Elai Davicioni

List of Publications by Year
in descending order

159 papers	11,724 citations	26567 56 h-index	30848 102 g-index
162 all docs	162 docs citations	162 times ranked	13702 citing authors

#	Article	IF	Citations
1	High intratumoral plasma cells content in primary prostate cancer defines a subset of tumors with potential susceptibility to immune-based treatments. Prostate Cancer and Prostatic Diseases, 2023, 26, 105-112.	2.0	2
2	A transcriptomic model for homologous recombination deficiency in prostate cancer. Prostate Cancer and Prostatic Diseases, 2022, 25, 659-665.	2.0	9
3	Subpathologies and genomic classifier for treatment individualization of post-prostatectomy radiotherapy. Urologic Oncology: Seminars and Original Investigations, 2022, 40, 5.e1-5.e13.	0.8	2
4	Antizyme Inhibitor 1 Regulates Matrikine Expression and Enhances the Metastatic Potential of Aggressive Primary Prostate Cancer. Molecular Cancer Research, 2022, 20, 527-541.	1.5	3
5	Variation in Molecularly Defined Prostate Tumor Subtypes by Self-identified Race. European Urology Open Science, 2022, 40, 19-26.	0.2	7
6	MYC drives aggressive prostate cancer by disrupting transcriptional pause release at androgen receptor targets. Nature Communications, 2022, 13, 2559.	5.8	56
7	Association between Incidental Pelvic Inflammation and Aggressive Prostate Cancer. Cancers, 2022, 14, 2734.	1.7	5
8	Genomic biomarkers to guide precision radiotherapy in prostate cancer. Prostate, 2022, 82, .	1.2	3
9	Somatic HOXB13 Expression Correlates with Metastatic Progression in Men with Localized Prostate Cancer Following Radical Prostatectomy. European Urology Oncology, 2021, 4, 955-962.	2.6	14
10	Prostate cancer in young men represents a distinct clinical phenotype: gene expression signature to predict early metastases. , 2021, 5, 50-61.		1
11	A comparative study of PCS and PAM50 prostate cancer classification schemes. Prostate Cancer and Prostatic Diseases, 2021, 24, 733-742.	2.0	14
12	A showcase study on personalized in silico drug response prediction based on the genetic landscape of muscle invasive bladder cancer. Scientific Reports, 2021, 11, 5849.	1.6	4
13	Validation of a 22-Gene Genomic Classifier in Patients With Recurrent Prostate Cancer. JAMA Oncology, 2021, 7, 544.	3.4	82
14	Expression of ISL1 and its partners in prostate cancer progression and neuroendocrine differentiation. Journal of Cancer Research and Clinical Oncology, 2021, 147, 2223-2231.	1.2	4
15	Tumor subtype defines distinct pathways of molecular and clinical progression in primary prostate cancer. Journal of Clinical Investigation, 2021, 131, .	3.9	17
16	Heterogeneity in Genomic Risk Assessment from Tissue Based Prognostic Signatures Used in the Biopsy Setting and the Impact of Magnetic Resonance Imaging Targeted Biopsy. Journal of Urology, 2021, 205, 1344-1351.	0.2	5
17	Comparative analysis of 1152 African-American and European-American men with prostate cancer identifies distinct genomic and immunological differences. Communications Biology, 2021, 4, 670.	2.0	50
18	Prostate-specific Membrane Antigen and Fluciclovine Transporter Genes are Associated with Variable Clinical Features and Molecular Subtypes of Primary Prostate Cancer. European Urology, 2021, 79, 717-721.	0.9	13

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19	Association of Molecular Subtypes With Differential Outcome to Apalutamide Treatment in Nonmetastatic Castration-Resistant Prostate Cancer. JAMA Oncology, 2021, 7, 1005.	3.4	21
