Francesca Demichelis

List of Publications by Year
in descending order

203	32,751	14644 66	6128 159
papers	citations	h-index	g-index

219	219	219	35830
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The landscape of somatic copy-number alteration across human cancers. Nature, 2010, 463, 899-905.	13.7	3,331
2	Integrative Clinical Genomics of Advanced Prostate Cancer. Cell, 2015, 161, 1215-1228.	13.5	2,660
3	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	13.5	2,435
4	Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. Nature Genetics, 2012, 44, 685-689.	9.4	1,300
5	Divergent clonal evolution of castration-resistant neuroendocrine prostate cancer. Nature Medicine, 2016, 22, 298-305.	15.2	1,193
6	The genomic complexity of primary human prostate cancer. Nature, 2011, 470, 214-220.	13.7	1,107
7	Punctuated Evolution of Prostate Cancer Genomes. Cell, 2013, 153, 666-677.	13.5	1,107
8	Assessing the significance of chromosomal aberrations in cancer: Methodology and application to glioma. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 20007-20012.	3.3	927
9	Genomic correlates of clinical outcome in advanced prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11428-11436.	3.3	839
10	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
11	SOX2 promotes lineage plasticity and antiandrogen resistance in TP53 - and RB1 -deficient prostate cancer. Science, 2017, 355, 84-88.	6.0	759
12	Personalized In Vitro and In Vivo Cancer Models to Guide Precision Medicine. Cancer Discovery, 2017, 7, 462-477.	7.7	735
13	Molecular Characterization of Neuroendocrine Prostate Cancer and Identification of New Drug Targets. Cancer Discovery, 2011, 1, 487-495.	7.7	725
14	The long tail of oncogenic drivers in prostate cancer. Nature Genetics, 2018, 50, 645-651.	9.4	601
15	TMPRSS2:ERG gene fusion associated with lethal prostate cancer in a watchful waiting cohort. Oncogene, 2007, 26, 4596-4599.	2.6	578
16	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
17	TMPRSS2:ERG Fusion-Associated Deletions Provide Insight into the Heterogeneity of Prostate Cancer. Cancer Research, 2006, 66, 8337-8341.	0.4	475
18	Rearrangements of the RAF kinase pathway in prostate cancer, gastric cancer and melanoma. Nature Medicine, 2010, 16, 793-798.	15.2	436

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19	Role of non-coding sequence variants in cancer. Nature Reviews Genetics, 2016, 17, 93-108.	7.7	420
20	TMPRSS2-ERG Fusion Prostate Cancer: An Early Molecular Event Associated With Invasion. American Journal of Surgical Pathology, 2007, 31, 882-888.	2.1	394
21	N-Myc Induces an EZH2-Mediated Transcriptional Program Driving Neuroendocrine Prostate Cancer. Cancer Cell, 2016, 30, 563-577.	7.7	394
22	A highly specific SpCas9 variant is identified by in vivo screening in yeast. Nature Biotechnology, 2018, 36, 265-271.	9.4	377
23	Plasma AR and abiraterone-resistant prostate cancer. Science Translational Medicine, 2015, 7, 312re10.	5.8	366
24	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
25	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
26	JAGGED1 Expression Is Associated with Prostate Cancer Metastasis and Recurrence. Cancer Research, 2004, 64, 6854-6857.	0.4	310
27	Antibody-Based Detection of ERG Rearrangement-Positive Prostate Cancer. Neoplasia, 2010, 12, 590-IN21.	2.3	305
28	The Role of SPINK1 in ETS Rearrangement-Negative Prostate Cancers. Cancer Cell, 2008, 13, 519-528.	7.7	303
29	Tumor clone dynamics in lethal prostate cancer. Science Translational Medicine, 2014, 6, 254ra125.	5.8	298
30	Estrogen-Dependent Signaling in a Molecularly Distinct Subclass of Aggressive Prostate Cancer. Journal of the National Cancer Institute, 2008, 100, 815-825.	3.0	286
31	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
32	Whole-Exome Sequencing of Metastatic Cancer and Biomarkers of Treatment Response. JAMA Oncology, 2015, 1, 466.	3.4	264
33	Clonal evolution of chemotherapy-resistant urothelial carcinoma. Nature Genetics, 2016, 48, 1490-1499.	9.4	250
34	Patient derived organoids to model rare prostate cancer phenotypes. Nature Communications, 2018, 9, 2404.	5.8	246
35	PCAT-1, a Long Noncoding RNA, Regulates BRCA2 and Controls Homologous Recombination in Cancer. Cancer Research, 2014, 74, 1651-1660.	0.4	237
36	EML4-ALK Fusion Lung Cancer: A Rare Acquired Event. Neoplasia, 2008, 10, 298-302.	2.3	231

