Xuhong Cao

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Integrative Clinical Genomics of Advanced Prostate Cancer. Cell, 2015, 161, 1215-1228.	13.5	2,660
2	The landscape of long noncoding RNAs in the human transcriptome. Nature Genetics, 2015, 47, 199-208.	9.4	2,410
3	The Landscape of Circular RNA in Cancer. Cell, 2019, 176, 869-881.e13.	13.5	1,095
4	Therapeutic targeting of BET bromodomain proteins in castration-resistant prostate cancer. Nature, 2014, 510, 278-282.	13.7	811
5	Integrative clinical genomics of metastatic cancer. Nature, 2017, 548, 297-303.	13.7	685
6	Liver metastasis restrains immunotherapy efficacy via macrophage-mediated T cell elimination. Nature Medicine, 2021, 27, 152-164.	15.2	451
7	Inactivation of CDK12 Delineates a Distinct Immunogenic Class of Advanced Prostate Cancer. Cell, 2018, 173, 1770-1782.e14.	13.5	400
8	Integrative Clinical Sequencing in the Management of Refractory or Relapsed Cancer in Youth. JAMA - Journal of the American Medical Association, 2015, 314, 913.	3.8	333
9	The Distinctive Mutational Spectra of Polyomavirus-Negative Merkel Cell Carcinoma. Cancer Research, 2015, 75, 3720-3727.	0.4	276
10	Oncogenic Role of THOR, a Conserved Cancer/Testis Long Non-coding RNA. Cell, 2017, 171, 1559-1572.e20.	13.5	200
11	The IncRNA landscape of breast cancer reveals a role for DSCAM-AS1 in breast cancer progression. Nature Communications, 2016, 7, 12791.	5.8	196
12	Analysis of the androgen receptor–regulated IncRNA landscape identifies a role for ARLNC1 in prostate cancer progression. Nature Genetics, 2018, 50, 814-824.	9.4	196
13	Distinct structural classes of activating FOXA1 alterations in advanced prostate cancer. Nature, 2019, 571, 413-418.	13.7	192
14	Targeting the MLL complex in castration-resistant prostate cancer. Nature Medicine, 2015, 21, 344-352.	15.2	165
15	The landscape of antisense gene expression in human cancers. Genome Research, 2015, 25, 1068-1079.	2.4	150
16	Development of a RNA-Seq Based Prognostic Signature in Lung Adenocarcinoma. Journal of the National Cancer Institute, 2017, 109, djw200.	3.0	150
17	Targeting transcriptional regulation of SARS-CoV-2 entry factors <i>ACE2</i> and <i>TMPRSS2</i> . Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	142
18	The use of exome capture RNA-seq for highly degraded RNA with application to clinical cancer sequencing. Genome Research, 2015, 25, 1372-1381.	2.4	139

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19	Single-cell analyses of renal cell cancers reveal insights into tumor microenvironment, cell of origin, and therapy response. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	136
20	The central role of EED in the orchestration of polycomb group complexes. Nature Communications, 2014, 5, 3127.	5.8	130
21	Transcriptome meta-analysis of lung cancer reveals recurrent aberrations in NRG1 and Hippo pathway genes. Nature Communications, 2014, 5, 5893.	5.8	121
22	The IncRNA <i>PCAT29</i> Inhibits Oncogenic Phenotypes in Prostate Cancer. Molecular Cancer Research, 2014, 12, 1081-1087.	1.5	119
23	Targeting SWI/SNF ATPases in enhancer-addicted prostate cancer. Nature, 2022, 601, 434-439.	13.7	110
24	Androgen receptor degraders overcome common resistance mechanisms developed during prostate cancer treatment. Neoplasia, 2020, 22, 111-119.	2.3	101
25	Prostate cancer cell–stromal cell crosstalk via FGFR1 mediates antitumor activity of dovitinib in bone metastases. Science Translational Medicine, 2014, 6, 252ra122.	5.8	86
26	Somatic Bi-allelic Loss of TSC Genes in Eosinophilic Solid and Cystic Renal Cell Carcinoma. European Urology, 2018, 74, 483-486.	0.9	86
27	Development of Peptidomimetic Inhibitors of the ERG Gene Fusion Product in Prostate Cancer. Cancer Cell, 2017, 31, 532-548.e7.	7.7	85
28	Targeting the MYCN–PARP–DNA Damage Response Pathway in Neuroendocrine Prostate Cancer. Clinical Cancer Research, 2018, 24, 696-707.	3.2	80
29	Inflammation-Induced Oxidative Stress Mediates Gene Fusion Formation in Prostate Cancer. Cell Reports, 2016, 17, 2620-2631.	2.9	68
30	Assessment of Clinical Benefit of Integrative Genomic Profiling in Advanced Solid Tumors. JAMA Oncology, 2021, 7, 525-533.	3.4	65
31	Next-generation RNA Sequencing–based Biomarker Characterization of Chromophobe Renal Cell Carcinoma and Related Oncocytic Neoplasms. European Urology, 2020, 78, 63-74.	0.9	57
32	<i>De novo</i> dominant <i>ASXL3</i> mutations alter H2A deubiquitination and transcription in Bainbridge–Ropers syndrome. Human Molecular Genetics, 2016, 25, 597-608.	1.4	56
33	Identification and Validation of PCAT14 as Prognostic Biomarker in Prostate Cancer. Neoplasia, 2016, 18, 489-499.	2.3	55
34	Autophagy inhibition by targeting PIKfyve potentiates response to immune checkpoint blockade in prostate cancer. Nature Cancer, 2021, 2, 978-993.	5.7	52
35	Expression of PDL1 (B7-H1) Before and After Neoadjuvant Chemotherapy in Urothelial Carcinoma. European Urology Focus, 2016, 1, 265-268.	1.6	45
36	Clinical validation of the Tempus xO assay. Oncotarget, 2018, 9, 25826-25832.	0.8	43

