Arul M Chinnaiyan

List of Publications by Year
in descending order

526 papers	110,073 citations	219 146 h-index	196 316 g-index
538 all docs	538 docs citations	538 times ranked	90509 citing authors

#	Article	IF	Citations
1	Recurrent Fusion of TMPRSS2 and ETS Transcription Factor Genes in Prostate Cancer. Science, 2005, 310, 644-648.	6.0	3,541
2	ONCOMINE: A Cancer Microarray Database and Integrated Data-Mining Platform. Neoplasia, 2004, 6, 1-6.	2.3	3,212
3	FLICE, A Novel FADD-Homologous ICE/CED-3â€"like Protease, Is Recruited to the CD95 (Fas/APO-1) Death-Inducing Signaling Complex. Cell, 1996, 85, 817-827.	13.5	2,944
4	Integrative Clinical Genomics of Advanced Prostate Cancer. Cell, 2015, 161, 1215-1228.	13.5	2,660
5	Inactivation of YAP oncoprotein by the Hippo pathway is involved in cell contact inhibition and tissue growth control. Genes and Development, 2007, 21, 2747-2761.	2.7	2,487
6	The polycomb group protein EZH2 is involved in progression of prostate cancer. Nature, 2002, 419, 624-629.	13.7	2,411
7	The landscape of long noncoding RNAs in the human transcriptome. Nature Genetics, 2015, 47, 199-208.	9.4	2,410
8	FADD, a novel death domain-containing protein, interacts with the death domain of fas and initiates apoptosis. Cell, 1995, 81, 505-512.	13.5	2,298
9	The mutational landscape of lethal castration-resistant prostate cancer. Nature, 2012, 487, 239-243.	13.7	2,128
10	Metabolomic profiles delineate potential role for sarcosine in prostate cancer progression. Nature, 2009, 457, 910-914.	13.7	1,944
11	TEAD mediates YAP-dependent gene induction and growth control. Genes and Development, 2008, 22, 1962-1971.	2.7	1,943
12	Oncomine 3.0: Genes, Pathways, and Networks in a Collection of 18,000 Cancer Gene Expression Profiles. Neoplasia, 2007, 9, 166-180.	2.3	1,847
13	DNA-Repair Defects and Olaparib in Metastatic Prostate Cancer. New England Journal of Medicine, 2015, 373, 1697-1708.	13.9	1,796
14	The Receptor for the Cytotoxic Ligand TRAIL. Science, 1997, 276, 111-113.	6.0	1,665
15	The Emergence of lncRNAs in Cancer Biology. Cancer Discovery, 2011, 1, 391-407.	7.7	1,612
16	Delineation of prognostic biomarkers in prostate cancer. Nature, 2001, 412, 822-826.	13.7	1,551
17	CD8+ T cells regulate tumour ferroptosis during cancer immunotherapy. Nature, 2019, 569, 270-274.	13.7	1,528
18	EZH2 is a marker of aggressive breast cancer and promotes neoplastic transformation of breast epithelial cells. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 11606-11611.	3.3	1,482

