Eliezer Van Allen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2491238/publications.pdf

Version: 2024-02-01

215 papers 46,541 citations

82 h-index 201 g-index

247 all docs

 $\begin{array}{c} 247 \\ \text{docs citations} \end{array}$

times ranked

247

55801 citing authors

#	Article	IF	CITATIONS
1	Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq. Science, 2016, 352, 189-196.	12.6	3,421
2	Integrative Clinical Genomics of Advanced Prostate Cancer. Cell, 2015, 161, 1215-1228.	28.9	2,660
3	Clonal neoantigens elicit T cell immunoreactivity and sensitivity to immune checkpoint blockade. Science, 2016, 351, 1463-1469.	12.6	2,445
4	Genomic correlates of response to CTLA-4 blockade in metastatic melanoma. Science, 2015, 350, 207-211.	12.6	2,275
5	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
6	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
7	Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. Nature Genetics, 2012, 44, 685-689.	21.4	1,300
8	Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. New England Journal of Medicine, 2016, 375, 443-453.	27.0	1,205
9	Divergent clonal evolution of castration-resistant neuroendocrine prostate cancer. Nature Medicine, 2016, 22, 298-305.	30.7	1,193
10	Punctuated Evolution of Prostate Cancer Genomes. Cell, 2013, 153, 666-677.	28.9	1,107
11	Genomic correlates of response to immune checkpoint therapies in clear cell renal cell carcinoma. Science, 2018, 359, 801-806.	12.6	898
12	A Cancer Cell Program Promotes T Cell Exclusion and Resistance to Checkpoint Blockade. Cell, 2018, 175, 984-997.e24.	28.9	892
13	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.	7.1	839
14	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. Cancer Discovery, 2015, 5, 1164-1177.	9.4	821
15	In vivo CRISPR screening identifies Ptpn2 as a cancer immunotherapy target. Nature, 2017, 547, 413-418.	27.8	792
16	The Genetic Landscape of Clinical Resistance to RAF Inhibition in Metastatic Melanoma. Cancer Discovery, 2014, 4, 94-109.	9.4	782
17	Tumor immune microenvironment characterization in clear cell renal cell carcinoma identifies prognostic and immunotherapeutically relevant messenger RNA signatures. Genome Biology, 2016, 17, 231.	8.8	746
18	Genomic Correlates of Immune-Cell Infiltrates in Colorectal Carcinoma. Cell Reports, 2016, 15, 857-865.	6.4	671

#	Article	IF	Citations
19	The long tail of oncogenic drivers in prostate cancer. Nature Genetics, 2018, 50, 645-651.	21.4	601
20	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. Nature Communications, 2017, 8, 1324.	12.8	584
21	Integrative molecular and clinical modeling of clinical outcomes to PD1 blockade in patients with metastatic melanoma. Nature Medicine, 2019, 25, 1916-1927.	30.7	541
22	Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. Nature Medicine, 2014, 20, 682-688.	30.7	508
23	Somatic <i>ERCC2</i> Mutations Correlate with Cisplatin Sensitivity in Muscle-Invasive Urothelial Carcinoma. Cancer Discovery, 2014, 4, 1140-1153.	9.4	506
24	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. Nature Biotechnology, 2014, 32, 479-484.	17.5	495
25	Interplay of somatic alterations and immune infiltration modulates response to PD-1 blockade in advanced clear cell renal cell carcinoma. Nature Medicine, 2020, 26, 909-918.	30.7	488
26	LSD1 Ablation Stimulates Anti-tumor Immunity and Enables Checkpoint Blockade. Cell, 2018, 174, 549-563.e19.	28.9	473
27	Mechanisms of Resistance to Immune Checkpoint Blockade: Why Does Checkpoint Inhibitor Immunotherapy Not Work for All Patients?. American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting, 2019, 39, 147-164.	3.8	459
28	Genomic correlates of response to immune checkpoint blockade in microsatellite-stable solid tumors. Nature Genetics, 2018, 50, 1271-1281.	21.4	438
29	A framework to rank genomic alterations as targets for cancer precision medicine: the ESMO Scale for Clinical Actionability of molecular Targets (ESCAT). Annals of Oncology, 2018, 29, 1895-1902.	1.2	424
30	MAP Kinase Pathway Alterations in <i>BRAF</i> -Mutant Melanoma Patients with Acquired Resistance to Combined RAF/MEK Inhibition. Cancer Discovery, 2014, 4, 61-68.	9.4	419
31	Loss of PTEN Is Associated with Resistance to Anti-PD-1 Checkpoint Blockade Therapy in Metastatic Uterine Leiomyosarcoma. Immunity, 2017, 46, 197-204.	14.3	400
32	<i>Ex Vivo</i> Profiling of PD-1 Blockade Using Organotypic Tumor Spheroids. Cancer Discovery, 2018, 8, 196-215.	9.4	392
33	RNF43 is frequently mutated in colorectal and endometrial cancers. Nature Genetics, 2014, 46, 1264-1266.	21.4	388
34	Complementary genomic approaches highlight the PI3K/mTOR pathway as a common vulnerability in osteosarcoma. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5564-73.	7.1	355
35	Somatic ERCC2 mutations are associated with a distinct genomic signature in urothelial tumors. Nature Genetics, 2016, 48, 600-606.	21.4	352
36	Genomic correlates of response to immune checkpoint blockade. Nature Medicine, 2019, 25, 389-402.	30.7	346

