Andrea Sboner

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

137	29,601	56	155
papers	citations	h-index	g-index
155	36,678 ext. citations	14.4	8.2
ext. papers		avg, IF	L-index

#	Paper	IF	Citations
137	Association of circulating tumor cell RB1 loss RNA signature with outcomes and immune phenotypes in men with mCRPC <i>Journal of Clinical Oncology</i> , 2022 , 40, 139-139	2.2	
136	Comparative genomics of primary prostate cancer and paired metastases: insights from 12 molecular case studies <i>Journal of Pathology</i> , 2022 ,	9.4	1
135	Opposing transcriptional programs of KLF5 and AR emerge during therapy for advanced prostate cancer. <i>Nature Communications</i> , 2021 , 12, 6377	17.4	О
134	G3BP1 inhibits Cul3 to amplify AR signaling and promote prostate cancer. <i>Nature Communications</i> , 2021 , 12, 6662	17.4	3
133	High Rates of Remission with the Initial Treatment of Oral Azacitidine Plus CHOP for Peripheral T-Cell Lymphoma (PTCL): Clinical Outcomes and Biomarker Analysis of a Multi-Center Phase II Study. <i>Blood</i> , 2021 , 138, 138-138	2.2	O
132	A Deep Learning Approach to Diagnostic Classification of Prostate Cancer Using Pathology-Radiology Fusion. <i>Journal of Magnetic Resonance Imaging</i> , 2021 , 54, 462-471	5.6	8
131	Targeting the epichaperome as an effective precision medicine approach in a novel PML-SYK fusion acute myeloid leukemia. <i>Npj Precision Oncology</i> , 2021 , 5, 44	9.8	6
130	Tumor subtype defines distinct pathways of molecular and clinical progression in primary prostate cancer. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	5
129	Androgen receptor variant shows heterogeneous expression in prostate cancer according to differentiation stage. <i>Communications Biology</i> , 2021 , 4, 785	6.7	Ο
128	CD38 in Advanced Prostate Cancers. European Urology, 2021, 79, 736-746	10.2	0
127	Temporal evolution of cellular heterogeneity during the progression to advanced AR-negative prostate cancer. <i>Nature Communications</i> , 2021 , 12, 3372	17.4	3
126	Integration of whole-exome and anchored PCR-based next generation sequencing significantly increases detection of actionable alterations in precision oncology. <i>Translational Oncology</i> , 2021 , 14, 100944	4.9	2
125	Limitations of Detecting Genetic Variants from the RNA Sequencing Data in Tissue and Fine-Needle Aspiration Samples. <i>Thyroid</i> , 2021 , 31, 589-595	6.2	4
124	Molecular medicine tumor board: whole-genome sequencing to inform on personalized medicine for a man with advanced prostate cancer. <i>Prostate Cancer and Prostatic Diseases</i> , 2021 , 24, 786-793	6.2	3
123	Patient-derived xenografts and organoids model therapy response in prostate cancer. <i>Nature Communications</i> , 2021 , 12, 1117	17.4	18
122	MicroRNA-1205 Regulation of FRYL in Prostate Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 647485	5.7	1
121	Functional comparison of exome capture-based methods for transcriptomic profiling of formalin-fixed paraffin-embedded tumors. <i>Npj Genomic Medicine</i> , 2021 , 6, 66	6.2	2