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19	Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. New England Journal of Medicine, 2016, 375, 443-453.	13.9	1,205
20	The Landscape of Circular RNA in Cancer. Cell, 2019, 176, 869-881.e13.	13.5	1,095
21	Genomic Loss of microRNA-101 Leads to Overexpression of Histone Methyltransferase EZH2 in Cancer. Science, 2008, 322, 1695-1699.	6.0	995
22	Development of Human Protein Reference Database as an Initial Platform for Approaching Systems Biology in Humans. Genome Research, 2003, 13, 2363-2371.	2.4	954
23	The Role of Non-coding RNAs in Oncology. Cell, 2019, 179, 1033-1055.	13.5	952
24	Transcriptome sequencing across a prostate cancer cohort identifies PCAT-1, an unannotated lincRNA implicated in disease progression. Nature Biotechnology, 2011, 29, 742-749.	9.4	950
25	Activating ESR1 mutations in hormone-resistant metastatic breast cancer. Nature Genetics, 2013, 45, 1446-1451.	9.4	925
26	Large-scale meta-analysis of cancer microarray data identifies common transcriptional profiles of neoplastic transformation and progression. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9309-9314.	3.3	874
27	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.	3.3	839
28	Integrative molecular concept modeling of prostate cancer progression. Nature Genetics, 2007, 39, 41-51.	9.4	837
29	Androgen-Independent Prostate Cancer Is a Heterogeneous Group of Diseases. Cancer Research, 2004, 64, 9209-9216.	0.4	816
30	Therapeutic targeting of BET bromodomain proteins in castration-resistant prostate cancer. Nature, 2014, 510, 278-282.	13.7	811
31	Androgen Receptor Regulates a Distinct Transcription Program in Androgen-Independent Prostate Cancer. Cell, 2009, 138, 245-256.	13.5	797
32	Transcriptome sequencing to detect gene fusions in cancer. Nature, 2009, 458, 97-101.	13.7	791
33	Distinct classes of chromosomal rearrangements create oncogenic ETS gene fusions in prostate cancer. Nature, 2007, 448, 595-599.	13.7	743
34	An Integrated Network of Androgen Receptor, Polycomb, and TMPRSS2-ERG Gene Fusions in Prostate Cancer Progression. Cancer Cell, 2010, 17, 443-454.	7.7	743
35	Integrative genomic and proteomic analysis of prostate cancer reveals signatures of metastatic progression. Cancer Cell, 2005, 8, 393-406.	7.7	731
36	Molecular Characterization of Neuroendocrine Prostate Cancer and Identification of New Drug Targets. Cancer Discovery, 2011, 1, 487-495.	7.7	725

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37	Integrative clinical genomics of metastatic cancer. Nature, 2017, 548, 297-303.	13.7	685
38	FADD/MORT1 Is a Common Mediator of CD95 (Fas/APO-1) and Tumor Necrosis Factor Receptor-induced Apoptosis. Journal of Biological Chemistry, 1996, 271, 4961-4965.	1.6	680
39	Identification of recurrent NAB2-STAT6 gene fusions in solitary fibrous tumor by integrative sequencing. Nature Genetics, 2013, 45, 180-185.	9.4	662
40	Signal Transduction by DR3, a Death Domain-Containing Receptor Related to TNFR-1 and CD95. Science, 1996, 274, 990-992.	6.0	625
41	The role of YAP transcription coactivator in regulating stem cell self-renewal and differentiation. Genes and Development, 2010, 24, 1106-1118.	2.7	621
42	Recurrent gene fusions in prostate cancer. Nature Reviews Cancer, 2008, 8, 497-511.	12.8	617
43	Identification of Targetable FGFR Gene Fusions in Diverse Cancers. Cancer Discovery, 2013, 3, 636-647.	7.7	614
44	Role of the TMPRSS2-ERG Gene Fusion in Prostate Cancer. Neoplasia, 2008, 10, 177-IN9.	2.3	608
45	The long noncoding RNA SChLAP1 promotes aggressive prostate cancer and antagonizes the SWI/SNF complex. Nature Genetics, 2013, 45, 1392-1398.	9.4	601
46	The long tail of oncogenic drivers in prostate cancer. Nature Genetics, 2018, 50, 645-651.	9.4	601
47	A Hierarchical Network of Transcription Factors Governs Androgen Receptor-Dependent Prostate Cancer Growth. Molecular Cell, 2007, 27, 380-392.	4.5	598
48	Autoantibody Signatures in Prostate Cancer. New England Journal of Medicine, 2005, 353, 1224-1235.	13.9	581
49	Radiotherapy and Immunotherapy Promote Tumoral Lipid Oxidation and Ferroptosis via Synergistic Repression of SLC7A11. Cancer Discovery, 2019, 9, 1673-1685.	7.7	566
50	Î±-Methylacyl Coenzyme A Racemase as a Tissue Biomarker for Prostate Cancer. JAMA - Journal of the American Medical Association, 2002, 287, 1662.	3.8	565
51	Molecular Ordering of the Cell Death Pathway. Journal of Biological Chemistry, 1996, 271, 4573-4576.	1.6	536
52	Personalized Oncology Through Integrative High-Throughput Sequencing: A Pilot Study. Science Translational Medicine, 2011, 3, 111ra121.	5.8	531
53	Meta-analysis of microarrays: interstudy validation of gene expression profiles reveals pathway dysregulation in prostate cancer. Cancer Research, 2002, 62, 4427-33.	0.4	511
54	TMPRSS2:ERG Fusion-Associated Deletions Provide Insight into the Heterogeneity of Prostate Cancer. Cancer Research, 2006, 66, 8337-8341.	0.4	475