#	Article	IF	Citations
37	Return of Genomic Results to Research Participants: The Floor, the Ceiling, and the Choices In Between. American Journal of Human Genetics, 2014, 94, 818-826.	6.2	342
38	A phase II trial of AS1411 (a novel nucleolin-targeted DNA aptamer) in metastatic renal cell carcinoma. Investigational New Drugs, 2014, 32, 178-187.	2.6	302
39	A Genome-Scale RNA Interference Screen Implicates NF1 Loss in Resistance to RAF Inhibition. Cancer Discovery, 2013, 3, 350-362.	9.4	299
40	Response and Acquired Resistance to Everolimus in Anaplastic Thyroid Cancer. New England Journal of Medicine, 2014, 371, 1426-1433.	27.0	290
41	Activating mTOR Mutations in a Patient with an Extraordinary Response on a Phase I Trial of Everolimus and Pazopanib. Cancer Discovery, 2014, 4, 546-553.	9.4	266
42	Clinical Acquired Resistance to RAF Inhibitor Combinations in <i>BRAF</i> -Mutant Colorectal Cancer through MAPK Pathway Alterations. Cancer Discovery, 2015, 5, 358-367.	9.4	265
43	Tumor and immune reprogramming during immunotherapy in advanced renal cell carcinoma. Cancer Cell, 2021, 39, 649-661.e5.	16.8	263
44	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. Cell, 2018, 174, 433-447.e19.	28.9	258
45	Assessing the clinical utility of cancer genomic and proteomic data across tumor types. Nature Biotechnology, 2014, 32, 644-652.	17.5	257
46	Next-generation sequencing to guide cancer therapy. Genome Medicine, 2015, 7, 80.	8.2	251
47	Intron retention is a source of neoepitopes in cancer. Nature Biotechnology, 2018, 36, 1056-1058.	17.5	212
48	Single-cell RNA sequencing reveals compromised immune microenvironment in precursor stages of multiple myeloma. Nature Cancer, 2020, 1, 493-506.	13.2	209
49	Clinical Validation of Chemotherapy Response Biomarker <i>ERCC2</i> in Muscle-Invasive Urothelial Bladder Carcinoma. JAMA Oncology, 2016, 2, 1094.	7.1	205
50	Change in neutrophil-to-lymphocyte ratio (NLR) in response to immune checkpoint blockade for metastatic renal cell carcinoma., 2018, 6, 5.		200
51	Mutations in TSC1, TSC2, and MTOR Are Associated with Response to Rapalogs in Patients with Metastatic Renal Cell Carcinoma. Clinical Cancer Research, 2016, 22, 2445-2452.	7.0	193
52	Beyond conventional immune-checkpoint inhibition — novel immunotherapies for renal cell carcinoma. Nature Reviews Clinical Oncology, 2021, 18, 199-214.	27.6	179
53	Identification of cancer driver genes based on nucleotide context. Nature Genetics, 2020, 52, 208-218.	21.4	170
54	Clinical Validation of <i>PBRM1</i> Alterations as a Marker of Immune Checkpoint Inhibitor Response in Renal Cell Carcinoma. JAMA Oncology, 2019, 5, 1631.	7.1	166

