

# Colin Collins

## List of Publications by Year in descending order

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64  
papers

9,073  
citations

87723

38  
h-index

118652

62  
g-index

65  
all docs

65  
docs citations

65  
times ranked

10857  
citing authors

#	ARTICLE	IF	CITATIONS
1	Modeling Androgen Deprivation Therapyâ€™s Induced Prostate Cancer Dormancy and Its Clinical Implications. <i>Molecular Cancer Research</i> , 2022, 20, 782-793.	1.5	10
2	ZRSR2 overexpression is a frequent and early event in castration-resistant prostate cancer development. <i>Prostate Cancer and Prostatic Diseases</i> , 2021, 24, 775-785.	2.0	0
3	Androgen receptor (AR) antagonism triggers acute succinateâ€™mediated adaptive responses to reactivate AR signaling. <i>EMBO Molecular Medicine</i> , 2021, 13, e13427.	3.3	11
4	The long noncoding RNA H19 regulates tumor plasticity in neuroendocrine prostate cancer. <i>Nature Communications</i> , 2021, 12, 7349.	5.8	51
5	Immune-focused multi-omics analysis of prostate cancer: leukocyte Ig-Like receptors are associated with disease progression. <i>Oncolmmunology</i> , 2020, 9, 1851950.	2.1	8
6	RNA Splicing of the BHC80 Gene Contributes to Neuroendocrine Prostate Cancer Progression. <i>European Urology</i> , 2019, 76, 157-166.	0.9	19
7	Widespread and Functional RNA Circularization in Localized Prostate Cancer. <i>Cell</i> , 2019, 176, 831-843.e22.	13.5	317
8	Patient-derived Hormone-naive Prostate Cancer Xenograft Models Reveal Growth Factor Receptor Bound Protein 10 as an Androgen Receptor-repressed Gene Driving the Development of Castration-resistant Prostate Cancer. <i>European Urology</i> , 2018, 73, 949-960.	0.9	19
9	SRRM4 Drives Neuroendocrine Transdifferentiation of Prostate Adenocarcinoma Under Androgen Receptor Pathway Inhibition. <i>European Urology</i> , 2017, 71, 68-78.	0.9	136
10	Quantification of large scale DNA organization for predicting prostate cancer recurrence. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2017, 91, 1164-1174.	1.1	10
11	miR-100-5p inhibition induces apoptosis in dormant prostate cancer cells and prevents the emergence of castration-resistant prostate cancer. <i>Scientific Reports</i> , 2017, 7, 4079.	1.6	37
12	Therapy-induced developmental reprogramming of prostate cancer cells and acquired therapy resistance. <i>Oncotarget</i> , 2017, 8, 18949-18967.	0.8	47
13	Establishment of a neuroendocrine prostate cancer model driven by the RNA splicing factor SRRM4. <i>Oncotarget</i> , 2017, 8, 66878-66888.	0.8	21
14	The role of epigenetics and long noncoding RNA MIAT in neuroendocrine prostate cancer. <i>Epigenomics</i> , 2016, 8, 721-731.	1.0	94
15	Whole-Exome Sequencing of Metastatic Cancer and Biomarkers of Treatment Response. <i>JAMA Oncology</i> , 2015, 1, 466.	3.4	264
16	The long non-coding RNA PCGEM1 is regulated by androgen receptor activity in vivo. <i>Molecular Cancer</i> , 2015, 14, 46.	7.9	71
17	Expression Profiling of Primary and Metastatic Ovarian Tumors Reveals Differences Indicative of Aggressive Disease. <i>PLoS ONE</i> , 2014, 9, e94476.	1.1	66
18	REST mediates androgen receptor actions on gene repression and predicts early recurrence of prostate cancer. <i>Nucleic Acids Research</i> , 2014, 42, 999-1015.	6.5	125