20	Molecular Characterization of Residual Bladder Cancer after Neoadjuvant Pembrolizumab. European Urology, 2021, 80, 149-159.	0.9	17
21	Molecular subtyping and immune-gene signatures identify a subset of early bladder tumors as candidates for single-agent immune-checkpoint inhibition. Urologic Oncology: Seminars and Original Investigations, 2021, 39, 734.e11-734.e17.	0.8	4
22	G3BP1 inhibits Cul3SPOP to amplify AR signaling and promote prostate cancer. Nature Communications, 2021, 12, 6662.	5.8	17
23	The long noncoding RNA H19 regulates tumor plasticity in neuroendocrine prostate cancer. Nature Communications, 2021, 12, 7349.	5.8	51
24	Decipher identifies men with otherwise clinically favorable-intermediate risk disease who may not be good candidates for active surveillance. Prostate Cancer and Prostatic Diseases, 2020, 23, 136-143.	2.0	36
25	Prospective study to define the clinical utility and benefit of Decipher testing in men following prostatectomy. Prostate Cancer and Prostatic Diseases, 2020, 23, 295-302.	2.0	30
26	Genomic and clinical characterization of stromal infiltration markers in prostate cancer. Cancer, 2020, 126, 1407-1412.	2.0	8
27	Validation of a genomic classifier for prediction of metastasis and prostate cancer-specific mortality in African-American men following radical prostatectomy in an equal access healthcare setting. Prostate Cancer and Prostatic Diseases, 2020, 23, 419-428.	2.0	22
28	Validation of a neuroendocrine-like classifier confirms poor outcomes in patients with bladder cancer treated with cisplatin-based neoadjuvant chemotherapy. Urologic Oncology: Seminars and Original Investigations, 2020, 38, 262-268.	0.8	15
29	Clinical Utility of a Genomic Classifier in Men Undergoing Radical Prostatectomy: The PRO-IMPACT Trial. Practical Radiation Oncology, 2020, 10, e82-e90.	1.1	19
30	Development and Validation of a Genomic Tool to Predict Seminal Vesicle Invasion in Adenocarcinoma of the Prostate. JCO Precision Oncology, 2020, 4, 1228-1238.	1.5	2
31	Identifying and treating *ROBO1*[−ve]/*DOCK1*[+ve] prostate cancer: An aggressive cancer subtype prevalent in African American patients. Prostate, 2020, 80, 1045-1057.	1.2	5
32	Development and Validation of a Novel TP53 Mutation Signature That Predicts Risk of Metastasis in Primary Prostate Cancer. Clinical Genitourinary Cancer, 2020, 19, 246-254.e5.	0.9	9
33	Diversity in Androgen Receptor Action Among Treatment-naïve Prostate Cancers Is Reflected in Treatment Response Predictions and Molecular Subtypes. European Urology Open Science, 2020, 22, 34-44.	0.2	7
34	Transcriptomic Heterogeneity of Gleason Grade Group 5 Prostate Cancer. European Urology, 2020, 78, 327-332.	0.9	18
35	Impact of Molecular Subtyping and Immune Infiltration on Pathological Response and Outcome Following Neoadjuvant Pembrolizumab in Muscle-invasive Bladder Cancer. European Urology, 2020, 77, 701-710.	0.9	128
36	Prognostic value of the SPOP mutant genomic subclass in prostate cancer. Urologic Oncology: Seminars and Original Investigations, 2020, 38, 418-422.	0.8	8

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37	Comprehensive Transcriptomic Profiling Identifies Breast Cancer Patients Who May Be Spared Adjuvant Systemic Therapy. Clinical Cancer Research, 2020, 26, 171-182.	3.2	14
38	Predictors of Prostate-specific Membrane Antigen (PSMA/FOLH1) Expression in a Genomic Database. Urology, 2020, 144, 117-122.	0.5	2
39	Performance of clinicopathologic models in men with high risk localized prostate cancer: impact of a 22-gene genomic classifier. Prostate Cancer and Prostatic Diseases, 2020, 23, 646-653.	2.0	17
