

# Luigi Marchionni

## List of Publications by Year in descending order

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Version: 2024-02-01

140  
papers

11,797  
citations

61687

45  
h-index

32181

105  
g-index

155  
all docs

155  
docs citations

155  
times ranked

23068  
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA-seq highlights differential regulated pathways involved in cell cycle and inflammation in orbitofacial neurofibromas. <i>Brain Pathology</i> , 2022, 32, e13007.	2.1	2
2	A robust and interpretable gene signature for predicting the lymph node status of primary T1/T2 oral cavity squamous cell carcinoma. <i>International Journal of Cancer</i> , 2022, 150, 450-460.	2.3	5
3	Building Tools for Machine Learning and Artificial Intelligence in Cancer Research: Best Practices and a Case Study with the PathML Toolkit for Computational Pathology. <i>Molecular Cancer Research</i> , 2022, 20, 202-206.	1.5	24
4	Precision health diagnostic and surveillance network uses S gene target failure (SGTF) combined with sequencing technologies to track emerging SARS-CoV-2 variants. <i>Immunity, Inflammation and Disease</i> , 2022, 10, .	1.3	4
5	Global microRNA profiling identified miR-10b-5p as a regulator of neurofibromatosis 1 (NF1) glioma migration. <i>Neuropathology and Applied Neurobiology</i> , 2021, 47, 96-107.	1.8	10
6	Plasma cells are enriched in localized prostate cancer in Black men and are associated with improved outcomes. <i>Nature Communications</i> , 2021, 12, 935.	5.8	56
7	An R package for divergence analysis of omics data. <i>PLoS ONE</i> , 2021, 16, e0249002.	1.1	2
8	Influenza Vaccination and COVID-19 Mortality in the USA: An Ecological Study. <i>Vaccines</i> , 2021, 9, 427.	2.1	54
9	Efficient representations of tumor diversity with paired DNA-RNA aberrations. <i>PLoS Computational Biology</i> , 2021, 17, e1008944.	1.5	2
10	Transcriptional landscape of PTEN loss in primary prostate cancer. <i>BMC Cancer</i> , 2021, 21, 856.	1.1	16
11	covid19census: U.S. and Italy COVID-19 metrics and other epidemiological data. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	0
12	Newly Identified Members of FGFR1 Splice Variants Engage in Cross-talk with AXL/AKT Axis in Salivary Adenoid Cystic Carcinoma. <i>Cancer Research</i> , 2021, 81, 1001-1013.	0.4	10
13	Identifying Personalized Metabolic Signatures in Breast Cancer. <i>Metabolites</i> , 2021, 11, 20.	1.3	7
14	A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021, 19, e3001419.	2.6	6
15	Host Blood Gene Signatures Can Detect the Progression to Severe and Cerebral Malaria. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 743616.	1.8	2
16	Whole Genome Sequencing Uncovers a Rare Germline Variant in ATM Associated with Familial Myeloproliferative Neoplasms. <i>Blood</i> , 2021, 138, 3592-3592.	0.6	0
17	Genetic Analysis of Small Well-differentiated Pancreatic Neuroendocrine Tumors Identifies Subgroups With Differing Risks of Liver Metastases. <i>Annals of Surgery</i> , 2020, 271, 566-573.	2.1	64
18	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	2.4	109

