

# Lars DyrskjÅ,t

## List of Publications by Year in descending order

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122  
papers

11,611  
citations

24978

57  
h-index

29081

104  
g-index

132  
all docs

132  
docs citations

132  
times ranked

15863  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Consensus Molecular Classification of Muscle-invasive Bladder Cancer. <i>European Urology</i> , 2020, 77, 420-433.	0.9	741
2	Analysis of Plasma Cell-Free DNA by Ultradeep Sequencing in Patients With Stages I to III Colorectal Cancer. <i>JAMA Oncology</i> , 2019, 5, 1124.	3.4	538
3	Comprehensive Transcriptional Analysis of Early-Stage Urothelial Carcinoma. <i>Cancer Cell</i> , 2016, 30, 27-42.	7.7	486
4	Diagnostic and Prognostic MicroRNAs in Stage II Colon Cancer. <i>Cancer Research</i> , 2008, 68, 6416-6424.	0.4	459
5	Identifying distinct classes of bladder carcinoma using microarrays. <i>Nature Genetics</i> , 2003, 33, 90-96.	9.4	452
6	Gene Expression in the Urinary Bladder. <i>Cancer Research</i> , 2004, 64, 4040-4048.	0.4	402
7	Genomic Profiling of MicroRNAs in Bladder Cancer: miR-129 Is Associated with Poor Outcome and Promotes Cell Death <i>in vitro</i> . <i>Cancer Research</i> , 2009, 69, 4851-4860.	0.4	349
8	Coordinated epigenetic repression of the miR-200 family and miR-205 in invasive bladder cancer. <i>International Journal of Cancer</i> , 2011, 128, 1327-1334.	2.3	335
9	Early Detection of Metastatic Relapse and Monitoring of Therapeutic Efficacy by Ultra-Deep Sequencing of Plasma Cell-Free DNA in Patients With Urothelial Bladder Carcinoma. <i>Journal of Clinical Oncology</i> , 2019, 37, 1547-1557.	0.8	298
10	Next-Generation Sequencing of RNA and DNA Isolated from Paired Fresh-Frozen and Formalin-Fixed Paraffin-Embedded Samples of Human Cancer and Normal Tissue. <i>PLoS ONE</i> , 2014, 9, e98187.	1.1	284
11	Comparative analysis of discrete exosome fractions obtained by differential centrifugation. <i>Journal of Extracellular Vesicles</i> , 2014, 3, 25011.	5.5	262
12	Cellular Disposal of miR23b by RAB27-Dependent Exosome Release Is Linked to Acquisition of Metastatic Properties. <i>Cancer Research</i> , 2014, 74, 5758-5771.	0.4	237
13	Detection of microRNAs in frozen tissue sections by fluorescence in situ hybridization using locked nucleic acid probes and tyramide signal amplification. <i>Nature Protocols</i> , 2007, 2, 2520-2528.	5.5	221
14	Pervasive chromosomal instability and karyotype order in tumour evolution. <i>Nature</i> , 2020, 587, 126-132.	13.7	221
15	Alternative Splicing in Colon, Bladder, and Prostate Cancer Identified by Exon Array Analysis. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1214-1224.	2.5	202
16	Emmprin and Survivin Predict Response and Survival following Cisplatin-Containing Chemotherapy in Patients with Advanced Bladder Cancer. <i>Clinical Cancer Research</i> , 2007, 13, 4407-4414.	3.2	198
17	Genetic Alterations in the Molecular Subtypes of Bladder Cancer: Illustration in the Cancer Genome Atlas Dataset. <i>European Urology</i> , 2017, 72, 354-365.	0.9	195
18	Gene Expression Signatures Predict Outcome in Non-Muscle-Invasive Bladder Carcinoma: A Multicenter Validation Study. <i>Clinical Cancer Research</i> , 2007, 13, 3545-3551.	3.2	189