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19	Identification of Ovarian Cancer Metastatic miRNAs. <i>PLoS ONE</i> , 2013, 8, e58226.	1.1	78
20	nFuse: Discovery of complex genomic rearrangements in cancer using high-throughput sequencing. <i>Genome Research</i> , 2012, 22, 2250-2261.	2.4	67
21	Isolation and genomic analysis of circulating tumor cells from castration resistant metastatic prostate cancer. <i>BMC Cancer</i> , 2012, 12, 78.	1.1	85
22	Detection of recurrent rearrangement breakpoints from copy number data. <i>BMC Bioinformatics</i> , 2011, 12, 114.	1.2	21
23	Comrad: detection of expressed rearrangements by integrated analysis of RNA-Seq and low coverage genome sequence data. <i>Bioinformatics</i> , 2011, 27, 1481-1488.	1.8	39
24	A Group of Genome-Based Biomarkers That Add to a Kattan Nomogram for Predicting Progression in Men with High-Risk Prostate Cancer. <i>Clinical Cancer Research</i> , 2010, 16, 195-202.	3.2	34
25	ZNF217 confers resistance to the pro-apoptotic signals of paclitaxel and aberrant expression of Aurora-A in breast cancer cells. <i>Molecular Cancer</i> , 2010, 9, 291.	7.9	42
26	Evaluation of Paired-End Sequencing Strategies for Detection of Genome Rearrangements in Cancer. <i>PLoS Computational Biology</i> , 2008, 4, e1000051.	1.5	72
27	Evaluation of Whole Genome Amplification Protocols for Array and Oligonucleotide CGH. <i>Diagnostic Molecular Pathology</i> , 2007, 16, 198-206.	2.1	11
28	TMPRSS2-ERG Fusion Prostate Cancer: An Early Molecular Event Associated With Invasion. <i>American Journal of Surgical Pathology</i> , 2007, 31, 882-888.	2.1	394
29	High resolution oligonucleotide CGH using DNA from archived prostate tissue. <i>Prostate</i> , 2007, 67, 1447-1455.	1.2	23
30	Genomic Profiling of Hormone-Na <sup>+</sup> ve Lymph Node Metastases in Patients with Prostate Cancer. <i>Neoplasia</i> , 2006, 8, 1083-1085.	2.3	21
31	Decoding the fine-scale structure of a breast cancer genome and transcriptome. <i>Genome Research</i> , 2006, 16, 394-404.	2.4	49
32	Integrating data on DNA copy number with gene expression levels and drug sensitivities in the NCI-60 cell line panel. <i>Molecular Cancer Therapeutics</i> , 2006, 5, 853-867.	1.9	157
33	High-resolution array comparative genomic hybridization of chromosome arm 8q: Evaluation of genetic progression markers for prostate cancer. <i>Genes Chromosomes and Cancer</i> , 2005, 44, 438-449.	1.5	85
34	Construction and application of a full-coverage, high-resolution, human chromosome 8q genomic microarray for comparative genomic hybridization. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2005, 63A, 10-19.	1.1	15
35	ZNF217 suppresses cell death associated with chemotherapy and telomere dysfunction. <i>Human Molecular Genetics</i> , 2005, 14, 3219-3225.	1.4	60
36	Overexpression, Amplification, and Androgen Regulation of TPD52 in Prostate Cancer. <i>Cancer Research</i> , 2004, 64, 3814-3822.	0.4	145