120	Validation of a Circulating Tumor DNA-Based Next-Generation Sequencing Assay in a Cohort of Patients with Solid tumors: A Proposed Solution for Decentralized Plasma Testing. <i>Oncologist</i> , 2021 , 26, e1971-e1981	5.7	1
119	Reshaping of the androgen-driven chromatin landscape in normal prostate cells by early cancer drivers and effect on therapeutic sensitivity. <i>Cell Reports</i> , 2021 , 36, 109625	10.6	4
118	Diversity in Androgen Receptor Action Among Treatment-nalle Prostate Cancers Is Reflected in Treatment Response Predictions and Molecular Subtypes. <i>European Urology Open Science</i> , 2020 , 22, 34-	449	2
117	Role of specialized composition of SWI/SNF complexes in prostate cancer lineage plasticity. <i>Nature Communications</i> , 2020 , 11, 5549	17.4	31
116	Identification of Distinct Heterogenic Subtypes and Molecular Signatures Associated with African Ancestry in Triple Negative Breast Cancer Using Quantified Genetic Ancestry Models in Admixed Race Populations. <i>Cancers</i> , 2020 , 12,	6.6	8
115	Building an international consortium for tracking coronavirus health status. <i>Nature Medicine</i> , 2020 , 26, 1161-1165	50.5	16
114	Fusions involving BCOR and CREBBP are rare events in infiltrating glioma. <i>Acta Neuropathologica Communications</i> , 2020 , 8, 80	7.3	3
113	SLFN11 Expression in Advanced Prostate Cancer and Response to Platinum-based Chemotherapy. <i>Molecular Cancer Therapeutics</i> , 2020 , 19, 1157-1164	6.1	23
112	Small Cell Carcinoma of the Ovary, Hypercalcemic Type (SCCOHT) beyond Mutations: A Comprehensive Genomic Analysis. <i>Cells</i> , 2020 , 9,	7.9	14
111	Integrative multiplatform molecular profiling of benign prostatic hyperplasia identifies distinct subtypes. <i>Nature Communications</i> , 2020 , 11, 1987	17.4	14
110	Circulating tumor DNA profile recognizes transformation to castration-resistant neuroendocrine prostate cancer. <i>Journal of Clinical Investigation</i> , 2020 , 130, 1653-1668	15.9	56
109	Circulating tumor DNA (ctDNA) to detect neuroendocrine prostate cancer genomic and DNA methylation changes <i>Journal of Clinical Oncology</i> , 2020 , 38, 8-8	2.2	
108	Performance Characteristics of a Targeted Sequencing Platform for Simultaneous Detection of Single Nucleotide Variants, Insertions/Deletions, Copy Number Alterations, and Gene Fusions in Cancer Genome. <i>Archives of Pathology and Laboratory Medicine</i> , 2020 , 144, 1535-1546	5	4
107	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. <i>Cell</i> , 2020 , 183, 197-210.e32	56.2	45
106	Common germline-somatic variant interactions in advanced urothelial cancer. <i>Nature Communications</i> , 2020 , 11, 6195	17.4	6
105	PARP Inhibition Suppresses GR-MYCN-CDK5-RB1-E2F1 Signaling and Neuroendocrine Differentiation in Castration-Resistant Prostate Cancer. <i>Clinical Cancer Research</i> , 2019 , 25, 6839-6851	12.9	22
104	Clinical features of neuroendocrine prostate cancer. European Journal of Cancer, 2019, 121, 7-18	7.5	79
103	Cancer-Specific Thresholds Adjust for Whole Exome Sequencing-based Tumor Mutational Burden Distribution. <i>JCO Precision Oncology</i> , 2019 , 3,	3.6	8

