasive molecular profiling. , 2017, , . | | 0 |
| 77 | Abstract 604: Accurate identification and prioritization of candidate neoantigens from integrated cancer exome and transcriptome sequencing of FFPE samples. , 2017, , . | | 0 |
| 78 | Genomic and Immunological Tumor Profiling Identifies Targetable Pathways and Extensive CD8+/PDL1+ Immune Infiltration in Inflammatory Breast Cancer Tumors. Molecular Cancer Therapeutics, 2016, 15, 1746-1756. | 1.9 | 45 |
| 79 | Oncogenic PIK3CA mutations reprogram glutamine metabolism in colorectal cancer. Nature Communications, 2016, 7, 11971. | 5.8 | 203 |
| 80 | Neoadjuvant anti-PD1, nivolumab, in early stage resectable non-small-cell lung cancer.. Journal of Clinical Oncology, 2016, 34, e20005-e20005. | 0.8 | 1 |
| 81 | Abstract 2773: Chronic cigarette smoke exposure of bronchial epithelial cells induces progressive epigenomic changes leading to transformation. , 2016, , . | | 0 |
| 82 | Abstract 3957: Optimized plasma collection procedures for liquid biopsy analyses in cancer. , 2016, , . | | 0 |
| 83 | Abstract 528: Identify and prioritize candidate neoantigens from cancer exome sequencing with unmatched accuracy. , 2016, , . | | 0 |
| 84 | Abstract A039: Accurate identification and prioritization of candidate neoantigens from cancer exome sequencing. , 2016, , . | | 0 |
| 85 | Clinical implications of genomic alterations in the tumour and circulation of pancreatic cancer patients. Nature Communications, 2015, 6, 7686. | 5.8 | 393 |
| 86 | Personalized genomic analyses for cancer mutation discovery and interpretation. Science Translational Medicine, 2015, 7, 283ra53. | 5.8 | 347 |
| 87 | Notch1 Mutations Are Drivers of Oral Tumorigenesis. Cancer Prevention Research, 2015, 8, 277-286. | 0.7 | 78 |
| 88 | The genomic landscape of response to EGFR blockade in colorectal cancer. Nature, 2015, 526, 263-267. | 13.7 | 398 |
| 89 | Beyond genomics: Critical evaluation of cell line utility for ovarian cancer research. Gynecologic Oncology, 2015, 139, 97-103. | 0.6 | 65 |
| 90 | Abstract 619: Identification of clinically actionable genomic alterations in the tumor and circulation of pancreatic cancer patients. , 2015, , . | | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 91 | Phase 1 trial of gemcitabine/nab-paclitaxel in combination with the autophagy inhibitor hydroxychloroquine in previously untreated patients with metastatic pancreatic adenocarcinoma.. Journal of Clinical Oncology, 2015, 33, e15213-e15213. | 0.8 | 4 |
| 92 | Personalized Genomic Analyses for Cancer Mutation Discovery and Interpretation.. Journal of Clinical Oncology, 2015, 33, 1529-1529. | 0.8 | 2 |
| 93 | Abstract 5246: Noninvasive detection of MET gene amplification in the circulation of cancer patients. , 2015, , . | | 0 |
| 94 | Abstract 3894: The importance of matched tumor and normal DNA for somatic mutation discovery and clinical interpretation. , 2015, , . | | 0 |
| 95 | Abstract 2405: A method for comprehensive genomic analysis of cell free DNA. , 2015, , . | | 0 |
| 96 | Abstract 3887: Genomic analysis identifies drug targetable pathways and predicts immune infiltration in inflammatory breast cancer tumors. , 2015, , . | | 0 |
| 97 | Abstract B1-62: Bumphunting analysis identifies PAX5 promoter methylation and p53 somatic mutations in genomic instability pathways linked to very poor survival in head and neck cancer. , 2015, , . | | 0 |
| 98 | Detection of Circulating Tumor DNA in Early- and Late-Stage Human Malignancies. Science Translational Medicine, 2014, 6, 224ra24. | 5.8 | 3,665 |
| 99 | Key tumor suppressor genes inactivated by â€œgreater promoterâ€•methylation and somatic mutations in head and neck cancer. Epigenetics, 2014, 9, 1031-1046. | 1.3 | 122 |
| 100 | Ganitumab (AMG 479) Inhibits IGF-IIâ€“Dependent Ovarian Cancer Growth and Potentiates Platinum-Based Chemotherapy. Clinical Cancer Research, 2014, 20, 2947-2958. | 3.2 | 41 |