#	Article	IF	CITATIONS
55	Compound Genomic Alterations of TP53, PTEN, and RB1 Tumor Suppressors in Localized and Metastatic Prostate Cancer. European Urology, 2019, 76, 89-97.	1.9	158
56	Biologically informed deep neural network for prostate cancer discovery. Nature, 2021, 598, 348-352.	27.8	158
57	Immunogenomic analyses associate immunological alterations with mismatch repair defects in prostate cancer. Journal of Clinical Investigation, 2018, 128, 4441-4453.	8.2	155
58	Whole-exome sequencing of cell-free DNA and circulating tumor cells in multiple myeloma. Nature Communications, 2018, 9, 1691.	12.8	153
59	The impact of tumor profiling approaches and genomic data strategies for cancer precision medicine. Genome Medicine, 2016, 8, 79.	8.2	151
60	A Functional Landscape of Resistance to ALK Inhibition in Lung Cancer. Cancer Cell, 2015, 27, 397-408.	16.8	150
61	Genomic evolution and chemoresistance in germ-cell tumours. Nature, 2016, 540, 114-118.	27.8	139
62	Metabolomic adaptations and correlates of survival to immune checkpoint blockade. Nature Communications, 2019, 10, 4346.	12.8	139
63	Tumor Mutational Burden and <i>PTEN</i> Alterations as Molecular Correlates of Response to PD-1/L1 Blockade in Metastatic Triple-Negative Breast Cancer. Clinical Cancer Research, 2020, 26, 2565-2572.	7.0	138
64	Genomic Approaches to Understanding Response and Resistance to Immunotherapy. Clinical Cancer Research, 2016, 22, 5642-5650.	7.0	134
65	Somatic Mutations and Neoepitope Homology in Melanomas Treated with CTLA-4 Blockade. Cancer Immunology Research, 2017, 5, 84-91.	3.4	126
66	Clinical Analysis and Interpretation of Cancer Genome Data. Journal of Clinical Oncology, 2013, 31, 1825-1833.	1.6	123
67	Genomics of response to immune checkpoint therapies for cancer: implications for precision medicine. Genome Medicine, 2018, 10, 93.	8.2	121
68	Association of High Tumor Mutation Burden in Non–Small Cell Lung Cancers With Increased Immune Infiltration and Improved Clinical Outcomes of PD-L1 Blockade Across PD-L1 Expression Levels. JAMA Oncology, 2022, 8, 1160.	7.1	117
69	Cancer-Germline Antigen Expression Discriminates Clinical Outcome to CTLA-4 Blockade. Cell, 2018, 173, 624-633.e8.	28.9	113
70	Tissue-resident memory and circulating T cells are early responders to pre-surgical cancer immunotherapy. Cell, 2022, 185, 2918-2935.e29.	28.9	113
71	Genomic Profiling of Smoldering Multiple Myeloma Identifies Patients at a High Risk of Disease Progression. Journal of Clinical Oncology, 2020, 38, 2380-2389.	1.6	110
72	Oncologists' and cancer patients' views on whole-exome sequencing and incidental findings: results from the CanSeq study. Genetics in Medicine, 2016, 18, 1011-1019.	2.4	108

#	Article	lF	Citations
73	Scaling computational genomics to millions of individuals with GPUs. Genome Biology, 2019, 20, 228.	8.8	108
74	<i>ERCC2</i> Helicase Domain Mutations Confer Nucleotide Excision Repair Deficiency and Drive Cisplatin Sensitivity in Muscle-Invasive Bladder Cancer. Clinical Cancer Research, 2019, 25, 977-988.	7.0	104
75	Mutational Analysis of 472 Urothelial Carcinoma Across Grades and Anatomic Sites. Clinical Cancer Research, 2019, 25, 2458-2470.	7.0	102
76	Processes and preliminary outputs for identification of actionable genes as incidental findings in genomic sequence data in the Clinical Sequencing Exploratory Research Consortium. Genetics in Medicine, 2013, 15, 860-867.	2.4	99
77	Mutational patterns in chemotherapy resistant muscle-invasive bladder cancer. Nature Communications, 2017, 8, 2193.	12.8	99
78	Assessment of Deep Natural Language Processing in Ascertaining Oncologic Outcomes From Radiology Reports. JAMA Oncology, 2019, 5, 1421.	7.1	99
79	Clonal hematopoiesis is associated with adverse outcomes in multiple myeloma patients undergoing transplant. Nature Communications, 2020, 11, 2996.	12.8	98
80	Exome Sequencing of African-American Prostate Cancer Reveals Loss-of-Function <i>ERF</i> Mutations. Cancer Discovery, 2017, 7, 973-983.	9.4	94
81	The Mutational Landscape of Circulating Tumor Cells in Multiple Myeloma. Cell Reports, 2017, 19, 218-224.	6.4	92
82	Genomic profiling of ER $<$ sup $>+sup> breast cancers after short-term estrogen suppression reveals alterations associated with endocrine resistance. Science Translational Medicine, 2017, 9, .$	12.4	91
83	Characterization of Clinical Cases of Collecting Duct Carcinoma of the Kidney Assessed by Comprehensive Genomic Profiling. European Urology, 2016, 70, 516-521.	1.9	90
84	Transcriptional mediators of treatment resistance in lethal prostate cancer. Nature Medicine, 2021, 27, 426-433.	30.7	90
85	Inherited DNA-Repair Defects in Colorectal Cancer. American Journal of Human Genetics, 2018, 102, 401-414.	6.2	89
86	The Clinical Activity of PD-1/PD-L1 Inhibitors in Metastatic Non–Clear Cell Renal Cell Carcinoma. Cancer Immunology Research, 2018, 6, 758-765.	3.4	89
87	Intrinsic Immunogenicity of Small Cell Lung Carcinoma Revealed by Its Cellular Plasticity. Cancer Discovery, 2021, 11, 1952-1969.	9.4	87
88	Effect of Eribulin With or Without Pembrolizumab on Progression-Free Survival for Patients With Hormone Receptor–Positive, <i>ERBB2</i> -Negative Metastatic Breast Cancer. JAMA Oncology, 2020, 6, 1598.	7.1	84
89	Integrative molecular characterization of sarcomatoid and rhabdoid renal cell carcinoma. Nature Communications, 2021, 12, 808.	12.8	84
90	Detection of circulating tumour DNA is associated with inferior outcomes in Ewing sarcoma and osteosarcoma: a report from the Children's Oncology Group. British Journal of Cancer, 2018, 119, 615-621.	6.4	83

