

Thomas A Sellers

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

5,078
citations

201674

27
h-index

182427

51
g-index

51
all docs

51
docs citations

51
times ranked

9123
citing authors

#	ARTICLE	IF	CITATIONS
1	Epidemiology of ovarian cancer: a review. <i>Cancer Biology and Medicine</i> , 2017, 14, 9-32.	3.0	981
2	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. <i>Nature Genetics</i> , 2018, 50, 928-936.	21.4	652
3	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , 2014, 46, 1103-1109.	21.4	408
4	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	21.4	356
5	CWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 362-370.	21.4	326
6	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. <i>Nature Genetics</i> , 2009, 41, 996-1000.	21.4	276
7	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. <i>Nature Genetics</i> , 2021, 53, 65-75.	21.4	264
8	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015, 47, 164-171.	21.4	221
9	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	9.4	157
10	A functional variant in <i>HOXA11-AS</i> , a novel long non-coding RNA, inhibits the oncogenic phenotype of epithelial ovarian cancer. <i>Oncotarget</i> , 2015, 6, 34745-34757.	1.8	98
11	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. <i>Nature Communications</i> , 2018, 9, 2256.	12.8	88
12	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	12.8	78
13	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. <i>Human Molecular Genetics</i> , 2015, 24, 5589-5602.	2.9	67
14	A Cross-Cancer Genetic Association Analysis of the DNA Repair and DNA Damage Signaling Pathways for Lung, Ovary, Prostate, Breast, and Colorectal Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 193-200.	2.5	66
15	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. <i>Nature Communications</i> , 2015, 6, 8234.	12.8	63
16	Super-Enhancer-Associated LncRNA UCA1 Interacts Directly with AMOT to Activate YAP Target Genes in Epithelial Ovarian Cancer. <i>IScience</i> , 2019, 17, 242-255.	4.1	60
17	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	6.3	57
18	A Large-Scale Analysis of Genetic Variants within Putative miRNA Binding Sites in Prostate Cancer. <i>Cancer Discovery</i> , 2015, 5, 368-379.	9.4	56

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19	Prediction of individual genetic risk to prostate cancer using a polygenic score. <i>Prostate</i> , 2015, 75, 1467-1474.	2.3	54
20	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2018, 78, 5419-5430.	0.9	54
21	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. <i>Nature Communications</i> , 2016, 7, 10979.	12.8	50
22	Genetic Data from Nearly 63,000 Women of European Descent Predicts DNA Methylation Biomarkers and Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2019, 79, 505-517.	0.9	49
23	Quantifying the Genetic Correlation between Multiple Cancer Types. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 1427-1435.	2.5	48
24	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. <i>PLoS ONE</i> , 2015, 10, e0128106.	2.5	44
25	Kernel canonical correlation analysis for assessing gene-gene interactions and application to ovarian cancer. <i>European Journal of Human Genetics</i> , 2014, 22, 126-131.	2.8	33
26	Genome-wide Analysis Identifies Novel Loci Associated with Ovarian Cancer Outcomes: Findings from the Ovarian Cancer Association Consortium. <i>Clinical Cancer Research</i> , 2015, 21, 5264-5276.	7.0	33
27	Common Genetic Variation and Susceptibility to Ovarian Cancer: Current Insights and Future Directions. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 395-404.	2.5	33
28	A Germline Variant at 8q24 Contributes to Familial Clustering of Prostate Cancer in Men of African Ancestry. <i>European Urology</i> , 2020, 78, 316-320.	1.9	32
29	Germline polymorphisms in an enhancer of <i>PSIP1</i> are associated with progression-free survival in epithelial ovarian cancer. <i>Oncotarget</i> , 2016, 7, 6353-6368.	1.8	29
30	Network-Based Integration of GWAS and Gene Expression Identifies a <i>HOX</i> -Centric Network Associated with Serous Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1574-1584.	2.5	28
31	MAFG is a potential therapeutic target to restore chemosensitivity in cisplatin-resistant cancer cells by increasing reactive oxygen species. <i>Translational Research</i> , 2018, 200, 1-17.	5.0	28
32	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. <i>Gynecologic Oncology</i> , 2019, 153, 343-355.	1.4	28
33	Genome-Wide Association Study of Prostate Cancer-Specific Survival. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1796-1800.	2.5	27
34	A Genetic Risk Score to Personalize Prostate Cancer Screening, Applied to Population Data. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1731-1738.	2.5	27
35	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). <i>Journal of Genetics and Genome Research</i> , 2015, 2, .	0.3	25
36	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. <i>British Journal of Cancer</i> , 2017, 116, 524-535.	6.4	23

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37	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. <i>Genetic Epidemiology</i> , 2015, 39, 689-697.	1.3	22
38	Correlation between germline mutations in MMR genes and microsatellite instability in ovarian cancer specimens. <i>Familial Cancer</i> , 2017, 16, 351-355.	1.9	18
39	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. <i>Human Molecular Genetics</i> , 2016, 25, 3600-3612.	2.9	17
40	The effect of sample size on polygenic hazard models for prostate cancer. <i>European Journal of Human Genetics</i> , 2020, 28, 1467-1475.	2.8	14
41	Variation in NF- κ B Signaling Pathways and Survival in Invasive Epithelial Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 1421-1427.	2.5	13
42	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. <i>Oncotarget</i> , 2016, 7, 72381-72394.	1.8	13
43	Cross-Cancer Genome-Wide Association Study of Endometrial Cancer and Epithelial Ovarian Cancer Identifies Genetic Risk Regions Associated with Risk of Both Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 217-228.	2.5	12
44	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. <i>PLoS ONE</i> , 2018, 13, e0197561.	2.5	9
45	Height, selected genetic markers and prostate cancer risk: results from the PRACTICAL consortium. <i>British Journal of Cancer</i> , 2017, 117, 734-743.	6.4	7
46	Evaluation of vitamin D biosynthesis and pathway target genes reveals UGT2A1/2 and EGFR polymorphisms associated with epithelial ovarian cancer in African American Women. <i>Cancer Medicine</i> , 2019, 8, 2503-2513.	2.8	6
47	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. <i>Oncotarget</i> , 2016, 7, 69097-69110.	1.8	5
48	The association of copy number variation and percent mammographic density. <i>BMC Research Notes</i> , 2015, 8, 297.	1.4	2
49	New Lung Cancer Susceptibility Locus Identified: Significance and Implications for Other Genome-Wide Association Studies. <i>Cancer Discovery</i> , 2012, 2, 110-111.	9.4	1