

# Francesca Demichelis

## List of Publications by Year in descending order

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203  
papers

32,751  
citations

14644

66  
h-index

6128

159  
g-index

219  
all docs

219  
docs citations

219  
times ranked

35830  
citing authors

#	ARTICLE	IF	CITATIONS
1	Plasma tumor <scp>DNA</scp> is associated with increased risk of venous thromboembolism in metastatic castration-resistant cancer patients. <i>International Journal of Cancer</i> , 2022, 150, 1166-1173.	2.3	4
2	Circulating RNAs in prostate cancer patients. <i>Cancer Letters</i> , 2022, 524, 57-69.	3.2	39
3	Allele-specific genomic data elucidate the role of somatic gain and copy-number neutral loss of heterozygosity in cancer. <i>Cell Systems</i> , 2022, 13, 183-193.e7.	2.9	13
4	Past, Current, and Future Strategies to Target ERG Fusion-Positive Prostate Cancer. <i>Cancers</i> , 2022, 14, 1118.	1.7	10
5	Comparative genomics of primary prostate cancer and paired metastases: insights from 12 molecular case studies. <i>Journal of Pathology</i> , 2022, 257, 274-284.	2.1	13
6	ETS-related gene (ERG) undermines genome stability in mouse prostate progenitors via Gsk3 <sup>Î²</sup> dependent Nrx3.1 degradation. <i>Cancer Letters</i> , 2022, 534, 215612.	3.2	6
7	Mutation "selection balance and compensatory mechanisms in tumour evolution. <i>Nature Reviews Genetics</i> , 2021, 22, 251-262.	7.7	38
8	Fast mutual exclusivity algorithm nominates potential synthetic lethal gene pairs through brute force matrix product computations. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4394-4403.	1.9	5
9	Combining molecular and functional imaging in metastatic castration-resistant prostate cancer (mCRPC).. <i>Journal of Clinical Oncology</i> , 2021, 39, 141-141.	0.8	0
10	Tumor subtype defines distinct pathways of molecular and clinical progression in primary prostate cancer. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	17
11	Association of plasma tumor DNA (ptDNA) with increased risk of venous thromboembolism (VTE) in metastatic castration resistant prostate cancer patients (mCRPC).. <i>Journal of Clinical Oncology</i> , 2021, 39, 5048-5048.	0.8	0
12	CD38 in Advanced Prostate Cancers. <i>European Urology</i> , 2021, 79, 736-746.	0.9	21
13	Therapy considerations in neuroendocrine prostate cancer: what next?. <i>Endocrine-Related Cancer</i> , 2021, 28, T67-T78.	1.6	33
14	Analytical protocol to identify local ancestry-associated molecular features in cancer. <i>STAR Protocols</i> , 2021, 2, 100766.	0.5	2
15	Charting differentially methylated regions in cancer with Rocker-meth. <i>Communications Biology</i> , 2021, 4, 1249.	2.0	7
16	ABEMUS: platform-specific and data-informed detection of somatic SNVs in cfDNA. <i>Bioinformatics</i> , 2020, 36, 2665-2674.	1.8	7
17	Two distinct immunopathological profiles in autopsy lungs of COVID-19. <i>Nature Communications</i> , 2020, 11, 5086.	5.8	230
18	Plasma tumour DNA as an early indicator of treatment response in metastatic castration-resistant prostate cancer. <i>British Journal of Cancer</i> , 2020, 123, 982-987.	2.9	22