#	Article	IF	Citations
91	Characterizing genomic alterations in cancer by complementary functional associations. Nature Biotechnology, 2016, 34, 539-546.	17.5	78
92	CSER and eMERGE: current and potential state of the display of genetic information in the electronic health record. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1231-1242.	4.4	73
93	<i>ATM</i> Loss Confers Greater Sensitivity to ATR Inhibition Than PARP Inhibition in Prostate Cancer. Cancer Research, 2020, 80, 2094-2100.	0.9	71
94	Early loss of mitochondrial complex I and rewiring of glutathione metabolism in renal oncocytoma. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6283-E6290.	7.1	70
95	Racial and Ethnic Disparities Among Participants in Precision Oncology Clinical Studies. JAMA Network Open, 2021, 4, e2133205.	5.9	70
96	Evolution of delayed resistance to immunotherapy in a melanoma responder. Nature Medicine, 2021, 27, 985-992.	30.7	67
97	Phase 2 trial of sunitinib and gemcitabine in patients with sarcomatoid and/or poorâ€risk metastatic renal cell carcinoma. Cancer, 2015, 121, 3435-3443.	4.1	64
98	Integrative Molecular Characterization of Resistance to Neoadjuvant Chemoradiation in Rectal Cancer. Clinical Cancer Research, 2019, 25, 5561-5571.	7.0	64
99	Tumor Mutational Load and Immune Parameters across Metastatic Renal Cell Carcinoma Risk Groups. Cancer Immunology Research, 2016, 4, 820-822.	3.4	63
100	A survey of informatics approaches to whole-exome and whole-genome clinical reporting in the electronic health record. Genetics in Medicine, 2013, 15, 824-832.	2.4	62
101	Convergent Therapeutic Strategies to Overcome the Heterogeneity of Acquired Resistance in <i>BRAF</i> V600E Colorectal Cancer. Cancer Discovery, 2018, 8, 417-427.	9.4	61
102	Long-term Benefit of PD-L1 Blockade in Lung Cancer Associated with <i>JAK3</i> Activation. Cancer Immunology Research, 2015, 3, 855-863.	3.4	60
103	Intrinsic Resistance to Immune Checkpoint Blockade in a Mismatch Repair–Deficient Colorectal Cancer. Cancer Immunology Research, 2019, 7, 1230-1236.	3.4	59
104	A model combining clinical and genomic factors to predict response to PD-1/PD-L1 blockade in advanced urothelial carcinoma. British Journal of Cancer, 2020, 122, 555-563.	6.4	59
105	Subtype heterogeneity and epigenetic convergence in neuroendocrine prostate cancer. Nature Communications, 2021, 12, 5775.	12.8	59
106	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.	3.0	58
107	Neoadjuvant-Intensive Androgen Deprivation Therapy Selects for Prostate Tumor Foci with Diverse Subclonal Oncogenic Alterations. Cancer Research, 2018, 78, 4716-4730.	0.9	56
108	Concurrent TP53 Mutations Facilitate Resistance Evolution in EGFR-Mutant Lung Adenocarcinoma. Journal of Thoracic Oncology, 2022, 17, 779-792.	1.1	50