40	Clinical-genomic Characterization Unveils More Aggressive Disease Features in Elderly Prostate Cancer Patients with Low-grade Disease. European Urology Focus, 2020, 7, 797-806.	1.6	1
41	A four‑gene transcript score to predict metastatic‑lethal progression in men treated for localized prostate cancer: Development and validation studies. Prostate, 2019, 79, 1589-1596.	1.2	8
42	Morphologic and genomic characterization of urothelial to sarcomatoid transition in muscle-invasive bladder cancer. Urologic Oncology: Seminars and Original Investigations, 2019, 37, 573.e19-573.e29.	0.8	13
43	Validation of the Decipher Test for Predicting Distant Metastatic Recurrence in Men with High-risk Nonmetastatic Prostate Cancer 10 Years After Surgery. European Urology Oncology, 2019, 2, 589-596.	2.6	19
44	Long non-coding RNAs identify a subset of luminal muscle-invasive bladder cancer patients with favorable prognosis. Genome Medicine, 2019, 11, 60.	3.6	36
45	Genomic Validation of 3-Tiered Clinical Subclassification of High-Risk Prostate Cancer. International Journal of Radiation Oncology Biology Physics, 2019, 105, 621-627.	0.4	10
46	The evolution of long noncoding RNA acceptance in prostate cancer initiation, progression, and its clinical utility in disease management. European Urology, 2019, 76, 546-559.	0.9	82
47	High-fat diet fuels prostate cancer progression by rewiring the metabolome and amplifying the MYC program. Nature Communications, 2019, 10, 4358.	5.8	109
48	Morphologic and genomic characterization of urothelial to sarcomatoid transition in muscle-invasive bladder cancer. Urologic Oncology: Seminars and Original Investigations, 2019, 37, 826-836.	0.8	33
49	Development of a predictive model for stromal content in prostate cancer samples to improve signature performance. Journal of Pathology, 2019, 249, 411-424.	2.1	3
50	FOXA1 mutations alter pioneering activity, differentiation and prostate cancer phenotypes. Nature, 2019, 571, 408-412.	13.7	163
51	Asporin Restricts Mesenchymal Stromal Cell Differentiation, Alters the Tumor Microenvironment, and Drives Metastatic Progression. Cancer Research, 2019, 79, 3636-3650.	0.4	47
52	Molecular Subtyping of Clinically Localized Urothelial Carcinoma Reveals Lower Rates of Pathological Upstaging at Radical Cystectomy Among Luminal Tumors. European Urology, 2019, 76, 200-206.	0.9	41
53	Novel RB1-Loss Transcriptomic Signature Is Associated with Poor Clinical Outcomes across Cancer Types. Clinical Cancer Research, 2019, 25, 4290-4299.	3.2	38
54	Correlation between MRI phenotypes and a genomic classifier of prostate cancer: preliminary findings. European Radiology, 2019, 29, 4861-4870.	2.3	23

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55	Molecular Characterization of Neuroendocrine-like Bladder Cancer. Clinical Cancer Research, 2019, 25, 3908-3920.	3.2	71
56	ARv7 Represses Tumor-Suppressor Genes in Castration-Resistant Prostate Cancer. Cancer Cell, 2019, 35, 401-413.e6.	7.7	127
57	Transcriptomic Heterogeneity of Androgen Receptor Activity Defines a <i>de novo</i> low AR-Active Subclass in Treatment Naïve Primary Prostate Cancer. Clinical Cancer Research, 2019, 25, 6721-6730.	3.2	74
58	Divergent Biological Response to Neoadjuvant Chemotherapy in Muscle-invasive Bladder Cancer. Clinical Cancer Research, 2019, 25, 5082-5093.	3.2	82