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19	Systematic Assessment of Tumor Purity and Its Clinical Implications. <i>JCO Precision Oncology</i> , 2020, 4, 995-1005.	1.5	23
20	Role of specialized composition of SWI/SNF complexes in prostate cancer lineage plasticity. <i>Nature Communications</i> , 2020, 11, 5549.	5.8	76
21	Inherited variant in NF1 promoter is associated with increased risk of IBD in an Algerian population and modulates SOX9 binding. <i>Cancer Reports</i> , 2020, 3, e1240.	0.6	5
22	Integrative multiplatform molecular profiling of benign prostatic hyperplasia identifies distinct subtypes. <i>Nature Communications</i> , 2020, 11, 1987.	5.8	29
23	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , 2020, 37, 639-654.e6.	7.7	151
24	Genome-wide plasma DNA methylation features of metastatic prostate cancer. <i>Journal of Clinical Investigation</i> , 2020, 130, 1991-2000.	3.9	68
25	Circulating tumor DNA profile recognizes transformation to castration-resistant neuroendocrine prostate cancer. <i>Journal of Clinical Investigation</i> , 2020, 130, 1653-1668.	3.9	122
26	Circulating tumor DNA (ctDNA) to detect neuroendocrine prostate cancer genomic and DNA methylation changes. <i>Journal of Clinical Oncology</i> , 2020, 38, 8-8.	0.8	0
27	Proteomic and genomic signatures of repeat instability in cancer and adjacent normal tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16987-16996.	3.3	14
28	Ploidy and Purity Adjusted Allele-Specific DNA Analysis Using CLONETv2. <i>Current Protocols in Bioinformatics</i> , 2019, 67, e81.	25.8	13
29	Integrative Molecular Analysis of Patients With Advanced and Metastatic Cancer. <i>JCO Precision Oncology</i> , 2019, 3, 1-12.	1.5	24
30	Genomic correlates of clinical outcome in advanced prostate cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11428-11436.	3.3	839
31	TPES: tumor purity estimation from SNVs. <i>Bioinformatics</i> , 2019, 35, 4433-4435.	1.8	22
32	Ultrasensitive detection of cancer biomarkers by nickel-based isolation of polydisperse extracellular vesicles from blood. <i>EBioMedicine</i> , 2019, 43, 114-126.	2.7	40
33	Core Biopsies from Prostate Cancer Patients in Active Surveillance Protocols Harbor PTEN and MYC Alterations. <i>European Urology Oncology</i> , 2019, 2, 277-285.	2.6	7
34	PaCBAM: fast and scalable processing of whole exome and targeted sequencing data. <i>BMC Genomics</i> , 2019, 20, 1018.	1.2	9
35	A Phase II Trial of the Aurora Kinase A Inhibitor Alisertib for Patients with Castration-resistant and Neuroendocrine Prostate Cancer: Efficacy and Biomarkers. <i>Clinical Cancer Research</i> , 2019, 25, 43-51.	3.2	177
36	RB1 Heterogeneity in Advanced Metastatic Castration-Resistant Prostate Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 687-697.	3.2	43

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37	The Genomics of Prostate Cancer: A Historic Perspective. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a034942.	2.9	11
38	Circulating tumor DNA fraction (ctDNA) as a surrogate predictive biomarker in metastatic castration-resistant prostate cancer (mCRPC).. Journal of Clinical Oncology, 2019, 37, 5039-5039.	0.8	1
39	Better screened than sorry!â€”an informed panel of inherited DNA repair gene variants for prostate cancer screening and prognostication. Annals of Translational Medicine, 2019, 7, S158-S158.	0.7	0
40	Abstract 2471: Pan-cancer catalog of Differentially Methylated Regions by Rocker-meth, a new computational method. , 2019, , .		0
41	A highly specific SpCas9 variant is identified by in vivo screening in yeast. Nature Biotechnology, 2018, 36, 265-271.	9.4	377
42	Tumor purity quantification by clonal DNA methylation signatures. Bioinformatics, 2018, 34, 1642-1649.	1.8	36
43	The Genomics of Prostate Cancer: emerging understanding with technologic advances. Modern Pathology, 2018, 31, 1-11.	2.9	47
44	The long tail of oncogenic drivers in prostate cancer. Nature Genetics, 2018, 50, 645-651.	9.4	601
45	Clinical and Genomic Characterization of Treatment-Emergent Small-Cell Neuroendocrine Prostate Cancer: A Multi-institutional Prospective Study. Journal of Clinical Oncology, 2018, 36, 2492-2503.	0.8	477
46	Large extracellular vesicles carry most of the tumour DNA circulating in prostate cancer patient plasma. Journal of Extracellular Vesicles, 2018, 7, 1505403.	5.5	286
47	Patient derived organoids to model rare prostate cancer phenotypes. Nature Communications, 2018, 9, 2404.	5.8	246
48	Abstract LB-022: Synthetic lethal pairs for cancer treatment by agnostic exploration of mutually exclusive genomics. , 2018, , .		0
49	Abstract IA19: Phenotype plasticityâ€”a novel mechanism of targeted therapy resistance. , 2018, , .		0
50	Abstract B040: Differential impact of RB status on E2F1 reprogramming in human cancer. , 2018, , .		0
51	Abstract IA03: Differential impact of RB pathway status on E2F1 reprogramming and disease progression in human prostate cancer. , 2018, , .		0
52	Abstract A078: Towards understanding noncanonical phosphatidylinositol kinases in the maintenance of prostate metabolism. , 2018, , .		0
53	Abstract A042: Modulation of translation regulation by N6-methyladenosine in prostate cancer. , 2018, , .		0
54	A novel brain tumour model in zebrafish reveals the role of YAP activation in MAPK/PI3K induced malignant growth. DMM Disease Models and Mechanisms, 2017, 10, 15-28.	1.2	58

