

Victor E Velculescu

List of Publications by Year in descending order

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Version: 2024-02-01

223
papers

95,235
citations

1172
111
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3323
184
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232
all docs

232
docs citations

232
times ranked

86656
citing authors

#	ARTICLE	IF	CITATIONS
1	Automated next-generation profiling of genomic alterations in human cancers. Nature Communications, 2022, 13, .	12.8	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.	0.9	0
4	Cell-free DNA (cfDNA) fragmentomes predict tumor burden in metastatic colorectal cancer (mCRC).. Journal of Clinical Oncology, 2022, 40, 3541-3541.	1.6	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.	1.6	1
6	Natural Language Processing Approaches for Retrieval of Clinically Relevant Genomic Information in Cancer. Studies in Health Technology and Informatics, 2022, , .	0.3	0
7	Reply to: Limitations of molecular testing in combination with computerized tomographic for lung cancer screening. Nature Communications, 2022, 13, .	12.8	0
8	Modeling cell-free DNA fragment size densities for non-invasive detection of cancer.. Journal of Clinical Oncology, 2021, 39, 3058-3058.	1.6	0
9	Immunogenomic features of pathologic response to neoadjuvant immune checkpoint blockade in esophageal cancer.. Journal of Clinical Oncology, 2021, 39, 4042-4042.	1.6	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.	27.8	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.	12.8	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.	30.7	62
16	<i>KRAS</i> A146 Mutations Are Associated With Distinct Clinical Behavior in Patients With Colorectal Liver Metastases. JCO Precision Oncology, 2021, 5, 1758-1767.	3.0	9
17	Multimodal genomic features predict outcome of immune checkpoint blockade in non-small-cell lung cancer. Nature Cancer, 2020, 1, 99-111.	13.2	141
18	Integrative Tumor and Immune Cell Multi-omic Analyses Predict Response to Immune Checkpoint Blockade in Melanoma. Cell Reports Medicine, 2020, 1, 100139.	6.5	45

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19	Combining PARP with ATR inhibition overcomes PARP inhibitor and platinum resistance in ovarian cancer models. <i>Nature Communications</i> , 2020, 11, 3726.	12.8	169
20	Inherited Rare, Deleterious Variants in ATM Increase Lung Adenocarcinoma Risk. <i>Journal of Thoracic Oncology</i> , 2020, 15, 1871-1879.	1.1	24
21	Conserved Interferon- γ Signaling Drives Clinical Response to Immune Checkpoint Blockade Therapy in Melanoma. <i>Cancer Cell</i> , 2020, 38, 500-515.e3.	16.8	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. <i>Nature Communications</i> , 2020, 11, 4085.	12.8	77
24	Diagnostic Strategies toward Clinical Implementation of Liquid Biopsy RAS/BRAF Circulating Tumor DNA Analyses in Patients with Metastatic Colorectal Cancer. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 1430-1437.	2.8	19
25	High-Throughput Prediction of MHC Class I and II Neoantigens with MHCnuggets. <i>Cancer Immunology Research</i> , 2020, 8, 396-408.	3.4	103
26	White blood cell and cell-free DNA analyses for detection of residual disease in gastric cancer. <i>Nature Communications</i> , 2020, 11, 525.	12.8	158
27	Compartmental Analysis of T-cell Clonal Dynamics as a Function of Pathologic Response to Neoadjuvant PD-1 Blockade in Resectable Non-Small Cell Lung Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 1327-1337.	7.0	90
28	Genome-wide investigation of intragenic DNA methylation identifies <i>ZMIZ1</i> gene as a prognostic marker in glioblastoma and multiple cancer types. <i>International Journal of Cancer</i> , 2019, 145, 3425-3435.	5.1	16
29	Phase I Study of Rapid Alternation of Sunitinib and Regorafenib for the Treatment of Tyrosine Kinase Inhibitor Refractory Gastrointestinal Stromal Tumors. <i>Clinical Cancer Research</i> , 2019, 25, 7287-7293.	7.0	37
30	Combined MEK and BCL-2/XL Inhibition Is Effective in High-Grade Serous Ovarian Cancer Patient-Derived Xenograft Models and BIM Levels Are Predictive of Responsiveness. <i>Molecular Cancer Therapeutics</i> , 2019, 18, 642-655.	4.1	39
31	Genome-wide cell-free DNA fragmentation in patients with cancer. <i>Nature</i> , 2019, 570, 385-389.	27.8	764
32	Circulating Tumor DNA as a Clinical Test in Resected Pancreatic Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 4973-4984.	7.0	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. <i>Clinical Cancer Research</i> , 2019, 25, 7024-7034.	7.0	104
35	Early Noninvasive Detection of Response to Targeted Therapy in Non-Small Cell Lung Cancer. <i>Cancer Research</i> , 2019, 79, 1204-1213.	0.9	75
36	Dynamics of Tumor and Immune Responses during Immune Checkpoint Blockade in Non-Small Cell Lung Cancer. <i>Cancer Research</i> , 2019, 79, 1214-1225.	0.9	226

