

# George S Bova

## List of Publications by Year in descending order

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Version: 2024-02-01

60  
papers

11,151  
citations

94381

37  
h-index

143943

57  
g-index

63  
all docs

63  
docs citations

63  
times ranked

14355  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Movember Global Action Plan 1 (GAP1): Unique Prostate Cancer Tissue Microarray Resource. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 715-727.	1.1	0
2	Combined Longitudinal Clinical and Autopsy Phenomic Assessment in Lethal Metastatic Prostate Cancer: Recommendations for Advancing Precision Medicine. <i>European Urology Open Science</i> , 2021, 30, 47-62.	0.2	2
3	Proteomic characterization of primary and metastatic prostate cancer reveals reduced proteinase activity in aggressive tumors. <i>Scientific Reports</i> , 2021, 11, 18936.	1.6	6
4	Subclone Eradication Analysis Identifies Targets for Enhanced Cancer Therapy and Reveals L1 Retrotransposition as a Dynamic Source of Cancer Heterogeneity. <i>Cancer Research</i> , 2021, 81, 4901-4909.	0.4	6
5	Prostate cancer evolution from multilineage primary to single lineage metastases with implications for liquid biopsy. <i>Nature Communications</i> , 2020, 11, 5070.	5.8	44
6	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. <i>Nature Genetics</i> , 2018, 50, 682-692.	9.4	182
7	Expression of neuroendocrine differentiation markers in lethal metastatic castration-resistant prostate cancer. <i>Pathology Research and Practice</i> , 2018, 214, 848-856.	1.0	19
8	Constitutively active androgen receptor splice variants AR-V3, AR-V7 and AR-V9 are co-expressed in castration-resistant prostate cancer metastases. <i>British Journal of Cancer</i> , 2018, 119, 347-356.	2.9	63
9	Human metastases under scrutiny. <i>Nature</i> , 2017, 548, 287-288.	13.7	2
10	The expression of AURKA is androgen regulated in castration-resistant prostate cancer. <i>Scientific Reports</i> , 2017, 7, 17978.	1.6	38
11	Appraising the relevance of DNA copy number loss and gain in prostate cancer using whole genome DNA sequence data. <i>PLoS Genetics</i> , 2017, 13, e1007001.	1.5	34
12	Microseminoprotein-Beta Expression in Different Stages of Prostate Cancer. <i>PLoS ONE</i> , 2016, 11, e0150241.	1.1	28
13	Integrated clinical, whole-genome, and transcriptome analysis of multisampled lethal metastatic prostate cancer. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a000752.	0.5	24
14	Mutational signatures of ionizing radiation in second malignancies. <i>Nature Communications</i> , 2016, 7, 12605.	5.8	214
15	Resolving complex research data management issues in biomedical laboratories: Qualitative study of an industry-academia collaboration. <i>Computer Methods and Programs in Biomedicine</i> , 2016, 126, 160-170.	2.6	5
16	The evolutionary history of lethal metastatic prostate cancer. <i>Nature</i> , 2015, 520, 353-357.	13.7	1,185
17	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. <i>ELife</i> , 2014, 3, .	2.8	318
18	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014, 345, 1251343.	6.0	348

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19	Loss of PTEN Is Associated with Aggressive Behavior in ERG-Positive Prostate Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013, 22, 2333-2344.	1.1	121
20	DNA Methylation Alterations Exhibit Intraindividual Stability and Interindividual Heterogeneity in Prostate Cancer Metastases. <i>Science Translational Medicine</i> , 2013, 5, 169ra10.	5.8	231
21	Genetic markers associated with early cancer-specific mortality following prostatectomy. <i>Cancer</i> , 2013, 119, 2405-2412.	2.0	81
22	Somatic Alterations Contributing to Metastasis of a Castration-Resistant Prostate Cancer. <i>Human Mutation</i> , 2013, 34, 1231-1241.	1.1	52
23	Clustering-Based Method for Developing a Genomic Copy Number Alteration Signature for Predicting the Metastatic Potential of Prostate Cancer. <i>Journal of Probability and Statistics</i> , 2012, 2012, 1-19.	0.3	3
24	Identification of novel CHD1-associated collaborative alterations of genomic structure and functional assessment of CHD1 in prostate cancer. <i>Oncogene</i> , 2012, 31, 3939-3948.	2.6	87
25	Detection and Verification of Glycosylation Patterns of Glycoproteins from Clinical Specimens Using Lectin Microarrays and Lectin-Based Immunosorbent Assays. <i>Analytical Chemistry</i> , 2011, 83, 8509-8516.	3.2	71
26	A DNA methylation microarray-based study identifies ERG as a gene commonly methylated in prostate cancer. <i>Epigenetics</i> , 2011, 6, 1248-1256.	1.3	16
27	Intragenic Rearrangement and Altered RNA Splicing of the Androgen Receptor in a Cell-Based Model of Prostate Cancer Progression. <i>Cancer Research</i> , 2011, 71, 2108-2117.	0.4	177
28	BACOM: <i>in silico</i> detection of genomic deletion types and correction of normal cell contamination in copy number data. <i>Bioinformatics</i> , 2011, 27, 1473-1480.	1.8	30
29	Androgen-induced TOP2B-mediated double-strand breaks and prostate cancer gene rearrangements. <i>Nature Genetics</i> , 2010, 42, 668-675.	9.4	539
30	Ligand-Independent Androgen Receptor Variants Derived from Splicing of Cryptic Exons Signify Hormone-Refractory Prostate Cancer. <i>Cancer Research</i> , 2009, 69, 16-22.	0.4	939
31	Copy number analysis indicates monoclonal origin of lethal metastatic prostate cancer. <i>Nature Medicine</i> , 2009, 15, 559-565.	15.2	596
32	DNA Hypomethylation Arises Later in Prostate Cancer Progression than CpG Island Hypermethylation and Contributes to Metastatic Tumor Heterogeneity. <i>Cancer Research</i> , 2008, 68, 8954-8967.	0.4	255
33	Roles for the Stem Cell-Associated Intermediate Filament Nestin in Prostate Cancer Migration and Metastasis. <i>Cancer Research</i> , 2007, 67, 9199-9206.	0.4	174
34	Optimal Molecular Profiling of Tissue and Tissue Components: Defining the Best Processing and Microdissection Methods for Biomedical Applications. <i>Molecular Biotechnology</i> , 2005, 29, 119-152.	1.3	20
35	Immortalizing the complexity of cancer metastasis: Genetic features of lethal metastatic pancreatic cancer obtained from rapid autopsy. <i>Cancer Biology and Therapy</i> , 2005, 4, 548-554.	1.5	132
36	Optimal molecular profiling of tissue and tissue components: defining the best processing and microdissection methods for biomedical applications. <i>Methods in Molecular Medicine</i> , 2005, 103, 15-66.	0.8	4