59	Genomic Classifier for Guiding Treatment of Intermediate-Risk Prostate Cancers to Dose-Escalated Image Guided Radiation Therapy Without Hormone Therapy. International Journal of Radiation Oncology Biology Physics, 2019, 103, 84-91.	0.4	36
60	Validation of the Decipher Test for predicting adverse pathology in candidates for prostate cancer active surveillance. Prostate Cancer and Prostatic Diseases, 2019, 22, 399-405.	2.0	53
61	Clinical and Genomic Implications of Luminal and Basal Subtypes Across Carcinomas. Clinical Cancer Research, 2019, 25, 2450-2457.	3.2	52
62	Low Tristetraprolin Expression Is Associated with Lethal Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 584-590.	1.1	8
63	The Immune Landscape of Prostate Cancer and Nomination of PD-L2 as a Potential Therapeutic Target. Journal of the National Cancer Institute, 2019, 111, 301-310.	3.0	142
64	Validation of a 10-gene molecular signature for predicting biochemical recurrence and clinical metastasis in localized prostate cancer. Journal of Cancer Research and Clinical Oncology, 2018, 144, 883-891.	1.2	24
65	Development and Validation of a 28-gene Hypoxia-related Prognostic Signature for Localized Prostate Cancer. EBioMedicine, 2018, 31, 182-189.	2.7	132
66	Validation of a Genomic Risk Classifier to Predict Prostate Cancer-specific Mortality in Men with Adverse Pathologic Features. European Urology, 2018, 73, 168-175.	0.9	53
67	Stromal Gene Expression is Predictive for Metastatic Primary Prostate Cancer. European Urology, 2018, 73, 524-532.	0.9	60
68	Transcriptome Wide Analysis of Magnetic Resonance Imaging-targeted Biopsy and Matching Surgical Specimens from High-risk Prostate Cancer Patients Treated with Radical Prostatectomy: The Target Must Be Hit. European Urology Focus, 2018, 4, 540-546.	1.6	18
69	Gene Expression Correlates of Site-specific Metastasis Among Men With Lymph Node Positive Prostate Cancer Treated With Radical Prostatectomy: A Case Series. Urology, 2018, 112, 29-32.	0.5	1
70	Performance of a Prostate Cancer Genomic Classifier in Predicting Metastasis in Men with Prostate-specific Antigen Persistence Postprostatectomy. European Urology, 2018, 74, 107-114.	0.9	54
71	Impact of the SPOP Mutant Subtype on the Interpretation of Clinical Parameters in Prostate Cancer. JCO Precision Oncology, 2018, 2018, 1-13.	1.5	29
72	Development and Validation of a Novel Integrated Clinical-Genomic Risk Group Classification for Localized Prostate Cancer. Journal of Clinical Oncology, 2018, 36, 581-590.	0.8	162

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73	Multiparametric Magnetic Resonance Imaging Features Identify Aggressive Prostate Cancer at the Phenotypic and Transcriptomic Level. Journal of Urology, 2018, 200, 1241-1249.	0.2	23
74	Development and Validation of a Prostate Cancer Genomic Signature that Predicts Early ADT Treatment Response Following Radical Prostatectomy. Clinical Cancer Research, 2018, 24, 3908-3916.	3.2	24
75	ETS2 is a prostate basal cell marker and is highly expressed in prostate cancers aberrantly expressing p63. Prostate, 2018, 78, 896-904.	1.2	13
76	The Diverse Genomic Landscape of Clinically Low-risk Prostate Cancer. European Urology, 2018, 74, 444-452.	0.9	55
77	The long noncoding RNA landscape of neuroendocrine prostate cancer and its clinical implications. GigaScience, 2018, 7, .	3.3	54
78	Tristetraprolin Is a Prognostic Biomarker for Poor Outcomes among Patients with Low-Grade Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1376-1383.	1.1	9
79	Pan-Cancer Analysis of Genomic Sequencing Among the Elderly. International Journal of Radiation Oncology Biology Physics, 2017, 98, 726-732.	0.4	11
