Stephanie A Bien

List of Publications by Year
in descending order

51 papers	3,047 citations	361413 20 h-index	214800 47 g-index
56 all docs	56 docs citations	56 times ranked	6670 citing authors

#	Article	IF	Citations
1	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. Diabetologia, 2022, 65, 477-489.	6.3	15
2	Predicted gene expression in ancestrally diverse populations leads to discovery of susceptibility loci for lifestyle and cardiometabolic traits. American Journal of Human Genetics, 2022, 109, 669-679.	6.2	5
3	Beyond GWAS of Colorectal Cancer: Evidence of Interaction with Alcohol Consumption and Putative Causal Variant for the 10q24.2 Region. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1077-1089.	2.5	6
4	OUP accepted manuscript. Journal of the National Cancer Institute, 2022, , .	6.3	0
5	Association of Body Mass Index With Colorectal Cancer Risk by Genome-Wide Variants. Journal of the National Cancer Institute, 2021, 113, 38-47.	6.3	14
6	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. Gastroenterology, 2021, 160, 1164-1178.e6.	1.3	36
7	Genetic Effects on Transcriptome Profiles in Colon Epithelium Provide Functional Insights for Genetic Risk Loci. Cellular and Molecular Gastroenterology and Hepatology, 2021, 12, 181-197.	4.5	18
8	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334.	12.1	44
9	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. Human Genetics and Genomics Advances, 2021, 2, 100029.	1.7	23
10	Multi-ethnic genome-wide association analyses of white blood cell and platelet traits in the Population Architecture using Genomics and Epidemiology (PAGE) study. BMC Genomics, 2021, 22, 432.	2.8	6
11	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. Genes, 2021, 12, 1049.	2.4	11
12	Full title: A largeâ€scale transcriptomeâ€wide association study (TWAS) of 10 blood cell phenotypes reveals complexities of TWAS fineâ€mapping. Genetic Epidemiology, 2021, , .	1.3	2
13	DNA repair and cancer in colon and rectum: Novel players in genetic susceptibility. International Journal of Cancer, 2020, 146, 363-372.	5.1	40
14	Colorectal cancer susceptibility variants and risk of conventional adenomas and serrated polyps: results from three cohort studies. International Journal of Epidemiology, 2020, 49, 259-269.	1.9	13
15	Cumulative Burden of Colorectal Cancerâ€“Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. Gastroenterology, 2020, 158, 1274-1286.e12.	1.3	110
16	Exploratory Genome-Wide Interaction Analysis of Nonsteroidal Anti-inflammatory Drugs and Predicted Gene Expression on Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1800-1808.	2.5	1
17	A general framework for functionally informed set-based analysis: Application to a large-scale colorectal cancer study. PLoS Genetics, 2020, 16, e1008947.	3.5	6
18	Ancestry-specific associations identified in genome-wide combined-phenotype study of red blood cell traits emphasize benefits of diversity in genomics. BMC Genomics, 2020, 21, 228.	2.8	19

#	Article	IF	Citations
19	Functional informed genomeâ€wide interaction analysis of body mass index, diabetes and colorectal cancer risk. Cancer Medicine, 2020, 9, 3563-3573.	2.8	7
20	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. PLoS Genetics, 2020, 16, e1008684.	3.5	17
21	Modeling the effect of prolonged ethanol exposure on global gene expression and chromatin accessibility in normal 3D colon organoids. PLoS ONE, 2020, 15, e0227116.	2.5	22
22	Title is missing!. , 2020, 16, e1008684.		0
23	Title is missing!. , 2020, 16, e1008684.		0
24	Title is missing!. , 2020, 16, e1008684.		0
25	Title is missing!. , 2020, 16, e1008684.		0
26	Title is missing!. , 2020, 16, e1008684.		0
27	Title is missing!. , 2020, 16, e1008684.		0
28	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	6.3	129
29	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
30	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	27.8	679
31	Genetic associations of breast and prostate cancer are enriched for regulatory elements identified in disease-related tissues. Human Genetics, 2019, 138, 1091-1104.	3.8	7
32	Moving from one to many: insights from the growing list of pleiotropic cancer risk genes. British Journal of Cancer, 2019, 120, 1087-1089.	6.4	14
33	The Future of Genomic Studies Must Be Globally Representative: Perspectives from PAGE. Annual Review of Genomics and Human Genetics, 2019, 20, 181-200.	6.2	33
34	Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. Human Genetics, 2019, 138, 307-326.	3.8	44
35	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. PLoS Genetics, 2019, 15, e1008500.	3.5	203
36	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	21.4	377

#	Article	IF	Citations
37	Determining Risk of Colorectal Cancer and Starting Age of Screening Based on Lifestyle, Environmental, and Genetic Factors. Gastroenterology, 2018, 154, 2152-2164.e19.	1.3	226
38	A Mixed-Effects Model for Powerful Association Tests in Integrative Functional Genomics. American Journal of Human Genetics, 2018, 102, 904-919.	6.2	30
39	Mendelian randomisation study of age at menarche and age at menopause and the risk of colorectal cancer. British Journal of Cancer, 2018, 118, 1639-1647.	6.4	16
40	Discovery, fine-mapping, and conditional analyses of genetic variants associated with C-reactive protein in multiethnic populations using the Metabochip in the Population Architecture using Genomics and Epidemiology (PAGE) study. Human Molecular Genetics, 2018, 27, 2940-2953.	2.9	16
41	Fine mapping of QT interval regions in global populations refines previously identified QT interval loci and identifies signals unique to African and Hispanic descent populations. Heart Rhythm, 2017, 14, 572-580.	0.7	19
42	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
43	Transethnic insight into the genetics of glycaemic traits: fine-mapping results from the Population Architecture using Genomics and Epidemiology (PAGE) consortium. Diabetologia, 2017, 60, 2384-2398.	6.3	20
44	Enrichment of colorectal cancer associations in functional regions: Insight for using epigenomics data in the analysis of whole genome sequence-imputed GWAS data. PLoS ONE, 2017, 12, e0186518.	2.5	8
45	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
46	Fine-Mapping of Common Genetic Variants Associated with Colorectal Tumor Risk Identified Potential Functional Variants. PLoS ONE, 2016, 11, e0157521.	2.5	8
47	Variant Discovery and Fine Mapping of Genetic Loci Associated with Blood Pressure Traits in Hispanics and African Americans. PLoS ONE, 2016, 11, e0164132.	2.5	24
48	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. American Journal of Human Genetics, 2016, 98, 229-242.	6.2	71
49	Genome-Wide Interaction Analyses between Genetic Variants and Alcohol Consumption and Smoking for Risk of Colorectal Cancer. PLoS Genetics, 2016, 12, e1006296.	3.5	38
50	Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array. PLoS ONE, 2016, 11, e0167758.	2.5	72
51	Genetic architecture of colorectal cancer. Gut, 2015, 64, 1623-1636.	12.1	152