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37	Neoadjuvant nivolumab plus concurrent chemoradiation in stage II/III esophageal/gastroesophageal junction cancer.. Journal of Clinical Oncology, 2019, 37, 142-142.	1.6	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.	1.6	2
39	Genome-wide cell-free DNA fragmentation profiling for early cancer detection.. Journal of Clinical Oncology, 2019, 37, 3018-3018.	1.6	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 for<i>in vivo</i> drug development. , 2019, , .		0
43	Neoadjuvant PD-1 Blockade in Resectable Lung Cancer. New England Journal of Medicine, 2018, 378, 1976-1986.	27.0	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.	2.1	33
45	Ipilimumab plus nivolumab and DNA-repair defects in AR-V7-expressing metastatic prostate cancer. Oncotarget, 2018, 9, 28561-28571.	1.8	129
46	<i>BRAF</i> Mutations Occur Infrequently in Ovarian Cancer but Suggest Responsiveness to BRAF and MEK Inhibition. JCO Precision Oncology, 2018, 2, 1-6.	3.0	6
47	Integrated Genomic, Epigenomic, and Expression Analyses of Ovarian Cancer Cell Lines. Cell Reports, 2018, 25, 2617-2633.	6.4	74
48	A machine learning approach for somatic mutation discovery. Science Translational Medicine, 2018, 10, .	12.4	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.	3.4	118
50	Abstract CT079: Neoadjuvant PD-1 blockade in resectable lung cancer. Cancer Research, 2018, 78, CT079-CT079.	0.9	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.	1.6	1
52	Circulating tumor DNA dynamics in resectable gastric cancer.. Journal of Clinical Oncology, 2018, 36, 4069-4069.	1.6	2
53	Immune checkpoint inhibition in elderly non-small cell lung cancer patients.. Journal of Clinical Oncology, 2018, 36, 137-137.	1.6	1
54	Pan-Cancer assessment of tumor mutational burden using a comprehensive genomic profiling assay.. Journal of Clinical Oncology, 2018, 36, 157-157.	1.6	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.	1.6	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 to immune 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.	9.4	1,235
61	Precancer Atlas to Drive Precision Prevention Trials. Cancer Research, 2017, 77, 1510-1541.	0.9	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.	3.8	12
63	Evolution of Neoantigen Landscape during Immune Checkpoint Blockade in Non-Small Cell Lung Cancer. Cancer Discovery, 2017, 7, 264-276.	9.4	706
64	Cancer DNA in the Circulation. JAMA - Journal of the American Medical Association, 2017, 318, 1272.	7.4	69
65	High grade serous ovarian carcinomas originate in the fallopian tube. Nature Communications, 2017, 8, 1093.	12.8	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.	16.8	162
67	Clinical study of genomic drivers in pancreatic ductal adenocarcinoma. British Journal of Cancer, 2017, 117, 572-582.	6.4	26
68	Direct detection of early-stage cancers using circulating tumor DNA. Science Translational Medicine, 2017, 9, .	12.4	808
69	Epigenetic Therapy Ties MYC Depletion to Reversing Immune Evasion and Treating Lung Cancer. Cell, 2017, 171, 1284-1300.e21.	28.9	366
70	The Effect of Preservative and Temperature on the Analysis of Circulating Tumor DNA. Clinical Cancer Research, 2017, 23, 2471-2477.	7.0	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.	7.0	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.	1.6	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.	4.1	45
79	Oncogenic PIK3CA mutations reprogram glutamine metabolism in colorectal cancer. Nature Communications, 2016, 7, 11971.	12.8	203
80	Neoadjuvant anti-PD1, nivolumab, in early stage resectable non-small-cell lung cancer.. Journal of Clinical Oncology, 2016, 34, e20005-e20005.	1.6	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.	12.8	393
86	Personalized genomic analyses for cancer mutation discovery and interpretation. Science Translational Medicine, 2015, 7, 283ra53.	12.4	347
87	Notch1 Mutations Are Drivers of Oral Tumorigenesis. Cancer Prevention Research, 2015, 8, 277-286.	1.5	78
88	The genomic landscape of response to EGFR blockade in colorectal cancer. Nature, 2015, 526, 263-267.	27.8	398
89	Beyond genomics: Critical evaluation of cell line utility for ovarian cancer research. Gynecologic Oncology, 2015, 139, 97-103.	1.4	65
90	Abstract 619: Identification of clinically actionable genomic alterations in the tumor and circulation of pancreatic cancer patients. , 2015, , .		3