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55	Genomic Hallmarks and Structural Variation in Metastatic Prostate Cancer. Cell, 2018, 174, 758-769.e9.	13.5	459
56	Liver metastasis restrains immunotherapy efficacy via macrophage-mediated T cell elimination. Nature Medicine, 2021, 27, 152-164.	15.2	451
57	Rearrangements of the RAF kinase pathway in prostate cancer, gastric cancer and melanoma. Nature Medicine, 2010, 16, 793-798.	15.2	436
58	TMPRSS2:ETV4 Gene Fusions Define a Third Molecular Subtype of Prostate Cancer. Cancer Research, 2006, 66, 3396-3400.	0.4	432
59	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	13.5	430
60	Host expression of PD-L1 determines efficacy of PD-L1 pathway blockadeâ€“mediated tumor regression. Journal of Clinical Investigation, 2018, 128, 805-815.	3.9	423
61	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. Cell, 2020, 182, 200-225.e35.	13.5	410
62	Expression of CXCR4 and CXCL12 (SDF-1) in human prostate cancers (PCa) in vivo. Journal of Cellular Biochemistry, 2003, 89, 462-473.	1.2	405
63	Inactivation of CDK12 Delineates a Distinct Immunogenic Class of Advanced Prostate Cancer. Cell, 2018, 173, 1770-1782.e14.	13.5	400
64	New class of microRNA targets containing simultaneous 5â€²-UTR and 3â€²-UTR interaction sites. Genome Research, 2009, 19, 1175-1183.	2.4	398
65	Mechanistic Rationale for Inhibition of Poly(ADP-Ribose) Polymerase in ETS Gene Fusion-Positive Prostate Cancer. Cancer Cell, 2011, 19, 664-678.	7.7	397
66	TMPRSS2-ERG Fusion Prostate Cancer: An Early Molecular Event Associated With Invasion. American Journal of Surgical Pathology, 2007, 31, 882-888.	2.1	394
67	Probabilistic model of the human protein-protein interaction network. Nature Biotechnology, 2005, 23, 951-959.	9.4	380
68	Beyond PSA: The Next Generation of Prostate Cancer Biomarkers. Science Translational Medicine, 2012, 4, 127rv3.	5.8	378
69	A First-Generation Multiplex Biomarker Analysis of Urine for the Early Detection of Prostate Cancer. Cancer Research, 2008, 68, 645-649.	0.4	369
70	Mechanisms of Enhanced Radiation Response following Epidermal Growth Factor Receptor Signaling Inhibition by Erlotinib (Tarceva). Cancer Research, 2005, 65, 3328-3335.	0.4	359
71	The cell-death machine. Current Biology, 1996, 6, 555-562.	1.8	358
72	Dual Roles of PARP-1 Promote Cancer Growth and Progression. Cancer Discovery, 2012, 2, 1134-1149.	7.7	354