#	Article	IF	Citations
37	Two distinct immunopathological profiles in autopsy lungs of COVID-19. Nature Communications, 2020, 11, 5086.	5.8	230
38	Molecular sampling of prostate cancer: a dilemma for predicting disease progression. BMC Medical Genomics, 2010, 3, 8.	0.7	219
39	Prostate cancer-associated mutations in speckle-type POZ protein (SPOP) regulate steroid receptor coactivator 3 protein turnover. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6997-7002.	3.3	210
40	Biology and evolution of poorly differentiated neuroendocrine tumors. Nature Medicine, 2017, 23, 664-673.	15.2	192
41	Large oncosomes mediate intercellular transfer of functional microRNA. Cell Cycle, 2013, 12, 3526-3536.	1.3	189
42	SLC45A3-ELK4 Is a Novel and Frequent Erythroblast Transformationâ€“Specific Fusion Transcript in Prostate Cancer. Cancer Research, 2009, 69, 2734-2738.	0.4	181
43	Discovery of non-ETS gene fusions in human prostate cancer using next-generation RNA sequencing. Genome Research, 2011, 21, 56-67.	2.4	179
44	A Phase II Trial of the Aurora Kinase A Inhibitor Alisertib for Patients with Castration-resistant and Neuroendocrine Prostate Cancer: Efficacy and Biomarkers. Clinical Cancer Research, 2019, 25, 43-51.	3.2	177
45	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. Cancer Cell, 2020, 37, 639-654.e6.	7.7	151
46	Epigenetic Repression of miR-31 Disrupts Androgen Receptor Homeostasis and Contributes to Prostate Cancer Progression. Cancer Research, 2013, 73, 1232-1244.	0.4	150
47	SPOP mutation leads to genomic instability in prostate cancer. ELife, 2015, 4, .	2.8	148
48	TMPRSS2-ERG Fusion Heterogeneity in Multifocal Prostate Cancer: Clinical and Biologic Implications. Urology, 2007, 70, 630-633.	0.5	146
49	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
50	FusionSeq: a modular framework for finding gene fusions by analyzing paired-end RNA-sequencing data. Genome Biology, 2010, 11, R104.	3.8	137
51	Genome-wide DNA Methylation Events in TMPRSS2â€“ERG Fusion-Negative Prostate Cancers Implicate an EZH2-Dependent Mechanism with miR-26a Hypermethylation. Cancer Discovery, 2012, 2, 1024-1035.	7.7	127
52	Circulating tumor DNA profile recognizes transformation to castration-resistant neuroendocrine prostate cancer. Journal of Clinical Investigation, 2020, 130, 1653-1668.	3.9	122
53	Molecular Characterization of TMPRSS2-ERG Gene Fusion in the NCI-H660 Prostate Cancer Cell Line: A New Perspective for an Old Model. Neoplasia, 2007, 9, 200-IN3.	2.3	119
54	N-myc Downstream Regulated Gene 1 (NDRG1) Is Fused to ERG in Prostate Cancer. Neoplasia, 2009, 11, 804-W18.	2.3	105