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55	<i>SOX2</i> promotes lineage plasticity and antiandrogen resistance in <i>TP53</i> - and <i>RB1</i> -deficient prostate cancer. <i>Science</i> , 2017, 355, 84-88.	6.0	759
56	EthSEQ: ethnicity annotation from whole exome sequencing data. <i>Bioinformatics</i> , 2017, 33, 2402-2404.	1.8	31
57	Exome Sequencing of African-American Prostate Cancer Reveals Loss-of-Function <i>ERF</i> Mutations. <i>Cancer Discovery</i> , 2017, 7, 973-983.	7.7	94
58	Hit and go CAS9 delivered through a lentiviral based self-limiting circuit. <i>Nature Communications</i> , 2017, 8, 15334.	5.8	75
59	Personalized <i>In Vitro</i> and <i>In Vivo</i> Cancer Models to Guide Precision Medicine. <i>Cancer Discovery</i> , 2017, 7, 462-477.	7.7	735
60	A germline FANCA alteration that is associated with increased sensitivity to DNA damaging agents. <i>Journal of Physical Education and Sports Management</i> , 2017, 3, a001487.	0.5	25
61	Inherited determinants of early recurrent somatic mutations in prostate cancer. <i>Nature Communications</i> , 2017, 8, 48.	5.8	23
62	High-throughput sequencing of two populations of extracellular vesicles provides an mRNA signature that can be detected in the circulation of breast cancer patients. <i>RNA Biology</i> , 2017, 14, 305-316.	1.5	43
63	Biology and evolution of poorly differentiated neuroendocrine tumors. <i>Nature Medicine</i> , 2017, 23, 664-673.	15.2	192
64	Next-Generation Rapid Autopsies Enable Tumor Evolution Tracking and Generation of Preclinical Models. <i>JCO Precision Oncology</i> , 2017, 2017, 1-13.	1.5	30
65	Differential impact of RB status on E2F1 reprogramming in human cancer. <i>Journal of Clinical Investigation</i> , 2017, 128, 341-358.	3.9	83
66	Whole exome sequencing (WES) of circulating tumor DNA (ctDNA) in patients with neuroendocrine prostate cancer (NEPC) informs tumor heterogeneity.. <i>Journal of Clinical Oncology</i> , 2017, 35, 5011-5011.	0.8	12
67	Punctuated evolution of copy-number alterations to define two molecular subtypes of muscle-invasive urothelial carcinoma.. <i>Journal of Clinical Oncology</i> , 2017, 35, 299-299.	0.8	0
68	Association of androgen receptor (AR) status in plasma DNA with outcome on enzalutamide (enza) or abiraterone (abi) for castration resistant prostate cancer (CRPC).. <i>Journal of Clinical Oncology</i> , 2017, 35, 5060-5060.	0.8	1
69	Abstract LB-232: Inherited determinants of early recurrent somatic mutations in prostate cancer. , 2017, , .		0
70	Abstract LB-122: Tumor heterogeneity in castration resistant neuroendocrine prostate cancer from whole exome sequencing of circulating tumor DNA. , 2017, , .		0
71	Abstract LB-085: RB loss-induced genome wide E2F1 reprogramming drive advanced prostate cancer. , 2017, , .		0
72	Abstract NG06: Genomic dissection of the clonal evolution dynamics of chemotherapy-resistant urothelial carcinoma. , 2017, , .		0