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37	Integration of high-resolution array comparative genomic hybridization analysis of chromosome 16q with expression array data refines common regions of loss at 16q23 and identifies underlying candidate tumor suppressor genes in prostate cancer. <i>Oncogene</i> , 2004, 23, 3487-3494.	2.6	78
38	Evolution of 8p loss in transformed human prostate epithelial cells. <i>Cancer Genetics and Cytogenetics</i> , 2004, 154, 36-43.	1.0	17
39	Evaluation of genetic patterns in different tumor areas of intermediate-grade prostatic adenocarcinomas by high-resolution genomic array analysis. <i>Genes Chromosomes and Cancer</i> , 2004, 39, 249-256.	1.5	46
40	Computational BAC clone contig assembly for comprehensive genome analysis. <i>Genes Chromosomes and Cancer</i> , 2004, 40, 66-71.	1.5	15
41	Whole genome scanning identifies genotypes associated with recurrence and metastasis in prostate tumors. <i>Human Molecular Genetics</i> , 2004, 13, 1303-1313.	1.4	171
42	Genome Amplification of Chromosome 20 in Breast Cancer. <i>Breast Cancer Research and Treatment</i> , 2003, 78, 337-345.	1.1	100
43	Chromosome aberrations in solid tumors. <i>Nature Genetics</i> , 2003, 34, 369-376.	9.4	702
44	High-Resolution Analysis of Paraffin-Embedded and Formalin-Fixed Prostate Tumors Using Comparative Genomic Hybridization to Genomic Microarrays. <i>American Journal of Pathology</i> , 2003, 162, 763-770.	1.9	76
45	Characterization of the novel amplified in breast cancer-1 (NABC1) gene product. <i>Experimental Cell Research</i> , 2003, 290, 402-413.	1.2	28
46	Reconstructing tumor genome architectures. <i>Bioinformatics</i> , 2003, 19, ii162-ii171.	1.8	58
47	End-sequence profiling: Sequence-based analysis of aberrant genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 7696-7701.	3.3	119
48	Protein elongation factor EEF1A2 is a putative oncogene in ovarian cancer. <i>Nature Genetics</i> , 2002, 31, 301-305.	9.4	220
49	Genome scanning with array CGH delineates regional alterations in mouse islet carcinomas. <i>Nature Genetics</i> , 2001, 29, 459-464.	9.4	268
50	Comprehensive Genome Sequence Analysis of a Breast Cancer Amplicon. <i>Genome Research</i> , 2001, 11, 1034-1042.	2.4	27
51	Quantitative mapping of amplicon structure by array CGH identifies CYP24 as a candidate oncogene. <i>Nature Genetics</i> , 2000, 25, 144-146.	9.4	555
52	Genome changes and gene expression in human solid tumors. <i>Carcinogenesis</i> , 2000, 21, 443-452.	1.3	174
53	PIK3CA is implicated as an oncogene in ovarian cancer. <i>Nature Genetics</i> , 1999, 21, 99-102.	9.4	1,041
54	High resolution analysis of DNA copy number variation using comparative genomic hybridization to microarrays. <i>Nature Genetics</i> , 1998, 20, 207-211.	9.4	2,066

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55	Zf9, a Kruppel-like transcription factor up-regulated in vivo during early hepatic fibrosis. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 9500-9505.	3.3	234
56	Genome Scanning and Gene Discovery in Breast and Ovarian Cancer. , 1998, , 65-72.		0
57	Genomic Organization, Sequence, and Chromosomal Localization of the Human Helix-Loop-Helix Id1 Gene. Biochemical and Biophysical Research Communications, 1997, 231, 628-634.	1.0	33
58	ESX: a structurally unique Ets overexpressed early during human breast tumorigenesis. Oncogene, 1997, 14, 1617-1622.	2.6	159
59	A physical map of chromosome 20 established using fluorescence in situ hybridization and digital image analysis. Genomics, 1995, 26, 134-137.	1.3	50
60	The human $\beta$ -subunit of rod photoreceptor cGMP phosphodiesterase: Complete retinal cDNA sequence and evidence for expression in brain. Genomics, 1992, 13, 698-704.	1.3	35
61	Exclusion of DNA changes in the $\beta$ -subunit of the cGMP phosphodiesterase gene as the cause for Huntington's disease. Nature Genetics, 1992, 1, 104-108.	9.4	12
62	Delineation of a 50 kilobase DNA segment containing the recombination site in a sporadic case of Huntington's disease. Nature Genetics, 1992, 2, 216-222.	9.4	7
63	Identification of multiple CpG islands and associated conserved sequences in a candidate region for the Huntington disease gene. Genomics, 1991, 11, 1113-1124.	1.3	21
64	Genomic organization and complete sequence of the human gene encoding the $\beta$ -subunit of the cGMP phosphodiesterase and its localisation to 4p16.3. Nucleic Acids Research, 1991, 19, 6263-6268.	6.5	57