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55	Exome Sequencing of African-American Prostate Cancer Reveals Loss-of-Function ERF Mutations. Cancer Discovery, 2017, 7, 973-983.	7.7	94
56	DIAPH3 governs the cellular transition to the amoeboid tumour phenotype. EMBO Molecular Medicine, 2012, 4, 743-760.	3.3	92
57	Defining Aggressive Prostate Cancer Using a 12-Gene Model. Neoplasia, 2006, 8, 59-68.	2.3	90
58	Distinct genomic aberrations associated with ERG rearranged prostate cancer. Genes Chromosomes and Cancer, 2009, 48, 366-380.	1.5	86
59	Differential impact of RB status on E2F1 reprogramming in human cancer. Journal of Clinical Investigation, 2017, 128, 341-358.	3.9	83
60	Caveolin-1 interacts with a lipid raft-associated population of fatty acid synthase. Cell Cycle, 2008, 7, 2257-2267.	1.3	80
61	Unraveling the clonal hierarchy of somatic genomic aberrations. Genome Biology, 2014, 15, 439.	3.8	80
62	M-CAM expression as marker of poor prognosis in epithelial ovarian cancer. International Journal of Cancer, 2006, 119, 1920-1926.	2.3	78
63	Role of specialized composition of SWI/SNF complexes in prostate cancer lineage plasticity. Nature Communications, 2020, 11, 5549.	5.8	76
64	Hit and go CAS9 delivered through a lentiviral based self-limiting circuit. Nature Communications, 2017, 8, 15334.	5.8	75
65	Integrative Microarray Analysis of Pathways Dysregulated in Metastatic Prostate Cancer. Cancer Research, 2007, 67, 10296-10303.	0.4	71
66	SNP panel identification assay (SPIA): a genetic-based assay for the identification of cell lines. Nucleic Acids Research, 2008, 36, 2446-2456.	6.5	68
67	Testing mutual exclusivity of ETS rearranged prostate cancer. Laboratory Investigation, 2011, 91, 404-412.	1.7	68
68	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
69	Genome-wide plasma DNA methylation features of metastatic prostate cancer. Journal of Clinical Investigation, 2020, 130, 1991-2000.	3.9	68
70	Genomic Correlates to the Newly Proposed Grading Prognostic Groups for Prostate Cancer. European Urology, 2016, 69, 557-560.	0.9	64
71	The virtual case: a new method to completely digitize cytological and histological slides. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2002, 441, 159-164.	1.4	62
72	Distinct ERG rearrangement prevalence in prostate cancer: higher frequency in young age and in low PSA prostate cancer. Prostate Cancer and Prostatic Diseases, 2013, 16, 132-138.	2.0	62

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73	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
74	ERG Rearrangement Metastasis Patterns in Locally Advanced Prostate Cancer. Urology, 2010, 75, 762-767.	0.5	56
75	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
76	A hierarchical NaÃ¯ve Bayes Model for handling sample heterogeneity in classification problems: an application to tissue microarrays. BMC Bioinformatics, 2006, 7, 514.	1.2	54
77	Molecular genetics of prostate cancer: emerging appreciation of genetic complexity. Histopathology, 2012, 60, 187-198.	1.6	52
78	ERG Cooperates with Androgen Receptor in Regulating Trefoil Factor 3 in Prostate Cancer Disease Progression. Neoplasia, 2010, 12, 1031-IN22.	2.3	51
79	ASEQ: fast allele-specific studies from next-generation sequencing data. BMC Medical Genomics, 2015, 8, 9.	0.7	51
80	Digital Storage of Glass Slides for Quality Assurance in Histopathology and Cytopathology. Journal of Telemedicine and Telecare, 2002, 8, 138-142.	1.4	50
81	TMPRSS2-ETS fusion prostate cancer: biological and clinical implications. Journal of Clinical Pathology, 2007, 60, 1185-1186.	1.0	49
82	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
83	The Genomics of Prostate Cancer: emerging understanding with technologic advances. Modern Pathology, 2018, 31, 1-11.	2.9	47
84	Automated immunofluorescence analysis defines microvessel area as a prognostic parameter in clear cell renal cell cancer. Human Pathology, 2007, 38, 1454-1462.	1.1	44
85	Association of cytokeratin 7 and 19 expression with genomic stability and favorable prognosis in clear cell renal cell cancer. International Journal of Cancer, 2008, 123, 569-576.	2.3	43
86	High-throughput sequencing of two populations of extracellular vesicles provides an mRNA signature that can be detected in the circulation of breast cancer patients. RNA Biology, 2017, 14, 305-316.	1.5	43
87	RB1 Heterogeneity in Advanced Metastatic Castration-Resistant Prostate Cancer. Clinical Cancer Research, 2019, 25, 687-697.	3.2	43
88	Ultrasensitive detection of cancer biomarkers by nickel-based isolation of polydisperse extracellular vesicles from blood. EBioMedicine, 2019, 43, 114-126.	2.7	40
89	Circulating RNAs in prostate cancer patients. Cancer Letters, 2022, 524, 57-69.	3.2	39
90	Mutationâ€“selection balance and compensatory mechanisms in tumour evolution. Nature Reviews Genetics, 2021, 22, 251-262.	7.7	38