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19	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , 2020, 30, 951-961.	2.4	29
20	GULP1 regulates the NRF2-KEAP1 signaling axis in urothelial carcinoma. <i>Science Signaling</i> , 2020, 13, .	1.6	19
21	Differential gene methylation and expression of HOX transcription factor family in orbitofacial neurofibroma. <i>Acta Neuropathologica Communications</i> , 2020, 8, 62.	2.4	7
22	Recounting the FANTOM CAGE-Associated Transcriptome. <i>Genome Research</i> , 2020, 30, 1073-1081.	2.4	35
23	<i>PTEN</i> Loss with <i>ERG</i> Negative Status is Associated with Lethal Disease after Radical Prostatectomy. <i>Journal of Urology</i> , 2020, 203, 344-350.	0.2	12
24	Abstract 4491: Characterizing long non-coding RNA expression of tumor-infiltrating lymphocytes across solid cancers. , 2020, , .		0
25	Abstract 2535: Screening <i>PTEN</i> -loss associated lncRNAs in prostate cancer. , 2020, , .		0
26	Abstract 3926: Establishment of patient-derived organoids asex vivotool to characterize the molecular mechanisms of SCLC chemo-radiation resistance. , 2020, , .		0
27	Abstract 4296: The EphA2/EGFR pathway dysregulation associates with poor prognosis and cetuximab treatment response in colorectal cancer. , 2020, , .		0
28	Combined extracts of <i>Echinacea angustifolia</i> DC. and <i>Zingiber officinale</i> Roscoe in softgel capsules: Pharmacokinetics and immunomodulatory effects assessed by gene expression profiling. <i>Phytomedicine</i> , 2019, 65, 153090.	2.3	12
29	<i>JAK3</i> Variant, Immune Signatures, DNA Methylation, and Social Determinants Linked to Survival Racial Disparities in Head and Neck Cancer Patients. <i>Cancer Prevention Research</i> , 2019, 12, 255-270.	0.7	19
30	CDK12 inactivation across solid tumors: an actionable genetic subtype. <i>Oncoscience</i> , 2019, 6, 312-316.	0.9	15
31	Look for methods, not conclusions. <i>Cell Death and Disease</i> , 2019, 10, 931.	2.7	1
32	Hedgehog/GLI1 activation leads to leukemic transformation of myelodysplastic syndrome in vivo and GLI1 inhibition results in antitumor activity. <i>Oncogene</i> , 2019, 38, 687-698.	2.6	21
33	Ezrin Promotes Stem Cell Properties in Pancreatic Ductal Adenocarcinoma. <i>Molecular Cancer Research</i> , 2019, 17, 929-936.	1.5	11
34	PDCD4 Is an Androgen-Repressed Tumor Suppressor that Regulates Prostate Cancer Growth and Castration Resistance. <i>Molecular Cancer Research</i> , 2019, 17, 618-627.	1.5	23
35	Abstract 908: Comprehensive analysis of alternative polyadenylation across cancer phenotypes. , 2019, , .		0
36	Bifunctional immune checkpoint-targeted antibody-ligand traps that simultaneously disable TGF $\beta$ enhance the efficacy of cancer immunotherapy. <i>Nature Communications</i> , 2018, 9, 741.	5.8	238

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37	Digitizing omics profiles by divergence from a baseline. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4545-4552.	3.3	23
38	Arsenic promotes the <scp>COX2/PGE2â€“SOX2</scp> axis to increase the malignant stemness properties of urothelial cells. International Journal of Cancer, 2018, 143, 113-126.	2.3	21
39	Genome-Wide Somatic Copy Number Alterations and Mutations in High-Grade Pancreatic Intraepithelial Neoplasia. American Journal of Pathology, 2018, 188, 1723-1733.	1.9	32
40	Cell-autonomous and cell non-autonomous downregulation of tumor suppressor DAB2IP by microRNA-149-3p promotes aggressiveness of cancer cells. Cell Death and Differentiation, 2018, 25, 1224-1238.	5.0	33
41	YAP1 and COX2 Coordinately Regulate Urothelial Cancer Stem-like Cells. Cancer Research, 2018, 78, 168-181.	0.4	77
42	Hypomethylation, endogenous retrovirus expression, and interferon signaling in testicular germ cell tumors. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8580-E8582.	3.3	13
43	PD-L1 Expression Heterogeneity in Nonâ€“Small Cell Lung Cancer: Defining Criteria for Harmonization between Biopsy Specimens and Whole Sections. Journal of Thoracic Oncology, 2018, 13, 1113-1120.	0.5	135
44	Epigenetically regulated PAX6 drives cancer cells toward a stem-like state via GLI-SOX2 signaling axis in lung adenocarcinoma. Oncogene, 2018, 37, 5967-5981.	2.6	42
45	Cell-type specific expression of oncogenic and tumor suppressive microRNAs in the human prostate and prostate cancer. Scientific Reports, 2018, 8, 7189.	1.6	41
46	Abstract 2297: Differential analysis of gene expression across the human genome using recount2 and FANTOM-CAT. , 2018, , .		2
47	Abstract 570: High-resolution microbiome profiling of 16SrRNA sequencing data, Microbiome Arrays, and expression arrays identifies differential bacterial communities in head and neck cancer patients treated with surgery, chemo-radiation, and PD-1 checkpoint blockade therapy. , 2018, , .		0
48	Abstract 2750: An epigenetic and immunologic approach to optimize therapy for HNSCC. , 2018, , .		0
49	Dysregulation of EGFR Pathway in EphA2 Cell Subpopulation Significantly Associates with Poor Prognosis in Colorectal Cancer. Clinical Cancer Research, 2017, 23, 159-170.	3.2	65
50	MicroRNA expression profiling of Xp11 renal cell carcinoma. Human Pathology, 2017, 67, 18-29.	1.1	25
51	PatternMarkers & GWCoGAPS for novel data-driven biomarkers via whole transcriptome NMF. Bioinformatics, 2017, 33, 1892-1894.	1.8	39
52	Selective analysis of cancer-cell intrinsic transcriptional traits defines novel clinically relevant subtypes of colorectal cancer. Nature Communications, 2017, 8, 15107.	5.8	213
53	Analysis of differential gene expression mediated by clozapine in human postmortem brains. Schizophrenia Research, 2017, 185, 58-66.	1.1	14
54	MicroRNAs, promising biomarkers in the diagnosis of Xp11 translocation RCCâ€“reply. Human Pathology, 2017, 68, 206-207.	1.1	0