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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.	1.6	4
92	Personalized Genomic Analyses for Cancer Mutation Discovery and Interpretation.. Journal of Clinical Oncology, 2015, 33, 1529-1529.	1.6	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.	12.4	3,665
99	Key tumor suppressor genes inactivated by Æœgreater promoterÆœ methylation and somatic mutations in head and neck cancer. Epigenetics, 2014, 9, 1031-1046.	2.7	122
100	Ganitumab (AMG 479) Inhibits IGF-IIÆœDependent Ovarian Cancer Growth and Potentiates Platinum-Based Chemotherapy. Clinical Cancer Research, 2014, 20, 2947-2958.	7.0	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.	12.8	149
103	Integrated Next-Generation Sequencing and Avatar Mouse Models for Personalized Cancer Treatment. Clinical Cancer Research, 2014, 20, 2476-2484.	7.0	140
104	Blood-Based Analyses of Cancer: Circulating Tumor Cells and Circulating Tumor DNA. Cancer Discovery, 2014, 4, 650-661.	9.4	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.	12.6	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.	4.1	93
108	Exome sequencing identifies frequent inactivating mutations in BAP1, ARID1A and PBRM1 in intrahepatic cholangiocarcinomas. Nature Genetics, 2013, 45, 1470-1473.	21.4	564

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109	<i>TERT</i> 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.	7.1	1,202
110	Integrated genomic analyses identify ARID1A and ARID1B alterations in the childhood cancer neuroblastoma. Nature Genetics, 2013, 45, 12-17.	21.4	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.	3.6	213
112	Amplification of the <i>MET</i> Receptor Drives Resistance to Anti-EGFR Therapies in Colorectal Cancer. Cancer Discovery, 2013, 3, 658-673.	9.4	585
113	Cancer detection using whole-genome sequencing of cell free DNA. Oncotarget, 2013, 4, 1119-1120.	1.8	11
114	Insights into therapeutic resistance from whole-genome analyses of circulating tumor DNA. Oncotarget, 2013, 4, 1856-1857.	1.8	39
115	Abstract LB-75: Blood-based molecular detection of acquired resistance to anti-EGFR therapies in colorectal cancer patients.. , 2013, , .		0
116	<i>ATM</i> Mutations in Patients with Hereditary Pancreatic Cancer. Cancer Discovery, 2012, 2, 41-46.	9.4	442
117	Somatic Mutations in CCK2R Alter Receptor Activity that Promote Oncogenic Phenotypes. Molecular Cancer Research, 2012, 10, 739-749.	3.4	16
118	Response to Comments on "The Predictive Capacity of Personal Genome Sequencing" Science Translational Medicine, 2012, 4, .	12.4	1
119	Comparative Genomic Analysis of Esophageal Adenocarcinoma and Squamous Cell Carcinoma. Cancer Discovery, 2012, 2, 899-905.	9.4	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.	7.0	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.	7.0	220
122	Detection of Chromosomal Alterations in the Circulation of Cancer Patients with Whole-Genome Sequencing. Science Translational Medicine, 2012, 4, 162ra154.	12.4	557
123	Rapid Characterization of Candidate Biomarkers for Pancreatic Cancer Using Cell Microarrays (CMAs). Journal of Proteome Research, 2012, 11, 5556-5563.	3.7	14
124	Low-grade serous carcinomas of the ovary contain very few point mutations. Journal of Pathology, 2012, 226, 413-420.	4.5	186
125	The Predictive Capacity of Personal Genome Sequencing. Science Translational Medicine, 2012, 4, 133ra58.	12.4	168
126	Somatic mutations in the chromatin remodeling gene <i>ARID1A</i> occur in several tumor types. Human Mutation, 2012, 33, 100-103.	2.5	263

