

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	A Consensus Molecular Classification of Muscle-invasive Bladder Cancer. <i>European Urology</i> , 2020, 77, 420-433.	1.9	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.	7.1	538
3	Comprehensive Transcriptional Analysis of Early-Stage Urothelial Carcinoma. <i>Cancer Cell</i> , 2016, 30, 27-42.	16.8	486
4	Diagnostic and Prognostic MicroRNAs in Stage II Colon Cancer. <i>Cancer Research</i> , 2008, 68, 6416-6424.	0.9	459
5	Identifying distinct classes of bladder carcinoma using microarrays. <i>Nature Genetics</i> , 2003, 33, 90-96.	21.4	452
6	Gene Expression in the Urinary Bladder. <i>Cancer Research</i> , 2004, 64, 4040-4048.	0.9	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.	0.9	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.	5.1	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.	1.6	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.	2.5	284
11	Comparative analysis of discrete exosome fractions obtained by differential centrifugation. <i>Journal of Extracellular Vesicles</i> , 2014, 3, 25011.	12.2	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.	0.9	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.	12.0	221
14	Pervasive chromosomal instability and karyotype order in tumour evolution. <i>Nature</i> , 2020, 587, 126-132.	27.8	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.	3.8	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.	7.0	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.	1.9	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.	7.0	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.	7.0	183
20	Genomic Alterations in Liquid Biopsies from Patients with Bladder Cancer. <i>European Urology</i> , 2016, 70, 75-82.	1.9	174
21	An integrated multi-omics analysis identifies prognostic molecular subtypes of non-muscle-invasive bladder cancer. <i>Nature Communications</i> , 2021, 12, 2301.	12.8	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.	1.9	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.	2.2	148
24	SOX4 Expression in Bladder Carcinoma: Clinical Aspects and In vitro Functional Characterization. <i>Cancer Research</i> , 2006, 66, 3434-3442.	0.9	146
25	MicroRNA profiles of prostate carcinoma detected by multiplatform microRNA screening. <i>International Journal of Cancer</i> , 2012, 130, 611-621.	5.1	141
26	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
27	A Molecular Signature in Superficial Bladder Carcinoma Predicts Clinical Outcome. <i>Clinical Cancer Research</i> , 2005, 11, 4029-4036.	7.0	136
28	Mutational Context and Diverse Clonal Development in Early and Late Bladder Cancer. <i>Cell Reports</i> , 2014, 7, 1649-1663.	6.4	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.	12.8	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.	3.3	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.	2.5	112
32	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
33	Adaptive differences in gene expression in European flounder (<i>Platichthys flesus</i>). <i>Molecular Ecology</i> , 2007, 16, 4674-4683.	3.9	111
34	Comprehensive multiregional analysis of molecular heterogeneity in bladder cancer. <i>Scientific Reports</i> , 2017, 7, 11702.	3.3	110
35	Molecular Profiling of ADAM12 in Human Bladder Cancer. <i>Clinical Cancer Research</i> , 2006, 12, 7359-7368.	7.0	108
36	Expression profiling of prostate cancer tissue delineates genes associated with recurrence after prostatectomy. <i>Scientific Reports</i> , 2015, 5, 16018.	3.3	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.	8.2	106
38	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
39	The functional role of the novel biomarker karyopherin β 2 (KPNA2) in cancer. <i>Cancer Letters</i> , 2013, 331, 18-23.	7.2	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.	5.1	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.	0.4	102
42	Genomic heterogeneity in bladder cancer: challenges and possible solutions to improve outcomes. <i>Nature Reviews Urology</i> , 2020, 17, 259-270.	3.8	100
43	Expression of TIP60 (tata-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
44	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
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.	7.0	87
46	Paired Exome Analysis Reveals Clonal Evolution and Potential Therapeutic Targets in Urothelial Carcinoma. <i>Cancer Research</i> , 2016, 76, 5894-5906.	0.9	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.	3.8	86
48	miRNAs associated with chemo-sensitivity in cell lines and in advanced bladder cancer. <i>BMC Medical Genomics</i> , 2012, 5, 40.	1.5	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.	12.2	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.	7.0	79
51	Identification of Differential Tumor Subtypes of T1 Bladder Cancer. <i>European Urology</i> , 2020, 78, 533-537.	1.9	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.	1.9	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.	3.8	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.	3.8	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.	1.9	70
56	Novel diagnostic and prognostic classifiers for prostate cancer identified by genome-wide microRNA profiling. <i>Oncotarget</i> , 2016, 7, 30760-30771.	1.8	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.	2.6	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.	2.8	57
59	Autophagy role(s) in response to oncogenes and DNA replication stress. <i>Cell Death and Differentiation</i> , 2020, 27, 1134-1153.	11.2	57
60	Representative Sequencing: Unbiased Sampling of Solid Tumor Tissue. <i>Cell Reports</i> , 2020, 31, 107550.	6.4	51
61	Optimized targeted sequencing of cell-free plasma DNA from bladder cancer patients. <i>Scientific Reports</i> , 2018, 8, 1917.	3.3	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.	5.5	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.	2.5	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.	5.1	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.	2.5	44