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55	Pharmacodynamic and pharmacokinetic neoadjuvant study of hedgehog pathway inhibitor Sonidegib (LDE-225) in men with high-risk localized prostate cancer undergoing prostatectomy. <i>Oncotarget</i> , 2017, 8, 104182-104192.	0.8	20
56	High-resolution microbiome profiling uncovers <i>Fusobacterium nucleatum</i> , <i>Lactobacillus gasseri/johnsonii</i> , and <i>Lactobacillus vaginalis</i> associated to oral and oropharyngeal cancer in saliva from HPV positive and HPV negative patients treated with surgery and chemo-radiation. <i>Oncotarget</i> , 2017, 8, 110931-110948.	0.8	79
57	Abstract 1018: High-resolution microbiome profiling and genome wide arrays uncover bacteria driven alterations of oncogenic and immune pathways in head and neck cancer patients treated with surgery, chemo-radiation and PD-1 checkpoint blockade therapy. , 2017, , .		5
58	The extracellular matrix and focal adhesion kinase signaling regulate cancer stem cell function in pancreatic ductal adenocarcinoma. <i>PLoS ONE</i> , 2017, 12, e0180181.	1.1	68
59	Synthesizer: Expediting synthesis studies from context-free data with information retrieval techniques. <i>PLoS ONE</i> , 2017, 12, e0175860.	1.1	0
60	Abstract 1742: Cancer cell-selective transcriptome analysis reveals new colorectal cancer molecular subtypes with improved biological resolution and superior predictive and prognostic performance. , 2017, , .		0
61	Abstract 1551:GULP1is an epigenetically altered and functional tumor suppressor in urothelial carcinoma through regulation of Nrf2-Keap1 signaling axis. , 2017, , .		0
62	Abstract 4551: Divergence analysis with coarse coding of omics data across cancer phenotypes. , 2017, , .		0
63	Alterations in cellular metabolome after pharmacological inhibition of N <sub>acetylcholine</sub> in glioblastoma cells. <i>International Journal of Cancer</i> , 2016, 138, 1246-1255.	2.3	32
64	MP03-01 CLINICAL, PATHOLOGIC AND GENOMIC PROFILES OF EXCEPTIONAL RESPONDERS TO ANTI-PD1 THERAPY IN RENAL CELL CARCINOMA. <i>Journal of Urology</i> , 2016, 195, .	0.2	1
65	Expression of HIV-1 matrix protein p17 and association with B-cell lymphoma in HIV-1 transgenic mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13168-13173.	3.3	26
66	Summary and Recommendations from the National Cancer Institute's Clinical Trials Planning Meeting on Novel Therapeutics for Non-Muscle Invasive Bladder Cancer. <i>Bladder Cancer</i> , 2016, 2, 165-202.	0.2	30
67	Human T <sub>H</sub> 17 Cells Lack HIV-Inhibitory RNases and Are Highly Permissive to Productive HIV Infection. <i>Journal of Virology</i> , 2016, 90, 7833-7847.	1.5	51
68	Whole-Genome Sequencing of Salivary Gland Adenoid Cystic Carcinoma. <i>Cancer Prevention Research</i> , 2016, 9, 265-274.	0.7	80
69	Germline Variants in Asporin Vary by Race, Modulate the Tumor Microenvironment, and Are Differentially Associated with Metastatic Prostate Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 448-458.	3.2	29
70	Tissue-based Genomics Augments Post-prostatectomy Risk Stratification in a Natural History Cohort of Intermediate- and High-Risk Men. <i>European Urology</i> , 2016, 69, 157-165.	0.9	206
71	Identification of miR-30b-3p and miR-30d-5p as direct regulators of androgen receptor signaling in prostate cancer by complementary functional microRNA library screening. <i>Oncotarget</i> , 2016, 7, 72593-72607.	0.8	71
72	Identification of novel immunomodulatory tumor biology through comprehensive characterization of a metastases-specific epigenome in patients with metachronous primary and metastatic urothelial carcinoma (UC) tumor pairs.. <i>Journal of Clinical Oncology</i> , 2016, 34, 452-452.	0.8	20

