## Elai Davicioni

List of Publications by Year in descending order

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159 papers 11,724 citations

<sup>26567</sup> 56 h-index

102 g-index

162 all docs

162 docs citations

162 times ranked 13702 citing authors

#	Article	IF	CITATIONS
1	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
2	The long noncoding RNA SChLAP1 promotes aggressive prostate cancer and antagonizes the SWI/SNF complex. Nature Genetics, 2013, 45, 1392-1398.	9.4	601
3	Discovery and Validation of a Prostate Cancer Genomic Classifier that Predicts Early Metastasis Following Radical Prostatectomy. PLoS ONE, 2013, 8, e66855.	1.1	524
4	The oestrogen receptor alpha-regulated lncRNA NEAT1 is a critical modulator of prostate cancer. Nature Communications, 2014, 5, 5383.	5.8	522
5	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
6	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
7	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
8	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
9	Molecular Classification of Rhabdomyosarcoma—Genotypic and Phenotypic Determinants of Diagnosis. American Journal of Pathology, 2009, 174, 550-564.	1.9	271
10	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
11	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
12	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
13	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
14	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
15	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
16	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
17	FOXA1 mutations alter pioneering activity, differentiation and prostate cancer phenotypes. Nature, 2019, 571, 408-412.	13.7	163
18	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

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19	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
20	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
21	DNA-PKcs-Mediated Transcriptional Regulation Drives Prostate Cancer Progression and Metastasis. Cancer Cell, 2015, 28, 97-113.	7.7	148
22	Integrated Classification of Prostate Cancer Reveals a Novel Luminal Subtype with Poor Outcome. Cancer Research, 2016, 76, 4948-4958.	0.4	147
23	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
24	Decipher Genomic Classifier Measured on Prostate Biopsy Predicts Metastasis Risk. Urology, 2016, 90, 148-152.	0.5	138
25	The Homeoprotein Six1 Transcriptionally Activates Multiple Protumorigenic Genes but Requires Ezrin to Promote Metastasis. Cancer Research, 2006, 66, 1982-1989.	0.4	132
26	Development and Validation of a 28-gene Hypoxia-related Prognostic Signature for Localized Prostate Cancer. EBioMedicine, 2018, 31, 182-189.	2.7	132
27	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
28	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
29	ARv7 Represses Tumor-Suppressor Genes in Castration-Resistant Prostate Cancer. Cancer Cell, 2019, 35, 401-413.e6.	7.7	127
30	Characterization of 1577 Primary Prostate Cancers Reveals Novel Biological and Clinicopathologic Insights into Molecular Subtypes. European Urology, 2015, 68, 555-567.	0.9	125
31	Prostate cancer radiomics and the promise of radiogenomics. Translational Cancer Research, 2016, 5, 432-447.	0.4	111
32	High-fat diet fuels prostate cancer progression by rewiring the metabolome and amplifying the MYC program. Nature Communications, 2019, 10, 4358.	5.8	109
33	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
34	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
35	Androgen Receptor Deregulation Drives Bromodomain-Mediated Chromatin Alterations in Prostate Cancer. Cell Reports, 2017, 19, 2045-2059.	2.9	99
36	MicroRNA-194 Promotes Prostate Cancer Metastasis by Inhibiting SOCS2. Cancer Research, 2017, 77, 1021-1034.	0.4	94

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37	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
38	TOP2A and EZH2 Provide Early Detection of an Aggressive Prostate Cancer Subgroup. Clinical Cancer Research, 2017, 23, 7072-7083.	3.2	87
39	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
40	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
41	Divergent Biological Response to Neoadjuvant Chemotherapy in Muscle-invasive Bladder Cancer. Clinical Cancer Research, 2019, 25, 5082-5093.	3.2	82
42	Validation of a 22-Gene Genomic Classifier in Patients With Recurrent Prostate Cancer. JAMA Oncology, 2021, 7, 544.	3.4	82
43	Quantitative Expression Profiling in Formalin-Fixed Paraffin-Embedded Samples by Affymetrix Microarrays. Journal of Molecular Diagnostics, 2010, 12, 409-417.	1.2	81
44	Racial Variations in Prostate Cancer Molecular Subtypes and Androgen Receptor Signaling Reflect Anatomic Tumor Location. European Urology, 2016, 70, 14-17.	0.9	79
45	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
46	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
47	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
48	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
49	Transcriptomic Heterogeneity of Androgen Receptor Activity Defines a <i>de novo</i> low AR-Active Subclass in Treatment Naà ve Primary Prostate Cancer. Clinical Cancer Research, 2019, 25, 6721-6730.	3.2	74
50	LSD1-Mediated Epigenetic Reprogramming Drives CENPE Expression and Prostate Cancer Progression. Cancer Research, 2017, 77, 5479-5490.	0.4	71
51	Molecular Characterization of Neuroendocrine-like Bladder Cancer. Clinical Cancer Research, 2019, 25, 3908-3920.	3.2	71
52	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
53	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
54	Lipid degradation promotes prostate cancer cell survival. Oncotarget, 2017, 8, 38264-38275.	0.8	64