80	Transcriptome evaluation of the relation between body mass index and prostate cancer outcomes. Cancer, 2017, 123, 2240-2247.	2.0	2
81	Cost-effectiveness of the Decipher Genomic Classifier to Guide Individualized Decisions for Early Radiation Therapy After Prostatectomy for Prostate Cancer. Clinical Genitourinary Cancer, 2017, 15, e299-e309.	0.9	25
82	Evaluation of a 24â€gene signature for prognosis of metastatic events and prostate cancerâ€specific mortality. BJU International, 2017, 119, 961-967.	1.3	6
83	Impact of Molecular Subtypes in Muscle-invasive Bladder Cancer on Predicting Response and Survival after Neoadjuvant Chemotherapy. European Urology, 2017, 72, 544-554.	0.9	638
84	Decipher test impacts decision making among patients considering adjuvant and salvage treatment after radical prostatectomy: Interim results from the Multicenter Prospective PROâ€IMPACT study. Cancer, 2017, 123, 2850-2859.	2.0	66
85	An Oncofetal Glycosaminoglycan Modification Provides Therapeutic Access to Cisplatin-resistant Bladder Cancer. European Urology, 2017, 72, 142-150.	0.9	38
86	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
87	Androgen Receptor Deregulation Drives Bromodomain-Mediated Chromatin Alterations in Prostate Cancer. Cell Reports, 2017, 19, 2045-2059.	2.9	99
88	Ability of a Genomic Classifier to Predict Metastasis and Prostate Cancer-specific Mortality after Radiation or Surgery based on Needle Biopsy Specimens. European Urology, 2017, 72, 845-852.	0.9	79
89	Comprehensive Determination of Prostate Tumor ETS Gene Status in Clinical Samples Using the CLIA Decipher Assay. Journal of Molecular Diagnostics, 2017, 19, 475-484.	1.2	16
90	MicroRNA-194 Promotes Prostate Cancer Metastasis by Inhibiting SOCS2. Cancer Research, 2017, 77, 1021-1034.	0.4	94

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91	LSD1-Mediated Epigenetic Reprogramming Drives CENPE Expression and Prostate Cancer Progression. Cancer Research, 2017, 77, 5479-5490.	0.4	71
92	TOP2A and EZH2 Provide Early Detection of an Aggressive Prostate Cancer Subgroup. Clinical Cancer Research, 2017, 23, 7072-7083.	3.2	87
93	Multi-institutional Analysis Shows that Low PCAT-14 Expression Associates with Poor Outcomes in Prostate Cancer. European Urology, 2017, 71, 257-266.	0.9	59
94	Molecular Analysis of Low Grade Prostate Cancer Using a Genomic Classifier of Metastatic Potential. Journal of Urology, 2017, 197, 122-128.	0.2	33
95	Gene expression signatures of neuroendocrine prostate cancer and primary small cell prostatic carcinoma. BMC Cancer, 2017, 17, 759.	1.1	57
96	Low PCA3 expression is a marker of poor differentiation in localized prostate tumors: exploratory analysis from 12,076 patients. Oncotarget, 2017, 8, 50804-50813.	0.8	29
97	Genomic Classifier Augments the Role of Pathological Features in Identifying Optimal Candidates for Adjuvant Radiation Therapy in Patients With Prostate Cancer: Development and Internal Validation of a Multivariable Prognostic Model. Journal of Clinical Oncology, 2017, 35, 1982-1990.	0.8	76
98	Individual Patient-Level Meta-Analysis of the Performance of the Decipher Genomic Classifier in High-Risk Men After Prostatectomy to Predict Development of Metastatic Disease. Journal of Clinical Oncology, 2017, 35, 1991-1998.	0.8	176
99	Lipid degradation promotes prostate cancer cell survival. Oncotarget, 2017, 8, 38264-38275.	0.8	64