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73	The bright side of dark matter: lncRNAs in cancer. Journal of Clinical Investigation, 2016, 126, 2775-2782.	3.9	353
74	Circulating Cell-Free DNA to Guide Prostate Cancer Treatment with PARP Inhibition. Cancer Discovery, 2017, 7, 1006-1017.	7.7	341
75	Induced Chromosomal Proximity and Gene Fusions in Prostate Cancer. Science, 2009, 326, 1230-1230.	6.0	334
76	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
77	ETS Gene Fusions in Prostate Cancer: From Discovery to Daily Clinical Practice. European Urology, 2009, 56, 275-286.	0.9	332
78	Urine <i>TMPRSS2:ERG</i> Fusion Transcript Stratifies Prostate Cancer Risk in Men with Elevated Serum PSA. Science Translational Medicine, 2011, 3, 94ra72.	5.8	313
79	JAGGED1 Expression Is Associated with Prostate Cancer Metastasis and Recurrence. Cancer Research, 2004, 64, 6854-6857.	0.4	310
80	Cancer mediates effector T cell dysfunction by targeting microRNAs and EZH2 via glycolysis restriction. Nature Immunology, 2016, 17, 95-103.	7.0	310
81	A Polycomb Repression Signature in Metastatic Prostate Cancer Predicts Cancer Outcome. Cancer Research, 2007, 67, 10657-10663.	0.4	308
82	Antibody-Based Detection of ERG Rearrangement-Positive Prostate Cancer. Neoplasia, 2010, 12, 590-IN21.	2.3	305
83	Urine TMPRSS2:ERG Plus PCA3 for Individualized Prostate Cancer Risk Assessment. European Urology, 2016, 70, 45-53.	0.9	304
84	The Role of SPINK1 in ETS Rearrangement-Negative Prostate Cancers. Cancer Cell, 2008, 13, 519-528.	7.7	303
85	Chimeric transcript discovery by paired-end transcriptome sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12353-12358.	3.3	302
86	Functionally recurrent rearrangements of the MAST kinase and Notch gene families in breast cancer. Nature Medicine, 2011, 17, 1646-1651.	15.2	301
87	Estrogen-Dependent Signaling in a Molecularly Distinct Subclass of Aggressive Prostate Cancer. Journal of the National Cancer Institute, 2008, 100, 815-825.	3.0	286
88	Comprehensive assessment of TMPRSS2 and ETS family gene aberrations in clinically localized prostate cancer. Modern Pathology, 2007, 20, 538-544.	2.9	281
89	Cancer SLC43A2 alters T cell methionine metabolism and histone methylation. Nature, 2020, 585, 277-282.	13.7	280
90	The Distinctive Mutational Spectra of Polyomavirus-Negative Merkel Cell Carcinoma. Cancer Research, 2015, 75, 3720-3727.	0.4	276

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91	Alpha-Methylacyl-CoA Racemase. American Journal of Surgical Pathology, 2002, 26, 926-931.	2.1	274
92	Ultraviolet Radiation-induced Apoptosis Is Mediated by Activation of CD-95 (Fas/APO-1). Journal of Biological Chemistry, 1997, 272, 25783-25786.	1.6	273
93	Identification of GATA3 as a Breast Cancer Prognostic Marker by Global Gene Expression Meta-analysis. Cancer Research, 2005, 65, 11259-11264.	0.4	272
94	Common Gene Rearrangements in Prostate Cancer. Journal of Clinical Oncology, 2011, 29, 3659-3668.	0.8	268
95	ICE-LAP3, a Novel Mammalian Homologue of the Caenorhabditis elegans Cell Death Protein Ced-3 Is Activated during Fas- and Tumor Necrosis Factor-induced Apoptosis. Journal of Biological Chemistry, 1996, 271, 1621-1625.	1.6	266
96	Expressed Pseudogenes in the Transcriptional Landscape of Human Cancers. Cell, 2012, 149, 1622-1634.	13.5	250
97	Multiplex Biomarker Approach for Determining Risk of Prostate-Specific Antigen-Defined Recurrence of Prostate Cancer. Journal of the National Cancer Institute, 2003, 95, 661-668.	3.0	249
98	Characterization of <i>TMPRSS2</i>-ETS Gene Aberrations in Androgen-Independent Metastatic Prostate Cancer. Cancer Research, 2008, 68, 3584-3590.	0.4	249
99	ICE-LAP6, a Novel Member of the ICE/Ced-3 Gene Family, Is Activated by the Cytotoxic T Cell Protease Granzyme B. Journal of Biological Chemistry, 1996, 271, 16720-16724.	1.6	246
100	PARP-1 Inhibition as a Targeted Strategy to Treat Ewing's Sarcoma. Cancer Research, 2012, 72, 1608-1613.	0.4	246
101	Characterization of TMPRSS2:ETV5 and SLC45A3:ETV5 Gene Fusions in Prostate Cancer. Cancer Research, 2008, 68, 73-80.	0.4	244
102	The Potential of MicroRNAs as Prostate Cancer Biomarkers. European Urology, 2016, 70, 312-322.	0.9	243
103	<i>PCAT-1</i>, a Long Noncoding RNA, Regulates BRCA2 and Controls Homologous Recombination in Cancer. Cancer Research, 2014, 74, 1651-1660.	0.4	237
104	A Role for FADD in T Cell Activation and Development. Immunity, 1998, 8, 439-449.	6.6	236
105	EML4-ALK Fusion Lung Cancer: A Rare Acquired Event. Neoplasia, 2008, 10, 298-302.	2.3	231
106	Activation of Mitogen-Activated Protein Kinase in Estrogen Receptor Î±â€"Positive Breast Cancer Cells In vitro Induces an In vivo Molecular Phenotype of Estrogen Receptor Î±â€"Negative Human Breast Tumors. Cancer Research, 2006, 66, 3903-3911.	0.4	226
107	RNA biomarkers associated with metastatic progression in prostate cancer: a multi-institutional high-throughput analysis of SChLAP1. Lancet Oncology, The, 2014, 15, 1469-1480.	5.1	226
108	Associations of Luminal and Basal Subtyping of Prostate Cancer With Prognosis and Response to Androgen Deprivation Therapy. JAMA Oncology, 2017, 3, 1663.	3.4	219