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19	Comprehensive Genome Methylation Analysis in Bladder Cancer: Identification and Validation of Novel Methylated Genes and Application of These as Urinary Tumor Markers. <i>Clinical Cancer Research</i> , 2011, 17, 5582-5592.	3.2	183
20	Genomic Alterations in Liquid Biopsies from Patients with Bladder Cancer. <i>European Urology</i> , 2016, 70, 75-82.	0.9	174
21	An integrated multi-omics analysis identifies prognostic molecular subtypes of non-muscle-invasive bladder cancer. <i>Nature Communications</i> , 2021, 12, 2301.	5.8	159
22	Liquid Biopsy Analysis of FGFR3 and PIK3CA Hotspot Mutations for Disease Surveillance in Bladder Cancer. <i>European Urology</i> , 2017, 71, 961-969.	0.9	154
23	Quantitative proteomics of fractionated membrane and lumen exosome proteins from isogenic metastatic and nonmetastatic bladder cancer cells reveal differential expression of EMT factors. <i>Proteomics</i> , 2014, 14, 699-712.	1.3	148
24	SOX4 Expression in Bladder Carcinoma: Clinical Aspects and In vitro Functional Characterization. <i>Cancer Research</i> , 2006, 66, 3434-3442.	0.4	146
25	MicroRNA profiles of prostate carcinoma detected by multiplatform microRNA screening. <i>International Journal of Cancer</i> , 2012, 130, 611-621.	2.3	141
26	Evaluation of two commercial global miRNA expression profiling platforms for detection of less abundant miRNAs. <i>BMC Genomics</i> , 2011, 12, 435.	1.2	140
27	A Molecular Signature in Superficial Bladder Carcinoma Predicts Clinical Outcome. <i>Clinical Cancer Research</i> , 2005, 11, 4029-4036.	3.2	136
28	Mutational Context and Diverse Clonal Development in Early and Late Bladder Cancer. <i>Cell Reports</i> , 2014, 7, 1649-1663.	2.9	128
29	Molecular correlates of cisplatin-based chemotherapy response in muscle invasive bladder cancer by integrated multi-omics analysis. <i>Nature Communications</i> , 2020, 11, 4858.	5.8	124
30	Profiling of long non-coding RNAs identifies LINC00958 and LINC01296 as candidate oncogenes in bladder cancer. <i>Scientific Reports</i> , 2017, 7, 395.	1.6	117
31	Diagnosis of Bladder Cancer Recurrence Based on Urinary Levels of EOMES, HOXA9, POU4F2, TWIST1, VIM, and ZNF154 Hypermethylation. <i>PLoS ONE</i> , 2012, 7, e46297.	1.1	112
32	Monitoring Treatment Response and Metastatic Relapse in Advanced Bladder Cancer by Liquid Biopsy Analysis. <i>European Urology</i> , 2018, 73, 535-540.	0.9	112
33	Adaptive differences in gene expression in European flounder ( <i>Platichthys flesus</i> ). <i>Molecular Ecology</i> , 2007, 16, 4674-4683.	2.0	111
34	Comprehensive multiregional analysis of molecular heterogeneity in bladder cancer. <i>Scientific Reports</i> , 2017, 7, 11702.	1.6	110
35	Molecular Profiling of ADAM12 in Human Bladder Cancer. <i>Clinical Cancer Research</i> , 2006, 12, 7359-7368.	3.2	108
36	Expression profiling of prostate cancer tissue delineates genes associated with recurrence after prostatectomy. <i>Scientific Reports</i> , 2015, 5, 16018.	1.6	108

