

Victor E Velculescu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7753232/publications.pdf>

Version: 2024-02-01

223
papers

95,235
citations

1163

111
h-index

3312

184
g-index

232
all docs

232
docs citations

232
times ranked

86656
citing authors

#	ARTICLE	IF	CITATIONS
1	WAF1, a potential mediator of p53 tumor suppression. <i>Cell</i> , 1993, 75, 817-825.	13.5	8,091
2	Cancer Genome Landscapes. <i>Science</i> , 2013, 339, 1546-1558.	6.0	6,507
3	<i>IDH1</i> and <i>IDH2</i> Mutations in Gliomas. <i>New England Journal of Medicine</i> , 2009, 360, 765-773.	13.9	5,285
4	An Integrated Genomic Analysis of Human Glioblastoma Multiforme. <i>Science</i> , 2008, 321, 1807-1812.	6.0	5,230
5	Core Signaling Pathways in Human Pancreatic Cancers Revealed by Global Genomic Analyses. <i>Science</i> , 2008, 321, 1801-1806.	6.0	3,755
6	Detection of Circulating Tumor DNA in Early- and Late-Stage Human Malignancies. <i>Science Translational Medicine</i> , 2014, 6, 224ra24.	5.8	3,665
7	The Consensus Coding Sequences of Human Breast and Colorectal Cancers. <i>Science</i> , 2006, 314, 268-274.	6.0	3,130
8	The Genomic Landscapes of Human Breast and Colorectal Cancers. <i>Science</i> , 2007, 318, 1108-1113.	6.0	3,049
9	High Frequency of Mutations of the <i>PIK3CA</i> Gene in Human Cancers. <i>Science</i> , 2004, 304, 554-554.	6.0	3,048
10	Distant metastasis occurs late during the genetic evolution of pancreatic cancer. <i>Nature</i> , 2010, 467, 1114-1117.	13.7	2,184
11	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	13.7	2,114
12	Genes Expressed in Human Tumor Endothelium. <i>Science</i> , 2000, 289, 1197-1202.	6.0	1,733
13	Exome Sequencing of Head and Neck Squamous Cell Carcinoma Reveals Inactivating Mutations in <i>NOTCH1</i> . <i>Science</i> , 2011, 333, 1154-1157.	6.0	1,568
14	<i>DAXX</i> / <i>ATRX</i> , <i>MEN1</i> , and mTOR Pathway Genes Are Frequently Altered in Pancreatic Neuroendocrine Tumors. <i>Science</i> , 2011, 331, 1199-1203.	6.0	1,504
15	Neoadjuvant PD-1 Blockade in Resectable Lung Cancer. <i>New England Journal of Medicine</i> , 2018, 378, 1976-1986.	13.9	1,495
16	Gene Expression Profiles in Normal and Cancer Cells. <i>Science</i> , 1997, 276, 1268-1272.	6.0	1,306
17	AACR Project GENIE: Powering Precision Medicine through an International Consortium. <i>Cancer Discovery</i> , 2017, 7, 818-831.	7.7	1,235
18	<i>TERT</i> promoter mutations occur frequently in gliomas and a subset of tumors derived from cells with low rates of self-renewal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6021-6026.	3.3	1,202