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73	Abstract 5035: MDB-seq screening of muscle-invasive urothelial carcinoma revealed unpredicted novel tumor suppressor genes. , 2016, , .		0
74	Abstract 4504: Developing a PTEN-ETS signature to improve molecular risk stratification in prostate cancer. , 2016, , .		0
75	A multi-omic analysis of human naïve CD4+ T cells. BMC Systems Biology, 2015, 9, 75.	3.0	43
76	Identification and Validation of Protein Biomarkers of Response to Neoadjuvant Platinum Chemotherapy in Muscle Invasive Urothelial Carcinoma. PLoS ONE, 2015, 10, e0131245.	1.1	42
77	Integration of Hedgehog and mutant FLT3 signaling in myeloid leukemia. Science Translational Medicine, 2015, 7, 291ra96.	5.8	50
78	Removal of Abnormal Myofilament <i>α</i> -GlcNAcylation Restores Ca <sup>2+</sup> Sensitivity in Diabetic Cardiac Muscle. Diabetes, 2015, 64, 3573-3587.	0.3	82
79	HES6 promotes prostate cancer aggressiveness independently of Notch signalling. Journal of Cellular and Molecular Medicine, 2015, 19, 1624-1636.	1.6	18
80	Notch Signaling Activation in Pediatric Low-Grade Astrocytoma. Journal of Neuropathology and Experimental Neurology, 2015, 74, 121-131.	0.9	6
81	Neutrophil to lymphocyte ratio (NLR) improves the risk assessment of ISS staging in newly diagnosed MM patients treated upfront with novel agents. Annals of Hematology, 2015, 94, 1875-1883.	0.8	47
82	Targeted sequencing reveals clonal genetic changes in the progression of early lung neoplasms and paired circulating DNA. Nature Communications, 2015, 6, 8258.	5.8	129
83	Only three driver gene mutations are required for the development of lung and colorectal cancers. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 118-123.	3.3	325
84	Identification of miR-145 targets through an integrated omics analysis. Molecular BioSystems, 2015, 11, 197-207.	2.9	21
85	switchBox: an R package for “Top Scoring Pairs classifier development. Bioinformatics, 2015, 31, 273-274.	1.8	40
86	Allogeneic Myeloma GVAX with Lenalidomide Enhances Progression Free Survival through the Generation of Tumor Specific Immunity in Patients in Near Complete Remission. Blood, 2015, 126, 4238-4238.	0.6	9
87	Abstract A10: In search of Kras resistance genes: Whole transcriptome analysis identifies critical pathways mediating resistance and sensitivity to oncogenic Kras. , 2015, , .		0
88	Abstract 3754: Predicting cancer phenotypes with mechanism-driven multi-omics data integration. , 2015, , .		2
89	Integrative Analysis of 1q23.3 Copy-Number Gain in Metastatic Urothelial Carcinoma. Clinical Cancer Research, 2014, 20, 1873-1883.	3.2	63
90	Key tumor suppressor genes inactivated by greater promoter methylation and somatic mutations in head and neck cancer. Epigenetics, 2014, 9, 1031-1046.	1.3	122

