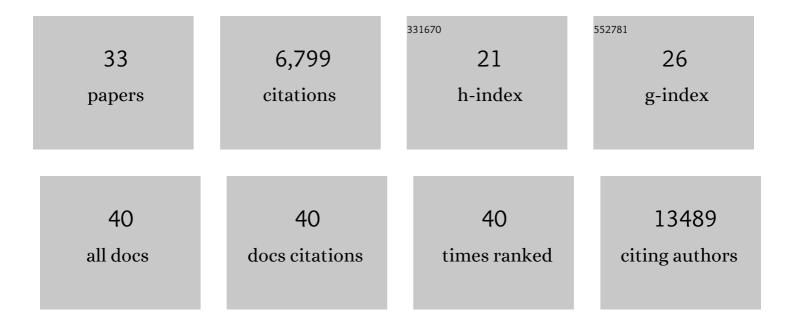
Simon G Coetzee

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
2	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	28.9	1,695
3	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
4	Granulocyte-Monocyte Progenitors and Monocyte-Dendritic Cell Progenitors Independently Produce Functionally Distinct Monocytes. Immunity, 2017, 47, 890-902.e4.	14.3	297
5	Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-Wide Meta-analysis. Gastroenterology, 2013, 144, 799-807.e24.	1.3	292
6	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
7	<i>motifbreakR</i> : an R/Bioconductor package for predicting variant effects at transcription factor binding sites. Bioinformatics, 2015, 31, 3847-3849.	4.1	208
8	Genome-wide association analyses in east Asians identify new susceptibility loci for colorectal cancer. Nature Genetics, 2013, 45, 191-196.	21.4	173
9	Comprehensive Functional Annotation of 77 Prostate Cancer Risk Loci. PLoS Genetics, 2014, 10, e1004102.	3.5	167
10	ONECUT2 is a targetable master regulator of lethal prostate cancer that suppresses the androgen axis. Nature Medicine, 2018, 24, 1887-1898.	30.7	113
11	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
12	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
13	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
14	Enrichment of risk SNPs in regulatory regions implicate diverse tissues in Parkinson's disease etiology. Scientific Reports, 2016, 6, 30509.	3.3	53
15	Opposing Effects of Runx2 and Estradiol on Breast Cancer Cell Proliferation: <i>In Vitro</i> Identification of Reciprocally Regulated Gene Signature Related to Clinical Letrozole Responsiveness. Clinical Cancer Research, 2012, 18, 901-911.	7.0	41
16	Comprehensive Functional Annotation of Seventy-One Breast Cancer Risk Loci. PLoS ONE, 2013, 8, e63925.	2.5	41
17	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
18	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics. 2015. 24. 3595-3607.	2.9	40

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#	Article	IF	CITATIONS
19	GENAVi: a shiny web application for gene expression normalization, analysis and visualization. BMC Genomics, 2019, 20, 745.	2.8	40
20	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
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	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. Gynecologic Oncology, 2019, 153, 343-355.	1.4	28
23	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. Cancer Research, 2019, 79, 467-481.	0.9	22
24	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
25	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
26	SIRT1 regulates Mxd1 during malignant melanoma progression. Oncotarget, 2017, 8, 114540-114553.	1.8	12
27	StateHub-StatePaintR: rapid and reproducible chromatin state evaluation for custom genome annotation. F1000Research, 0, 7, 214.	1.6	5
28	StateHub-StatePaintR: rapid and reproducible chromatin state evaluation for custom genome annotation. F1000Research, 0, 7, 214.	1.6	4
29	The Functionality of Prostate Cancer Predisposition Risk Regions Is Revealed by AR Enhancers. , 2013, , 59-84.		1
30	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
31	Granulocyte-Monocyte Progenitors and Monocyte-Dendritic Cell Progenitors Independently Produce Functionally Distinct Monocytes. Experimental Hematology, 2018, 64, S111.	0.4	0
32	A molecular taxonomy of tumors independent of tissue-of-origin. IScience, 2021, 24, 103084.	4.1	0
33	Interleukin-6 Promoter and Receptor Polymorphisms, Body Mass Index and Risk of Multiple Myeloma Blood, 2005, 106, 5101-5101.	1.4	0