#	ARTICLE	IF	CITATIONS
19	RAF/RAS oncogenes and mismatch-repair status. <i>Nature</i> , 2002, 418, 934-934.	13.7	1,110
20	Frequent Mutations of Chromatin Remodeling Gene <i>ARID1A</i> in Ovarian Clear Cell Carcinoma. <i>Science</i> , 2010, 330, 228-231.	6.0	1,090
21	Characterization of the Yeast Transcriptome. <i>Cell</i> , 1997, 88, 243-251.	13.5	1,009
22	The colorectal microRNAome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 3687-3692.	3.3	890
23	Mutant PIK3CA promotes cell growth and invasion of human cancer cells. <i>Cancer Cell</i> , 2005, 7, 561-573.	7.7	818
24	Direct detection of early-stage cancers using circulating tumor DNA. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	808
25	Glucose Deprivation Contributes to the Development of <i>KRAS</i> Pathway Mutations in Tumor Cells. <i>Science</i> , 2009, 325, 1555-1559.	6.0	797
26	Genome-wide cell-free DNA fragmentation in patients with cancer. <i>Nature</i> , 2019, 570, 385-389.	13.7	764
27	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.	3.3	720
28	Analysis of human transcriptomes. <i>Nature Genetics</i> , 1999, 23, 387-388.	9.4	719
29	Exomic Sequencing Identifies <i>PALB2</i> as a Pancreatic Cancer Susceptibility Gene. <i>Science</i> , 2009, 324, 217-217.	6.0	713
30	Evolution of Neoantigen Landscape during Immune Checkpoint Blockade in Non-Small Cell Lung Cancer. <i>Cancer Discovery</i> , 2017, 7, 264-276.	7.7	706
31	The Genetic Landscape of the Childhood Cancer Medulloblastoma. <i>Science</i> , 2011, 331, 435-439.	6.0	652
32	Allelic Variation in Human Gene Expression. <i>Science</i> , 2002, 297, 1143-1143.	6.0	618
33	Using the transcriptome to annotate the genome. <i>Nature Biotechnology</i> , 2002, 20, 508-512.	9.4	603
34	A Phosphatase Associated with Metastasis of Colorectal Cancer. <i>Science</i> , 2001, 294, 1343-1346.	6.0	601
35	The PIK3CA gene is mutated with high frequency in human breast cancers. <i>Cancer Biology and Therapy</i> , 2004, 3, 772-775.	1.5	594
36	Blood-Based Analyses of Cancer: Circulating Tumor Cells and Circulating Tumor DNA. <i>Cancer Discovery</i> , 2014, 4, 650-661.	7.7	594

#	ARTICLE	IF	CITATIONS
37	Germline mutations of the gene encoding bone morphogenetic protein receptor 1A in juvenile polyposis. <i>Nature Genetics</i> , 2001, 28, 184-187.	9.4	591
38	Amplification of the <i>MET</i> Receptor Drives Resistance to Anti-EGFR Therapies in Colorectal Cancer. <i>Cancer Discovery</i> , 2013, 3, 658-673.	7.7	585
39	Exome sequencing identifies frequent inactivating mutations in BAP1, ARID1A and PBRM1 in intrahepatic cholangiocarcinomas. <i>Nature Genetics</i> , 2013, 45, 1470-1473.	9.4	564
40	Detection of Chromosomal Alterations in the Circulation of Cancer Patients with Whole-Genome Sequencing. <i>Science Translational Medicine</i> , 2012, 4, 162ra154.	5.8	557
41	High grade serous ovarian carcinomas originate in the fallopian tube. <i>Nature Communications</i> , 2017, 8, 1093.	5.8	515
42	Inactivation of hCDC4 can cause chromosomal instability. <i>Nature</i> , 2004, 428, 77-81.	13.7	512
43	Mutations in a signalling pathway. <i>Nature</i> , 2005, 436, 792-792.	13.7	510
44	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.	6.0	504
45	Mutational Analysis of the Tyrosine Phosphatome in Colorectal Cancers. <i>Science</i> , 2004, 304, 1164-1166.	6.0	498
46	The Antisense Transcriptomes of Human Cells. <i>Science</i> , 2008, 322, 1855-1857.	6.0	489
47	Mutations in <i>CIC</i> and <i>FUBP1</i> Contribute to Human Oligodendroglioma. <i>Science</i> , 2011, 333, 1453-1455.	6.0	485
48	Distinct epigenetic changes in the stromal cells of breast cancers. <i>Nature Genetics</i> , 2005, 37, 899-905.	9.4	476
49	Activating Mutations of the Noonan Syndrome-Associated SHP2/PTPN11 Gene in Human Solid Tumors and Adult Acute Myelogenous Leukemia. <i>Cancer Research</i> , 2004, 64, 8816-8820.	0.4	472
50	Heteroplasmic mitochondrial DNA mutations in normal and tumour cells. <i>Nature</i> , 2010, 464, 610-614.	13.7	470
51	Development of Personalized Tumor Biomarkers Using Massively Parallel Sequencing. <i>Science Translational Medicine</i> , 2010, 2, 20ra14.	5.8	447
52	<i>ATM</i> Mutations in Patients with Hereditary Pancreatic Cancer. <i>Cancer Discovery</i> , 2012, 2, 41-46.	7.7	442
53	Mutational Analysis of the Tyrosine Kinome in Colorectal Cancers. <i>Science</i> , 2003, 300, 949-949.	6.0	436
54	Oncogenic Mutations of PIK3CA in Human Cancers. <i>Cell Cycle</i> , 2004, 3, 1221-1224.	1.3	435