#	Article	IF	CITATIONS
109	Genomic Predictors of Good Outcome, Recurrence, or Progression in High-Grade T1 Non–Muscle-Invasive Bladder Cancer. Cancer Research, 2020, 80, 4476-4486.	0.9	49
110	Inactivation of <i>Fbxw7</i> Impairs dsRNA Sensing and Confers Resistance to PD-1 Blockade. Cancer Discovery, 2020, 10, 1296-1311.	9.4	49
111	Mammalian SWI/SNF Complex Genomic Alterations and Immune Checkpoint Blockade in Solid Tumors. Cancer Immunology Research, 2020, 8, 1075-1084.	3.4	47
112	PLZF, a Tumor Suppressor Genetically Lost in Metastatic Castration-Resistant Prostate Cancer, Is a Mediator of Resistance to Androgen Deprivation Therapy. Cancer Research, 2015, 75, 1944-1948.	0.9	46
113	Assigning clinical meaning to somatic and germ-line whole-exome sequencing data in a prospective cancer precision medicine study. Genetics in Medicine, 2017, 19, 787-795.	2.4	46
114	CREB5 Promotes Resistance to Androgen-Receptor Antagonists and Androgen Deprivation in Prostate Cancer. Cell Reports, 2019, 29, 2355-2370.e6.	6.4	45
115	Accelerating precision medicine in metastatic prostate cancer. Nature Cancer, 2020, 1, 1041-1053.	13.2	45
116	Phase II study of tivantinib (ARQ 197) in patients with metastatic triple-negative breast cancer. Investigational New Drugs, 2015, 33, 1108-1114.	2.6	44
117	Genomic Correlate of Exceptional Erlotinib Response in Head and Neck Squamous Cell Carcinoma. JAMA Oncology, 2015, 1, 238.	7.1	44
118	Genomic Evolution after Chemoradiotherapy in Anal Squamous Cell Carcinoma. Clinical Cancer Research, 2017, 23, 3214-3222.	7.0	44
119	Prevalence of pathogenic germline cancer risk variants in high-risk urothelial carcinoma. Genetics in Medicine, 2020, 22, 709-718.	2.4	44
120	Association of Inherited Pathogenic Variants in Checkpoint Kinase 2 (<i>CHEK2</i>) With Susceptibility to Testicular Germ Cell Tumors. JAMA Oncology, 2019, 5, 514.	7.1	43
121	Transcriptional profiling of primary prostate tumor in metastatic hormone-sensitive prostate cancer and association with clinical outcomes: correlative analysis of the E3805 CHAARTED trial. Annals of Oncology, 2021, 32, 1157-1166.	1.2	43
122	Discovery and Features of an Alkylating Signature in Colorectal Cancer. Cancer Discovery, 2021, 11, 2446-2455.	9.4	42
123	Decomposing Oncogenic Transcriptional Signatures to Generate Maps of Divergent Cellular States. Cell Systems, 2017, 5, 105-118.e9.	6.2	40
124	Inherited TP53 Variants and Risk of Prostate Cancer. European Urology, 2022, 81, 243-250.	1.9	40
125	Integrative clinical and molecular characterization of translocation renal cell carcinoma. Cell Reports, 2022, 38, 110190.	6.4	40
126	CoMut: visualizing integrated molecular information with comutation plots. Bioinformatics, 2020, 36, 4348-4349.	4.1	39

#	Article	IF	Citations
127	Functional Precision Medicine Identifies New Therapeutic Candidates for Medulloblastoma. Cancer Research, 2020, 80, 5393-5407.	0.9	38
128	Natural Language Processing to Ascertain Cancer Outcomes From Medical Oncologist Notes. JCO Clinical Cancer Informatics, 2020, 4, 680-690.	2.1	37
129	Whole-Exome Sequencing in Two Extreme Phenotypes of Response to VEGF-Targeted Therapies in Patients With Metastatic Clear Cell Renal Cell Carcinoma. Journal of the National Comprehensive Cancer Network: JNCCN, 2016, 14, 820-824.	4.9	36
130	Integrated molecular drivers coordinate biological and clinical states in melanoma. Nature Genetics, 2020, 52, 1373-1383.	21.4	36
131	Germline Features Associated with Immune Infiltration in Solid Tumors. Cell Reports, 2020, 30, 2900-2908.e4.	6.4	35
132	Systematic genomic and translational efficiency studies of uveal melanoma. PLoS ONE, 2017, 12, e0178189.	2.5	34
133	Detection of Pathogenic Variants With Germline Genetic Testing Using Deep Learning vs Standard Methods in Patients With Prostate Cancer and Melanoma. JAMA - Journal of the American Medical Association, 2020, 324, 1957.	7.4	33
134	Genome-wide analysis of somatic noncoding mutation patterns in cancer. Science, 2022, 376, eabg5601.	12.6	33
135	Successful whole-exome sequencing from a prostate cancer bone metastasis biopsy. Prostate Cancer and Prostatic Diseases, 2014, 17, 23-27.	3.9	30
136	Summary and Recommendations from the National Cancer Institute's Clinical Trials Planning Meeting on Novel Therapeutics for Non-Muscle Invasive Bladder Cancer. Bladder Cancer, 2016, 2, 165-202.	0.4	30
137	Clinical Efficacy and Molecular Response Correlates of the WEE1 Inhibitor Adavosertib Combined with Cisplatin in Patients with Metastatic Triple-Negative Breast Cancer. Clinical Cancer Research, 2021, 27, 983-991.	7.0	29
138	Everolimus and pazopanib (E/P) benefit genomically selected patients with metastatic urothelial carcinoma. British Journal of Cancer, 2018, 119, 707-712.	6.4	28
139	Genomic determinants of cancer immunotherapy. Current Opinion in Immunology, 2016, 41, 32-38.	5.5	27
140	Targeting the innate immunoreceptor RIG-I overcomes melanoma-intrinsic resistance to T cell immunotherapy. Journal of Clinical Investigation, 2020, 130, 4266-4281.	8.2	27
141	Implications of Selection Bias Due to Delayed Study Entry in Clinical Genomic Studies. JAMA Oncology, 2022, 8, 287.	7.1	27
142	A Systematic Framework to Rapidly Obtain Data on Patients with Cancer and COVID-19: CCC19 Governance, Protocol, and Quality Assurance. Cancer Cell, 2020, 38, 761-766.	16.8	26
143	Novel secondary hormonal therapy in advanced prostate cancer: an update. Current Opinion in Urology, 2009, 19, 315-321.	1.8	25
144	Genomic Heterogeneity and Exceptional Response to Dual Pathway Inhibition in Anaplastic Thyroid Cancer. Clinical Cancer Research, 2017, 23, 2367-2373.	7.0	24