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91	Clear cell papillary renal cell carcinoma: micro-RNA expression profiling and comparison with clear cell renal cell carcinoma and papillary renal cell carcinoma. <i>Human Pathology</i> , 2014, 45, 1130-1138.	1.1	61
92	H2S Increases Survival during Sepsis: Protective Effect of CHOP Inhibition. <i>Journal of Immunology</i> , 2014, 192, 1806-1814.	0.4	68
93	Correction: H2S Increases Survival During Sepsis: Protective Effect of CHOP Inhibition. <i>Journal of Immunology</i> , 2014, 192, 3991-3991.	0.4	1
94	An expression-guided screen for small molecules targeting aggressive prostate cancer.. <i>Journal of Clinical Oncology</i> , 2014, 32, e16081-e16081.	0.8	0
95	Abstract 1465: Phase specific microRNA deregulation of oncogenesis and stemness in a mouse model of sporadic CRC. , 2014, , .		0
96	Abstract 2482: Key tumor suppressor genes inactivated by promoter methylation and somatic mutations in head and neck cancer. , 2014, , .		1
97	Abstract 5342: Hardwiring mechanism into predicting cancer phenotypes by computational learning. , 2014, , .		0
98	A simple and reproducible breast cancer prognostic test. <i>BMC Genomics</i> , 2013, 14, 336.	1.2	45
99	Combination treatment with ABT-737 and chloroquine in preclinical models of small cell lung cancer. <i>Molecular Cancer</i> , 2013, 12, 16.	7.9	42
100	MicroRNA profiling in pediatric pilocytic astrocytoma reveals biologically relevant targets, including PBX3, NFIB, and METAP2. <i>Neuro-Oncology</i> , 2013, 15, 69-82.	0.6	56
101	Isolation of microarray-quality RNA from primary human cells after intracellular immunostaining and fluorescence-activated cell sorting. <i>Journal of Immunological Methods</i> , 2013, 391, 22-30.	0.6	11
102	High Levels of CD2 Expression Identify HIV-1 Latently Infected Resting Memory CD4 <sup>+</sup> T Cells in Virally Suppressed Subjects. <i>Journal of Virology</i> , 2013, 87, 9148-9158.	1.5	91
103	ERK Phosphorylation Is Predictive of Resistance to IGF-1R Inhibition in Small Cell Lung Cancer. <i>Molecular Cancer Therapeutics</i> , 2013, 12, 1131-1139.	1.9	33
104	Analysis of the genomic response of human prostate cancer cells to histone deacetylase inhibitors. <i>Epigenetics</i> , 2013, 8, 907-920.	1.3	32
105	Next-Generation Sequence Analysis of Cancer Xenograft Models. <i>PLoS ONE</i> , 2013, 8, e74432.	1.1	30
106	Association of Promoter Methylation of VGF and PGP9.5 with Ovarian Cancer Progression. <i>PLoS ONE</i> , 2013, 8, e70878.	1.1	34
107	MYC Is Activated by USP2a-Mediated Modulation of MicroRNAs in Prostate Cancer. <i>Cancer Discovery</i> , 2012, 2, 236-247.	7.7	82
108	Secreted protein, acidic and rich in cysteine-like 1 (SPARCL1) is down regulated in aggressive prostate cancers and is prognostic for poor clinical outcome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14977-14982.	3.3	49