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91	Digital storage of glass slides for quality assurance in histopathology and cytopathology. Journal of Telemedicine and Telecare, 2002, 8, 138-142.	1.4	38
92	Robotic Telepathology for Intraoperative Remote Diagnosis Using a Still-Imagingâ€“Based System. American Journal of Clinical Pathology, 2001, 116, 744-752.	0.4	36
93	Variants at IRX4 as prostate cancer expression quantitative trait loci. European Journal of Human Genetics, 2014, 22, 558-563.	1.4	36
94	Tumor purity quantification by clonal DNA methylation signatures. Bioinformatics, 2018, 34, 1642-1649.	1.8	36
95	Next Generation Sequencing of Prostate Cancer from a Patient Identifies a Deficiency of Methylthioadenosine Phosphorylase, an Exploitable Tumor Target. Molecular Cancer Therapeutics, 2012, 11, 775-783.	1.9	34
96	Therapy considerations in neuroendocrine prostate cancer: what next?. Endocrine-Related Cancer, 2021, 28, T67-T78.	1.6	33
97	Genome-Wide Linkage Analysis of TMPRSS2-ERG Fusion in Familial Prostate Cancer. Cancer Research, 2009, 69, 640-646.	0.4	32
98	Recurrent Prostate Cancer Genomic Alterations Predict Response to Brachytherapy Treatment. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 594-600.	1.1	31
99	EthSEQ: ethnicity annotation from whole exome sequencing data. Bioinformatics, 2017, 33, 2402-2404.	1.8	31
100	The Lethal Clone in Prostate Cancer: Redefining the Index. European Urology, 2014, 66, 395-397.	0.9	30
101	Next-Generation Rapid Autopsies Enable Tumor Evolution Tracking and Generation of Preclinical Models. JCO Precision Oncology, 2017, 2017, 1-13.	1.5	30
102	Integrative multiplatform molecular profiling of benign prostatic hyperplasia identifies distinct subtypes. Nature Communications, 2020, 11, 1987.	5.8	29
103	Second Generation Imaging of Nuclear/Cytoplasmic HIV-1 Complexes. AIDS Research and Human Retroviruses, 2014, 30, 717-726.	0.5	26
104	Genetic predisposition to prostate cancer: Update and future perspectives. Urologic Oncology: Seminars and Original Investigations, 2015, 33, 75-84.	0.8	26
105	Impact of constitutional copy number variants on biological pathway evolution. BMC Evolutionary Biology, 2013, 13, 19.	3.2	25
106	A germline FANCA alteration that is associated with increased sensitivity to DNA damaging agents. Journal of Physical Education and Sports Management, 2017, 3, a001487.	0.5	25
107	Integrative Molecular Analysis of Patients With Advanced and Metastatic Cancer. JCO Precision Oncology, 2019, 3, 1-12.	1.5	24
108	Inherited determinants of early recurrent somatic mutations in prostate cancer. Nature Communications, 2017, 8, 48.	5.8	23