#	Article	IF	Citations
145	The role of site-specific therapy for cancers of unknown of primary: A meta-analysis. European Journal of Cancer, 2020, 127, 118-122.	2.8	24
146	Molecular features of exceptional response to neoadjuvant anti-androgen therapy in high-risk localized prostate cancer. Cell Reports, 2021, 36, 109665.	6.4	24
147	Precision medicine for advanced prostate cancer. Current Opinion in Urology, 2016, 26, 231-239.	1.8	23
148	Exome sequencing reveals recurrent germ line variants in patients with familial Waldenström macroglobulinemia. Blood, 2016, 127, 2598-2606.	1.4	22
149	CD38 in Advanced Prostate Cancers. European Urology, 2021, 79, 736-746.	1.9	21
150	FiTAc-seq: fixed-tissue ChIP-seq for H3K27ac profiling and super-enhancer analysis of FFPE tissues. Nature Protocols, 2020, 15, 2503-2518.	12.0	20
151	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.	5.9	20
152	Nivolumab in combination with cabozantinib for metastatic triple-negative breast cancer: a phase II and biomarker study. Npj Breast Cancer, 2021, 7, 110.	5.2	20
153	Off-Label Use of Rituximab in a Multipayer Insurance System. Journal of Oncology Practice, 2011, 7, 76-79.	2.5	19
154	Identification of a Synthetic Lethal Relationship between Nucleotide Excision Repair Deficiency and Irofulven Sensitivity in Urothelial Cancer. Clinical Cancer Research, 2021, 27, 2011-2022.	7.0	19
155	Molecular correlates of response to eribulin and pembrolizumab in hormone receptor-positive metastatic breast cancer. Nature Communications, 2021, 12, 5563.	12.8	19
156	Integrating molecular profiles into clinical frameworks through the Molecular Oncology Almanac to prospectively guide precision oncology. Nature Cancer, 2021, 2, 1102-1112.	13.2	19
157	Germline predisposition to pediatric Ewing sarcoma is characterized by inherited pathogenic variants in DNA damage repair genes. American Journal of Human Genetics, 2022, 109, 1026-1037.	6.2	19
158	A comparative assessment of clinical whole exome and transcriptome profiling across sequencing centers: implications for precision cancer medicine. Oncotarget, 2016, 7, 52888-52899.	1.8	18
159	Phase II Multicenter Study of Enzalutamide in Metastatic Castration-Resistant Prostate Cancer to Identify Mechanisms Driving Resistance. Clinical Cancer Research, 2021, 27, 3610-3619.	7.0	17
160	RAF1 amplification drives a subset of bladder tumors and confers sensitivity to MAPK-directed therapeutics. Journal of Clinical Investigation, 2021, 131, .	8.2	17
161	Artificial intelligence-aided clinical annotation of a large multi-cancer genomic dataset. Nature Communications, 2021, 12, 7304.	12.8	17
162	A phase 1 study of buparlisib and bevacizumab in patients with metastatic renal cell carcinoma progressing on vascular endothelial growth factorâ€targeted therapies. Cancer, 2016, 122, 2389-2398.	4.1	16