#	ARTICLE	IF	CITATIONS
55	Cancer-Specific High-Throughput Annotation of Somatic Mutations: Computational Prediction of Driver Missense Mutations. <i>Cancer Research</i> , 2009, 69, 6660-6667.	0.4	416
56	Frequent Activating Mutations of PIK3CA in Ovarian Clear Cell Carcinoma. <i>American Journal of Pathology</i> , 2009, 174, 1597-1601.	1.9	409
57	The genomic landscape of response to EGFR blockade in colorectal cancer. <i>Nature</i> , 2015, 526, 263-267.	13.7	398
58	Clinical implications of genomic alterations in the tumour and circulation of pancreatic cancer patients. <i>Nature Communications</i> , 2015, 6, 7686.	5.8	393
59	Inactivating mutations of the chromatin remodeling gene ARID2 in hepatocellular carcinoma. <i>Nature Genetics</i> , 2011, 43, 828-829.	9.4	392
60	Integrated genomic analyses identify ARID1A and ARID1B alterations in the childhood cancer neuroblastoma. <i>Nature Genetics</i> , 2013, 45, 12-17.	9.4	374
61	Epitope Landscape in Breast and Colorectal Cancer. <i>Cancer Research</i> , 2008, 68, 889-892.	0.4	373
62	Epigenetic Therapy Ties MYC Depletion to Reversing Immune Evasion and Treating Lung Cancer. <i>Cell</i> , 2017, 171, 1284-1300.e21.	13.5	366
63	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.	3.3	361
64	Personalized genomic analyses for cancer mutation discovery and interpretation. <i>Science Translational Medicine</i> , 2015, 7, 283ra53.	5.8	347
65	Comparative Genomic Analysis of Esophageal Adenocarcinoma and Squamous Cell Carcinoma. <i>Cancer Discovery</i> , 2012, 2, 899-905.	7.7	342
66	Genetic Progression and the Waiting Time to Cancer. <i>PLoS Computational Biology</i> , 2007, 3, e225.	1.5	337
67	<i>SMAD4</i> Gene Mutations Are Associated with Poor Prognosis in Pancreatic Cancer. <i>Clinical Cancer Research</i> , 2009, 15, 4674-4679.	3.2	335
68	Mutations of PIK3CA in Anaplastic Oligodendrogliomas, High-Grade Astrocytomas, and Medulloblastomas. <i>Cancer Research</i> , 2004, 64, 5048-5050.	0.4	318
69	Sensitive digital quantification of DNA methylation in clinical samples. <i>Nature Biotechnology</i> , 2009, 27, 858-863.	9.4	317
70	Somatic Mutations of EGFR in Colorectal Cancers and Glioblastomas. <i>New England Journal of Medicine</i> , 2004, 351, 2883-2883.	13.9	290
71	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.	3.3	285
72	Somatic mutations in the chromatin remodeling gene <i>ARID1A</i> occur in several tumor types. <i>Human Mutation</i> , 2012, 33, 100-103.	1.1	263

#	ARTICLE	IF	CITATIONS
73	Implications of micro-RNA profiling for cancer diagnosis. <i>Oncogene</i> , 2006, 25, 6220-6227.	2.6	247
74	Expression of p16 and Retinoblastoma Determines Response to CDK4/6 Inhibition in Ovarian Cancer. <i>Clinical Cancer Research</i> , 2011, 17, 1591-1602.	3.2	247
75	Transcriptional programs of neoantigen-specific TIL in anti-PD-1-treated lung cancers. <i>Nature</i> , 2021, 596, 126-132.	13.7	234
76	Dynamics of Tumor and Immune Responses during Immune Checkpoint Blockade in Non-“Small Cell Lung Cancer. <i>Cancer Research</i> , 2019, 79, 1214-1225.	0.4	226
77	Clinical Significance of the Genetic Landscape of Pancreatic Cancer and Implications for Identification of Potential Long-term Survivors. <i>Clinical Cancer Research</i> , 2012, 18, 6339-6347.	3.2	220
78	Digital karyotyping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16156-16161.	3.3	215
79	Exomic Sequencing of Medullary Thyroid Cancer Reveals Dominant and Mutually Exclusive Oncogenic Mutations in RET and RAS. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2013, 98, E364-E369.	1.8	213
80	Analysing uncharted transcriptomes with SAGE. <i>Trends in Genetics</i> , 2000, 16, 423-425.	2.9	206
81	Oncogenic PIK3CA mutations reprogram glutamine metabolism in colorectal cancer. <i>Nature Communications</i> , 2016, 7, 11971.	5.8	203
82	Conserved Interferon- β Signaling Drives Clinical Response to Immune Checkpoint Blockade Therapy in Melanoma. <i>Cancer Cell</i> , 2020, 38, 500-515.e3.	7.7	203
83	Changes in Gene Expression Associated with Developmental Arrest and Longevity in <i>Caenorhabditis elegans</i> . <i>Genome Research</i> , 2001, 11, 1346-1352.	2.4	202
84	Recurrent KRAS codon 146 mutations in human colorectal cancer. <i>Cancer Biology and Therapy</i> , 2006, 5, 928-932.	1.5	200
85	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.	3.3	190
86	Low-grade serous carcinomas of the ovary contain very few point mutations. <i>Journal of Pathology</i> , 2012, 226, 413-420.	2.1	186
87	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
88	Digital karyotyping identifies thymidylate synthase amplification as a mechanism of resistance to 5-fluorouracil in metastatic colorectal cancer patients. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 3089-3094.	3.3	175
89	Prevalence of somatic alterations in the colorectal cancer cell genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 3076-3080.	3.3	174
90	Three Classes of Genes Mutated In Colorectal Cancers with Chromosomal Instability. <i>Cancer Research</i> , 2004, 64, 2998-3001.	0.4	174