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55	Stromal Gene Expression is Predictive for Metastatic Primary Prostate Cancer. European Urology, 2018, 73, 524-532.	0.9	60
56	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
57	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
58	Gene expression signatures of neuroendocrine prostate cancer and primary small cell prostatic carcinoma. BMC Cancer, 2017, 17, 759.	1.1	57
59	Cyclin D1 Loss Distinguishes Prostatic Small-Cell Carcinoma from Most Prostatic Adenocarcinomas. Clinical Cancer Research, 2015, 21, 5619-5629.	3.2	56
60	MYC drives aggressive prostate cancer by disrupting transcriptional pause release at androgen receptor targets. Nature Communications, 2022, 13, 2559.	5.8	56
61	The Diverse Genomic Landscape of Clinically Low-risk Prostate Cancer. European Urology, 2018, 74, 444-452.	0.9	55
62	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
63	The long noncoding RNA landscape of neuroendocrine prostate cancer and its clinical implications. GigaScience, 2018, 7, .	3.3	54
64	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
65	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
66	Effect of a genomic classifier test on clinical practice decisions for patients with highâ€risk prostate cancer after surgery. BJU International, 2015, 115, 419-429.	1.3	52
67	Clinical and Genomic Implications of Luminal and Basal Subtypes Across Carcinomas. Clinical Cancer Research, 2019, 25, 2450-2457.	3.2	52
68	The long noncoding RNA H19 regulates tumor plasticity in neuroendocrine prostate cancer. Nature Communications, 2021, 12, 7349.	5.8	51
69	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
70	Inferring cancer subnetwork markers using density-constrained biclustering. Bioinformatics, 2010, 26, i625-i631.	1.8	49
71	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
72	Asporin Restricts Mesenchymal Stromal Cell Differentiation, Alters the Tumor Microenvironment, and Drives Metastatic Progression. Cancer Research, 2019, 79, 3636-3650.	0.4	47

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73	Therapy-induced developmental reprogramming of prostate cancer cells and acquired therapy resistance. Oncotarget, 2017, 8, 18949-18967.	0.8	47
74	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
75	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
76	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
77	The Landscape of Prognostic Outlier Genes in High-Risk Prostate Cancer. Clinical Cancer Research, 2016, 22, 1777-1786.	3.2	42
78	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
79	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
80	An Oncofetal Glycosaminoglycan Modification Provides Therapeutic Access to Cisplatin-resistant Bladder Cancer. European Urology, 2017, 72, 142-150.	0.9	38
81	Novel RB1-Loss Transcriptomic Signature Is Associated with Poor Clinical Outcomes across Cancer Types. Clinical Cancer Research, 2019, 25, 4290-4299.	3.2	38
82	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
83	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
84	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
85	Genomic and epigenomic analysis of high-risk prostate cancer reveals changes in hydroxymethylation and TET1. Oncotarget, 2016, 7, 24326-24338.	0.8	33
86	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
87	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
88	Molecular Analysis of Low Grade Prostate Cancer Using a Genomic Classifier of Metastatic Potential. Journal of Urology, 2017, 197, 122-128.	0.2	33
89	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
90	Retinoic acid induces leukemia cell G 1 arrest and transition into differentiation by inhibiting cyclinâ€dependent kinaseâ€activating kinase binding and phosphorylation of PML/RAR. FASEB Journal, 2006, 20, 2142-2144.	0.2	32

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91	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
92	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
93	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
94	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
95	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
96	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
97	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
98	Androgen-Regulated SPARCL1 in the Tumor Microenvironment Inhibits Metastatic Progression. Cancer Research, 2015, 75, 4322-4334.	0.4	23
99	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
100	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
101	Correlation between MRI phenotypes and a genomic classifier of prostate cancer: preliminary findings. European Radiology, 2019, 29, 4861-4870.	2.3	23
102	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
103	Diagnostic and Prognostic Sarcoma Signatures. Molecular Diagnosis and Therapy, 2008, 12, 359-374.	1.6	21
104	Association of Molecular Subtypes With Differential Outcome to Apalutamide Treatment in Nonmetastatic Castration-Resistant Prostate Cancer. JAMA Oncology, 2021, 7, 1005.	3.4	21
105	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
106	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
107	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
108	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