#	Article	IF	CITATIONS
163	Somatic Copy Number Abnormalities and Mutations in PI3K/AKT/mTOR Pathway Have Prognostic Significance for Overall Survival in Platinum Treated Locally Advanced or Metastatic Urothelial Tumors. PLoS ONE, 2015, 10, e0124711.	2.5	16
164	Tumor Mutations Across Racial Groups in a Real-World Data Registry. JCO Precision Oncology, 2021, 5, 1654-1658.	3.0	16
165	Molecular profiling identifies targeted therapy opportunities in pediatric solid cancer. Nature Medicine, 2022, 28, 1581-1589.	30.7	16
166	Genetic Effect of Chemotherapy Exposure in Children of Testicular Cancer Survivors. Clinical Cancer Research, 2016, 22, 2183-2189.	7.0	15
167	The fuzzy world of precision medicine: deliberations of a precision medicine tumor board. Personalized Medicine, 2017, 14, 37-50.	1.5	15
168	Impact of Pathogenic Germline DNA Damage Repair alterations on Response to Intense Neoadjuvant Androgen Deprivation Therapy in High-risk Localized Prostate Cancer. European Urology, 2021, 80, 295-303.	1.9	15
169	Autocrine Canonical Wnt Signaling Primes Noncanonical Signaling through ROR1 in Metastatic Castration-Resistant Prostate Cancer. Cancer Research, 2022, 82, 1518-1533.	0.9	15
170	Genomic attributes of homology-directed DNA repair deficiency in metastatic prostate cancer. JCI Insight, 2021, 6, .	5.0	15
171	Interactive or static reports to guide clinical interpretation of cancer genomics. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 458-464.	4.4	14
172	Genomic Evolutionary Patterns of Leiomyosarcoma and Liposarcoma. Clinical Cancer Research, 2019, 25, 5135-5142.	7.0	14
173	A phase 2 trial of buparlisib in patients with platinumâ€resistant metastatic urothelial carcinoma. Cancer, 2020, 126, 4532-4544.	4.1	14
174	Genomic Resistance Patterns to Second-Generation Androgen Blockade in Paired Tumor Biopsies of Metastatic Castration-Resistant Prostate Cancer. JCO Precision Oncology, 2017, 1, 1-11.	3.0	13
175	Phase I Trial of a Tablet Formulation of Pilaralisib, a Panâ€Class I PI3K Inhibitor, in Patients with Advanced Solid Tumors. Oncologist, 2018, 23, 401.	3.7	13
176	Predicting immunotherapy response through genomics. Current Opinion in Genetics and Development, 2021, 66, 1-9.	3.3	12
177	Genomic Features of Muscle-invasive Bladder Cancer Arising After Prostate Radiotherapy. European Urology, 2022, 81, 466-473.	1.9	12
178	Insights into Immune Escape During Tumor Evolution and Response to Immunotherapy Using a Rat Model of Breast Cancer. Cancer Immunology Research, 2022, 10, 680-697.	3.4	12
179	Toward Molecularly Driven Precision Medicine in Lung Adenocarcinoma. Cancer Discovery, 2017, 7, 555-557.	9.4	11
180	Gene Fusions Create Partner and Collateral Dependencies Essential to Cancer Cell Survival. Cancer Research, 2021, 81, 3971-3984.	0.9	11

#	Article	IF	Citations
181	Multidimensional Molecular Profiling of Metastatic Triple-Negative Breast Cancer and Immune Checkpoint Inhibitor Benefit. JCO Precision Oncology, 2022, , .	3.0	11
182	Engaging Patients in Precision Oncology: Development and Usability of a Web-Based Patient-Facing Genomic Sequencing Report. JCO Precision Oncology, 2020, 4, 307-318.	3.0	10
183	CREB5 reprograms FOXA1 nuclear interactions to promote resistance to androgen receptor-targeting therapies. ELife, 2022, 11 , .	6.0	10
184	Germ Cell Tumor Molecular Heterogeneity Revealed Through Analysis of Primary and Metastasis Pairs. JCO Precision Oncology, 2020, 4, 1307-1320.	3.0	9
185	Integrated genomic characterization of oral carcinomas in post-hematopoietic stem cell transplantation survivors. Oral Oncology, 2018, 81, 1-9.	1.5	8
186	Whole-Exome Sequencing and Targeted Deep Sequencing of cfDNA Enables a Comprehensive Mutational Profiling of Multiple Myeloma. Blood, 2016, 128, 197-197.	1.4	8
187	Delivering on the promise of precision cancer medicine. Genome Medicine, 2016, 8, 110.	8.2	7
188	Cancer Moonshot Immuno-Oncology Translational Network (IOTN): accelerating the clinical translation of basic discoveries for improving immunotherapy and immunoprevention of cancer., 2020, 8, e000796.		7
189	Dissecting the immunogenomic biology of cancer for biomarker development. Nature Reviews Clinical Oncology, 2021, 18, 133-134.	27.6	7
190	Moving Toward Personalized Medicine in Castration-Resistant Prostate Cancer. Urologic Clinics of North America, 2012, 39, 483-490.	1.8	6
191	The Potential and Challenges of Expanded Germline Testing in Clinical Oncology. JAMA - Journal of the American Medical Association, 2017, 318, 801.	7.4	6
192	The Role of Clonal Hematopoiesis of Indeterminate Potential (CHIP) in Multiple Myeloma: Immunomodulator Maintenance Post Autologous Stem Cell Transplant (ASCT) Predicts Better Outcome. Blood, 2018, 132, 749-749.	1.4	6
193	A Process Framework for Ethically Deploying Artificial Intelligence in Oncology. Journal of Clinical Oncology, 2022, 40, 3907-3911.	1.6	6
194	Phase 2 trial of sunitinib and gemcitabine in patients with sarcomatoid and/or poor-risk metastatic renal cell carcinoma. Michaelson MD, McKay RR, Werner L, Atkins MB, Van Allen EM, Olivier KM, Song J, Signoretti S, McDermott DF, Choueiri TK.Cancer. 2015 Oct 1;121(19):3435-43. [Epub 2015 Jun 8]. doi: 10.1002/cncr.29503 Urologic Oncology: Seminars and Original Investigations, 2017, 35, 117-118.	1.6	5
195	Tumor Evolution: A Problem of Histocompatibility. Cell, 2017, 171, 1252-1253.	28.9	5
196	Evaluating the molecular diagnostic yield of joint genotyping–based approach for detecting rare germline pathogenic and putative loss-of-function variants. Genetics in Medicine, 2021, 23, 918-926.	2.4	5
197	Re: Floris H. Groenendijk, Jeroen de Jong, Elisabeth E. Fransen van de Putte, et al. ERBB2 Mutations Characterize a Subgroup of Muscle-invasive Bladder Cancers with Excellent Response to Neoadjuvant Chemotherapy. Eur Urol. In press. http://dx.doi.org/10.1016/j.eururo.2015.01.014. European Urology, 2015, 68. e31-e32.	1.9	4
198	Clinical Inflection Point Detection on the Basis of EHR Data to Identify Clinical Trial–Ready Patients With Cancer. JCO Clinical Cancer Informatics, 2021, 5, 622-630.	2.1	3