#	ARTICLE	IF	CITATIONS
91	Combining PARP with ATR inhibition overcomes PARP inhibitor and platinum resistance in ovarian cancer models. <i>Nature Communications</i> , 2020, 11, 3726.	5.8	169
92	The Predictive Capacity of Personal Genome Sequencing. <i>Science Translational Medicine</i> , 2012, 4, 133ra58.	5.8	168
93	Sequence mutations and amplification of PIK3CA and AKT2 genes in purified ovarian serous neoplasms. <i>Cancer Biology and Therapy</i> , 2006, 5, 779-785.	1.5	165
94	Chronic Cigarette Smoke-Induced Epigenomic Changes Precede Sensitization of Bronchial Epithelial Cells to Single-Step Transformation by KRAS Mutations. <i>Cancer Cell</i> , 2017, 32, 360-376.e6.	7.7	162
95	Detection and characterization of lung cancer using cell-free DNA fragmentomes. <i>Nature Communications</i> , 2021, 12, 5060.	5.8	161
96	White blood cell and cell-free DNA analyses for detection of residual disease in gastric cancer. <i>Nature Communications</i> , 2020, 11, 525.	5.8	158
97	PRL-3 expression in metastatic cancers. <i>Clinical Cancer Research</i> , 2003, 9, 5607-15.	3.2	155
98	The Effect of Preservative and Temperature on the Analysis of Circulating Tumor DNA. <i>Clinical Cancer Research</i> , 2017, 23, 2471-2477.	3.2	154
99	Genomic analyses of gynaecologic carcinosarcomas reveal frequent mutations in chromatin remodelling genes. <i>Nature Communications</i> , 2014, 5, 5006.	5.8	149
100	Serial Assessment of Human Tumor Burdens in Mice by the Analysis of Circulating DNA. <i>Cancer Research</i> , 2007, 67, 9364-9370.	0.4	147
101	Multimodal genomic features predict outcome of immune checkpoint blockade in non-small-cell lung cancer. <i>Nature Cancer</i> , 2020, 1, 99-111.	5.7	141
102	Convergence of Mutation and Epigenetic Alterations Identifies Common Genes in Cancer That Predict for Poor Prognosis. <i>PLoS Medicine</i> , 2008, 5, e114.	3.9	141
103	Integrated Next-Generation Sequencing and Avatar Mouse Models for Personalized Cancer Treatment. <i>Clinical Cancer Research</i> , 2014, 20, 2476-2484.	3.2	140
104	Mutant Metabolic Enzymes Are at the Origin of Gliomas. <i>Cancer Research</i> , 2009, 69, 9157-9159.	0.4	132
105	Ipilimumab plus nivolumab and DNA-repair defects in AR-V7-expressing metastatic prostate cancer. <i>Oncotarget</i> , 2018, 9, 28561-28571.	0.8	129
106	The genome and transcriptomes of the anti-tumor agent <i>Clostridium novyi-NT</i> . <i>Nature Biotechnology</i> , 2006, 24, 1573-1580.	9.4	128
107	Inactivating germ-line and somatic mutations in polypeptide <i>N</i> -acetylgalactosaminyltransferase 12 in human colon cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12921-12925.	3.3	128
108	Genetic Mutations Associated with Cigarette Smoking in Pancreatic Cancer. <i>Cancer Research</i> , 2009, 69, 3681-3688.	0.4	126