| 101 | Circulating tumor DNA analysis as a real-time method for monitoring tumor burden in melanoma patients undergoing treatment with immune checkpoint blockade. , 2014, 2, 42. | | 186 |
| 102 | Genomic analyses of gynaecologic carcinosarcomas reveal frequent mutations in chromatin remodelling genes. Nature Communications, 2014, 5, 5006. | 5.8 | 149 |
| 103 | Integrated Next-Generation Sequencing and Avatar Mouse Models for Personalized Cancer Treatment. Clinical Cancer Research, 2014, 20, 2476-2484. | 3.2 | 140 |
| 104 | Blood-Based Analyses of Cancer: Circulating Tumor Cells and Circulating Tumor DNA. Cancer Discovery, 2014, 4, 650-661. | 7.7 | 594 |
| 105 | Abstract 2482: Key tumor suppressor genes inactivated by promoter methylation and somatic mutations in head and neck cancer. , 2014, , . | | 1 |
| 106 | Cancer Genome Landscapes. Science, 2013, 339, 1546-1558. | 6.0 | 6,507 |
| 107 | Therapeutic Potential of the Poly(ADP-ribose) Polymerase Inhibitor Rucaparib for the Treatment of Sporadic Human Ovarian Cancer. Molecular Cancer Therapeutics, 2013, 12, 1002-1015. | 1.9 | 93 |
| 108 | Exome sequencing identifies frequent inactivating mutations in BAP1, ARID1A and PBRM1 in intrahepatic cholangiocarcinomas. Nature Genetics, 2013, 45, 1470-1473. | 9.4 | 564 |

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|---|---|---|---|
| 109 | TERT promoter mutations occur frequently in gliomas and a subset of tumors derived from cells with low rates of self-renewal. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6021-6026. | 3.3 | 1,202 |
| 110 | Integrated genomic analyses identify ARID1A and ARID1B alterations in the childhood cancer neuroblastoma. Nature Genetics, 2013, 45, 12-17. | 9.4 | 374 |
| 111 | Exomic Sequencing of Medullary Thyroid Cancer Reveals Dominant and Mutually Exclusive Oncogenic Mutations in RET and RAS. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E364-E369. | 1.8 | 213 |
| 112 | Amplification of the MET Receptor Drives Resistance to Anti-EGFR Therapies in Colorectal Cancer. Cancer Discovery, 2013, 3, 658-673. | 7.7 | 585 |
| 113 | Cancer detection using whole-genome sequencing of cell free DNA. Oncotarget, 2013, 4, 1119-1120. | 0.8 | 11 |
| 114 | Insights into therapeutic resistance from whole-genome analyses of circulating tumor DNA. Oncotarget, 2013, 4, 1856-1857. | 0.8 | 39 |
| 115 | Abstract LB-75: Blood-based molecular detection of acquired resistance to anti-EGFR therapies in colorectal cancer patients.. , 2013, , . | | 0 |
| 116 | ATM Mutations in Patients with Hereditary Pancreatic Cancer. Cancer Discovery, 2012, 2, 41-46. | 7.7 | 442 |
| 117 | Somatic Mutations in CCK2R Alter Receptor Activity that Promote Oncogenic Phenotypes. Molecular Cancer Research, 2012, 10, 739-749. | 1.5 | 16 |
| 118 | Response to Comments on â€œThe Predictive Capacity of Personal Genome Sequencingâ€• Science Translational Medicine, 2012, 4, . | 5.8 | 1 |
| 119 | Comparative Genomic Analysis of Esophageal Adenocarcinoma and Squamous Cell Carcinoma. Cancer Discovery, 2012, 2, 899-905. | 7.7 | 342 |
| 120 | Genetic Basis of Pancreas Cancer Development and Progression: Insights from Whole-Exome and Whole-Genome Sequencing. Clinical Cancer Research, 2012, 18, 4257-4265. | 3.2 | 122 |
| 121 | Clinical Significance of the Genetic Landscape of Pancreatic Cancer and Implications for Identification of Potential Long-term Survivors. Clinical Cancer Research, 2012, 18, 6339-6347. | 3.2 | 220 |
| 122 | Detection of Chromosomal Alterations in the Circulation of Cancer Patients with Whole-Genome Sequencing. Science Translational Medicine, 2012, 4, 162ra154. | 5.8 | 557 |
| 123 | Rapid Characterization of Candidate Biomarkers for Pancreatic Cancer Using Cell Microarrays (CMAs). Journal of Proteome Research, 2012, 11, 5556-5563. | 1.8 | 14 |
| 124 | Lowâ€grade serous carcinomas of the ovary contain very few point mutations. Journal of Pathology, 2012, 226, 413-420. | 2.1 | 186 |
