

Lars Dyrskj t

List of Publications by Year in descending order

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Version: 2024-02-01

122
papers

11,611
citations

25034

57
h-index

29157

104
g-index

132
all docs

132
docs citations

132
times ranked

15863
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	5.4	5
2	Sensitivity and Specificity in Urine Bladder Cancer Markers – Is it that Simple?. <i>Bladder Cancer</i> , 2022, 8, 1-4.	0.4	1
3	Characterizing molecular subtypes of high-risk nonmuscle-invasive bladder cancer in African American patients.. <i>Journal of Clinical Oncology</i> , 2022, 40, 527-527.	1.6	0
4	Immune Contexture and Differentiation Features Predict Outcome in Bladder Cancer. <i>European Urology Oncology</i> , 2022, 5, 203-213.	5.4	14
5	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.	1.6	7
6	Classifying cGAS-STING Activity Links Chromosomal Instability with Immunotherapy Response in Metastatic Bladder Cancer. <i>Cancer Research Communications</i> , 2022, 2, 762-771.	1.7	6
7	PAI-1 is a potential transcriptional silencer that supports bladder cancer cell activity. <i>Scientific Reports</i> , 2022, 12, .	3.3	3
8	Targeting natural splicing plasticity of APOBEC3B restricts its expression and mutagenic activity. <i>Communications Biology</i> , 2021, 4, 386.	4.4	7
9	An integrated multi-omics analysis identifies prognostic molecular subtypes of non-muscle-invasive bladder cancer. <i>Nature Communications</i> , 2021, 12, 2301.	12.8	159
10	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.	6.4	6
11	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.	5.4	31
12	Refinement of an Established Procedure and Its Application for Identification of Hypoxia in Prostate Cancer Xenografts. <i>Cancers</i> , 2021, 13, 2602.	3.7	2
13	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.	1.6	9
14	The exon-junction complex helicase eIF4A3 controls cell fate via coordinated regulation of ribosome biogenesis and translational output. <i>Science Advances</i> , 2021, 7, .	10.3	25
15	Reply to: Reconciling differences in impact of molecular subtyping on response to cisplatin-based chemotherapy. <i>Nature Communications</i> , 2021, 12, 4834.	12.8	3
16	SPTAN1, APC, and FGFR3 Mutation Status and APOBEC Mutation Signatures are Predictive of Mitomycin C Response in Non-muscle-invasive Bladder Cancer. <i>European Urology Open Science</i> , 2021, 34, 59-67.	0.4	1
17	Stage-stratified molecular profiling of non-muscle-invasive bladder cancer enhances biological, clinical, and therapeutic insight. <i>Cell Reports Medicine</i> , 2021, 2, 100472.	6.5	13
18	A Consensus Molecular Classification of Muscle-invasive Bladder Cancer. <i>European Urology</i> , 2020, 77, 420-433.	1.9	741

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19	Autophagy role(s) in response to oncogenes and DNA replication stress. <i>Cell Death and Differentiation</i> , 2020, 27, 1134-1153.	11.2	57
20	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. <i>Eur Urol</i> 2019, 76:9â€“13. <i>European Urology</i> , 2020, 77, e26-e27.	1.9	3
21	Re: Aurélie Kamoun, Aurélien de Reyni'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.	1.9	29
22	Identification of Differential Tumor Subtypes of T1 Bladder Cancer. <i>European Urology</i> , 2020, 78, 533-537.	1.9	77
23	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.	8.2	106
24	The DaBlaCa-13 Study: Short-term, Intensive Chemoresection Versus Standard Adjuvant Intravesical Instillations in Non-muscle-invasive Bladder Cancer: A Randomised Controlled Trial. <i>European Urology</i> , 2020, 78, 856-862.	1.9	20
25	Pervasive chromosomal instability and karyotype order in tumour evolution. <i>Nature</i> , 2020, 587, 126-132.	27.8	221
26	Molecular correlates of cisplatin-based chemotherapy response in muscle invasive bladder cancer by integrated multi-omics analysis. <i>Nature Communications</i> , 2020, 11, 4858.	12.8	124
27	The effect of surgical trauma on circulating free DNA levels in cancer patients: implications for studies of circulating tumor DNA. <i>Molecular Oncology</i> , 2020, 14, 1670-1679.	4.6	89
28	Representative Sequencing: Unbiased Sampling of Solid Tumor Tissue. <i>Cell Reports</i> , 2020, 31, 107550.	6.4	51
29	Converging Roads to Early Bladder Cancer. <i>European Urology</i> , 2020, 78, 127-130.	1.9	5
30	Genomic heterogeneity in bladder cancer: challenges and possible solutions to improve outcomes. <i>Nature Reviews Urology</i> , 2020, 17, 259-270.	3.8	100
31	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. <i>Eur Urol</i> 2020;77:434â€“5. <i>European Urology</i> , 2020, 77, 436-438.	1.9	1
32	Mutational Analysis of Field Cancerization in Bladder Cancer. <i>Bladder Cancer</i> , 2020, 6, 253-264.	0.4	12
33	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.	7.1	538
34	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.	1.6	298
35	Identification of ADAM12 as a Novel Basigin Sheddase. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1957.	4.1	15
36	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.	3.7	16