#	ARTICLE	IF	CITATIONS
109	Genetic Basis of Pancreas Cancer Development and Progression: Insights from Whole-Exome and Whole-Genome Sequencing. <i>Clinical Cancer Research</i> , 2012, 18, 4257-4265.	3.2	122
110	Key tumor suppressor genes inactivated by CpG promoter methylation and somatic mutations in head and neck cancer. <i>Epigenetics</i> , 2014, 9, 1031-1046.	1.3	122
111	A multidimensional analysis of genes mutated in breast and colorectal cancers. <i>Genome Research</i> , 2007, 17, 1304-1318.	2.4	121
112	The Mutation-Associated Neoantigen Functional Expansion of Specific T Cells (MANAFEST) Assay: A Sensitive Platform for Monitoring Antitumor Immunity. <i>Cancer Immunology Research</i> , 2018, 6, 888-899.	1.6	118
113	Circulating Tumor DNA as a Clinical Test in Resected Pancreatic Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 4973-4984.	3.2	118
114	Precancer Atlas to Drive Precision Prevention Trials. <i>Cancer Research</i> , 2017, 77, 1510-1541.	0.4	116
115	Identification of OTX2 as a medulloblastoma oncogene whose product can be targeted by all-trans retinoic acid. <i>Cancer Research</i> , 2005, 65, 919-24.	0.4	115
116	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2598-2603.	3.3	113
117	Neoadjuvant nivolumab plus ipilimumab in resectable non-small cell lung cancer. , 2020, 8, e001282.		108
118	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.	3.2	104
119	High-Throughput Prediction of MHC Class I and II Neoantigens with MHCnuggets. <i>Cancer Immunology Research</i> , 2020, 8, 396-408.	1.6	103
120	<i>NORF5/HUG1</i> Is a Component of the <i>MEC1</i> -Mediated Checkpoint Response to DNA Damage and Replication Arrest in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 1999, 19, 7041-7049.	1.1	95
121	Establishment of Patient-Derived Tumor Xenograft Models of Epithelial Ovarian Cancer for Preclinical Evaluation of Novel Therapeutics. <i>Clinical Cancer Research</i> , 2017, 23, 1263-1273.	3.2	95
122	Therapeutic Potential of the Poly(ADP-ribose) Polymerase Inhibitor Rucaparib for the Treatment of Sporadic Human Ovarian Cancer. <i>Molecular Cancer Therapeutics</i> , 2013, 12, 1002-1015.	1.9	93
123	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.	3.2	90
124	Somatic Mutations of PPP2R1A in Ovarian and Uterine Carcinomas. <i>American Journal of Pathology</i> , 2011, 178, 1442-1447.	1.9	88
125	Somatic mutations of <i>GUCY2F</i> , <i>EPHA3</i> , and <i>NTRK3</i> in human cancers. <i>Human Mutation</i> , 2006, 27, 1060-1061.	1.1	87
126	Design and analysis issues in genome-wide somatic mutation studies of cancer. <i>Genomics</i> , 2009, 93, 17-21.	1.3	83