102	Integrative Molecular Analysis of Patients With Advanced and Metastatic Cancer. <i>JCO Precision Oncology</i> , 2019 , 3,	3.6	15
101	FOXA1 mutations alter pioneering activity, differentiation and prostate cancer phenotypes. <i>Nature</i> , 2019 , 571, 408-412	50.4	81
100	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	11.5	383
99	Identification of a therapeutic target using molecular sequencing for treatment of recurrent uterine serous adenocarcinoma. <i>Gynecologic Oncology Reports</i> , 2019 , 28, 54-57	1.3	5
98	Delta-like protein 3 expression and therapeutic targeting in neuroendocrine prostate cancer. <i>Science Translational Medicine</i> , 2019 , 11,	17.5	56
97	CHD1 Loss Alters AR Binding at Lineage-Specific Enhancers and Modulates Distinct Transcriptional Programs to Drive Prostate Tumorigenesis. <i>Cancer Cell</i> , 2019 , 35, 603-617.e8	24.3	29
96	N-Myc-mediated epigenetic reprogramming drives lineage plasticity in advanced prostate cancer. Journal of Clinical Investigation, 2019 , 129, 3924-3940	15.9	55
95	Clinical and molecular analysis of patients treated with prostate-specific membrane antigen (PSMA)-targeted radionuclide therapy <i>Journal of Clinical Oncology</i> , 2019 , 37, 272-272	2.2	5
94	Oncogenic Addiction to ERBB2 Signaling Predicts Response to Trastuzumab in Urothelial Cancer. Journal of the National Comprehensive Cancer Network: JNCCN, 2019 , 17, 194-200	7.3	3
93	The genomic landscape of metastatic clear cell renal cell carcinoma (ccRCC) after treatment with systemic therapy <i>Journal of Clinical Oncology</i> , 2019 , 37, 675-675	2.2	
92	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	12.9	110
91	Low Tristetraprolin Expression Is Associated with Lethal Prostate Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 584-590	4	4
90	Bone biopsy protocol for advanced prostate cancer in the era of precision medicine. <i>Cancer</i> , 2018 , 124, 1008-1015	6.4	24
89	The long tail of oncogenic drivers in prostate cancer. <i>Nature Genetics</i> , 2018 , 50, 645-651	36.3	380
88	Biallelic tumour suppressor loss and DNA repair defects in de novo small-cell prostate carcinoma. <i>Journal of Pathology</i> , 2018 , 246, 244-253	9.4	21
87	Suppression of insulin feedback enhances the efficacy of PI3K inhibitors. <i>Nature</i> , 2018 , 560, 499-503	50.4	277
86	Patient derived organoids to model rare prostate cancer phenotypes. <i>Nature Communications</i> , 2018 , 9, 2404	17.4	149
85	SPOP mutation drives prostate neoplasia without stabilizing oncogenic transcription factor ERG. Journal of Clinical Investigation, 2018, 128, 381-386	15.9	23

(2016-2018)

84	Risk of venous thromboembolism, survival, and expression of procoagulant genes in neuroendocrine versus castration-resistant prostate cancer <i>Journal of Clinical Oncology</i> , 2018 , 36, e170) 39 -e1	7039
83	Targeting the Epichaperome As an Effective Precision Medicine Approach in a Novel PML-SYK Fusion Acute Myeloid Leukemia. <i>Blood</i> , 2018 , 132, 1435-1435	2.2	1
82	Gene Fusions. Molecular Pathology Library, 2018 , 137-151		
81	BRCA2-Associated Prostate Cancer in a Patient With Spinal and Bulbar Muscular Atrophy. <i>JCO Precision Oncology</i> , 2018 , 2,	3.6	2
80	Impact of the SPOP Mutant Subtype on the Interpretation of Clinical Parameters in Prostate Cancer. <i>JCO Precision Oncology</i> , 2018 , 2018,	3.6	17
79	TBIO-15. UTILIZING A HISTOLOGY-SPECIFIC SEQUENCING ALGORITHM FOR PRECISION NEURO-ONCOLOGY. <i>Neuro-Oncology</i> , 2018 , 20, i183-i183	1	78
78	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018 , 362,	33.3	277
77	ZFX Mediates Non-canonical Oncogenic Functions of the Androgen Receptor Splice Variant 7 in Castrate-Resistant Prostate Cancer. <i>Molecular Cell</i> , 2018 , 72, 341-354.e6	17.6	38
76	CD38 is methylated in prostate cancer and regulates extracellular NAD. <i>Cancer & Metabolism</i> , 2018 , 6, 13	5.4	18
75	Personalized and Cancer Models to Guide Precision Medicine. Cancer Discovery, 2017, 7, 462-477	24.4	477
74	SPOP Mutation Drives Prostate Tumorigenesis In Vivo through Coordinate Regulation of PI3K/mTOR and AR Signaling. <i>Cancer Cell</i> , 2017 , 31, 436-451	24.3	116
73	Identification of novel prostate cancer drivers using RegNetDriver: a framework for integration of genetic and epigenetic alterations with tissue-specific regulatory network. <i>Genome Biology</i> , 2017 , 18, 141	18.3	20
72	Next-Generation Rapid Autopsies Enable Tumor Evolution Tracking and Generation of Preclinical Models. <i>JCO Precision Oncology</i> , 2017 , 2017,	3.6	23
71	Impact of Therapy on Genomics and Transcriptomics in High-Risk Prostate Cancer Treated with Neoadjuvant Docetaxel and Androgen Deprivation Therapy. <i>Clinical Cancer Research</i> , 2017 , 23, 6802-68	1 ¹ 1 ^{2.9}	50
70	Aberrant Activation of a Gastrointestinal Transcriptional Circuit in Prostate Cancer Mediates Castration Resistance. <i>Cancer Cell</i> , 2017 , 32, 792-806.e7	24.3	39
69	Inherited determinants of early recurrent somatic mutations in prostate cancer. <i>Nature Communications</i> , 2017 , 8, 48	17.4	16
68	The cancer precision medicine knowledge base for structured clinical-grade mutations and interpretations. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2017 , 24, 513-519	8.6	66
67	Clonal evolution of chemotherapy-resistant urothelial carcinoma. <i>Nature Genetics</i> , 2016 , 48, 1490-1499	36.3	161