66	Spatial and temporal clonal evolution during development of metastatic urothelial carcinoma. <i>Molecular Oncology</i> , 2016, 10, 1450-1460.	4.6	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.	2.8	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.	1.2	41
69	Snail1 is overexpressed in prostate cancer. <i>Apmis</i> , 2009, 117, 196-204.	2.0	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.	3.1	39
71	Increased expression of transcription factor TFAP2 \pm correlates with chemosensitivity in advanced bladder cancer. <i>BMC Cancer</i> , 2011, 11, 135.	2.6	35
72	Exosomes of invasive urothelial carcinoma cells are characterized by a specific miRNA expression signature. <i>Oncotarget</i> , 2017, 8, 58278-58291.	1.8	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.	1.9	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.	5.4	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.	2.6	30
76	Re: Aurélien Kamoun, Aurélien de Reyniès, Yves Allory, et al. A Consensus Molecular Classification of Muscle-invasive Bladder Cancer. <i>Eur Urol</i> 2020;77:420–33. <i>European Urology</i> , 2020, 77, e105-e106.	1.9	29
77	High miR-449b expression in prostate cancer is associated with biochemical recurrence after radical prostatectomy. <i>BMC Cancer</i> , 2014, 14, 859.	2.6	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.	1.5	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.	7.0	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, .	10.3	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.	2.6	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.	5.1	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.	7.0	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.	5.1	22
85	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
86	Biology of nonmuscle-invasive bladder cancer. <i>Current Opinion in Urology</i> , 2018, 28, 598-603.	1.8	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.	1.8	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.	3.5	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.	3.7	16
90	Chromosomal imbalance in the progression of high-risk non-muscle invasive bladder cancer. <i>BMC Cancer</i> , 2009, 9, 149.	2.6	15

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91	Toward personalized management in bladder cancer: the promise of novel molecular taxonomy. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2017, 471, 271-280.	2.8	15
92	Challenges in the Diagnosis of Urothelial Carcinoma Variants: Can Emerging Molecular Data Complement Pathology Review?. Urology, 2017, 102, 7-16.	1.0	15
93	Identification of ADAM12 as a Novel Basigin Sheddase. International Journal of Molecular Sciences, 2019, 20, 1957.	4.1	15
94	Immune Contexture and Differentiation Features Predict Outcome in Bladder Cancer. European Urology Oncology, 2022, 5, 203-213.	5.4	14
95	Stage-stratified molecular profiling of non-muscle-invasive bladder cancer enhances biological, clinical, and therapeutic insight. Cell Reports Medicine, 2021, 2, 100472.	6.5	13
96	Mutational Analysis of Field Cancerization in Bladder Cancer. Bladder Cancer, 2020, 6, 253-264.	0.4	12
97	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
98	Gene Networks Modified by Sulphonylureas in Beta Cells: A Pathway-based Analysis of Insulin Secretion and Cell Death. Basic and Clinical Pharmacology and Toxicology, 2012, 111, 254-261.	2.5	10
99	Recent developments in molecular profiling of bladder cancer. Current Opinion in Urology, 2006, 16, 377-381.	1.8	9
100	STAG2 as a prognostic biomarker in low-grade non-muscle invasive bladder cancer. Urologic Oncology: Seminars and Original Investigations, 2021, 39, 438.e1-438.e9.	1.6	9
101	Molecular Subtypes of Bladder Cancer: Academic Exercise or Clinical Relevance?. European Urology, 2019, 75, 433-434.	1.9	8
102	Targeting natural splicing plasticity of APOBEC3B restricts its expression and mutagenic activity. Communications Biology, 2021, 4, 386.	4.4	7
103	Characterizing molecular subtypes of high-risk non-muscle-invasive bladder cancer in African American patients. Urologic Oncology: Seminars and Original Investigations, 2022, 40, 410.e19-410.e27.	1.6	7
104	Bioinformatic identification of FGF, p38-MAPK, and calcium signalling pathways associated with carcinoma in situ in the urinary bladder. BMC Cancer, 2008, 8, 37.	2.6	6
105	A miRNA signature predicts benefit from addition of hypoxia-modifying therapy to radiation treatment in invasive bladder cancer. British Journal of Cancer, 2021, 125, 85-93.	6.4	6
106	Classifying cGAS-STING Activity Links Chromosomal Instability with Immunotherapy Response in Metastatic Bladder Cancer. Cancer Research Communications, 2022, 2, 762-771.	1.7	6
107	Converging Roads to Early Bladder Cancer. European Urology, 2020, 78, 127-130.	1.9	5
108	Genome-wide Meta-analysis Identifies Novel Genes Associated with Recurrence and Progression in Non-muscle-invasive Bladder Cancer. European Urology Oncology, 2022, 5, 70-83.	5.4	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.	3.8	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.	1.9	3
112	Reply to: Reconciling differences in impact of molecular subtyping on response to cisplatin-based chemotherapy. Nature Communications, 2021, 12, 4834.	12.8	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, .	3.3	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.	3.7	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.	1.9	1
118	Sensitivity and Specificity in Urine Bladder Cancer Markers – Is it that Simple?. Bladder Cancer, 2022, 8, 1-4.	0.4	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.	0.4	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.	0.1	0
122	Characterizing molecular subtypes of high-risk nonmuscle-invasive bladder cancer in African American patients.. Journal of Clinical Oncology, 2022, 40, 527-527.	1.6	0