#	ARTICLE	IF	CITATIONS
127	A machine learning approach for somatic mutation discovery. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	80
128	Notch1 Mutations Are Drivers of Oral Tumorigenesis. <i>Cancer Prevention Research</i> , 2015, 8, 277-286.	0.7	78
129	Genomic characterization of malignant progression in neoplastic pancreatic cysts. <i>Nature Communications</i> , 2020, 11, 4085.	5.8	77
130	Early Noninvasive Detection of Response to Targeted Therapy in Nonâ€“Small Cell Lung Cancer. <i>Cancer Research</i> , 2019, 79, 1204-1213.	0.4	75
131	Integrated Genomic, Epigenomic, and Expression Analyses of Ovarian Cancer Cell Lines. <i>Cell Reports</i> , 2018, 25, 2617-2633.	2.9	74
132	Cancer DNA in the Circulation. <i>JAMA - Journal of the American Medical Association</i> , 2017, 318, 1272.	3.8	69
133	Beyond genomics: Critical evaluation of cell line utility for ovarian cancer research. <i>Gynecologic Oncology</i> , 2015, 139, 97-103.	0.6	65
134	Patient-oriented gene set analysis for cancer mutation data. <i>Genome Biology</i> , 2010, 11, R112.	13.9	63
135	Durvalumab with platinum-pemetrexed for unresectable pleural mesothelioma: survival, genomic and immunologic analyses from the phase 2 PrE0505 trial. <i>Nature Medicine</i> , 2021, 27, 1910-1920.	15.2	62
136	Defining the blueprint of the cancer genome. <i>Carcinogenesis</i> , 2008, 29, 1087-1091.	1.3	57
137	Sodium ion channel mutations in glioblastoma patients correlate with shorter survival. <i>Molecular Cancer</i> , 2011, 10, 17.	7.9	51
138	Homozygous deletion of MKK4 in ovarian serous carcinoma. <i>Cancer Biology and Therapy</i> , 2006, 5, 630-634.	1.5	48
139	AMERSHAM PHARMACIA BIOTECH & SCIENCE PRIZE:Tantalizing Transcriptomes--SAGE and Its Use in Global Gene Expression Analysis. <i>Science</i> , 1999, 286, 1491-1492.	6.0	47
140	Mutational analysis of gene families in human cancer. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 5-12.	1.5	47
141	Genomic and Immunological Tumor Profiling Identifies Targetable Pathways and Extensive CD8+/PDL1+ Immune Infiltration in Inflammatory Breast Cancer Tumors. <i>Molecular Cancer Therapeutics</i> , 2016, 15, 1746-1756.	1.9	45
142	Integrative Tumor and Immune Cell Multi-omic Analyses Predict Response to Immune Checkpoint Blockade in Melanoma. <i>Cell Reports Medicine</i> , 2020, 1, 100139.	3.3	45
143	Persistent mutant oncogene specific T cells in two patients benefitting from anti-PD-1. , 2019, 7, 40.		42
144	Ganitumab (AMG 479) Inhibits IGF-IIâ€“Dependent Ovarian Cancer Growth and Potentiates Platinum-Based Chemotherapy. <i>Clinical Cancer Research</i> , 2014, 20, 2947-2958.	3.2	41

#	ARTICLE	IF	CITATIONS
145	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.	1.9	39
146	Insights into therapeutic resistance from whole-genome analyses of circulating tumor DNA. <i>Oncotarget</i> , 2013, 4, 1856-1857.	0.8	39
147	High-throughput gene expression analysis using SAGE. <i>Drug Discovery Today</i> , 1998, 3, 152-159.	3.2	38
148	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.	3.2	37
149	Peripheral blood immune cell dynamics reflect antitumor immune responses and predict clinical response to immunotherapy. , 2022, 10, e004688.		34
150	Gene expression analysis goes digital. <i>Nature Biotechnology</i> , 2007, 25, 878-880.	9.4	33
151	Genome-wide linkage scan for colorectal cancer susceptibility genes supports linkage to chromosome 3q. <i>BMC Cancer</i> , 2008, 8, 87.	1.1	33
152	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. <i>JCO Clinical Cancer Informatics</i> , 2018, 2, 1-14.	1.0	33
153	Sequence analysis of 515 kinase genes in chronic lymphocytic leukemia. <i>Leukemia</i> , 2011, 25, 1908-1910.	3.3	28
154	Identification of microbial DNA in human cancer. <i>BMC Medical Genomics</i> , 2009, 2, 22.	0.7	26
155	Clinical study of genomic drivers in pancreatic ductal adenocarcinoma. <i>British Journal of Cancer</i> , 2017, 117, 572-582.	2.9	26
156	Neoadjuvant nivolumab in early-stage, resectable non-small cell lung cancers.. <i>Journal of Clinical Oncology</i> , 2017, 35, 8508-8508.	0.8	25
157	Inherited Rare, Deleterious Variants in ATM Increase Lung Adenocarcinoma Risk. <i>Journal of Thoracic Oncology</i> , 2020, 15, 1871-1879.	0.5	24
158	Abstract NG01: Evolution of neoantigen landscape during immune checkpoint blockade in non-small cell lung cancer. , 2017, , .		23
159	Digital karyotyping. <i>Nature Protocols</i> , 2007, 2, 1973-1986.	5.5	22
160	Neoadjuvant nivolumab plus concurrent chemoradiation in stage II/III esophageal/gastroesophageal junction cancer.. <i>Journal of Clinical Oncology</i> , 2019, 37, 142-142.	0.8	21
161	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.	1.2	19
162	Somatic Mutations in CCK2R Alter Receptor Activity that Promote Oncogenic Phenotypes. <i>Molecular Cancer Research</i> , 2012, 10, 739-749.	1.5	16