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109	Systematic Assessment of Tumor Purity and Its Clinical Implications. JCO Precision Oncology, 2020, 4, 995-1005.	1.5	23
110	TPES: tumor purity estimation from SNVs. Bioinformatics, 2019, 35, 4433-4435.	1.8	22
111	Plasma tumour DNA as an early indicator of treatment response in metastatic castration-resistant prostate cancer. British Journal of Cancer, 2020, 123, 982-987.	2.9	22
112	Skp2 expression is associated with high risk and elevated Ki67 expression in gastrointestinal stromal tumours. BMC Cancer, 2008, 8, 134.	1.1	21
113	CD38 in Advanced Prostate Cancers. European Urology, 2021, 79, 736-746.	0.9	21
114	Digital Pathology: Science Fiction?. International Journal of Surgical Pathology, 2000, 8, 261-263.	0.4	20
115	User attitudes in analyzing digital slides in a quality control test bed: A preliminary study. Computer Methods and Programs in Biomedicine, 2006, 82, 177-186.	2.6	20
116	Testing a Multigene Signature of Prostate Cancer Death in the Swedish Watchful Waiting Cohort. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1682-1688.	1.1	19
117	TMABoost: An Integrated System for Comprehensive Management of Tissue Microarray Data. IEEE Transactions on Information Technology in Biomedicine, 2006, 10, 19-27.	3.6	18
118	Intrapatient heterogeneity in prostate cancer. Nature Reviews Urology, 2015, 12, 430-431.	1.9	18
119	Optimizing copy number variation analysis using genome-wide short sequence oligonucleotide arrays. Nucleic Acids Research, 2010, 38, 3275-3286.	6.5	17
120	Tumor subtype defines distinct pathways of molecular and clinical progression in primary prostate cancer. Journal of Clinical Investigation, 2021, 131, .	3.9	17
121	A Computational Framework Discovers New Copy Number Variants with Functional Importance. PLoS ONE, 2011, 6, e17539.	1.1	16
122	A Comparative Study of ERG Status Assessment on DNA, mRNA, and Protein Levels Using Unique Samples from a Swedish Biopsy Cohort. Applied Immunohistochemistry and Molecular Morphology, 2014, 22, 136-141.	0.6	15
123	An automated procedure to properly handle digital images in large scale Tissue Microarray experiments. Computer Methods and Programs in Biomedicine, 2005, 79, 197-208.	2.6	14
124	Proteomic and genomic signatures of repeat instability in cancer and adjacent normal tissues. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16987-16996.	3.3	14
125	Ploidyâ€•and Purityâ€Adjusted Alleleâ€Specific DNA Analysis Using CLONETv2. Current Protocols in Bioinformatics, 2019, 67, e81.	25.8	13
126	Allele-specific genomic data elucidate the role of somatic gain and copy-number neutral loss of heterozygosity in cancer. Cell Systems, 2022, 13, 183-193.e7.	2.9	13