#	Article	IF	Citations
199	Enrichment of FGFR3-TACC3 Fusions in Patients With Bladder Cancer Who Are Young, Asian, or Have Never Smoked. JCO Precision Oncology, 2018, 2, 1-11.	3.0	2
200	Driver Mutation in Waldenstrom's Macroglobullinemia and Their Clonal Heterogeneity during Progression and Relapse. Blood, 2016, 128, 1092-1092.	1.4	2
201	OUP accepted manuscript. Oncologist, 2022, , .	3.7	2
202	A Role in Transition. Annals of Internal Medicine, 2009, 151, 427.	3.9	1
203	One Day Later. Journal of General Internal Medicine, 2010, 25, 882-883.	2.6	1
204	Genomic profiling of smoldering multiple myeloma identifies patients at a high risk of disease progression Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e5-e6.	0.4	1
205	Single-Cell RNA Sequencing Reveals Compromised Immune Microenvironment in Precursor Stages of Multiple Myeloma. Blood, 2018, 132, 2603-2603.	1.4	1
206	Towards a Better Understanding of Antibody-Drug Conjugates in Urothelial Carcinoma. European Urology Oncology, 2022, 5, 719-721.	5.4	1
207	Implementation of a prostate cancerâ€specific targeted sequencing panel for credentialing of patientâ€derived cell lines and genomic characterization of patient samples. Prostate, 2022, , .	2.3	1
208	Linking a Trio of Molecular Features in Clear-Cell Renal Cell Carcinoma. Cancer Immunology Research, 2022, , .	3.4	1
209	Paracentesis by Moonlight. JAMA - Journal of the American Medical Association, 2011, 305, 1635.	7.4	0
210	The Paradox of Positive Thinking. Journal of Clinical Oncology, 2011, 29, 2730-2731.	1.6	0
211	Finding the edge of the seat. Nature Medicine, 2019, 25, 1328-1328.	30.7	0
212	Single-cell RNA sequencing reveals compromised immune microenvironment in precursor stages of multiple myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e27.	0.4	0
213	Re: Russell E.N. Becker, Alexa R. Meyer, Aaron Brant, et al. Clinical Restaging and Tumor Sequencing are Inaccurate Indicators of Response to Neoadjuvant Chemotherapy for Muscle-invasive Bladder Cancer. Eur Urol. In press. https://doi.org/10.1016/j.eururo.2020.07.016. European Urology, 2021, 79, e56-e57.	1.9	0
214	Whole Exome Sequencing and Targeted Sequencing Reveal the Heterogeneity of Genomic Evolution and Mutational Profile in Smoldering Multiple Myeloma. Blood, 2016, 128, 237-237.	1.4	0
215	Integrated Analysis of Germ Cell Tumors. Methods in Molecular Biology, 2021, 2195, 181-187.	0.9	0