#	ARTICLE	IF	CITATIONS
163	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.	2.3	16
164	Large-scale identification of novel transcripts in the human genome. <i>Genome Research</i> , 2007, 17, 287-292.	2.4	15
165	Rapid Characterization of Candidate Biomarkers for Pancreatic Cancer Using Cell Microarrays (CMAs). <i>Journal of Proteome Research</i> , 2012, 11, 5556-5563.	1.8	14
166	Circulating Tumor DNA for Mutation Detection and Identification of Mechanisms of Resistance in Non-Small Cell Lung Cancer. <i>Molecular Diagnosis and Therapy</i> , 2017, 21, 375-384.	1.6	12
167	Cancer detection using whole-genome sequencing of cell free DNA. <i>Oncotarget</i> , 2013, 4, 1119-1120.	0.8	11
168	Functional Synergies yet Distinct Modulators Affected by Genetic Alterations in Common Human Cancers. <i>Cancer Research</i> , 2011, 71, 3471-3481.	0.4	10
169	<i>KRAS</i> A146 Mutations Are Associated With Distinct Clinical Behavior in Patients With Colorectal Liver Metastases. <i>JCO Precision Oncology</i> , 2021, 5, 1758-1767.	1.5	9
170	Transcriptome PETs: A genome's best friends. <i>Nature Methods</i> , 2005, 2, 93-94.	9.0	8
171	Automated next-generation profiling of genomic alterations in human cancers. <i>Nature Communications</i> , 2022, 13, .	5.8	8
172	<i>BRAF</i> Mutations Occur Infrequently in Ovarian Cancer but Suggest Responsiveness to BRAF and MEK Inhibition. <i>JCO Precision Oncology</i> , 2018, 2, 1-6.	1.5	6
173	Understanding the Enemy. <i>Science Translational Medicine</i> , 2011, 3, 98ps37.	5.8	4
174	Abstract CT079: Neoadjuvant PD-1 blockade in resectable lung cancer. <i>Cancer Research</i> , 2018, 78, CT079-CT079.	0.4	4
175	Phase 1 trial of gemcitabine/nab-paclitaxel in combination with the autophagy inhibitor hydroxychloroquine in previously untreated patients with metastatic pancreatic adenocarcinoma.. <i>Journal of Clinical Oncology</i> , 2015, 33, e15213-e15213.	0.8	4
176	TRAB: Testing Whether Mutation Frequencies Are Above an Unknown Background. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2008, 7, Article11.	0.2	3
177	Abstract 619: Identification of clinically actionable genomic alterations in the tumor and circulation of pancreatic cancer patients. , 2015, , .		3
178	Circulating tumor DNA dynamics in resectable gastric cancer.. <i>Journal of Clinical Oncology</i> , 2018, 36, 4069-4069.	0.8	2
179	Early shifts in immune cell subsets to predict response to immune checkpoint blockade in non-small cell lung cancer (NSCLC).. <i>Journal of Clinical Oncology</i> , 2019, 37, 105-105.	0.8	2
180	Personalized Genomic Analyses for Cancer Mutation Discovery and Interpretation.. <i>Journal of Clinical Oncology</i> , 2015, 33, 1529-1529.	0.8	2