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109	Transcriptomic Heterogeneity of Gleason Grade Group 5 Prostate Cancer. European Urology, 2020, 78, 327-332.	0.9	18
110	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
111	Genomic "Dark Matter―in Prostate Cancer: Exploring the Clinical Utility of ncRNA as Biomarkers. Frontiers in Genetics, 2012, 3, 23.	1.1	17
112	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
113	Tumor subtype defines distinct pathways of molecular and clinical progression in primary prostate cancer. Journal of Clinical Investigation, 2021, 131, .	3.9	17
114	Molecular Characterization of Residual Bladder Cancer after Neoadjuvant Pembrolizumab. European Urology, 2021, 80, 149-159.	0.9	17
115	G3BP1 inhibits Cul3SPOP to amplify AR signaling and promote prostate cancer. Nature Communications, 2021, 12, 6662.	5.8	17
116	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
117	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
118	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
119	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
120	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
121	<i>AXIN2</i> expression predicts prostate cancer recurrence and regulates invasion and tumor growth. Prostate, 2016, 76, 597-608.	1.2	14
122	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
123	Comprehensive Transcriptomic Profiling Identifies Breast Cancer Patients Who May Be Spared Adjuvant Systemic Therapy. Clinical Cancer Research, 2020, 26, 171-182.	3.2	14
124	A comparative study of PCS and PAM50 prostate cancer classification schemes. Prostate Cancer and Prostatic Diseases, 2021, 24, 733-742.	2.0	14
125	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
126	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

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127	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
128	Pan-Cancer Analysis of Genomic Sequencing Among the Elderly. International Journal of Radiation Oncology Biology Physics, 2017, 98, 726-732.	0.4	11
129	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
130	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
131	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
132	A transcriptomic model for homologous recombination deficiency in prostate cancer. Prostate Cancer and Prostatic Diseases, 2022, 25, 659-665.	2.0	9
133	A fourâ€gene transcript score to predict metastaticâ€lethal progression in men treated for localized prostate cancer: Development and validation studies. Prostate, 2019, 79, 1589-1596.	1.2	8
134	Low Tristetraprolin Expression Is Associated with Lethal Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 584-590.	1.1	8
135	Genomic and clinical characterization of stromal infiltration markers in prostate cancer. Cancer, 2020, 126, 1407-1412.	2.0	8
136	Prognostic value of the SPOP mutant genomic subclass in prostate cancer. Urologic Oncology: Seminars and Original Investigations, 2020, 38, 418-422.	0.8	8
137	Diversity in Androgen Receptor Action Among Treatment-na $\tilde{A}$ -ve Prostate Cancers Is Reflected in Treatment Response Predictions and Molecular Subtypes. European Urology Open Science, 2020, 22, 34-44.	0.2	7
138	Variation in Molecularly Defined Prostate Tumor Subtypes by Self-identified Race. European Urology Open Science, 2022, 40, 19-26.	0.2	7
139	Evolving transcriptomic fingerprint based on genomeâ€wide data as prognostic tools in prostate cancer. Biology of the Cell, 2015, 107, 232-244.	0.7	6
140	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
141	Identifying and treating <i>ROBO1</i> <sup>â^ve</sup> / <i>DOCK1</i> <sup>+ve</sup> prostate cancer: An aggressive cancer subtype prevalent in African American patients. Prostate, 2020, 80, 1045-1057.	1.2	5
142	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
143	Association between Incidental Pelvic Inflammation and Aggressive Prostate Cancer. Cancers, 2022, 14, 2734.	1.7	5
144	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

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145	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
146	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
147	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
148	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
149	Genomic biomarkers to guide precision radiotherapy in prostate cancer. Prostate, 2022, 82, .	1.2	3
150	Transcriptome evaluation of the relation between body mass index and prostate cancer outcomes. Cancer, 2017, 123, 2240-2247.	2.0	2
151	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
152	Predictors of Prostate-specific Membrane Antigen (PSMA/FOLH1) Expression in a Genomic Database. Urology, 2020, 144, 117-122.	0.5	2
153	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
154	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
155	2239 CLINICAL AND GENOMIC ANALYSIS OF METASTATIC DISEASE PROGRESSION IN A BACKGROUND OF BIOCHEMICAL RECURRENCE. Journal of Urology, 2013, 189, .	0.2	1
156	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
157	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
158	Prostate cancer in young men represents a distinct clinical phenotype: gene expression signature to predict early metastases., 2021, 5, 50-61.		1
159	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