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127	Abstract 2628: Genome-wide sequencing identifies ATM as 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.	1.6	0
129	Mutations in <i>CIC</i> and <i>FUBP1</i> Contribute to Human Oligodendroglioma. Science, 2011, 333, 1453-1455.	12.6	485
130	Inactivating mutations of the chromatin remodeling gene ARID2 in hepatocellular carcinoma. Nature Genetics, 2011, 43, 828-829.	21.4	392
131	The Genetic Landscape of the Childhood Cancer Medulloblastoma. Science, 2011, 331, 435-439.	12.6	652
132	Somatic Mutations of PPP2R1A in Ovarian and Uterine Carcinomas. American Journal of Pathology, 2011, 178, 1442-1447.	3.8	88
133	<i>DAXX</i> / <i>ATRX</i> , <i>MEN1</i> , and mTOR Pathway Genes Are Frequently Altered in Pancreatic Neuroendocrine Tumors. Science, 2011, 331, 1199-1203.	12.6	1,504
134	Exome Sequencing of Head and Neck Squamous Cell Carcinoma Reveals Inactivating Mutations in <i>NOTCH1</i> . Science, 2011, 333, 1154-1157.	12.6	1,568
135	Sodium ion channel mutations in glioblastoma patients correlate with shorter survival. Molecular Cancer, 2011, 10, 17.	19.2	51
136	Expression of p16 and Retinoblastoma Determines Response to CDK4/6 Inhibition in Ovarian Cancer. Clinical Cancer Research, 2011, 17, 1591-1602.	7.0	247
137	Understanding the Enemy. Science Translational Medicine, 2011, 3, 98ps37.	12.4	4
138	Functional Synergies yet Distinct Modulators Affected by Genetic Alterations in Common Human Cancers. Cancer Research, 2011, 71, 3471-3481.	0.9	10
139	Sequence analysis of 515 kinase genes in chronic lymphocytic leukemia. Leukemia, 2011, 25, 1908-1910.	7.2	28
140	Heteroplasmic mitochondrial DNA mutations in normal and tumour cells. Nature, 2010, 464, 610-614.	27.8	470
141	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
142	Distant metastasis occurs late during the genetic evolution of pancreatic cancer. Nature, 2010, 467, 1114-1117.	27.8	2,184
143	Development of Personalized Tumor Biomarkers Using Massively Parallel Sequencing. Science Translational Medicine, 2010, 2, 20ra14.	12.4	447
144	Genetic inactivation of <i>AKT1</i> , <i>AKT2</i> , and <i>PDPK1</i> 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.	7.1	113