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109	Long Noncoding RNAs in Cancer: From Function to Translation. Trends in Cancer, 2015, 1, 93-109.	3.8	218
110	The Long Non-Coding RNA PCAT-1 Promotes Prostate Cancer Cell Proliferation through cMyc. Neoplasia, 2014, 16, 900-908.	2.3	216
111	Noninvasive Detection of TMPRSS2:ERG Fusion Transcripts in the Urine of Men with Prostate Cancer. Neoplasia, 2006, 8, 885-888.	2.3	212
112	Development and Validation of a Scalable Next-Generation Sequencing System for Assessing Relevant Somatic Variants in Solid Tumors. Neoplasia, 2015, 17, 385-399.	2.3	212
113	Fluorescence in situ hybridization study shows association of PTEN deletion with ERG rearrangement during prostate cancer progression. Modern Pathology, 2009, 22, 1083-1093.	2.9	209
114	Prevalence of <i>TMPRSS2-ERG</i> Fusion Prostate Cancer among Men Undergoing Prostate Biopsy in the United States. Clinical Cancer Research, 2009, 15, 4706-4711.	3.2	205
115	Integrative Genomics Analysis Reveals Silencing of Î²-Adrenergic Signaling by Polycomb in Prostate Cancer. Cancer Cell, 2007, 12, 419-431.	7.7	204
116	A Germline DNA Polymorphism Enhances Alternative Splicing of the KLF6 Tumor Suppressor Gene and Is Associated with Increased Prostate Cancer Risk. Cancer Research, 2005, 65, 1213-1222.	0.4	202
117	Cancer transcriptome profiling at the juncture of clinical translation. Nature Reviews Genetics, 2018, 19, 93-109.	7.7	202
118	Oncogenic Role of THOR, a Conserved Cancer/Testis Long Non-coding RNA. Cell, 2017, 171, 1559-1572.e20.	13.5	200
119	Nod1 acts as an intracellular receptor to stimulate chemokine production and neutrophil recruitment in vivo. Journal of Experimental Medicine, 2006, 203, 203-213.	4.2	199
120	The DNA methylation landscape of advanced prostate cancer. Nature Genetics, 2020, 52, 778-789.	9.4	198
121	Metastasis suppressor gene Raf kinase inhibitor protein (RKIP) is a novel prognostic marker in prostate cancer. Prostate, 2006, 66, 248-256.	1.2	197
122	Heterogeneity of <i>TMPRSS2</i> Gene Rearrangements in Multifocal Prostate Adenocarcinoma: Molecular Evidence for an Independent Group of Diseases. Cancer Research, 2007, 67, 7991-7995.	0.4	197
123	The lncRNA landscape of breast cancer reveals a role for DSCAM-AS1 in breast cancer progression. Nature Communications, 2016, 7, 12791.	5.8	196
124	Analysis of the androgen receptorâ€“regulated lncRNA landscape identifies a role for ARLNC1 in prostate cancer progression. Nature Genetics, 2018, 50, 814-824.	9.4	196
125	Distinct structural classes of activating FOXA1 alterations in advanced prostate cancer. Nature, 2019, 571, 413-418.	13.7	192
126	Coordinated Regulation of Polycomb Group Complexes through microRNAs in Cancer. Cancer Cell, 2011, 20, 187-199.	7.7	191