66	Development and validation of a whole-exome sequencing test for simultaneous detection of point mutations, indels and copy-number alterations for precision cancer care. <i>Npj Genomic Medicine</i> , 2016 , 1,	6.2	51
65	A primer on precision medicine informatics. <i>Briefings in Bioinformatics</i> , 2016 , 17, 145-53	13.4	30
64	Patient-Level DNA Damage and Repair Pathway Profiles and Prognosis After Prostatectomy for High-Risk Prostate Cancer. <i>JAMA Oncology</i> , 2016 , 2, 471-80	13.4	38
63	Divergent clonal evolution of castration-resistant neuroendocrine prostate cancer. <i>Nature Medicine</i> , 2016 , 22, 298-305	50.5	775
62	The metabolic/pH sensor soluble adenylyl cyclase is a tumor suppressor protein. <i>Oncotarget</i> , 2016 , 7, 45597-45607	3.3	13
61	N-Myc Induces an EZH2-Mediated Transcriptional Program Driving Neuroendocrine Prostate Cancer. <i>Cancer Cell</i> , 2016 , 30, 563-577	24.3	256
60	MAGI3-AKT3 fusion in breast cancer amended. <i>Nature</i> , 2015 , 520, E11-2	50.4	20
59	ASEQ: fast allele-specific studies from next-generation sequencing data. <i>BMC Medical Genomics</i> , 2015 , 8, 9	3.7	38
58	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-25	56.2	1713
57	Alternative transcription initiation leads to expression of a novel ALK isoform in cancer. <i>Nature</i> , 2015 , 526, 453-7	50.4	144
56	SPOP mutation leads to genomic instability in prostate cancer. <i>ELife</i> , 2015 , 4,	8.9	110
55	Integrative clinical genomics of advanced prostate cancer. <i>Cell</i> , 2015 , 161, 1215-1228	56.2	1765
54	Whole-Exome Sequencing of Metastatic Cancer and Biomarkers of Treatment Response. <i>JAMA Oncology</i> , 2015 , 1, 466-74	13.4	207
53	SPOP mutations in prostate cancer across demographically diverse patient cohorts. <i>Neoplasia</i> , 2014 , 16, 14-20	6.4	113
52	Novel ZC3H7B-BCOR, MEAF6-PHF1, and EPC1-PHF1 fusions in ossifying fibromyxoid tumorsmolecular characterization shows genetic overlap with endometrial stromal sarcoma. <i>Genes Chromosomes and Cancer</i> , 2014 , 53, 183-93	5	117
51	PRC2 is recurrently inactivated through EED or SUZ12 loss in malignant peripheral nerve sheath tumors. <i>Nature Genetics</i> , 2014 , 46, 1227-32	36.3	348
50	Organoid cultures derived from patients with advanced prostate cancer. <i>Cell</i> , 2014 , 159, 176-187	56.2	847
49	MTSS1 is a metastasis driver in a subset of human melanomas. <i>Nature Communications</i> , 2014 , 5, 3465	17.4	43