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37	Hedgehog signalling in prostate regeneration, neoplasia and metastasis. <i>Nature</i> , 2004, 431, 707-712.	13.7	959
38	Hypermethylation of CpG Islands in Primary and Metastatic Human Prostate Cancer. <i>Cancer Research</i> , 2004, 64, 1975-1986.	0.4	467
39	Xq27-28 deletions in prostate carcinoma. <i>Genes Chromosomes and Cancer</i> , 2003, 37, 381-388.	1.5	14
40	Evaluation of Non-Formalin Tissue Fixation for Molecular Profiling Studies. <i>American Journal of Pathology</i> , 2002, 160, 449-457.	1.9	274
41	Germline mutations and sequence variants of the macrophage scavenger receptor 1 gene are associated with prostate cancer risk. <i>Nature Genetics</i> , 2002, 32, 321-325.	9.4	318
42	Increased fatty acid synthase as a therapeutic target in androgen-independent prostate cancer progression. <i>Prostate</i> , 2001, 47, 102-110.	1.2	137
43	Methylation and mutational analysis of p27kip1 in prostate carcinoma. <i>Prostate</i> , 2001, 48, 248-253.	1.2	35
44	Detection and analysis of $\beta$ -catenin mutations in prostate cancer. <i>Prostate</i> , 2000, 45, 323-334.	1.2	167
45	LOSS OF HETEROZYGOSITY AT 12P12-13 IN PRIMARY AND METASTATIC PROSTATE ADENOCARCINOMA. <i>Journal of Urology</i> , 2000, 164, 192-196.	0.2	55
46	Deletion mapping at 12p12-13 in metastatic prostate cancer. , 1999, 25, 270-276.		42
47	Evidence for a prostate cancer susceptibility locus on the X chromosome.. <i>Nature Genetics</i> , 1998, 20, 175-179.	9.4	641
48	BIOLOGICAL AGGRESSIVENESS OF HEREDITARY PROSTATE CANCER: LONG-TERM EVALUATION FOLLOWING RADICAL PROSTATECTOMY. <i>Journal of Urology</i> , 1998, 160, 660-663.	0.2	69
49	VITAMIN D RECEPTOR POLYMORPHISMS AND LETHAL PROSTATE CANCER. <i>Journal of Urology</i> , 1998, 160, 1405-1409.	0.2	56
50	Deletional, mutational, and methylation analyses of CDKN2 (p16/MTS1) in primary and metastatic prostate cancer. <i>Genes Chromosomes and Cancer</i> , 1997, 19, 90-96.	1.5	169
51	DNA methylation, molecular genetic, and linkage studies in prostate cancer. <i>Prostate</i> , 1996, 29, 36-44.	1.2	29
52	Review of allelic loss and gain in prostate cancer. <i>World Journal of Urology</i> , 1996, 14, 338-46.	1.2	62
53	Molecular genetics and chromosomal alterations in prostate cancer. <i>Cancer</i> , 1995, 75, 2004-2012.	2.0	31
54	Allelic loss of the retinoblastoma gene in primary human prostatic adenocarcinomas. <i>Prostate</i> , 1995, 26, 35-39.	1.2	123

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55	Frequency of homozygous deletion at p16/CDKN2 in primary human tumours. <i>Nature Genetics</i> , 1995, 11, 210-212.	9.4	593
56	TaqI polymorphism of the human MXI1 gene. <i>Human Molecular Genetics</i> , 1994, 3, 2266-2266.	1.4	0
57	Hereditary Prostate Cancer: Epidemiologic and Clinical Features. <i>Journal of Urology</i> , 1993, 150, 797-802.	0.2	519
58	Homozygous deletion and frequent allelic loss of chromosome 8p22 loci in human prostate cancer. <i>Cancer Research</i> , 1993, 53, 3869-73.	0.4	283
59	Methods of radical prostatectomy specimen processing: a novel technique for harvesting fresh prostate cancer tissue and review of processing techniques. <i>Modern Pathology</i> , 1993, 6, 201-7.	2.9	53
60	Lethal Metastatic Human Prostate Cancer: Autopsy Studies and Characteristics of Metastases. , 0, , 39-60.		2