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127	Comparative genomics of primary prostate cancer and paired metastases: insights from 12 molecular case studies. Journal of Pathology, 2022, 257, 274-284.	2.1	13
128	Nine-Gene Molecular Signature Is Not Associated with Prostate Cancer Death in a Watchful Waiting Cohort. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 249-251.	1.1	12
129	Whole exome sequencing (WES) of circulating tumor DNA (ctDNA) in patients with neuroendocrine prostate cancer (NEPC) informs tumor heterogeneity.. Journal of Clinical Oncology, 2017, 35, 5011-5011.	0.8	12
130	The Genomics of Prostate Cancer: A Historic Perspective. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a034942.	2.9	11
131	Internet-based Profiler system as integrative framework to support translational research. BMC Bioinformatics, 2005, 6, 304.	1.2	10
132	Past, Current, and Future Strategies to Target ERG Fusion-Positive Prostate Cancer. Cancers, 2022, 14, 1118.	1.7	10
133	Defining order and timing of mutations during cancer progression: the TO-DAG probabilistic graphical model. Frontiers in Genetics, 2015, 6, 309.	1.1	9
134	PaCBAM: fast and scalable processing of whole exome and targeted sequencing data. BMC Genomics, 2019, 20, 1018.	1.2	9
135	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. Human Pathology, 2013, 44, 2282-2292.	1.1	8
136	Core Biopsies from Prostate Cancer Patients in Active Surveillance Protocols Harbor PTEN and MYC Alterations. European Urology Oncology, 2019, 2, 277-285.	2.6	7
137	ABEMUS: platform-specific and data-informed detection of somatic SNVs in cfDNA. Bioinformatics, 2020, 36, 2665-2674.	1.8	7
138	Charting differentially methylated regions in cancer with Rocker-meth. Communications Biology, 2021, 4, 1249.	2.0	7
139	In silico identification and functional validation of allele-dependent AR enhancers. Oncotarget, 2015, 6, 4816-4828.	0.8	6
140	Transcriptional regulation and prostate cancer risk loci.. Journal of Clinical Oncology, 2013, 31, 1554-1554.	0.8	6
141	ETS-related gene (ERG) undermines genome stability in mouse prostate progenitors via Gsk3Î² dependent Nkx3.1 degradation. Cancer Letters, 2022, 534, 215612.	3.2	6
142	A step toward functionally characterized prostate cancer molecular subtypes. Nature Medicine, 2013, 19, 966-967.	15.2	5
143	Molecular Archeology: Unearthing Androgen-Induced Structural Rearrangements in Prostate Cancer Genomes. Cancer Cell, 2013, 23, 133-135.	7.7	5
144	Inherited variant in NFÎºBâ€‹1 promoter is associated with increased risk of IBD in an Algerian population and modulates SOX9 binding. Cancer Reports, 2020, 3, e1240.	0.6	5

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145	Fast mutual exclusivity algorithm nominates potential synthetic lethal gene pairs through brute force matrix product computations. Computational and Structural Biotechnology Journal, 2021, 19, 4394-4403.	1.9	5
146	Response to â€˜TMPRSS2-ERG gene fusions are infrequent in prostatic ductal adenocarcinomasâ€™. Modern Pathology, 2009, 22, 1398-1399.	2.9	4
147	Voices of biotech. Nature Biotechnology, 2016, 34, 270-275.	9.4	4
148	Plasma tumor <scp>DNA</scp> is associated with increased risk of venous thromboembolism in metastatic castrationâ€resistant cancer patients. International Journal of Cancer, 2022, 150, 1166-1173.	2.3	4
149	Defining a molecular subclass of treatment resistant prostate cancer.. Journal of Clinical Oncology, 2015, 33, 5004-5004.	0.8	3
150	Accuracy of telepathology. Journal of Telemedicine and Telecare, 2004, 10, 123-124.	1.4	2
151	Active Sampling for Knowledge Discovery from Biomedical Data. Lecture Notes in Computer Science, 2005, , 343-354.	1.0	2
152	Allele-Specific Genomics is an Orthogonal Feature in the Landscape of Primary Tumors Phenotypes. SSRN Electronic Journal, 0, , .	0.4	2
153	Analytical protocol to identify local ancestry-associated molecular features in cancer. STAR Protocols, 2021, 2, 100766.	0.5	2
154	MP24-13 WITHDRAWN: RECURRENT PROSTATE CANCER GENOMIC ALTERATIONS PREDICT RESPONSE TO BRACHYTHERAPY TREATMENT. Journal of Urology, 2014, 191, .	0.2	1
155	Abstract 4017: Dissecting the clonal hierarchy of cancer-driving genomic lesions.. , 2013, , .		1
156	Whole exome sequencing to reveal chemotherapy-driven evolution of platinum-resistant metastatic urothelial cancer.. Journal of Clinical Oncology, 2015, 33, 4513-4513.	0.8	1
157	Combining Supervised and Unsupervised Methods to Support Early Diagnosis of Hepatocellular Carcinoma. Lecture Notes in Computer Science, 2003, , 239-243.	1.0	1
158	Precision medicine program for whole-exome sequencing (WES) provides new insight on platinum sensitivity in advanced prostate cancer (PCa).. Journal of Clinical Oncology, 2015, 33, 158-158.	0.8	1
159	Abstract 1108: SPOP mutation leads to genomic instability in prostate cancer. , 2015, , .		1
160	Abstract 4745: Precision cancer medicine program for whole-exome sequencing of metastatic tumors reveals biomarkers of response. , 2015, , .		1
161	Abstract NG01: SPOP mutation is associated with genomic instability in prostate cancer. , 2015, , .		1
162	Association of androgen receptor (AR) status in plasma DNA with outcome on enzalutamide (enza) or abiraterone (abi) for castration resistant prostate cancer (CRPC).. Journal of Clinical Oncology, 2017, 35, 5060-5060.	0.8	1