100	Therapy-induced developmental reprogramming of prostate cancer cells and acquired therapy resistance. Oncotarget, 2017, 8, 18949-18967.	0.8	47
101	Evaluation of a genomic classifier in radical prostatectomy patients with lymph node metastasis. Research and Reports in Urology, 2016, Volume 8, 77-84.	0.6	16
102	Genomic and epigenomic analysis of high-risk prostate cancer reveals changes in hydroxymethylation and TET1. Oncotarget, 2016, 7, 24326-24338.	0.8	33
103	*AXIN2* expression predicts prostate cancer recurrence and regulates invasion and tumor growth. Prostate, 2016, 76, 597-608.	1.2	14
104	SPINK1 Defines a Molecular Subtype of Prostate Cancer in Men with More Rapid Progression in an at Risk, Natural History Radical Prostatectomy Cohort. Journal of Urology, 2016, 196, 1436-1444.	0.2	38
105	Prediction of Lymph Node Metastasis in Patients with Bladder Cancer Using Whole Transcriptome Gene Expression Signatures. Journal of Urology, 2016, 196, 1036-1041.	0.2	33
106	Development and validation of a 24-gene predictor of response to postoperative radiotherapy in prostate cancer: a matched, retrospective analysis. Lancet Oncology, The, 2016, 17, 1612-1620.	5.1	182
107	Integrated Classification of Prostate Cancer Reveals a Novel Luminal Subtype with Poor Outcome. Cancer Research, 2016, 76, 4948-4958.	0.4	147
108	Decipher Genomic Classifier Measured on Prostate Biopsy Predicts Metastasis Risk. Urology, 2016, 90, 148-152.	0.5	138

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109	Utilization of a Genomic Classifier for Prediction of Metastasis Following Salvage Radiation Therapy after Radical Prostatectomy. European Urology, 2016, 70, 588-596.	0.9	69
110	Patient-Level DNA Damage and Repair Pathway Profiles and Prognosis After Prostatectomy for High-Risk Prostate Cancer. JAMA Oncology, 2016, 2, 471.	3.4	46
111	Racial Variations in Prostate Cancer Molecular Subtypes and Androgen Receptor Signaling Reflect Anatomic Tumor Location. European Urology, 2016, 70, 14-17.	0.9	79
112	Validation of a Genomic Classifier for Predicting Post-Prostatectomy Recurrence in a Community Based Health Care Setting. Journal of Urology, 2016, 195, 1748-1753.	0.2	33
113	The Landscape of Prognostic Outlier Genes in High-Risk Prostate Cancer. Clinical Cancer Research, 2016, 22, 1777-1786.	3.2	42
114	Application of a Clinical Whole-Transcriptome Assay for Staging and Prognosis of Prostate Cancer Diagnosed in Needle Core Biopsy Specimens. Journal of Molecular Diagnostics, 2016, 18, 395-406.	1.2	46
115	Utility of Risk Models in Decision Making After Radical Prostatectomy: Lessons from a Natural History Cohort of Intermediate- and High-Risk Men. European Urology, 2016, 69, 496-504.	0.9	23
116	Germline Variants in Asporin Vary by Race, Modulate the Tumor Microenvironment, and Are Differentially Associated with Metastatic Prostate Cancer. Clinical Cancer Research, 2016, 22, 448-458.	3.2	29
117	Tissue-based Genomics Augments Post-prostatectomy Risk Stratification in a Natural History Cohort of Intermediate- and High-Risk Men. European Urology, 2016, 69, 157-165.	0.9	206
118	Association of multiparametric MRI quantitative imaging features with prostate cancer gene expression in MRI-targeted prostate biopsies. Oncotarget, 2016, 7, 53362-53376.	0.8	90
119	Prostate cancer radiomics and the promise of radiogenomics. Translational Cancer Research, 2016, 5, 432-447.	0.4	111
120	Evolving transcriptomic fingerprint based on genome‐wide data as prognostic tools in prostate cancer. Biology of the Cell, 2015, 107, 232-244.	0.7	6