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37	Transcriptome-wide profiles of circular RNA and RNA-binding protein interactions reveal effects on circular RNA biogenesis and cancer pathway expression. <i>Genome Medicine</i> , 2020, 12, 112.	3.6	106
38	Circular RNA expression is abundant and correlated to aggressiveness in early-stage bladder cancer. <i>Npj Genomic Medicine</i> , 2017, 2, 36.	1.7	105
39	The functional role of the novel biomarker karyopherin Î± 2 (KPNA2) in cancer. <i>Cancer Letters</i> , 2013, 331, 18-23.	3.2	104
40	Tumor-promoting macrophages induce the expression of the macrophage-specific receptor CD163 in malignant cells. <i>International Journal of Cancer</i> , 2012, 131, 2320-2331.	2.3	103
41	Validation of a DNA Methylation-Mutation Urine Assay to Select Patients with Hematuria for Cystoscopy. <i>Journal of Urology</i> , 2017, 197, 590-595.	0.2	102
42	Genomic heterogeneity in bladder cancer: challenges and possible solutions to improve outcomes. <i>Nature Reviews Urology</i> , 2020, 17, 259-270.	1.9	100
43	Expression of TIP60 (tata-interactive protein) and MRE11 (meiotic recombination 11 homolog) predict treatment-specific outcome of localised invasive bladder cancer. <i>BJU International</i> , 2012, 110, E1228-36.	1.3	92
44	The effect of surgical trauma on circulating free DNA levels in cancer patientsâ€”implications for studies of circulating tumor DNA. <i>Molecular Oncology</i> , 2020, 14, 1670-1679.	2.1	89
45	Role of Activating Fibroblast Growth Factor Receptor 3 Mutations in the Development of Bladder Tumors. <i>Clinical Cancer Research</i> , 2005, 11, 7709-7719.	3.2	87
46	Paired Exome Analysis Reveals Clonal Evolution and Potential Therapeutic Targets in Urothelial Carcinoma. <i>Cancer Research</i> , 2016, 76, 5894-5906.	0.4	87
47	Cathepsin E, Maspin, Plk1, and Survivin Are Promising Prognostic Protein Markers for Progression in Non-Muscle Invasive Bladder Cancer. <i>American Journal of Pathology</i> , 2012, 180, 1824-1834.	1.9	86
48	miRNAs associated with chemo-sensitivity in cell lines and in advanced bladder cancer. <i>BMC Medical Genomics</i> , 2012, 5, 40.	0.7	86
49	Tumour exosomes display differential mechanical and complement activation properties dependent on malignant state: implications in endothelial leakiness. <i>Journal of Extracellular Vesicles</i> , 2015, 4, 29685.	5.5	86
50	Molecular Markers Increase Precision of the European Association of Urology Non-Muscle-Invasive Bladder Cancer Progression Risk Groups. <i>Clinical Cancer Research</i> , 2018, 24, 1586-1593.	3.2	79
51	Identification of Differential Tumor Subtypes of T1 Bladder Cancer. <i>European Urology</i> , 2020, 78, 533-537.	0.9	77
52	Prognostic Impact of a 12-gene Progression Score in Non-muscle-invasive Bladder Cancer: A Prospective Multicentre Validation Study. <i>European Urology</i> , 2017, 72, 461-469.	0.9	74
53	Alternative Splicing of SLC39A14 in Colorectal Cancer is Regulated by the Wnt Pathway. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.002998.	2.5	73
54	Multicenter Validation of Cyclin D1, MCM7, TRIM29, and UBE2C as Prognostic Protein Markers in Non-Muscle-Invasive Bladder Cancer. <i>American Journal of Pathology</i> , 2013, 182, 339-349.	1.9	71