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127	Molecular Signatures of Sepsis. American Journal of Pathology, 2001, 159, 1199-1209.	1.9	190
128	Treatment-Dependent Androgen Receptor Mutations in Prostate Cancer Exploit Multiple Mechanisms to Evade Therapy. Cancer Research, 2009, 69, 4434-4442.	0.4	190
129	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. Cancer Cell, 2021, 39, 361-379.e16.	7.7	189
130	Role of CED-4 in the activation of CED-3. Nature, 1997, 388, 728-729.	13.7	185
131	The Apoptosome: Heart and Soul of the Cell Death Machine. Neoplasia, 1999, 1, 5-15.	2.3	182
132	Combining urinary detection of TMPRSS2:ERG and PCA3 with serum PSA to predict diagnosis of prostate cancer. Urologic Oncology: Seminars and Original Investigations, 2013, 31, 566-571.	0.8	181
133	Discovery of non-ETS gene fusions in human prostate cancer using next-generation RNA sequencing. Genome Research, 2011, 21, 56-67.	2.4	179
134	Comparative analysis of circulating tumor DNA stability In K3EDTA, Streck, and CellSave blood collection tubes. Clinical Biochemistry, 2016, 49, 1354-1360.	0.8	175
135	Whole genome scanning identifies genotypes associated with recurrence and metastasis in prostate tumors. Human Molecular Genetics, 2004, 13, 1303-1313.	1.4	171
136	Tumor cell-selective regulation of NOXA by c-MYC in response to proteasome inhibition. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19488-19493.	3.3	171
137	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	13.5	170
138	Targeting Androgen Receptor and DNA Repair in Metastatic Castration-Resistant Prostate Cancer: Results From NCI 9012. Journal of Clinical Oncology, 2018, 36, 991-999.	0.8	169
139	FIZZ1 Stimulation of Myofibroblast Differentiation. American Journal of Pathology, 2004, 164, 1315-1326.	1.9	168
140	A precision oncology approach to the pharmacological targeting of mechanistic dependencies in neuroendocrine tumors. Nature Genetics, 2018, 50, 979-989.	9.4	168
141	Deep sequencing reveals distinct patterns of DNA methylation in prostate cancer. Genome Research, 2011, 21, 1028-1041.	2.4	166
142	Targeting the MLL complex in castration-resistant prostate cancer. Nature Medicine, 2015, 21, 344-352.	15.2	165
143	Dysregulation of the Annexin Family Protein Family Is Associated with Prostate Cancer Progression. American Journal of Pathology, 2003, 162, 255-261.	1.9	162
144	Mining for regulatory programs in the cancer transcriptome. Nature Genetics, 2005, 37, 579-583.	9.4	158

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145	TACO produces robust multisample transcriptome assemblies from RNA-seq. Nature Methods, 2017, 14, 68-70.	9.0	157
146	Immunogenomic analyses associate immunological alterations with mismatch repair defects in prostate cancer. Journal of Clinical Investigation, 2018, 128, 4441-4453.	3.9	155
147	C5a-Induced Gene Expression in Human Umbilical Vein Endothelial Cells. American Journal of Pathology, 2004, 164, 849-859.	1.9	152
148	<i>ESR1</i> Mutations in Circulating Plasma Tumor DNA from Metastatic Breast Cancer Patients. Clinical Cancer Research, 2016, 22, 993-999.	3.2	152
149	SPOP Mutation Drives Prostate Tumorigenesis InÂVivo through Coordinate Regulation of PI3K/mTOR and AR Signaling. Cancer Cell, 2017, 31, 436-451.	7.7	152
150	Transcriptome analysis of HER2 reveals a molecular connection to fatty acid synthesis. Cancer Research, 2003, 63, 132-9.	0.4	151
151	The landscape of antisense gene expression in human cancers. Genome Research, 2015, 25, 1068-1079.	2.4	150
152	Development of a RNA-Seq Based Prognostic Signature in Lung Adenocarcinoma. Journal of the National Cancer Institute, 2017, 109, djw200.	3.0	150
153	Copy number and targeted mutational analysis reveals novel somatic events in metastatic prostate tumors. Genome Research, 2011, 21, 47-55.	2.4	148
154	Circulating microRNA Profiling Identifies a Subset of Metastatic Prostate Cancer Patients with Evidence of Cancer-Associated Hypoxia. PLoS ONE, 2013, 8, e69239.	1.1	147
155	The Role of Calpain in the Proteolytic Cleavage of E-cadherin in Prostate and Mammary Epithelial Cells. Journal of Biological Chemistry, 2003, 278, 1372-1379.	1.6	146
156	Overexpression, Amplification, and Androgen Regulation of TPD52 in Prostate Cancer. Cancer Research, 2004, 64, 3814-3822.	0.4	145
157	Quantitative Determination of Expression of the Prostate Cancer Protein Î±-Methylacyl-CoA Racemase Using Automated Quantitative Analysis (AQUA). American Journal of Pathology, 2004, 164, 831-840.	1.9	145
158	The Lethal Phenotype of Cancer: The Molecular Basis of Death Due to Malignancy. Ca-A Cancer Journal for Clinicians, 2007, 57, 225-241.	157.7	145
159	Metabolism unhinged: IDH mutations in cancer. Nature Medicine, 2011, 17, 291-293.	15.2	144
160	Lowered H3K27me3 and DNA hypomethylation define poorly prognostic pediatric posterior fossa ependymomas. Science Translational Medicine, 2016, 8, 366ra161.	5.8	144
161	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
162	AGTR1 overexpression defines a subset of breast cancer and confers sensitivity to losartan, an AGTR1 antagonist. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10284-10289.	3.3	140