121	Genomic Classifier Identifies Men With Adverse Pathology After Radical Prostatectomy Who Benefit From Adjuvant Radiation Therapy. Journal of Clinical Oncology, 2015, 33, 944-951.	0.8	196
122	A Genomic Classifier Improves Prediction of Metastatic Disease Within 5 Years After Surgery in Node-negative High-risk Prostate Cancer Patients Managed by Radical Prostatectomy Without Adjuvant Therapy. European Urology, 2015, 67, 778-786.	0.9	162
123	Clinical and genomic analysis of metastatic prostate cancer progression with a background of postoperative biochemical recurrence. BJU International, 2015, 116, 556-567.	1.3	19
124	Effect of a genomic classifier test on clinical practice decisions for patients with high‐risk prostate cancer after surgery. BJU International, 2015, 115, 419-429.	1.3	52
125	Characterization of 1577 Primary Prostate Cancers Reveals Novel Biological and Clinicopathologic Insights into Molecular Subtypes. European Urology, 2015, 68, 555-567.	0.9	125
126	DNA-PKcs-Mediated Transcriptional Regulation Drives Prostate Cancer Progression and Metastasis. Cancer Cell, 2015, 28, 97-113.	7.7	148

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127	Novel Biomarker Signature That May Predict Aggressive Disease in African American Men With Prostate Cancer. Journal of Clinical Oncology, 2015, 33, 2789-2796.	0.8	127
128	Cyclin D1 Loss Distinguishes Prostatic Small-Cell Carcinoma from Most Prostatic Adenocarcinomas. Clinical Cancer Research, 2015, 21, 5619-5629.	3.2	56
129	Androgen-Regulated SPARCL1 in the Tumor Microenvironment Inhibits Metastatic Progression. Cancer Research, 2015, 75, 4322-4334.	0.4	23
130	Combined Value of Validated Clinical and Genomic Risk Stratification Tools for Predicting Prostate Cancer Mortality in a High-risk Prostatectomy Cohort. European Urology, 2015, 67, 326-333.	0.9	178
131	The lncRNAs <i>PCGEM1</i> and <i>PRNCR1</i> are not implicated in castration resistant prostate cancer. Oncotarget, 2014, 5, 1434-1438.	0.8	106
132	Tumour genomic and microenvironmental heterogeneity for integrated prediction of 5-year biochemical recurrence of prostate cancer: a retrospective cohort study. Lancet Oncology, The, 2014, 15, 1521-1532.	5.1	291
133	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
134	The oestrogen receptor alpha-regulated lncRNA NEAT1 is a critical modulator of prostate cancer. Nature Communications, 2014, 5, 5383.	5.8	522
135	Discovery and Validation of Novel Expression Signature for Postcystectomy Recurrence in High-Risk Bladder Cancer. Journal of the National Cancer Institute, 2014, 106, .	3.0	46
136	Genomic Prostate Cancer Classifier Predicts Biochemical Failure and Metastases in Patients After Postoperative Radiation Therapy. International Journal of Radiation Oncology Biology Physics, 2014, 89, 1038-1046.	0.4	149
137	The long noncoding RNA SChLAP1 promotes aggressive prostate cancer and antagonizes the SWI/SNF complex. Nature Genetics, 2013, 45, 1392-1398.	9.4	601
138	2239 CLINICAL AND GENOMIC ANALYSIS OF METASTATIC DISEASE PROGRESSION IN A BACKGROUND OF BIOCHEMICAL RECURRENCE. Journal of Urology, 2013, 189, .	0.2	1
139	Validation of a Genomic Classifier that Predicts Metastasis Following Radical Prostatectomy in an At Risk Patient Population. Journal of Urology, 2013, 190, 2047-2053.	0.2	280
140	Whole-Transcriptome Profiling of Thyroid Nodules Identifies Expression-Based Signatures for Accurate Thyroid Cancer Diagnosis. Journal of Clinical Endocrinology and Metabolism, 2013, 98, 4072-4079.	1.8	15
