John S Witte

List of Publications by Year
in descending order

96 papers	8,221 citations	76196 40 h-index	53109 85 g-index
100 all docs	100 docs citations	100 times ranked	16560 citing authors

#	Article	IF	Citations
1	Residential particulate matter, proximity to major roads, traffic density and traffic volume as risk factors for preterm birth in California. Paediatric and Perinatal Epidemiology, 2022, 36, 70-79.	0.8	8
2	Genetic Analysis of Lung Cancer and the Germline Impact on Somatic Mutation Burden. Journal of the National Cancer Institute, 2022, 114, 1159-1166.	3.0	8
3	A Large-Scale Association Study Detects Novel Rare Variants, Risk Genes, Functional Elements, and Polygenic Architecture of Prostate Cancer Susceptibility. Cancer Research, 2021, 81, 1695-1703.	0.4	15
4	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	9.4	264
5	Cross-cancer evaluation of polygenic risk scores for 16 cancer types in two large cohorts. Nature Communications, 2021, 12, 970.	5.8	50
6	Detecting methylation quantitative trait loci using a methylation random field method. Briefings in Bioinformatics, 2021, 22, .	3.2	2
7	A genomeâ€wide association study of prostate cancer in Latinos. International Journal of Cancer, 2020, 146, 1819-1826.	2.3	24
8	Immune-mediated genetic pathways resulting in pulmonary function impairment increase lung cancer susceptibility. Nature Communications, 2020, 11, 27.	5.8	23
9	The landscape of host genetic factors involved in immune response to common viral infections. Genome Medicine, 2020, 12, 93.	3.6	65
10	Genomewide Metaâ€Analysis Validates a Role for S1PR1 in Microtubule Targeting Agentâ€Induced Sensory Peripheral Neuropathy. Clinical Pharmacology and Therapeutics, 2020, 108, 625-634.	2.3	25
11	Age-of-onset information helps identify 76 genetic variants associated with allergic disease. PLoS Genetics, 2020, 16, e1008725.	1.5	27
12	Genetic Determinants of Blood Cell Traits Play a Role in Susceptibility to Acute Lymphoblastic Leukemia. Blood, 2020, 136, 10-11.	0.6	0
13	Association of imputed prostate cancer transcriptome with disease risk reveals novel mechanisms. Nature Communications, 2019, 10, 3107.	5.8	28
14	Identification of Novel Susceptibility Loci and Genes for Prostate Cancer Risk: A Transcriptome-Wide Association Study in Over 140,000 European Descendants. Cancer Research, 2019, 79, 3192-3204.	0.4	43
15	Newborn Metabolic Profile Associated with Hyperbilirubinemia With and Without Kernicterus. Clinical and Translational Science, 2019, 12, 28-38.	1.5	9
16	A Pharmacogenetic Prediction Model of Progressionâ€Free Survival in Breast Cancer using Genomeâ€Wide Genotyping Data from CALGB 40502 (Alliance). Clinical Pharmacology and Therapeutics, 2019, 105, 738-745.	2.3	11
17	Identification of Pleiotropic Cancer Susceptibility Variants from Genome-Wide Association Studies Reveals Functional Characteristics. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 75-85.	1.1	25
18	Detecting Rare Mutations with Heterogeneous Effects Using a Family-Based Genetic Random Field Method. Genetics, 2018, 210, 463-476.	1.2	4

#	Article	IF	Citations
19	An efficient Bayesian meta-analysis approach for studying cross-phenotype genetic associations. PLoS Genetics, 2018, 14, e1007139.	1.5	40
20	Genome-wide association study of prostate-specific antigen levels identifies novel loci independent of prostate cancer. Nature Communications, 2017, 8, 14248.	5.8	58
21	Familial Risk and Heritability of Colorectal Cancer in the Nordic Twin Study of Cancer. Clinical Gastroenterology and Hepatology, 2017, 15, 1256-1264.	2.4	77
22	Investigating the Genetic Architecture of the PR Interval Using Clinical Phenotypes. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	8
23	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. Nature Genetics, 2017, 49, 1752-1757.	9.4	432
24	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. Journal of the National Cancer Institute, 2017, 109, .	3.0	57
25	Cis-eQTL-based trans-ethnic meta-analysis reveals novel genes associated with breast cancer risk. PLoS Genetics, 2017, 13, e1006690.	1.5	61
26	Up For A Challenge (U4C): Stimulating innovation in breast cancer genetic epidemiology. PLoS Genetics, 2017, 13, e1006945.	1.5	3
27	Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. PLoS Genetics, 2017, 13, e1006719.	1.5	98
28	Testing Allele Transmission of an SNP Set Using a Familyâ€Based Generalized Genetic Random Field Method. Genetic Epidemiology, 2016, 40, 341-351.	0.6	4
29	Joint effects of genetic variants and residential proximity to pesticide applications on hypospadias risk. Birth Defects Research Part A: Clinical and Molecular Teratology, 2016, 106, 653-658.	1.6	13
30	Association of common genetic variation in the protein C pathway genes with clinical outcomes in acute respiratory distress syndrome. Critical Care, 2016, 20, 151.	2.5	25
31	A Meta-analysis of Multiple Myeloma Risk Regions in African and European Ancestry Populations Identifies Putatively Functional Loci. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1609-1618.	1.1	18
32	Sequence variation in folate pathway genes and risks of human cleft lip with or without cleft palate. American Journal of Medical Genetics, Part A, 2016, 170, 2777-2787.	0.7	15
33	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	5.8	50
34	Prostate Cancer Susceptibility in Men of African Ancestry at 8q24. Journal of the National Cancer Institute, 2016, 108, djv431.	3.0	111
35	Mutational Landscape of Aggressive Prostate Tumors in African American Men. Cancer Research, 2016, 76, 1860-1868.	0.4	61
36	MDS-associated somatic mutations and clonal hematopoiesis are common in idiopathic cytopenias of undetermined significance. Blood, 2015, 126, 2355-2361.	0.6	280