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37	APOBEC-mediated Mutagenesis as a Likely Cause of FGFR3 S249C Mutation Over-representation in Bladder Cancer. <i>European Urology</i> , 2019, 76, 9-13.	1.9	34
38	Large-scale genomic comparison of UTUC and bladder tumours. <i>Nature Reviews Urology</i> , 2019, 16, 149-150.	3.8	3
39	Molecular Subtypes of Bladder Cancer: Academic Exercise or Clinical Relevance?. <i>European Urology</i> , 2019, 75, 433-434.	1.9	8
40	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
41	Molecular Markers Increase Precision of the European Association of Urology Nonâ€Muscle-Invasive Bladder Cancer Progression Risk Groups. <i>Clinical Cancer Research</i> , 2018, 24, 1586-1593.	7.0	79
42	Optimized targeted sequencing of cell-free plasma DNA from bladder cancer patients. <i>Scientific Reports</i> , 2018, 8, 1917.	3.3	50
43	Monitoring Treatment Response and Metastatic Relapse in Advanced Bladder Cancer by Liquid Biopsy Analysis. <i>European Urology</i> , 2018, 73, 535-540.	1.9	112
44	Biology of nonmuscle-invasive bladder cancer. <i>Current Opinion in Urology</i> , 2018, 28, 598-603.	1.8	19
45	STAG2 Is a Biomarker for Prediction of Recurrence and Progression in Papillary Nonâ€Muscle-Invasive Bladder Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 4145-4153.	7.0	23
46	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.	5.5	47
47	Liquid Biopsy Analysis of FGFR3 and PIK3CA Hotspot Mutations for Disease Surveillance in Bladder Cancer. <i>European Urology</i> , 2017, 71, 961-969.	1.9	154
48	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.	2.8	15
49	Genetic Alterations in the Molecular Subtypes of Bladder Cancer: Illustration in the Cancer Genome Atlas Dataset. <i>European Urology</i> , 2017, 72, 354-365.	1.9	195
50	Profiling of long non-coding RNAs identifies LINC00958 and LINC01296 as candidate oncogenes in bladder cancer. <i>Scientific Reports</i> , 2017, 7, 395.	3.3	117
51	Comprehensive multiregional analysis of molecular heterogeneity in bladder cancer. <i>Scientific Reports</i> , 2017, 7, 11702.	3.3	110
52	Circular RNA expression is abundant and correlated to aggressiveness in early-stage bladder cancer. <i>Npj Genomic Medicine</i> , 2017, 2, 36.	3.8	105
53	Validation of a DNA Methylation-Mutation Urine Assay to Select Patients with Hematuria for Cystoscopy. <i>Journal of Urology</i> , 2017, 197, 590-595.	0.4	102
54	Challenges in the Diagnosis of Urothelial Carcinoma Variants: Can Emerging Molecular Data Complement Pathology Review?. <i>Urology</i> , 2017, 102, 7-16.	1.0	15