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55	High Expression of Karyopherin-1 $\pm$ 2 Defines Poor Prognosis in Non-Muscle-Invasive Bladder Cancer and in Patients with Invasive Bladder Cancer Undergoing Radical Cystectomy. <i>European Urology</i> , 2011, 59, 841-848.	0.9	70
56	Novel diagnostic and prognostic classifiers for prostate cancer identified by genome-wide microRNA profiling. <i>Oncotarget</i> , 2016, 7, 30760-30771.	0.8	70
57	Prediction and diagnosis of bladder cancer recurrence based on urinary content of hTERT, SENP1, PPP1CA, and MCM5 transcripts. <i>BMC Cancer</i> , 2010, 10, 646.	1.1	60
58	Tumor-specific usage of alternative transcription start sites in colorectal cancer identified by genome-wide exon array analysis. <i>BMC Genomics</i> , 2011, 12, 505.	1.2	57
59	Autophagy role(s) in response to oncogenes and DNA replication stress. <i>Cell Death and Differentiation</i> , 2020, 27, 1134-1153.	5.0	57
60	Representative Sequencing: Unbiased Sampling of Solid Tumor Tissue. <i>Cell Reports</i> , 2020, 31, 107550.	2.9	51
61	Optimized targeted sequencing of cell-free plasma DNA from bladder cancer patients. <i>Scientific Reports</i> , 2018, 8, 1917.	1.6	50
62	Discordant molecular subtype classification in the basal-squamous subtype of bladder tumors and matched lymph-node metastases. <i>Modern Pathology</i> , 2018, 31, 1869-1881.	2.9	47
63	Risk Prediction Scores for Recurrence and Progression of Non-Muscle Invasive Bladder Cancer: An International Validation in Primary Tumours. <i>PLoS ONE</i> , 2014, 9, e96849.	1.1	46
64	Consistent genomic alterations in carcinoma <i>in situ</i> of the urinary bladder confirm the presence of two major pathways in bladder cancer development. <i>International Journal of Cancer</i> , 2009, 125, 2095-2103.	2.3	45
65	External Validation of a Multiplex Urinary Protein Panel for the Detection of Bladder Cancer in a Multicenter Cohort. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 1804-1812.	1.1	44
66	Spatial and temporal clonal evolution during development of metastatic urothelial carcinoma. <i>Molecular Oncology</i> , 2016, 10, 1450-1460.	2.1	44
67	Isolation of Microarray-Grade Total RNA, MicroRNA, and DNA from a Single PAXgene Blood RNA Tube. <i>Journal of Molecular Diagnostics</i> , 2007, 9, 452-458.	1.2	41
68	Next-generation sequencing identifies germline MRE11A variants as markers of radiotherapy outcomes in muscle-invasive bladder cancer. <i>Annals of Oncology</i> , 2014, 25, 877-883.	0.6	41
69	Snail1 is overexpressed in prostate cancer. <i>Apmis</i> , 2009, 117, 196-204.	0.9	40
70	Classification of bladder cancer by microarray expression profiling: towards a general clinical use of microarrays in cancer diagnostics. <i>Expert Review of Molecular Diagnostics</i> , 2003, 3, 635-647.	1.5	39
71	Increased expression of transcription factor TFAP2 $\pm$ correlates with chemosensitivity in advanced bladder cancer. <i>BMC Cancer</i> , 2011, 11, 135.	1.1	35
72	Exosomes of invasive urothelial carcinoma cells are characterized by a specific miRNA expression signature. <i>Oncotarget</i> , 2017, 8, 58278-58291.	0.8	35