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73	Abstract 4165:SOX2promotes lineage plasticity and antiandrogen resistance inTP53andRB1deficient prostate cancer. , 2017, , .		0
74	Abstract 1749: Stability of copy-number profiles defines two molecular subtypes during urothelial carcinomaâ€™s evolution. , 2017, , .		0
75	N-Myc Induces an EZH2-Mediated Transcriptional Program Driving Neuroendocrine Prostate Cancer. Cancer Cell, 2016, 30, 563-577.	7.7	394
76	Clonal evolution of chemotherapy-resistant urothelial carcinoma. Nature Genetics, 2016, 48, 1490-1499.	9.4	250
77	Development and validation of a whole-exome sequencing test for simultaneous detection of point mutations, indels and copy-number alterations for precision cancer care. Npj Genomic Medicine, 2016, 1, .	1.7	68
78	Role of non-coding sequence variants in cancer. Nature Reviews Genetics, 2016, 17, 93-108.	7.7	420
79	Genomic Correlates to the Newly Proposed Grading Prognostic Groups for Prostate Cancer. European Urology, 2016, 69, 557-560.	0.9	64
80	Divergent clonal evolution of castration-resistant neuroendocrine prostate cancer. Nature Medicine, 2016, 22, 298-305.	15.2	1,193
81	Voices of biotech. Nature Biotechnology, 2016, 34, 270-275.	9.4	4
82	Abstract 887: N-Myc drives neuroendocrine prostate cancer. , 2016, , .		0
83	MP66-01 SPOP MUTATION LEADS TO GENOMIC INSTABILITY IN PROSTATE CANCER. Journal of Urology, 2015, 193, .	0.2	0
84	Defining order and timing of mutations during cancer progression: the TO-DAG probabilistic graphical model. Frontiers in Genetics, 2015, 6, 309.	1.1	9
85	SPOP mutation leads to genomic instability in prostate cancer. ELife, 2015, 4, .	2.8	148
86	Integrative Clinical Genomics of Advanced Prostate Cancer. Cell, 2015, 161, 1215-1228.	13.5	2,660
87	Whole-Exome Sequencing of Metastatic Cancer and Biomarkers of Treatment Response. JAMA Oncology, 2015, 1, 466.	3.4	264
88	ASEQ: fast allele-specific studies from next-generation sequencing data. BMC Medical Genomics, 2015, 8, 9.	0.7	51
89	Plasma <i>AR</i> and abiraterone-resistant prostate cancer. Science Translational Medicine, 2015, 7, 312re10.	5.8	366
90	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	13.5	2,435

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91	Inpatient heterogeneity in prostate cancer. <i>Nature Reviews Urology</i> , 2015, 12, 430-431.	1.9	18
92	Genetic predisposition to prostate cancer: Update and future perspectives. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2015, 33, 75-84.	0.8	26
93	Whole exome sequencing to reveal chemotherapy-driven evolution of platinum-resistant metastatic urothelial cancer.. <i>Journal of Clinical Oncology</i> , 2015, 33, 4513-4513.	0.8	1
94	Defining a molecular subclass of treatment resistant prostate cancer.. <i>Journal of Clinical Oncology</i> , 2015, 33, 5004-5004.	0.8	3
95	<i>In silico</i> identification and functional validation of allele-dependent AR enhancers. <i>Oncotarget</i> , 2015, 6, 4816-4828.	0.8	6
96	Precision medicine program for whole-exome sequencing (WES) provides new insight on platinum sensitivity in advanced prostate cancer (PCa).. <i>Journal of Clinical Oncology</i> , 2015, 33, 158-158.	0.8	1
97	Abstract 1108: SPOP mutation leads to genomic instability in prostate cancer. , 2015, , .		1
98	Abstract 5269: Myxofibrosarcoma: A move toward Precision Medicine. , 2015, , .		0
99	Abstract 4745: Precision cancer medicine program for whole-exome sequencing of metastatic tumors reveals biomarkers of response. , 2015, , .		1
100	Abstract NG01: SPOP mutation is associated with genomic instability in prostate cancer. , 2015, , .		1
101	Abstract LB-018: Defining a molecular subclass of treatment-resistant prostate cancer. , 2015, , .		0
102	Unraveling the clonal hierarchy of somatic genomic aberrations. <i>Genome Biology</i> , 2014, 15, 439.	3.8	80
103	Recurrent Prostate Cancer Genomic Alterations Predict Response to Brachytherapy Treatment. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 594-600.	1.1	31
104	Tumor clone dynamics in lethal prostate cancer. <i>Science Translational Medicine</i> , 2014, 6, 254ra125.	5.8	298
105	A Comparative Study of ERG Status Assessment on DNA, mRNA, and Protein Levels Using Unique Samples from a Swedish Biopsy Cohort. <i>Applied Immunohistochemistry and Molecular Morphology</i> , 2014, 22, 136-141.	0.6	15
106	Variants at IRX4 as prostate cancer expression quantitative trait loci. <i>European Journal of Human Genetics</i> , 2014, 22, 558-563.	1.4	36
107	MP24-13 WITHDRAWN: RECURRENT PROSTATE CANCER GENOMIC ALTERATIONS PREDICT RESPONSE TO BRACHYTHERAPY TREATMENT. <i>Journal of Urology</i> , 2014, 191, .	0.2	1
108	MP41-06 SPOP MUTATIONS IN PROSTATE CANCER ACROSS DEMOGRAPHICALLY DIVERSE PATIENT COHORTS.. <i>Journal of Urology</i> , 2014, 191, .	0.2	0