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109	E4 Modeling HIV-1 Latency In Vitro. Journal of Acquired Immune Deficiency Syndromes (1999), 2012, 59, 83.	0.9	0
110	Oncogene amplification in male breast cancer: analysis by multiplex ligation-dependent probe amplification. Breast Cancer Research and Treatment, 2012, 135, 49-58.	1.1	53
111	Wnt signaling through beta-catenin is required for prostate lineage specification. Developmental Biology, 2012, 371, 246-255.	0.9	48
112	Regulation of Lipid Metabolism by Dicer Revealed through SILAC Mice. Journal of Proteome Research, 2012, 11, 2193-2205.	1.8	26
113	Sox9 is required for prostate development and prostate cancer initiation. Oncotarget, 2012, 3, 651-663.	0.8	52
114	Abstract 1913: Epithelial mesenchymal transition: A mechanism of resistance to VEGF pathway inhibition in genitourinary cancers. , 2012, , .		0
115	External validation of somatic copy number alteration (SCNA) at chromosome 1q23.3 in advanced urothelial carcinoma (UC).. Journal of Clinical Oncology, 2012, 30, 4585-4585.	0.8	0
116	Integrating diverse genomic data using gene sets. Genome Biology, 2011, 12, R105.	13.9	52
117	Molecular Effects of Genistein on Male Urethral Development. Journal of Urology, 2011, 185, 1894-1899.	0.2	26
118	Effects of Age and Heart Failure on Human Cardiac Stem Cell Function. American Journal of Pathology, 2011, 179, 349-366.	1.9	183
119	Dimeric naphthoquinones, a novel class of compounds with prostate cancer cytotoxicity. BJU International, 2011, 108, 447-454.	1.3	15
120	Gene expression pathways of high grade localized prostate cancer. Prostate, 2011, 71, 1568-1577.	1.2	77
121	In Vivo Liver Regeneration Potential of Human Induced Pluripotent Stem Cells from Diverse Origins. Science Translational Medicine, 2011, 3, 82ra39.	5.8	211
122	An EGFR-ERK-SOX9 Signaling Cascade Links Urothelial Development and Regeneration to Cancer. Cancer Research, 2011, 71, 3812-3821.	0.4	101
123	A novel role of IL-17 producing lymphocytes in mediating lytic bone disease in multiple myeloma. Blood, 2010, 116, 3554-3563.	0.6	187
124	The Notch Target Hes1 Directly Modulates Gli1 Expression and Hedgehog Signaling: A Potential Mechanism of Therapeutic Resistance. Clinical Cancer Research, 2010, 16, 6060-6070.	3.2	146
125	Methylation profiles of endometrioid and serous endometrial cancers. Endocrine-Related Cancer, 2010, 17, 663-673.	1.6	30
126	Downregulation of Homologous Recombination DNA Repair Genes by HDAC Inhibition in Prostate Cancer Is Mediated through the E2F1 Transcription Factor. PLoS ONE, 2010, 5, e11208.	1.1	140



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127	The ordering of expression among a few genes can provide simple cancer biomarkers and signal BRCA1 mutations. <i>BMC Bioinformatics</i> , 2009, 10, 256.	1.2	34
128	Differentiation of a Highly Tumorigenic Basal Cell Compartment in Urothelial Carcinoma. <i>Stem Cells</i> , 2009, 27, 1487-1495.	1.4	117
129	A Primary Xenograft Model of Small-Cell Lung Cancer Reveals Irreversible Changes in Gene Expression Imposed by Culture <i>in vitro</i> . <i>Cancer Research</i> , 2009, 69, 3364-3373.	0.4	406
130	Androgen-induced programs for prostate epithelial growth and invasion arise in embryogenesis and are reactivated in cancer. <i>Oncogene</i> , 2008, 27, 7180-7191.	2.6	151
131	Systematic Review: Gene Expression Profiling Assays in Early-Stage Breast Cancer. <i>Annals of Internal Medicine</i> , 2008, 148, 358.	2.0	135
132	Are Short-Term or Long-Term Recurrence Rates More Important in Breast Cancer Screening?. <i>Annals of Internal Medicine</i> , 2008, 149, 357.	2.0	1
133	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	6.0	3,227
134	Discovery of 342 putative new genes from the analysis of 5' end-sequenced full-length-enriched cDNA human transcripts. <i>Genomics</i> , 2005, 85, 739-751.	1.3	5
135	hGTSE-1 Expression Stimulates Cytoplasmic Localization of p53. <i>Journal of Biological Chemistry</i> , 2004, 279, 11744-11752.	1.6	44
136	Gene expression profiling of advanced ovarian cancer: characterization of a molecular signature involving fibroblast growth factor 2. <i>Oncogene</i> , 2004, 23, 8171-8183.	2.6	75
137	LNCIB human full-length cDNAs collection: towards a better comprehension of the human transcriptome. <i>Comptes Rendus - Biologies</i> , 2003, 326, 967-970.	0.1	2
138	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.	13.7	1,548
139	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001, 409, 685-690.	13.7	653
140	Optimized Cross-Study Analysis of Microarray-Based Predictors. , 0, , 398-422.		1