| 125 | The Predictive Capacity of Personal Genome Sequencing. Science Translational Medicine, 2012, 4, 133ra58. | 5.8 | 168 |
| 126 | Somatic mutations in the chromatin remodeling gene ARID1A occur in several tumor types. Human Mutation, 2012, 33, 100-103. | 1.1 | 263 |

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|---|---|---|---|
| 127 | Abstract 2628: Genome-wide sequencing identifiesATMas a pancreatic cancer susceptibility gene. , 2012, , . | | 0 |
| 128 | Integrated next-generation sequencing and patient-derived xenografts to personalized cancer treatment.. Journal of Clinical Oncology, 2012, 30, 3068-3068. | 0.8 | 0 |
| 129 | Mutations in CIC and FUBP1 Contribute to Human Oligodendroglioma. Science, 2011, 333, 1453-1455. | 6.0 | 485 |
| 130 | Inactivating mutations of the chromatin remodeling gene ARID2 in hepatocellular carcinoma. Nature Genetics, 2011, 43, 828-829. | 9.4 | 392 |
| 131 | The Genetic Landscape of the Childhood Cancer Medulloblastoma. Science, 2011, 331, 435-439. | 6.0 | 652 |
| 132 | Somatic Mutations of PPP2R1A in Ovarian and Uterine Carcinomas. American Journal of Pathology, 2011, 178, 1442-1447. | 1.9 | 88 |
| 133 | DAXX / ATRX , MEN1 , and mTOR Pathway Genes Are Frequently Altered in Pancreatic Neuroendocrine Tumors. Science, 2011, 331, 1199-1203. | 6.0 | 1,504 |
| 134 | Exome Sequencing of Head and Neck Squamous Cell Carcinoma Reveals Inactivating Mutations in NOTCH1. Science, 2011, 333, 1154-1157. | 6.0 | 1,568 |
| 135 | Sodium ion channel mutations in glioblastoma patients correlate with shorter survival. Molecular Cancer, 2011, 10, 17. | 7.9 | 51 |
| 136 | Expression of p16 and Retinoblastoma Determines Response to CDK4/6 Inhibition in Ovarian Cancer. Clinical Cancer Research, 2011, 17, 1591-1602. | 3.2 | 247 |
| 137 | Understanding the Enemy. Science Translational Medicine, 2011, 3, 98ps37. | 5.8 | 4 |
| 138 | Functional Synergies yet Distinct Modulators Affected by Genetic Alterations in Common Human Cancers. Cancer Research, 2011, 71, 3471-3481. | 0.4 | 10 |
| 139 | Sequence analysis of 515 kinase genes in chronic lymphocytic leukemia. Leukemia, 2011, 25, 1908-1910. | 3.3 | 28 |
| 140 | Heteroplasmic mitochondrial DNA mutations in normal and tumour cells. Nature, 2010, 464, 610-614. | 13.7 | 470 |
| 141 | International network of cancer genome projects. Nature, 2010, 464, 993-998. | 13.7 | 2,114 |
| 142 | Distant metastasis occurs late during the genetic evolution of pancreatic cancer. Nature, 2010, 467, 1114-1117. | 13.7 | 2,184 |
| 143 | Development of Personalized Tumor Biomarkers Using Massively Parallel Sequencing. Science Translational Medicine, 2010, 2, 20ra14. | 5.8 | 447 |
| 144 | Genetic inactivation of AKT1 , AKT2 , and PDPK1 in human colorectal cancer cells clarifies their roles in tumor growth regulation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2598-2603. | 3.3 | 113 |

| # | Article | IF | Citations |
|---|---|---|---|
| 145 | Frequent Mutations of Chromatin Remodeling Gene ARID1A in Ovarian Clear Cell Carcinoma. Science, 2010, 330, 228-231. | 6.0 | 1,090 |
| 146 | Patient-oriented gene set analysis for cancer mutation data. Genome Biology, 2010, 11, R112. | 13.9 | 63 |
| 147 | Exomic Sequencing Identifies PALB2 as a Pancreatic Cancer Susceptibility Gene. Science, 2009, 324, 217-217. | 6.0 | 713 |
| 148 | Mutant Metabolic Enzymes Are at the Origin of Gliomas. Cancer Research, 2009, 69, 9157-9159. | 0.4 | 132 |
| 149 | Genetic Mutations Associated with Cigarette Smoking in Pancreatic Cancer. Cancer Research, 2009, 69, 3681-3688. | 0.4 | 126 |
| 150 | SMAD4 Gene Mutations Are Associated with Poor Prognosis in Pancreatic Cancer. Clinical Cancer Research, 2009, 15, 4674-4679. | 3.2 | 335 |
| 151 | Inactivating germ-line and somatic mutations in polypeptide N -acetylgalactosaminyltransferase 12 in human colon cancers. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12921-12925. | 3.3 | 128 |