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73	APOBEC-mediated Mutagenesis as a Likely Cause of FGFR3 S249C Mutation Over-representation in Bladder Cancer. <i>European Urology</i> , 2019, 76, 9-13.	0.9	34
74	Clinical Utility of Cell-free and Circulating Tumor DNA in Kidney and Bladder Cancer: A Critical Review of Current Literature. <i>European Urology Oncology</i> , 2021, 4, 893-903.	2.6	31
75	High frequency of tumor cells with nuclear Egr-1 protein expression in human bladder cancer is associated with disease progression. <i>BMC Cancer</i> , 2009, 9, 385.	1.1	30
76	Re: AurÃ©lie Kamoun, AurÃ©lien de ReyniÃ©s, Yves Allory, et al. A Consensus Molecular Classification of Muscle-invasive Bladder Cancer. <i>Eur Urol</i> 2020;77:420â€“33. <i>European Urology</i> , 2020, 77, e105-e106.	0.9	29
77	High miR-449b expression in prostate cancer is associated with biochemical recurrence after radical prostatectomy. <i>BMC Cancer</i> , 2014, 14, 859.	1.1	28
78	Increased cell motility and invasion upon knockdown of lipolysis stimulated lipoprotein receptor (LSR) in SW780 bladder cancer cells. <i>BMC Medical Genomics</i> , 2008, 1, 31.	0.7	27
79	Genetic and Epigenetic <i>SLC18A2</i> Silencing in Prostate Cancer Is an Independent Adverse Predictor of Biochemical Recurrence after Radical Prostatectomy. <i>Clinical Cancer Research</i> , 2009, 15, 1400-1410.	3.2	26
80	The exon-junction complex helicase eIF4A3 controls cell fate via coordinated regulation of ribosome biogenesis and translational output. <i>Science Advances</i> , 2021, 7, .	4.7	25
81	High expression of GEM and EDNRA is associated with metastasis and poor outcome in patients with advanced bladder cancer. <i>BMC Cancer</i> , 2014, 14, 638.	1.1	24
82	Downregulation of zinc finger protein 132 in prostate cancer is associated with aberrant promoter hypermethylation and poor prognosis. <i>International Journal of Cancer</i> , 2012, 130, 885-895.	2.3	23
83	STAG2 Is a Biomarker for Prediction of Recurrence and Progression in Papillary Non-Muscle-Invasive Bladder Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 4145-4153.	3.2	23
84	Chromosomal deletion, promoter hypermethylation and downregulation of <i>FYN</i> in prostate cancer. <i>International Journal of Cancer</i> , 2008, 122, 509-519.	2.3	22
85	The DaBlaCa-13 Study: Short-term, Intensive Chemoresection Versus Standard Adjuvant Intravesical Instillations in Non-muscle-invasive Bladder Cancerâ€”A Randomised Controlled Trial. <i>European Urology</i> , 2020, 78, 856-862.	0.9	20
86	Biology of nonmuscle-invasive bladder cancer. <i>Current Opinion in Urology</i> , 2018, 28, 598-603.	0.9	19
87	Association of MMP-2, RB and PAI-1 with decreased recurrence-free survival and overall survival in bladder cancer patients. <i>Oncotarget</i> , 2017, 8, 99707-99721.	0.8	19
88	The Splicing Efficiency of Activating HRAS Mutations Can Determine Costello Syndrome Phenotype and Frequency in Cancer. <i>PLoS Genetics</i> , 2016, 12, e1006039.	1.5	18
89	Androgen Receptor mRNA Expression in Urothelial Carcinoma of the Bladder: A Retrospective Analysis of Two Independent Cohorts. <i>Translational Oncology</i> , 2019, 12, 661-668.	1.7	16
90	Chromosomal imbalance in the progression of high-risk non-muscle invasive bladder cancer. <i>BMC Cancer</i> , 2009, 9, 149.	1.1	15

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91	Toward personalized management in bladder cancer: the promise of novel molecular taxonomy. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2017, 471, 271-280.	1.4	15
92	Challenges in the Diagnosis of Urothelial Carcinoma Variants: Can Emerging Molecular Data Complement Pathology Review?. <i>Urology</i> , 2017, 102, 7-16.	0.5	15
93	Identification of ADAM12 as a Novel Basigin Sheddase. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1957.	1.8	15
94	Immune Contexture and Differentiation Features Predict Outcome in Bladder Cancer. <i>European Urology Oncology</i> , 2022, 5, 203-213.	2.6	14
95	Stage-stratified molecular profiling of non-muscle-invasive bladder cancer enhances biological, clinical, and therapeutic insight. <i>Cell Reports Medicine</i> , 2021, 2, 100472.	3.3	13
96	Mutational Analysis of Field Cancerization in Bladder Cancer. <i>Bladder Cancer</i> , 2020, 6, 253-264.	0.2	12
97	Smarcc1 expression: A significant predictor of disease-specific survival in patients with clinically localized prostate cancer treated with no intention to cure. <i>Scandinavian Journal of Urology and Nephrology</i> , 2011, 45, 91-96.	1.4	10
98	Gene Networks Modified by Sulphonylureas in Beta Cells: A Pathway-based Analysis of Insulin Secretion and Cell Death. <i>Basic and Clinical Pharmacology and Toxicology</i> , 2012, 111, 254-261.	1.2	10
99	Recent developments in molecular profiling of bladder cancer. <i>Current Opinion in Urology</i> , 2006, 16, 377-381.	0.9	9
100	STAG2 as a prognostic biomarker in low-grade non-muscle invasive bladder cancer. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2021, 39, 438.e1-438.e9.	0.8	9
101	Molecular Subtypes of Bladder Cancer: Academic Exercise or Clinical Relevance?. <i>European Urology</i> , 2019, 75, 433-434.	0.9	8
102	Targeting natural splicing plasticity of APOBEC3B restricts its expression and mutagenic activity. <i>Communications Biology</i> , 2021, 4, 386.	2.0	7
103	Characterizing molecular subtypes of high-risk non-muscle-invasive bladder cancer in African American patients. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2022, 40, 410.e19-410.e27.	0.8	7
104	Bioinformatic identification of FGF, p38-MAPK, and calcium signalling pathways associated with carcinoma in situ in the urinary bladder. <i>BMC Cancer</i> , 2008, 8, 37.	1.1	6
105	A miRNA signature predicts benefit from addition of hypoxia-modifying therapy to radiation treatment in invasive bladder cancer. <i>British Journal of Cancer</i> , 2021, 125, 85-93.	2.9	6
106	Classifying cGAS-STING Activity Links Chromosomal Instability with Immunotherapy Response in Metastatic Bladder Cancer. <i>Cancer Research Communications</i> , 2022, 2, 762-771.	0.7	6
107	Converging Roads to Early Bladder Cancer. <i>European Urology</i> , 2020, 78, 127-130.	0.9	5
108	Genome-wide Meta-analysis Identifies Novel Genes Associated with Recurrence and Progression in Non-muscle-invasive Bladder Cancer. <i>European Urology Oncology</i> , 2022, 5, 70-83.	2.6	5