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55	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.	1.9	74
56	Exosomes of invasive urothelial carcinoma cells are characterized by a specific miRNA expression signature. <i>Oncotarget</i> , 2017, 8, 58278-58291.	1.8	35
57	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.	1.8	19
58	The Splicing Efficiency of Activating HRAS Mutations Can Determine Costello Syndrome Phenotype and Frequency in Cancer. <i>PLoS Genetics</i> , 2016, 12, e1006039.	3.5	18
59	Paired Exome Analysis Reveals Clonal Evolution and Potential Therapeutic Targets in Urothelial Carcinoma. <i>Cancer Research</i> , 2016, 76, 5894-5906.	0.9	87
60	Spatial and temporal clonal evolution during development of metastatic urothelial carcinoma. <i>Molecular Oncology</i> , 2016, 10, 1450-1460.	4.6	44
61	Comprehensive Transcriptional Analysis of Early-Stage Urothelial Carcinoma. <i>Cancer Cell</i> , 2016, 30, 27-42.	16.8	486
62	Genomic Alterations in Liquid Biopsies from Patients with Bladder Cancer. <i>European Urology</i> , 2016, 70, 75-82.	1.9	174
63	Novel diagnostic and prognostic classifiers for prostate cancer identified by genome-wide microRNA profiling. <i>Oncotarget</i> , 2016, 7, 30760-30771.	1.8	70
64	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.	12.2	86
65	Expression profiling of prostate cancer tissue delineates genes associated with recurrence after prostatectomy. <i>Scientific Reports</i> , 2015, 5, 16018.	3.3	108
66	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.	2.5	284
67	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.	2.5	46
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.	1.2	41
69	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.	2.6	24
70	High miR-449b expression in prostate cancer is associated with biochemical recurrence after radical prostatectomy. <i>BMC Cancer</i> , 2014, 14, 859.	2.6	28
71	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.	2.2	148
72	Cellular Disposal of miR23b by RAB27-Dependent Exosome Release Is Linked to Acquisition of Metastatic Properties. <i>Cancer Research</i> , 2014, 74, 5758-5771.	0.9	237

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73	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.	2.5	44
74	Mutational Context and Diverse Clonal Development in Early and Late Bladder Cancer. <i>Cell Reports</i> , 2014, 7, 1649-1663.	6.4	128
75	Comparative analysis of discrete exosome fractions obtained by differential centrifugation. <i>Journal of Extracellular Vesicles</i> , 2014, 3, 25011.	12.2	262
76	The functional role of the novel biomarker karyopherin β 2 (KPNA2) in cancer. <i>Cancer Letters</i> , 2013, 331, 18-23.	7.2	104
77	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.	3.8	71
78	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.	3.8	86
79	miRNAs associated with chemo-sensitivity in cell lines and in advanced bladder cancer. <i>BMC Medical Genomics</i> , 2012, 5, 40.	1.5	86
80	Expression of TIP60 (tata box-interacting protein) and MRE11 (meiotic recombination 11 homolog) predict treatment-specific outcome of localised invasive bladder cancer. <i>BJU International</i> , 2012, 110, E1228-36.	2.5	92
81	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.	2.5	112
82	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.	5.1	103
83	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.	2.5	10
84	MicroRNA profiles of prostate carcinoma detected by multiplatform microRNA screening. <i>International Journal of Cancer</i> , 2012, 130, 611-621.	5.1	141
85	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.	5.1	23
86	Expression Profiling of Hereditary versus Sporadic Prostate Cancer Suggests CYR61, EGR3, KLF6 and SNF1LK as Differentially Expressed Genes. <i>Open Journal of Urology</i> , 2012, 02, 55-66.	0.1	0
87	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.	7.0	183
88	Evaluation of two commercial global miRNA expression profiling platforms for detection of less abundant miRNAs. <i>BMC Genomics</i> , 2011, 12, 435.	2.8	140
89	High Expression of Karyopherin- β 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.	1.9	70
90	Increased expression of transcription factor TFAP2 β correlates with chemosensitivity in advanced bladder cancer. <i>BMC Cancer</i> , 2011, 11, 135.	2.6	35