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145	Frequent Mutations of Chromatin Remodeling Gene <i>ARID1A</i> in Ovarian Clear Cell Carcinoma. Science, 2010, 330, 228-231.	12.6	1,090
146	Patient-oriented gene set analysis for cancer mutation data. Genome Biology, 2010, 11, R112.	9.6	63
147	Exomic Sequencing Identifies <i>PALB2</i> as a Pancreatic Cancer Susceptibility Gene. Science, 2009, 324, 217-217.	12.6	713
148	Mutant Metabolic Enzymes Are at the Origin of Gliomas. Cancer Research, 2009, 69, 9157-9159.	0.9	132
149	Genetic Mutations Associated with Cigarette Smoking in Pancreatic Cancer. Cancer Research, 2009, 69, 3681-3688.	0.9	126
150	<i>SMAD4</i> Gene Mutations Are Associated with Poor Prognosis in Pancreatic Cancer. Clinical Cancer Research, 2009, 15, 4674-4679.	7.0	335
151	Inactivating germ-line and somatic mutations in polypeptide <i>N</i> -acetylgalactosaminyltransferase 12 in human colon cancers. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12921-12925.	7.1	128
152	Identification of microbial DNA in human cancer. BMC Medical Genomics, 2009, 2, 22.	1.5	26
153	Sensitive digital quantification of DNA methylation in clinical samples. Nature Biotechnology, 2009, 27, 858-863.	17.5	317
154	Design and analysis issues in genome-wide somatic mutation studies of cancer. Genomics, 2009, 93, 17-21.	2.9	83
155	<i>IDH1</i> and <i>IDH2</i> Mutations in Gliomas. New England Journal of Medicine, 2009, 360, 765-773.	27.0	5,285
156	Glucose Deprivation Contributes to the Development of <i>KRAS</i> Pathway Mutations in Tumor Cells. Science, 2009, 325, 1555-1559.	12.6	797
157	Frequent Activating Mutations of PIK3CA in Ovarian Clear Cell Carcinoma. American Journal of Pathology, 2009, 174, 1597-1601.	3.8	409
158	Cancer-Specific High-Throughput Annotation of Somatic Mutations: Computational Prediction of Driver Missense Mutations. Cancer Research, 2009, 69, 6660-6667.	0.9	416
159	Abstract B232: Preclinical evaluation of AMG479 a fully human insulin-like growth factor receptor-1 (IGFR1) antibody in ovarian cancer cells. , 2009, , .		0
160	An Integrated Genomic Analysis of Human Glioblastoma Multiforme. Science, 2008, 321, 1807-1812.	12.6	5,230
161	Genome-wide linkage scan for colorectal cancer susceptibility genes supports linkage to chromosome 3q. BMC Cancer, 2008, 8, 87.	2.6	33
162	The Antisense Transcriptomes of Human Cells. Science, 2008, 322, 1855-1857.	12.6	489

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163	Core Signaling Pathways in Human Pancreatic Cancers Revealed by Global Genomic Analyses. <i>Science</i> , 2008, 321, 1801-1806.	12.6	3,755
164	Epitope Landscape in Breast and Colorectal Cancer. <i>Cancer Research</i> , 2008, 68, 889-892.	0.9	373
165	Chromatid cohesion defects may underlie chromosome instability in human colorectal cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3443-3448.	7.1	361
166	Defining the blueprint of the cancer genome. <i>Carcinogenesis</i> , 2008, 29, 1087-1091.	2.8	57
167	TRAB: Testing Whether Mutation Frequencies Are Above an Unknown Background. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2008, 7, Article11.	0.6	3
168	Integrated analysis of homozygous deletions, focal amplifications, and sequence alterations in breast and colorectal cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16224-16229.	7.1	285
169	Comparative lesion sequencing provides insights into tumor evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4283-4288.	7.1	720
170	Convergence of Mutation and Epigenetic Alterations Identifies Common Genes in Cancer That Predict for Poor Prognosis. <i>PLoS Medicine</i> , 2008, 5, e114.	8.4	141
171	Large-scale identification of novel transcripts in the human genome. <i>Genome Research</i> , 2007, 17, 287-292.	5.5	15
172	Identification of STAT3 as a substrate of receptor protein tyrosine phosphatase T. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 4060-4064.	7.1	190
173	Genetic Progression and the Waiting Time to Cancer. <i>PLoS Computational Biology</i> , 2007, 3, e225.	3.2	337
174	Serial Assessment of Human Tumor Burdens in Mice by the Analysis of Circulating DNA. <i>Cancer Research</i> , 2007, 67, 9364-9370.	0.9	147
175	A multidimensional analysis of genes mutated in breast and colorectal cancers. <i>Genome Research</i> , 2007, 17, 1304-1318.	5.5	121
176	The Structure of a Human p110 α /p85 β Complex Elucidates the Effects of Oncogenic PI3K β Mutations. <i>Science</i> , 2007, 318, 1744-1748.	12.6	504
177	Gene expression analysis goes digital. <i>Nature Biotechnology</i> , 2007, 25, 878-880.	17.5	33
178	Digital karyotyping. <i>Nature Protocols</i> , 2007, 2, 1973-1986.	12.0	22
179	The Genomic Landscapes of Human Breast and Colorectal Cancers. <i>Science</i> , 2007, 318, 1108-1113.	12.6	3,049
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