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163	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
164	CAVEOLIN-1 INTERACTS WITH A LIPID RAFT-ASSOCIATED POPULATION OF FATTY ACID SYNTHASE IN PROSTATE CANCER. Journal of Urology, 2008, 179, 456-457.	0.2	0
165	608 COMBINING DNA-SEQ AND RNA-SEQ FOR DISCOVERY OF NOVEL MUTATIONS IN HUMAN PROSTATE CANCER. Journal of Urology, 2011, 185, .	0.2	0
166	1314 RECURRENT MUTATIONS IN SPOP DEFINE A DISTINCT MOLECULAR CLASS OF PROSTATE CANCER. Journal of Urology, 2012, 187, .	0.2	0
167	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
168	200 DEFINING THE MECHANISTIC BASIS OF SPOP MUTATIONS IN PROSTATE CANCER. Journal of Urology, 2013, 189, .	0.2	0
169	MP41-06 SPOP MUTATIONS IN PROSTATE CANCER ACROSS DEMOGRAPHICALLY DIVERSE PATIENT COHORTS.. Journal of Urology, 2014, 191, .	0.2	0
170	MP66-01 SPOP MUTATION LEADS TO GENOMIC INSTABILITY IN PROSTATE CANCER. Journal of Urology, 2015, 193, .	0.2	0
171	Combining molecular and functional imaging in metastatic castration-resistant prostate cancer (mCRPC).. Journal of Clinical Oncology, 2021, 39, 141-141.	0.8	0
172	Association of plasma tumor DNA (ptDNA) with increased risk of venous thromboembolism (VTE) in metastatic castration resistant prostate cancer patients (mCRPC).. Journal of Clinical Oncology, 2021, 39, 5048-5048.	0.8	0
173	Abstract LB-21: Emergence of castration resistant prostate cancer class defined by recurrentERGfusion. , 2010, , .		0
174	Abstract 1139: Complete characterization of prostate cancer genomes by massively parallel sequencing. , 2010, , .		0
175	Abstract 2743: Accelerating the exploration of novel gene fusion events in prostate cancer. , 2010, , .		0
176	Abstract 2227: Concordance ofERGgene rearrangements andERGprotein expression in low grade PIN lesions in prostate needle biopsies. , 2011, , .		0
177	Abstract 2218: Integrated diagnostic methods for detection of multiple gene rearrangements in prostate cancer tissue specimens. , 2011, , .		0
178	Abstract 3925: Characterization of complex chromosomal aberrations in prostate cancer from whole genome sequencing. , 2011, , .		0
179	Abstract 957: Aurora kinase and N-myc are involved in neuroendocrine differentiation of prostate cancer and are new drug targets. , 2011, , .		0
180	Abstract LB-246: Recurrent inactivating mutations in SPOP define a molecular subset of prostate cancer. , 2011, , .		0

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181	Abstract 2222: Oncogene-mediated alterations in chromatin conformation. , 2012, , .		0
182	Abstract 486: The novel tumor suppressorDIAPH3governs transition to an amoeboid phenotype. , 2012, , .		0
183	Abstract 4601: Punctuated evolution of prostate cancer genomes.. , 2013, , .		0
184	Abstract 3952: Recurrent prostate cancer genomic alterations predict response to brachytherapy treatment. , 2014, , .		0
185	Abstract 5269: Myxofibrosarcoma: A move toward Precision Medicine. , 2015, , .		0
186	Abstract LB-018: Defining a molecular subclass of treatment-resistant prostate cancer. , 2015, , .		0
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