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91	Tumor-specific usage of alternative transcription start sites in colorectal cancer identified by genome-wide exon array analysis. BMC Genomics, 2011, 12, 505.	2.8	57
92	Coordinated epigenetic repression of the miR-200 family and miR-205 in invasive bladder cancer. International Journal of Cancer, 2011, 128, 1327-1334.	5.1	335
93	Alternative Splicing of SLC39A14 in Colorectal Cancer is Regulated by the Wnt Pathway. Molecular and Cellular Proteomics, 2011, 10, M110.002998.	3.8	73
94	Smarcc1 expression: A significant predictor of disease-specific survival in patients with clinically localized prostate cancer treated with no intention to cure. Scandinavian Journal of Urology and Nephrology, 2011, 45, 91-96.	1.4	10
95	Prediction and diagnosis of bladder cancer recurrence based on urinary content of hTERT, SENP1, PPP1CA, and MCM5 transcripts. BMC Cancer, 2010, 10, 646.	2.6	60
96	DNA Microarrays and Genetic Testing. , 2010, , 247-265.		2
97	Genomic Profiling of MicroRNAs in Bladder Cancer: miR-129 Is Associated with Poor Outcome and Promotes Cell Death <i>in vitro</i> . Cancer Research, 2009, 69, 4851-4860.	0.9	349
98	Genetic and Epigenetic <i>SLC18A2</i> Silencing in Prostate Cancer Is an Independent Adverse Predictor of Biochemical Recurrence after Radical Prostatectomy. Clinical Cancer Research, 2009, 15, 1400-1410.	7.0	26
99	Chromosomal imbalance in the progression of high-risk non-muscle invasive bladder cancer. BMC Cancer, 2009, 9, 149.	2.6	15
100	High frequency of tumor cells with nuclear Egr-1 protein expression in human bladder cancer is associated with disease progression. BMC Cancer, 2009, 9, 385.	2.6	30
101	Consistent genomic alterations in carcinoma <i>in situ</i> of the urinary bladder confirm the presence of two major pathways in bladder cancer development. International Journal of Cancer, 2009, 125, 2095-2103.	5.1	45
102	Snail1 is overexpressed in prostate cancer. Apmis, 2009, 117, 196-204.	2.0	40
103	Increased cell motility and invasion upon knockdown of lipolysis stimulated lipoprotein receptor (LSR) in SW780 bladder cancer cells. BMC Medical Genomics, 2008, 1, 31.	1.5	27
104	Chromosomal deletion, promoter hypermethylation and downregulation of <i>FYN</i> in prostate cancer. International Journal of Cancer, 2008, 122, 509-519.	5.1	22
105	Bioinformatic identification of FGF, p38-MAPK, and calcium signalling pathways associated with carcinoma <i>in situ</i> in the urinary bladder. BMC Cancer, 2008, 8, 37.	2.6	6
106	Gene signatures for risk-adapted treatment of bladder cancer. Scandinavian Journal of Urology and Nephrology, 2008, 42, 166-174.	1.4	3
107	Alternative Splicing in Colon, Bladder, and Prostate Cancer Identified by Exon Array Analysis. Molecular and Cellular Proteomics, 2008, 7, 1214-1224.	3.8	202
108	Diagnostic and Prognostic MicroRNAs in Stage II Colon Cancer. Cancer Research, 2008, 68, 6416-6424.	0.9	459

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109	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.	2.8	41
110	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.	7.0	198
111	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.	12.0	221
112	Adaptive differences in gene expression in European flounder (<i>Platichthys flesus</i>). <i>Molecular Ecology</i> , 2007, 16, 4674-4683.	3.9	111
113	Gene Expression Signatures Predict Outcome in Non-Muscle-Invasive Bladder Carcinoma: A Multicenter Validation Study. <i>Clinical Cancer Research</i> , 2007, 13, 3545-3551.	7.0	189
114	Recent developments in molecular profiling of bladder cancer. <i>Current Opinion in Urology</i> , 2006, 16, 377-381.	1.8	9
115	Molecular Profiling of ADAM12 in Human Bladder Cancer. <i>Clinical Cancer Research</i> , 2006, 12, 7359-7368.	7.0	108
116	SOX4 Expression in Bladder Carcinoma: Clinical Aspects and In vitro Functional Characterization. <i>Cancer Research</i> , 2006, 66, 3434-3442.	0.9	146
117	Microarrays for Gene Expression Profiling Fabrication of Oligonucleotide Microarrays, Isolation of RNA, Fluorescent Labeling of cRNA, Hybridization, and Scanning. , 2006, , 83-93.		0
118	Role of Activating Fibroblast Growth Factor Receptor 3 Mutations in the Development of Bladder Tumors. <i>Clinical Cancer Research</i> , 2005, 11, 7709-7719.	7.0	87
119	A Molecular Signature in Superficial Bladder Carcinoma Predicts Clinical Outcome. <i>Clinical Cancer Research</i> , 2005, 11, 4029-4036.	7.0	136
120	Gene Expression in the Urinary Bladder. <i>Cancer Research</i> , 2004, 64, 4040-4048.	0.9	402
121	Identifying distinct classes of bladder carcinoma using microarrays. <i>Nature Genetics</i> , 2003, 33, 90-96.	21.4	452
122	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.	3.1	39