#	Article	IF	Citations
37	Developments in our understanding of the genetic basis of birth defects. Birth Defects Research Part A: Clinical and Molecular Teratology, 2015, 103, 680-691.	1.6	30
38	Detecting geneâ€“environment interactions in human birth defects: Study designs and statistical methods. Birth Defects Research Part A: Clinical and Molecular Teratology, 2015, 103, 692-702.	1.6	5
39	Methodological Considerations in Estimation of Phenotype Heritability Using Genome-Wide SNP Data, Illustrated by an Analysis of the Heritability of Height in a Large Sample of African Ancestry Adults. PLoS ONE, 2015, 10, e0131106.	1.1	2
40	A Large Multiethnic Genome-Wide Association Study of Prostate Cancer Identifies Novel Risk Variants and Substantial Ethnic Differences. Cancer Discovery, 2015, 5, 878-891.	7.7	111
41	Generalizability of established prostate cancer risk variants in men of <scp>A</scp>frican ancestry. International Journal of Cancer, 2015, 136, 1210-1217.	2.3	62
42	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. Human Molecular Genetics, 2015, 24, 5603-5618.	1.4	50
43	Imputation of the Rare HOXB13 G84E Mutation and Cancer Risk in a Large Population-Based Cohort. PLoS Genetics, 2015, 11, e1004930.	1.5	36
44	Replication and Heritability of Prostate Cancer Risk Variants: Impact of Population-Specific Factors. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 938-943.	1.1	13
45	Strategies for Imputing and Analyzing Rare Variants in Association Studies. Trends in Genetics, 2015, 31, 556-563.	2.9	27
46	Cross Cancer Genomic Investigation of Inflammation Pathway for Five Common Cancers: Lung, Ovary, Prostate, Breast, and Colorectal Cancer. Journal of the National Cancer Institute, 2015, 107, djv246.	3.0	63
47	Polymorphisms of an Innate Immune Gene, Toll-Like Receptor 4, and Aggressive Prostate Cancer Risk: A Systematic Review and Meta-Analysis. PLoS ONE, 2014, 9, e110569.	1.1	24
48	Leveraging population admixture to characterize the heritability of complex traits. Nature Genetics, 2014, 46, 1356-1362.	9.4	69
49	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	9.4	408
50	Genome-wide Scan of 29,141 African Americans Finds No Evidence of Directional Selection since Admixture. American Journal of Human Genetics, 2014, 95, 437-444.	2.6	69
51	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
52	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. Nature Genetics, 2013, 45, 690-696.	9.4	232
53	HOXB13 Mutation and Prostate Cancer: Studies of Siblings and Aggressive Disease. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 675-680.	1.1	40
54	Mechanistic Phenotypes: An Aggregative Phenotyping Strategy to Identify Disease Mechanisms Using GWAS Data. PLoS ONE, 2013, 8, e81503.	1.1	15