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109	Gene signatures for risk-adapted treatment of bladder cancer. Scandinavian Journal of Urology and Nephrology, 2008, 42, 166-174.	1.4	3
110	Large-scale genomic comparison of UTUC and bladder tumours. Nature Reviews Urology, 2019, 16, 149-150.	1.9	3
111	Reply to Alexander Yang, Vincent L. Cannataro, Jeffrey P. Townsend's Letter to the Editor, re: Ming-Jun Shi, Xiang-Yu Meng, Philippe Lamy, et al. APOBEC-mediated Mutagenesis as a Likely Cause of FGFR3 S249C Mutation Over-representation in Bladder Cancer. Eur Urol 2019, 76:9-13. European Urology, 2020, 77, e26-e27.	0.9	3
112	Reply to: Reconciling differences in impact of molecular subtyping on response to cisplatin-based chemotherapy. Nature Communications, 2021, 12, 4834.	5.8	3
113	Abstract 913: Early detection of metastatic relapse and monitoring of therapeutic efficacy by ultra-deep sequencing of plasma cell-free DNA in patients with urothelial bladder carcinoma. , 2019, , .		3
114	PAI-1 is a potential transcriptional silencer that supports bladder cancer cell activity. Scientific Reports, 2022, 12, .	1.6	3
115	DNA Microarrays and Genetic Testing. , 2010, , 247-265.		2
116	Refinement of an Established Procedure and Its Application for Identification of Hypoxia in Prostate Cancer Xenografts. Cancers, 2021, 13, 2602.	1.7	2
117	Reply To Kenneth B. Yatai, Mark J. Dunning, Dennis Wang. Consensus Genomic Subtypes of Muscle-invasive Bladder Cancer: A Step in the Right Direction but Still a Long Way To Go. Eur Urol 2020;77:434-435. European Urology, 2020, 77, 436-438.	0.9	1
118	Sensitivity and Specificity in Urine Bladder Cancer Markers " Is it that Simple?. Bladder Cancer, 2022, 8, 1-4.	0.2	1
119	SPTAN1, APC, and FGFR3 Mutation Status and APOBEC Mutation Signatures are Predictive of Mitomycin C Response in Non-muscle-invasive Bladder Cancer. European Urology Open Science, 2021, 34, 59-67.	0.2	1
120	Microarrays for Gene Expression ProfilingFabrication of Oligonucleotide Microarrays, Isolation of RNA, Fluorescent Labeling of cRNA, Hybridization, and Scanning. , 2006, , 83-93.		0
121	Expression Profiling of Hereditary versus Sporadic Prostate Cancer Suggests CYR61, EGR3, KLF6 and SNF1LK as Differentially Expressed Genes. Open Journal of Urology, 2012, 02, 55-66.	0.0	0
122	Characterizing molecular subtypes of high-risk nonmuscle-invasive bladder cancer in African American patients.. Journal of Clinical Oncology, 2022, 40, 527-527.	0.8	0