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163	Therapeutic Targeting of SPINK1-Positive Prostate Cancer. Science Translational Medicine, 2011, 3, 72ra17.	5.8	140
164	A Fluorescence <i>In situ</i> Hybridization Screen for E26 Transformationâ€“Specific Aberrations: Identification of DDX5-ETV4 Fusion Protein in Prostate Cancer. Cancer Research, 2008, 68, 7629-7637.	0.4	139
165	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
166	Changes in Differential Gene Expression because of Warm Ischemia Time of Radical Prostatectomy Specimens. American Journal of Pathology, 2002, 161, 1743-1748.	1.9	138
167	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. American Journal of Human Genetics, 2016, 98, 1051-1066.	2.6	137
168	BET Bromodomain Inhibitors Enhance Efficacy and Disrupt Resistance to AR Antagonists in the Treatment of Prostate Cancer. Molecular Cancer Research, 2016, 14, 324-331.	1.5	137
169	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
170	The Role of Sarcosine Metabolism in Prostate Cancer Progression. Neoplasia, 2013, 15, 491-IN13.	2.3	134
171	Translating cancer genomes and transcriptomes for precision oncology. Ca-A Cancer Journal for Clinicians, 2016, 66, 75-88.	157.7	133
172	Targeting of microRNA-142-3p in dendritic cells regulates endotoxin-induced mortality. Blood, 2011, 117, 6172-6183.	0.6	132
173	Characterization of the EZH2-MMSET Histone Methyltransferase Regulatory Axis in Cancer. Molecular Cell, 2013, 49, 80-93.	4.5	130
174	The central role of EED in the orchestration of polycomb group complexes. Nature Communications, 2014, 5, 3127.	5.8	130
175	TRIP13 promotes error-prone nonhomologous end joining and induces chemoresistance in head and neck cancer. Nature Communications, 2014, 5, 4527.	5.8	129
176	Melanoma Proliferation and Chemoresistance Controlled by the DEK Oncogene. Cancer Research, 2009, 69, 6405-6413.	0.4	127
177	Landscape of gene fusions in epithelial cancers: seq and ye shall find. Genome Medicine, 2015, 7, 129.	3.6	127
178	The Role of Metastasis-Associated Protein 1 in Prostate Cancer Progression. Cancer Research, 2004, 64, 825-829.	0.4	126
179	Genetic and epigenetic loss of microRNA-31 leads to feed-forward expression of EZH2 in melanoma. Oncotarget, 2012, 3, 1011-1025.	0.8	126
180	Delineation, Functional Validation, and Bioinformatic Evaluation of Gene Expression in Thyroid Follicular Carcinomas with the PAX8-PPARG Translocation. Clinical Cancer Research, 2006, 12, 1983-1993.	3.2	125

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181	Molecular Concepts Analysis Links Tumors, Pathways, Mechanisms, and Drugs. Neoplasia, 2007, 9, 443-IN9.	2.3	124
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