141	Discovery and Validation of a Prostate Cancer Genomic Classifier that Predicts Early Metastasis Following Radical Prostatectomy. PLoS ONE, 2013, 8, e66855.	1.1	524
142	Impact of a genomic classifier of metastatic risk on postoperative treatment recommendations for prostate cancer patients: a report from the DECIDE study group. Oncotarget, 2013, 4, 600-609.	0.8	58
143	Secreted protein, acidic and rich in cysteine-like 1 (SPARCL1) is down regulated in aggressive prostate cancers and is prognostic for poor clinical outcome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14977-14982.	3.3	49
144	Transcriptome-Wide Detection of Differentially Expressed Coding and Non-Coding Transcripts and Their Clinical Significance in Prostate Cancer. Journal of Oncology, 2012, 2012, 1-11.	0.6	14

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145	Genomic "Dark Matter" in Prostate Cancer: Exploring the Clinical Utility of ncRNA as Biomarkers. Frontiers in Genetics, 2012, 3, 23.	1.1	17
146	Progression of ductal carcinoma in situ to invasive breast cancer is associated with gene expression programs of EMT and myoepithelia. Breast Cancer Research and Treatment, 2012, 133, 1009-1024.	1.1	77
147	Clinical and genomic analysis of metastatic disease progression in a background of biochemical recurrence.. Journal of Clinical Oncology, 2012, 30, 90-90.	0.8	1
148	Prognostic Significance and Tumor Biology of Regional Lymph Node Disease in Patients With Rhabdomyosarcoma: A Report From the Children's Oncology Group. Journal of Clinical Oncology, 2011, 29, 1304-1311.	0.8	102
149	Inferring cancer subnetwork markers using density-constrained biclustering. Bioinformatics, 2010, 26, i625-i631.	1.8	49
150	Gene Expression Profiling for Survival Prediction in Pediatric Rhabdomyosarcomas: A Report From the Children's Oncology Group. Journal of Clinical Oncology, 2010, 28, 1240-1246.	0.8	78
151	Quantitative Expression Profiling in Formalin-Fixed Paraffin-Embedded Samples by Affymetrix Microarrays. Journal of Molecular Diagnostics, 2010, 12, 409-417.	1.2	81
152	Translational Activation of Snail1 and Other Developmentally Regulated Transcription Factors by YB-1 Promotes an Epithelial-Mesenchymal Transition. Cancer Cell, 2009, 15, 402-415.	7.7	400
153	Molecular Classification of Rhabdomyosarcoma—Genotypic and Phenotypic Determinants of Diagnosis. American Journal of Pathology, 2009, 174, 550-564.	1.9	271
154	Diagnostic and Prognostic Sarcoma Signatures. Molecular Diagnosis and Therapy, 2008, 12, 359-374.	1.6	21
155	Histone Deacetylase 1 Gene Expression and Sensitization of Multidrug-Resistant Neuroblastoma Cell Lines to Cytotoxic Agents by Depsipeptide. Journal of the National Cancer Institute, 2007, 99, 1107-1119.	3.0	85
156	Transgenic mice expressing PAX3-FKHR have multiple defects in muscle development, including ectopic skeletal myogenesis in the developing neural tube. Transgenic Research, 2006, 15, 595-614.	1.3	17
157	Identification of a PAX-FKHR Gene Expression Signature that Defines Molecular Classes and Determines the Prognosis of Alveolar Rhabdomyosarcomas. Cancer Research, 2006, 66, 6936-6946.	0.4	286
158	The Homeoprotein Six1 Transcriptionally Activates Multiple Protumorigenic Genes but Requires Ezrin to Promote Metastasis. Cancer Research, 2006, 66, 1982-1989.	0.4	132
159	Retinoic acid induces leukemia cell G 1 arrest and transition into differentiation by inhibiting cyclin-dependent kinase-activating kinase binding and phosphorylation of PML/RAR. FASEB Journal, 2006, 20, 2142-2144.	0.2	32