#	ARTICLE	IF	CITATIONS
181	Response to Comments on "The Predictive Capacity of Personal Genome Sequencing" Science Translational Medicine, 2012, 4, .	5.8	1
182	Abstract LB-102: Landscape analysis of the initial data release from AACR Project GENIE. , 2017, , .		1
183	Neoadjuvant anti-PD1, nivolumab, in early stage resectable non-small-cell lung cancer.. Journal of Clinical Oncology, 2016, 34, e20005-e20005.	0.8	1
184	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
185	Immune checkpoint inhibition in elderly non-small cell lung cancer patients.. Journal of Clinical Oncology, 2018, 36, 137-137.	0.8	1
186	Abstract 2482: Key tumor suppressor genes inactivated by promoter methylation and somatic mutations in head and neck cancer. , 2014, , .		1
187	Pan-Cancer assessment of tumor mutational burden using a comprehensive genomic profiling assay.. Journal of Clinical Oncology, 2018, 36, 157-157.	0.8	1
188	Genome-wide cell-free DNA fragmentation profiling for early cancer detection.. Journal of Clinical Oncology, 2019, 37, 3018-3018.	0.8	1
189	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
190	Modeling cell-free DNA fragment size densities for non-invasive detection of cancer.. Journal of Clinical Oncology, 2021, 39, 3058-3058.	0.8	0
191	Immunogenomic features of pathologic response to neoadjuvant immune checkpoint blockade in esophageal cancer.. Journal of Clinical Oncology, 2021, 39, 4042-4042.	0.8	0
192	Abstract 1617: Sex-specific genomic determinants of response to immunotherapy. , 2021, , .		0
193	Abstract 540: Molecular response evaluation of patients with metastatic colorectal cancer using circulating tumor DNA. , 2021, , .		0
194	Abstract 570: Detecting cancer using genome-wide cfDNA nucleosomal fragmentation in a prospective multi cancer cohort. , 2021, , .		0
195	Abstract B232: Preclinical evaluation of AMG479 a fully human insulin-like growth factor receptor-1 (IGFR1) antibody in ovarian cancer cells. , 2009, , .		0
196	Abstract 2628: Genome-wide sequencing identifies ATM as a pancreatic cancer susceptibility gene. , 2012, , .		0
197	Integrated next-generation sequencing and patient-derived xenografts to personalized cancer treatment.. Journal of Clinical Oncology, 2012, 30, 3068-3068.	0.8	0
198	Abstract LB-75: Blood-based molecular detection of acquired resistance to anti-EGFR therapies in colorectal cancer patients.. , 2013, , .		0

#	ARTICLE	IF	CITATIONS
199	Abstract 5246: Noninvasive detection of MET gene amplification in the circulation of cancer patients. , 2015, , .		0
200	Abstract 3894: The importance of matched tumor and normal DNA for somatic mutation discovery and clinical interpretation. , 2015, , .		0
201	Abstract 2405: A method for comprehensive genomic analysis of cell free DNA. , 2015, , .		0
202	Abstract 3887: Genomic analysis identifies drug targetable pathways and predicts immune infiltration in inflammatory breast cancer tumors. , 2015, , .		0
203	Abstract B1-62: Bumhunting 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
204	Abstract 2773: Chronic cigarette smoke exposure of bronchial epithelial cells induces progressive epigenomic changes leading to transformation. , 2016, , .		0
205	Abstract 3957: Optimized plasma collection procedures for liquid biopsy analyses in cancer. , 2016, , .		0
206	Abstract 528: Identify and prioritize candidate neoantigens from cancer exome sequencing with unmatched accuracy. , 2016, , .		0
207	Abstract A039: Accurate identification and prioritization of candidate neoantigens from cancer exome sequencing. , 2016, , .		0
208	Abstract LB-246: Detection of circulating tumor DNA in early stage cancers. , 2017, , .		0
209	Abstract 4954: Clinical validation of a cell-free DNA liquid biopsy approach for noninvasive molecular profiling. , 2017, , .		0
210	Abstract 604: Accurate identification and prioritization of candidate neoantigens from integrated cancer exome and transcriptome sequencing of FFPE samples. , 2017, , .		0
211	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
212	Abstract 4596: Early noninvasive prediction of response to targeted therapy in non-small cell lung cancer. , 2018, , .		0
213	Abstract 3271: A machine learning approach for somatic mutation discovery. , 2018, , .		0
214	Abstract 3668: ctDNA and TCR dynamics predict response to immune checkpoint blockade in non-small cell lung cancer. , 2018, , .		0
215	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
216	Abstract 3977: Clinical validation of cell-free circulating tumor DNA to detect therapy resistance and disease progression in metastatic colorectal cancer patients. , 2019, , .		0

#	ARTICLE	IF	CITATIONS
217	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
218	Amplification in DNA Copy Numbers as a Mechanism of Acquired Drug Resistance. , 2006, , 531-540.		0
219	Abstract 1065: Comprehensive molecular and experimental characterization of ovarian clear cell carcinoma cell lines for <i>in vivo</i> drug development. , 2019, , .		0
220	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
221	Cell-free DNA (cfDNA) fragmentomes predict tumor burden in metastatic colorectal cancer (mCRC).. Journal of Clinical Oncology, 2022, 40, 3541-3541.	0.8	0
222	Natural Language Processing Approaches for Retrieval of Clinically Relevant Genomic Information in Cancer. Studies in Health Technology and Informatics, 2022, , .	0.2	0
223	Reply to: Limitations of molecular testing in combination with computerized tomographic for lung cancer screening. Nature Communications, 2022, 13, .	5.8	0