| 152 | Identification of microbial DNA in human cancer. BMC Medical Genomics, 2009, 2, 22. | 0.7 | 26 |
| 153 | Sensitive digital quantification of DNA methylation in clinical samples. Nature Biotechnology, 2009, 27, 858-863. | 9.4 | 317 |
| 154 | Design and analysis issues in genome-wide somatic mutation studies of cancer. Genomics, 2009, 93, 17-21. | 1.3 | 83 |
| 155 | IDH1andIDH2Mutations in Gliomas. New England Journal of Medicine, 2009, 360, 765-773. | 13.9 | 5,285 |
| 156 | Glucose Deprivation Contributes to the Development of KRAS Pathway Mutations in Tumor Cells. Science, 2009, 325, 1555-1559. | 6.0 | 797 |
| 157 | Frequent Activating Mutations of PIK3CA in Ovarian Clear Cell Carcinoma. American Journal of Pathology, 2009, 174, 1597-1601. | 1.9 | 409 |
| 158 | Cancer-Specific High-Throughput Annotation of Somatic Mutations: Computational Prediction of Driver Missense Mutations. Cancer Research, 2009, 69, 6660-6667. | 0.4 | 416 |
| 159 | Abstract B232: Preclinical evaluation of AMG479 a fully human insulinâ€like growth factor receptorâ€1 (IGFR1) antibody in ovarian cancer cells. , 2009, , . | | 0 |
| 160 | An Integrated Genomic Analysis of Human Glioblastoma Multiforme. Science, 2008, 321, 1807-1812. | 6.0 | 5,230 |
| 161 | Genome-wide linkage scan for colorectal cancer susceptibility genes supports linkage to chromosome 3q. BMC Cancer, 2008, 8, 87. | 1.1 | 33 |
| 162 | The Antisense Transcriptomes of Human Cells. Science, 2008, 322, 1855-1857. | 6.0 | 489 |

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|---|---|---|---|
| 163 | Core Signaling Pathways in Human Pancreatic Cancers Revealed by Global Genomic Analyses. Science, 2008, 321, 1801-1806. | 6.0 | 3,755 |
| 164 | Epitope Landscape in Breast and Colorectal Cancer. Cancer Research, 2008, 68, 889-892. | 0.4 | 373 |
| 165 | Chromatid cohesion defects may underlie chromosome instability in human colorectal cancers. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3443-3448. | 3.3 | 361 |
| 166 | Defining the blueprint of the cancer genome. Carcinogenesis, 2008, 29, 1087-1091. | 1.3 | 57 |
| 167 | TRAB: Testing Whether Mutation Frequencies Are Above an Unknown Background. Statistical Applications in Genetics and Molecular Biology, 2008, 7, Article11. | 0.2 | 3 |
| 168 | Integrated analysis of homozygous deletions, focal amplifications, and sequence alterations in breast and colorectal cancers. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16224-16229. | 3.3 | 285 |
| 169 | Comparative lesion sequencing provides insights into tumor evolution. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4283-4288. | 3.3 | 720 |
| 170 | Convergence of Mutation and Epigenetic Alterations Identifies Common Genes in Cancer That Predict for Poor Prognosis. PLoS Medicine, 2008, 5, e114. | 3.9 | 141 |
| 171 | Large-scale identification of novel transcripts in the human genome. Genome Research, 2007, 17, 287-292. | 2.4 | 15 |
| 172 | Identification of STAT3 as a substrate of receptor protein tyrosine phosphatase T. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 4060-4064. | 3.3 | 190 |
| 173 | Genetic Progression and the Waiting Time to Cancer. PLoS Computational Biology, 2007, 3, e225. | 1.5 | 337 |
| 174 | Serial Assessment of Human Tumor Burdens in Mice by the Analysis of Circulating DNA. Cancer Research, 2007, 67, 9364-9370. | 0.4 | 147 |
| 175 | A multidimensional analysis of genes mutated in breast and colorectal cancers. Genome Research, 2007, 17, 1304-1318. | 2.4 | 121 |
| 176 | The Structure of a Human p110Î±/p85Î± Complex Elucidates the Effects of Oncogenic PI3KÎ± Mutations. Science, 2007, 318, 1744-1748. | 6.0 | 504 |
| 177 | Gene expression analysis goes digital. Nature Biotechnology, 2007, 25, 878-880. | 9.4 | 33 |
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