Simon G Coetzee

List of Publications by Year
in descending order

33 papers	6,799 citations	331670 21 h-index	552781 26 g-index
40 all docs	40 docs citations	40 times ranked	13489 citing authors

#	Article	IF	Citations
1	A molecular taxonomy of tumors independent of tissue-of-origin. IScience, 2021, 24, 103084.	4.1	0
2	Ovarian Cancer Risk Variants Are Enriched in Histotype-Specific Enhancers and Disrupt Transcription Factor Binding Sites. American Journal of Human Genetics, 2020, 107, 622-635.	6.2	14
3	GENAVi: a shiny web application for gene expression normalization, analysis and visualization. BMC Genomics, 2019, 20, 745.	2.8	40
4	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. Gynecologic Oncology, 2019, 153, 343-355.	1.4	28
5	A Study of High-Grade Serous Ovarian Cancer Origins Implicates the SOX18 Transcription Factor in Tumor Development. Cell Reports, 2019, 29, 3726-3735.e4.	6.4	39
6	ELMER v.2: an R/Bioconductor package to reconstruct gene regulatory networks from DNA methylation and transcriptome profiles. Bioinformatics, 2019, 35, 1974-1977.	4.1	87
7	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. Cancer Research, 2019, 79, 467-481.	0.9	22
8	ONECUT2 is a targetable master regulator of lethal prostate cancer that suppresses the androgen axis. Nature Medicine, 2018, 24, 1887-1898.	30.7	113
9	Granulocyte-Monocyte Progenitors and Monocyte-Dendritic Cell Progenitors Independently Produce Functionally Distinct Monocytes. Experimental Hematology, 2018, 64, S111.	0.4	0
10	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
11	Granulocyte-Monocyte Progenitors and Monocyte-Dendritic Cell Progenitors Independently Produce Functionally Distinct Monocytes. Immunity, 2017, 47, 890-902.e4.	14.3	297
12	SIRT1 regulates Mxd1 during malignant melanoma progression. Oncotarget, 2017, 8, 114540-114553.	1.8	12
13	Independent production of distinct monocyte subsets by granulocyte-monocyte progenitors (GMPS) and monocyte-dendritic cell progenitors (MDPS). Experimental Hematology, 2016, 44, S76.	0.4	0
14	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	28.9	1,695
15	Enrichment of risk SNPs in regulatory regions implicate diverse tissues in Parkinson's disease etiology. Scientific Reports, 2016, 6, 30509.	3.3	53
16	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	2.9	40
17	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
18	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582

#	Article	IF	Citations
19	*motifbreakR*: an R/Bioconductor package for predicting variant effects at transcription factor binding sites. Bioinformatics, 2015, 31, 3847-3849.	4.1	208
20	Comprehensive Functional Annotation of 77 Prostate Cancer Risk Loci. PLoS Genetics, 2014, 10, e1004102.	3.5	167
21	Identification and characterization of functional risk variants for colorectal cancer mapping to chromosome 11q23.1. Human Molecular Genetics, 2014, 23, 2198-2209.	2.9	36
22	Nucleosome positioning and histone modifications define relationships between regulatory elements and nearby gene expression in breast epithelial cells. BMC Genomics, 2014, 15, 331.	2.8	40
23	Genome-wide association analyses in east Asians identify new susceptibility loci for colorectal cancer. Nature Genetics, 2013, 45, 191-196.	21.4	173
24	Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-Wide Meta-analysis. Gastroenterology, 2013, 144, 799-807.e24.	1.3	292
25	A rare variant, which destroys a FoxA1 site at 8q24, is associated with prostate cancer risk. Cell Cycle, 2013, 12, 379-380.	2.6	20
26	The Functionality of Prostate Cancer Predisposition Risk Regions Is Revealed by AR Enhancers. , 2013, , 59-84.		1
27	Comprehensive Functional Annotation of Seventy-One Breast Cancer Risk Loci. PLoS ONE, 2013, 8, e63925.	2.5	41
28	Opposing Effects of Runx2 and Estradiol on Breast Cancer Cell Proliferation: *In Vitro* Identification of Reciprocally Regulated Gene Signature Related to Clinical Letrozole Responsiveness. Clinical Cancer Research, 2012, 18, 901-911.	7.0	41
29	FunciSNP: an R/bioconductor tool integrating functional non-coding data sets with genetic association studies to identify candidate regulatory SNPs. Nucleic Acids Research, 2012, 40, e139-e139.	14.5	97
30	Interleukin-6-Related Genotypes, Body Mass Index, and Risk of Multiple Myeloma and Plasmacytoma. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 2285-2291.	2.5	57
31	Interleukin-6 Promoter and Receptor Polymorphisms, Body Mass Index and Risk of Multiple Myeloma.. Blood, 2005, 106, 5101-5101.	1.4	0
32	StateHub-StatePaintR: rapid and reproducible chromatin state evaluation for custom genome annotation. F1000Research, 0, 7, 214.	1.6	5
33	StateHub-StatePaintR: rapid and reproducible chromatin state evaluation for custom genome annotation. F1000Research, 0, 7, 214.	1.6	4