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37	KRAS Engages AGO2 to Enhance Cellular Transformation. Cell Reports, 2016, 14, 1448-1461.	2.9	41
38	Age and Gender Associations of Virus Positivity in Merkel Cell Carcinoma Characterized Using a Novel RNA <i>In Situ</i> Hybridization Assay. Clinical Cancer Research, 2017, 23, 5622-5630.	3.2	31
39	An essential role for Argonaute 2 in EGFR-KRAS signaling in pancreatic cancer development. Nature Communications, 2020, 11, 2817.	5.8	29
40	Functional and Mechanistic Interrogation of BET Bromodomain Degraders for the Treatment of Metastatic Castration-resistant Prostate Cancer. Clinical Cancer Research, 2019, 25, 4038-4048.	3.2	26
41	Mechanistic Support for Combined MET and AR Blockade in Castration-Resistant Prostate Cancer. Neoplasia, 2016, 18, 1-9.	2.3	25
42	MiPanda: A Resource for Analyzing and Visualizing Next-Generation Sequencing Transcriptomics Data. Neoplasia, 2018, 20, 1144-1149.	2.3	20
43	Next generation sequencing of extraskeletal myxoid chondrosarcoma. Oncotarget, 2017, 8, 21770-21777.	0.8	20
44	A comparative assessment of clinical whole exome and transcriptome profiling across sequencing centers: implications for precision cancer medicine. Oncotarget, 2016, 7, 52888-52899.	0.8	18
45	Multi-focal sequencing of a diffuse intrinsic pontine glioma establishes PTEN loss as an early event. Npj Precision Oncology, 2017, 1, 32.	2.3	17
46	Genetic diversity of NDUFV1-dependent mitochondrial complex I deficiency. European Journal of Human Genetics, 2018, 26, 1582-1587.	1.4	15
47	AGO2 promotes tumor progression in KRAS-driven mouse models of non–small cell lung cancer. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	14
48	Blood-brain barrier–adapted precision medicine therapy for pediatric brain tumors. Translational Research, 2017, 188, 27.e1-27.e14.	2.2	12
49	Clinically Integrated Sequencing Alters Therapy in Children and Young Adults With High-Risk Glial Brain Tumors. JCO Precision Oncology, 2018, 2, 1-34.	1.5	10
50	Characterizing the Therapeutic Potential of a Potent BET Degrader in Merkel Cell Carcinoma. Neoplasia, 2019, 21, 322-330.	2.3	10
51	Viral Status Predicts the Patterns of Genome Methylation and Decitabine Response in Merkel Cell Carcinoma. Journal of Investigative Dermatology, 2022, 142, 641-652.	0.3	9
52	Cancer Cell Intrinsic and Immunologic Phenotypes Determine Clinical Outcomes in Basal-like Breast Cancer. Clinical Cancer Research, 2021, 27, 3079-3093.	3.2	8
53	Tomlins et al. reply. Nature, 2009, 457, E2-E3.	13.7	6
54	Identification of clinically actionable pharmacogenetic variants during tumor genetic profiling in pediatric cancer patients Journal of Clinical Oncology, 2016, 34, 1583-1583.	0.8	2

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55	Comprehensive molecular profiling of pretreatment metastatic castration resistant prostate cancer (CRPC): Secondary data from NCI 9012, a randomized ETS fusion-stratified phase II trial Journal of Clinical Oncology, 2014, 32, e16038-e16038.	0.8	1
56	DIPG-38. ID1 EXPRESSION CORRELATES WITH H3F3A K27M MUTATION AND EXTRA-PONTINE INVASION IN DIPG. Neuro-Oncology, 2018, 20, i56-i56.	0.6	0
57	Genome-Wide Binding Studies of Acetyl-STAT3 Demonstrates a Novel Regulatory Pathway in Dendritic Cells. Blood, 2015, 126, 647-647.	0.6	0
58	DIPG-59. UPREGULATION OF PRENATAL PONTINE ID1 SIGNALING IN DIPG. Neuro-Oncology, 2020, 22, iii298-iii299.	0.6	0