(2011-2014)

48	Unraveling the clonal hierarchy of somatic genomic aberrations. <i>Genome Biology</i> , 2014 , 15, 439	18.3	61
47	The oestrogen receptor alpha-regulated lncRNA NEAT1 is a critical modulator of prostate cancer. <i>Nature Communications</i> , 2014 , 5, 5383	17.4	432
46	Epigenomic alterations in localized and advanced prostate cancer. <i>Neoplasia</i> , 2013 , 15, 373-83	6.4	59
45	Integrative annotation of variants from 1092 humans: application to cancer genomics. <i>Science</i> , 2013 , 342, 1235587	33.3	281
44	Novel MIR143-NOTCH fusions in benign and malignant glomus tumors. <i>Genes Chromosomes and Cancer</i> , 2013 , 52, 1075-87	5	99
43	Identification of molecular tumor markers in renal cell carcinomas with TFE3 protein expression by RNA sequencing. <i>Neoplasia</i> , 2013 , 15, 1231-40	6.4	28
42	Punctuated evolution of prostate cancer genomes. <i>Cell</i> , 2013 , 153, 666-77	56.2	862
41	Novel YAP1-TFE3 fusion defines a distinct subset of epithelioid hemangioendothelioma. <i>Genes Chromosomes and Cancer</i> , 2013 , 52, 775-84	5	349
40	Recurrent NCOA2 gene rearrangements in congenital/infantile spindle cell rhabdomyosarcoma. <i>Genes Chromosomes and Cancer</i> , 2013 , 52, 538-50	5	143
39	Re: Stoehr et al. Lack of evidence for frequent MED12 p.L1224F mutation in prostate tumours from Caucasian patients. J Pathol 2013; 230: 453-456. <i>Journal of Pathology</i> , 2013 , 231, 271	9.4	1
38	VAT: a computational framework to functionally annotate variants in personal genomes within a cloud-computing environment. <i>Bioinformatics</i> , 2012 , 28, 2267-9	7.2	55
37	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
36	Genomic analysis of the hydrocarbon-producing, cellulolytic, endophytic fungus Ascocoryne sarcoides. <i>PLoS Genetics</i> , 2012 , 8, e1002558	6	64
35	IQSeq: integrated isoform quantification analysis based on next-generation sequencing. <i>PLoS ONE</i> , 2012 , 7, e29175	3.7	5
34	Molecular characterization of neuroendocrine prostate cancer and identification of new drug targets. <i>Cancer Discovery</i> , 2011 , 1, 487-95	24.4	550
33	Identification of a disease-defining gene fusion in epithelioid hemangioendothelioma. <i>Science Translational Medicine</i> , 2011 , 3, 98ra82	17.5	252
32	A userß guide to the encyclopedia of DNA elements (ENCODE). PLoS Biology, 2011, 9, e1001046	9.7	1060
31	The genomic complexity of primary human prostate cancer. <i>Nature</i> , 2011 , 470, 214-20	50.4	984