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109	Second Generation Imaging of Nuclear/Cytoplasmic HIV-1 Complexes. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, 717-726.	0.5	26
110	PCAT-1, a Long Noncoding RNA, Regulates BRCA2 and Controls Homologous Recombination in Cancer. <i>Cancer Research</i> , 2014, 74, 1651-1660.	0.4	237
111	The Lethal Clone in Prostate Cancer: Redefining the Index. <i>European Urology</i> , 2014, 66, 395-397.	0.9	30
112	Abstract 3952: Recurrent prostate cancer genomic alterations predict response to brachytherapy treatment. , 2014, , .		0
113	Impact of constitutional copy number variants on biological pathway evolution. <i>BMC Evolutionary Biology</i> , 2013, 13, 19.	3.2	25
114	A step toward functionally characterized prostate cancer molecular subtypes. <i>Nature Medicine</i> , 2013, 19, 966-967.	15.2	5
115	Molecular Archeology: Unearthing Androgen-Induced Structural Rearrangements in Prostate Cancer Genomes. <i>Cancer Cell</i> , 2013, 23, 133-135.	7.7	5
116	200 DEFINING THE MECHANISTIC BASIS OF SPOP MUTATIONS IN PROSTATE CANCER. <i>Journal of Urology</i> , 2013, 189, .	0.2	0
117	V-ets erythroblastosis virus E26 oncogene homolog (avian)/Trefoil factor 3/high-molecular-weight cytokeratin triple immunostain: a novel tissue-based biomarker in prostate cancer with potential clinical application. <i>Human Pathology</i> , 2013, 44, 2282-2292.	1.1	8
118	Punctuated Evolution of Prostate Cancer Genomes. <i>Cell</i> , 2013, 153, 666-677.	13.5	1,107
119	Prostate cancer-associated mutations in speckle-type POZ protein (SPOP) regulate steroid receptor coactivator 3 protein turnover. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6997-7002.	3.3	210
120	Large oncosomes mediate intercellular transfer of functional microRNA. <i>Cell Cycle</i> , 2013, 12, 3526-3536.	1.3	189
121	Distinct ERG rearrangement prevalence in prostate cancer: higher frequency in young age and in low PSA prostate cancer. <i>Prostate Cancer and Prostatic Diseases</i> , 2013, 16, 132-138.	2.0	62
122	Epigenetic Repression of miR-31 Disrupts Androgen Receptor Homeostasis and Contributes to Prostate Cancer Progression. <i>Cancer Research</i> , 2013, 73, 1232-1244.	0.4	150
123	Abstract 4017: Dissecting the clonal hierarchy of cancer-driving genomic lesions.. , 2013, , .		1
124	Abstract 4601: Punctuated evolution of prostate cancer genomes.. , 2013, , .		0
125	Transcriptional regulation and prostate cancer risk loci.. <i>Journal of Clinical Oncology</i> , 2013, 31, 1554-1554.	0.8	6
126	Next Generation Sequencing of Prostate Cancer from a Patient Identifies a Deficiency of Methylthioadenosine Phosphorylase, an Exploitable Tumor Target. <i>Molecular Cancer Therapeutics</i> , 2012, 11, 775-783.	1.9	34