#	Article	IF	Citations
55	Commentary. Epidemiology, 2012, 23, 910-911.	1.2	1
56	Association of the Innate Immunity and Inflammation Pathway with Advanced Prostate Cancer Risk. PLoS ONE, 2012, 7, e51680.	1.1	61
57	Hereditary Prostate Cancer and Genetic Risk. , 2012, , 79-101.		0
58	Genome-wide association study of prostate cancer in men of African ancestry identifies a susceptibility locus at 17q21. Nature Genetics, 2011, 43, 570-573.	9.4	198
59	Parallel biocomputing. Source Code for Biology and Medicine, 2011, 6, 4.	1.7	0
60	Use of principal components to aggregate rare variants in case-control and family-based association studies in the presence of multiple covariates. BMC Proceedings, 2011, 5, S29.	1.8	5
61	The landscape of recombination in African Americans. Nature, 2011, 476, 170-175.	13.7	319
62	Characterizing Genetic Risk at Known Prostate Cancer Susceptibility Loci in African Americans. PLoS Genetics, 2011, 7, e1001387.	1.5	117
63	Identification, Replication, and Fine-Mapping of Loci Associated with Adult Height in Individuals of African Ancestry. PLoS Genetics, 2011, 7, e1002298.	1.5	93
64	trans-Fatty acid intake and increased risk of advanced prostate cancer: modification by RNASEL R462Q variant. Carcinogenesis, 2007, 28, 1232-1236.	1.3	30
65	Microsatellite markers for genome-wide association studies. Nature Reviews Genetics, 2007, 8, 164-164.	7.7	7
66	Coverage and Power in Genomewide Association Studies. American Journal of Human Genetics, 2006, 78, 884-888.	2.6	44
67	A gene-centric approach to genome-wide association studies. Nature Reviews Genetics, 2006, 7, 885-891.	7.7	93
68	Likelihood Modelling: Genetic Mapping of Complex Traits. , 2005, , 339-359.		0
69	Comprehensive evaluation of the association between prostate cancer and genotypes/haplotypes in CYP17A1, CYP3A4, and SRD5A2. European Journal of Human Genetics, 2004, 12, 321-332.	1.4	46
70	Hereditary Prostate Cancer and Genetic Risk. , 2004, , 57-69.		0
71	Haplotype Tagging Single Nucleotide Polymorphisms and Association Studies. Human Heredity, 2003, 56, 48-55.	0.4	57
72	Relation between tumour necrosis factor polymorphism TNFÎ±-308 and risk of asthma. European Journal of Human Genetics, 2002, 10, 82-85.	1.4	120

#	Article	IF	Citations
73	RNASEL Arg462Gln variant is implicated in up to 13% of prostate cancer cases. Nature Genetics, 2002, 32, 581-583.	9.4	280
74	Introduction: Analysis of Sequence Data and Population Structure. Genetic Epidemiology, 2001, 21, S600-1.	0.6	13
75	Impact of Preadjusting a Quantitative Phenotype Prior to Sib-Pair Linkage Analysis when GeneÃ—Environment Interaction Exists. Genetic Epidemiology, 2001, 21, S837-S842.	0.6	0
76	Hierarchical Modeling of the Relation Between Sequence Variants and a Quantitative Trait: Addressing Multiple Comparison and Population Stratification Issues. Genetic Epidemiology, 2001, 21, S668-S673.	0.6	7
77	Predicting Quantitative Trait Levels by Modeling SNP Interaction. Genetic Epidemiology, 2001, 21, S608-S613.	0.6	2
78	On the relative sample size required for multiple comparisons. , 2000, 19, 369-372.		41
79	Replication linkage study for prostate cancer susceptibility genes. Prostate, 2000, 45, 106-114.	1.2	35
80	CYP3A activity in African American and European American men: Population differences and functional effect of the CYP3A4*1B 5â€²-promoter region polymorphism. Clinical Pharmacology and Therapeutics, 2000, 68, 82-91.	2.3	214
81	Correlations of individual plasma carotenoid concentrations in free-living older adults. Nutrition Research, 2000, 20, 955-965.	1.3	1
82	Linkage Disequilibrium and Allele-Frequency Distributions for 114 Single-Nucleotide Polymorphisms in Five Populations. American Journal of Human Genetics, 2000, 66, 216-234.	2.6	193
83	Likelihood-based approach to estimating twin concordance for dichotomous traits. , 1999, 16, 290-304.		76
84	Genetic mapping of complex traits. , 1999, 18, 2961-2981.		35
85	Model-based and model-free multipoint genome-wide linkage analysis of alcoholism. Genetic Epidemiology, 1999, 17, S175-S180.	0.6	1
86	A nested approach to evaluating dose-response and trend. Annals of Epidemiology, 1997, 7, 188-193.	0.9	41
87	Diet and premenopausal bilateral breast cancer: A case-control study. Breast Cancer Research and Treatment, 1997, 42, 243-251.	1.1	124
88	Meat preparation and colorectal adenomas in a large sigmoidoscopy-based case-control study in California (United States). Cancer Causes and Control, 1997, 8, 175-183.	0.8	88
89	Modeling age of onset and residual familial correlations for the linkage analysis of bipolar disorder. Genetic Epidemiology, 1997, 14, 675-680.	0.6	6
90	A sigmoidoscopy-based caseâ€“control study of polyps: macronutrients, fiber and meat consumption. , 1997, 73, 497-502.		33

#	Article	IF	Citations
91	Relation of Vegetable, Fruit, and Grain Consumption to Colorectal Adenomatous Polyps. American Journal of Epidemiology, 1996, 144, 1015-1025.	1.6	165
92	SIMULATION STUDY OF HIERARCHICAL REGRESSION. , 1996, 15, 1161-1170.		46
93	Association within twin pairs for a dichotomous trait. , 1996, 13, 489-499.		14
94	Genetic dissection of complex traits. Nature Genetics, 1996, 12, 355-356.	9.4	119
95	Genetic epidemiologic analysis of quantitative phenotypes using gibbs sampling. Genetic Epidemiology, 1995, 12, 753-758.	0.6	7
96	Hierarchical Regression Analysis Applied to a Study of Multiple Dietary Exposures and Breast Cancer. Epidemiology, 1994, 5, 612-621.	1.2	96