30	The real cost of sequencing: higher than you think!. Genome Biology, 2011, 12, 125	18.3	247
29	Discovery of non-ETS gene fusions in human prostate cancer using next-generation RNA sequencing. <i>Genome Research</i> , 2011 , 21, 56-67	9.7	156
28	Diverse protein kinase interactions identified by protein microarrays reveal novel connections between cellular processes. <i>Genes and Development</i> , 2011 , 25, 767-78	12.6	51
27	RSEQtools: a modular framework to analyze RNA-Seq data using compact, anonymized data summaries. <i>Bioinformatics</i> , 2011 , 27, 281-3	7.2	89
26	Genomics and privacy: implications of the new reality of closed data for the field. <i>PLoS Computational Biology</i> , 2011 , 7, e1002278	5	56
25	Optimizing copy number variation analysis using genome-wide short sequence oligonucleotide arrays. <i>Nucleic Acids Research</i> , 2010 , 38, 3275-86	20.1	15
24	Integrative analysis of the Caenorhabditis elegans genome by the modENCODE project. <i>Science</i> , 2010 , 330, 1775-87	33.3	744
23	FusionSeq: a modular framework for finding gene fusions by analyzing paired-end RNA-sequencing data. <i>Genome Biology</i> , 2010 , 11, R104	18.3	121
22	Comparison and calibration of transcriptome data from RNA-Seq and tiling arrays. <i>BMC Genomics</i> , 2010 , 11, 383	4.5	88
21	Molecular sampling of prostate cancer: a dilemma for predicting disease progression. <i>BMC Medical Genomics</i> , 2010 , 3, 8	3.7	169
20	Distinct genomic aberrations associated with ERG rearranged prostate cancer. <i>Genes Chromosomes and Cancer</i> , 2009 , 48, 366-80	5	72
19	Robust-linear-model normalization to reduce technical variability in functional protein microarrays. <i>Journal of Proteome Research</i> , 2009 , 8, 5451-64	5.6	55
18	N-myc downstream regulated gene 1 (NDRG1) is fused to ERG in prostate cancer. <i>Neoplasia</i> , 2009 , 11, 804-11	6.4	92
17	The role of disorder in interaction networks: a structural analysis. <i>Molecular Systems Biology</i> , 2008 , 4, 179	12.2	167
16	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, 569-76	7.5	32
15	Estrogen-dependent signaling in a molecularly distinct subclass of aggressive prostate cancer. Journal of the National Cancer Institute, 2008 , 100, 815-25	9.7	251
14	UbcH10 expression may be a useful tool in the prognosis of ovarian carcinomas. <i>Oncogene</i> , 2007 , 26, 2136-40	9.2	61
13	Comparing classical pathways and modern networks: towards the development of an edge ontology. <i>Trends in Biochemical Sciences</i> , 2007 , 32, 320-31	10.3	49

LIST OF PUBLICATIONS

-	12	Integrative microarray analysis of pathways dysregulated in metastatic prostate cancer. <i>Cancer Research</i> , 2007 , 67, 10296-303	10.1	64	
	11	UbcH10 is overexpressed in malignant breast carcinomas. <i>European Journal of Cancer</i> , 2007 , 43, 2729-3	5 7.5	56	
-	10	TMABoost: an integrated system for comprehensive management of tissue microarray data. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2006 , 10, 19-27		17	
٩	9	An automated procedure to properly handle digital images in large scale tissue microarray experiments. <i>Computer Methods and Programs in Biomedicine</i> , 2005 , 79, 197-208	6.9	13	
8	8	Clinical validation of an automated system for supporting the early diagnosis of melanoma. <i>Skin Research and Technology</i> , 2004 , 10, 184-92	1.9	13	
7	7	A multiple classifier system for early melanoma diagnosis. <i>Artificial Intelligence in Medicine</i> , 2003 , 27, 29-44	7.4	75	
(6	Automatic model selection in cost-sensitive boosting. <i>Information Fusion</i> , 2003 , 4, 3-10	16.7	14	
!	5	Analysis of user-satisfaction with the use of a teleconsultation system in oncology. <i>Informatics for Health and Social Care</i> , 2003 , 28, 73-84		17	
4	4	Combining Supervised and Unsupervised Methods to Support Early Diagnosis of Hepatocellular Carcinoma. <i>Lecture Notes in Computer Science</i> , 2003 , 239-243	0.9		
	3	Role of Specialized Composition of SWI/SNF Complexes in Prostate Cancer Lineage Plasticity		1	
1	2	Novel patterns of complex structural variation revealed across thousands of cancer genome graphs		8	
-	1	SPOP mutation confers sensitivity to AR-targeted therapy in prostate cancer by reshaping the androgen-driven chromatin landscape		2	