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127	Oncogene-mediated alterations in chromatin conformation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9083-9088.	3.3	142
128	Identification of functionally active, low frequency copy number variants at 15q21.3 and 12q21.31 associated with prostate cancer risk. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6686-6691.	3.3	49
129	1314 RECURRENT MUTATIONS IN SPOP DEFINE A DISTINCT MOLECULAR CLASS OF PROSTATE CANCER. Journal of Urology, 2012, 187, .	0.2	0
130	2223 ERG GENE REARRANGEMENT IS MORE FREQUENT IN EARLY-ONSET PROSTATE CANCER AND IS ASSOCIATED WITH LOWER PSA SERUM LEVELS IN YOUNGER PATIENTS IN A PSA SCREENING COHORT. Journal of Urology, 2012, 187, .	0.2	0
131	Genome-wide DNA Methylation Events in <i>TPRSS2-ERG</i> Fusion-Negative Prostate Cancers Implicate an EZH2-Dependent Mechanism with <i>miR-26a</i> Hypermethylation. Cancer Discovery, 2012, 2, 1024-1035.	7.7	127
132	Large Oncosomes in Human Prostate Cancer Tissues and in the Circulation of Mice with Metastatic Disease. American Journal of Pathology, 2012, 181, 1573-1584.	1.9	321
133	Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. Nature Genetics, 2012, 44, 685-689.	9.4	1,300
134	DIAPH3 governs the cellular transition to the amoeboid tumour phenotype. EMBO Molecular Medicine, 2012, 4, 743-760.	3.3	92
135	Molecular genetics of prostate cancer: emerging appreciation of genetic complexity. Histopathology, 2012, 60, 187-198.	1.6	52
136	Abstract 2222: Oncogene-mediated alterations in chromatin conformation. , 2012, , .		0
137	Abstract 486: The novel tumor suppressor DIAPH3 governs transition to an amoeboid phenotype. , 2012, , .		0
138	Discovery of non-ETS gene fusions in human prostate cancer using next-generation RNA sequencing. Genome Research, 2011, 21, 56-67.	2.4	179
139	Molecular Characterization of Neuroendocrine Prostate Cancer and Identification of New Drug Targets. Cancer Discovery, 2011, 1, 487-495.	7.7	725
140	608 COMBINING DNA-SEQ AND RNA-SEQ FOR DISCOVERY OF NOVEL MUTATIONS IN HUMAN PROSTATE CANCER. Journal of Urology, 2011, 185, .	0.2	0
141	A Computational Framework Discovers New Copy Number Variants with Functional Importance. PLoS ONE, 2011, 6, e17539.	1.1	16
142	Testing mutual exclusivity of ETS rearranged prostate cancer. Laboratory Investigation, 2011, 91, 404-412.	1.7	68
143	The genomic complexity of primary human prostate cancer. Nature, 2011, 470, 214-220.	13.7	1,107
144	Abstract 2227: Concordance of ERG gene rearrangements and ERG protein expression in low grade PIN lesions in prostate needle biopsies. , 2011, , .		0

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145	Abstract 2218: Integrated diagnostic methods for detection of multiple gene rearrangements in prostate cancer tissue specimens. , 2011, , .		0
146	Abstract 3925: Characterization of complex chromosomal aberrations in prostate cancer from whole genome sequencing. , 2011, , .		0
147	Abstract 957: Aurora kinase and N-myc are involved in neuroendocrine differentiation of prostate cancer and are new drug targets. , 2011, , .		0
148	Abstract LB-246: Recurrent inactivating mutations in SPOP define a molecular subset of prostate cancer. , 2011, , .		0
149	Molecular sampling of prostate cancer: a dilemma for predicting disease progression. BMC Medical Genomics, 2010, 3, 8.	0.7	219
150	The landscape of somatic copy-number alteration across human cancers. Nature, 2010, 463, 899-905.	13.7	3,331
151	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	9.4	795
152	Rearrangements of the RAF kinase pathway in prostate cancer, gastric cancer and melanoma. Nature Medicine, 2010, 16, 793-798.	15.2	436
153	Optimizing copy number variation analysis using genome-wide short sequence oligonucleotide arrays. Nucleic Acids Research, 2010, 38, 3275-3286.	6.5	17
154	Genetic Variation of Genes Involved in Dihydrotestosterone Metabolism and the Risk of Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 229-239.	1.1	55
155	FusionSeq: a modular framework for finding gene fusions by analyzing paired-end RNA-sequencing data. Genome Biology, 2010, 11, R104.	3.8	137
156	ERG Rearrangement Metastasis Patterns in Locally Advanced Prostate Cancer. Urology, 2010, 75, 762-767.	0.5	56
157	Antibody-Based Detection of ERG Rearrangement-Positive Prostate Cancer. Neoplasia, 2010, 12, 590-IN21.	2.3	305
158	ERG Cooperates with Androgen Receptor in Regulating Trefoil Factor 3 in Prostate Cancer Disease Progression. Neoplasia, 2010, 12, 1031-IN22.	2.3	51
159	Abstract LB-21: Emergence of castration resistant prostate cancer class defined by recurrentERGFusion. , 2010, , .		0
160	Abstract 1139: Complete characterization of prostate cancer genomes by massively parallel sequencing. , 2010, , .		0
161	Abstract 2743: Accelerating the exploration of novel gene fusion events in prostate cancer. , 2010, , .		0
162	Oncosome Formation in Prostate Cancer: Association with a Region of Frequent Chromosomal Deletion in Metastatic Disease. Cancer Research, 2009, 69, 5601-5609.	0.4	325

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163	SLC45A3-ELK4 Is a Novel and Frequent Erythroblast Transformationâ€“Specific Fusion Transcript in Prostate Cancer. <i>Cancer Research</i> , 2009, 69, 2734-2738.	0.4	181
164	Genome-Wide Linkage Analysis of <i>TMPRSS2-ERG</i> Fusion in Familial Prostate Cancer. <i>Cancer Research</i> , 2009, 69, 640-646.	0.4	32
165	Distinct genomic aberrations associated with <i>ERG</i> rearranged prostate cancer. <i>Genes Chromosomes and Cancer</i> , 2009, 48, 366-380.	1.5	86
166	Response to <i>TMPRSS2-ERG</i> gene fusions are infrequent in prostatic ductal adenocarcinomasâ€™. <i>Modern Pathology</i> , 2009, 22, 1398-1399.	2.9	4
167	N-myc Downstream Regulated Gene 1 (NDRG1) Is Fused to ERG in Prostate Cancer. <i>Neoplasia</i> , 2009, 11, 804-W18.	2.3	105
168	Skp2 expression is associated with high risk and elevated Ki67 expression in gastrointestinal stromal tumours. <i>BMC Cancer</i> , 2008, 8, 134.	1.1	21
169	The Role of SPINK1 in ETS Rearrangement-Negative Prostate Cancers. <i>Cancer Cell</i> , 2008, 13, 519-528.	7.7	303
170	Association of cytokeratin 7 and 19 expression with genomic stability and favorable prognosis in clear cell renal cell cancer. <i>International Journal of Cancer</i> , 2008, 123, 569-576.	2.3	43
171	CAVEOLIN-1 INTERACTS WITH A LIPID RAFT-ASSOCIATED POPULATION OF FATTY ACID SYNTHASE IN PROSTATE CANCER. <i>Journal of Urology</i> , 2008, 179, 456-457.	0.2	0
172	EML4-ALK Fusion Lung Cancer: A Rare Acquired Event. <i>Neoplasia</i> , 2008, 10, 298-302.	2.3	231
173	SNP panel identification assay (SPIA): a genetic-based assay for the identification of cell lines. <i>Nucleic Acids Research</i> , 2008, 36, 2446-2456.	6.5	68
174	Caveolin-1 interacts with a lipid raft-associated population of fatty acid synthase. <i>Cell Cycle</i> , 2008, 7, 2257-2267.	1.3	80
175	Nine-Gene Molecular Signature Is Not Associated with Prostate Cancer Death in a Watchful Waiting Cohort. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008, 17, 249-251.	1.1	12
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