Paul Scheet

List of Publications by Year
in descending order

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103 papers	22,518 citations	38742 50 h-index	32842 100 g-index
105 all docs	105 docs citations	105 times ranked	36077 citing authors

#	Article	IF	Citations
1	Evaluation of COVID-19 Mortality and Adverse Outcomes in US Patients With or Without Cancer. JAMA Oncology, 2022, 8, 69.	7.1	136
2	Chromosomal imbalances detected via RNA-sequencing in 28 cancers. Bioinformatics, 2022, 38, 1483-1490.	4.1	3
3	A whole-exome case-control association study to characterize the contribution of rare coding variation to pancreatic cancer risk. Human Genetics and Genomics Advances, 2022, 3, 100078.	1.7	0
4	Association of clonal hematopoiesis mutations with clinical outcomes: A systematic review and metaâ€analysis. American Journal of Hematology, 2022, 97, 411-420.	4.1	11
5	Chronic Exposure to Waterpipe Smoke Elicits Immunomodulatory and Carcinogenic Effects in the Lung. Cancer Prevention Research, 2022, 15, 423-434.	1.5	1
6	Evolution of DNA methylome from precancerous lesions to invasive lung adenocarcinomas. Nature Communications, 2021, 12, 687.	12.8	30
7	Single-Cell Expression Landscape of SARS-CoV-2 Receptor ACE2 and Host Proteases in Normal and Malignant Lung Tissues from Pulmonary Adenocarcinoma Patients. Cancers, 2021, 13, 1250.	3.7	7
8	Resolving the Spatial and Cellular Architecture of Lung Adenocarcinoma by Multiregion Single-Cell Sequencing. Cancer Discovery, 2021, 11, 2506-2523.	9.4	68
9	Immune evolution from preneoplasia to invasive lung adenocarcinomas and underlying molecular features. Nature Communications, 2021, 12, 2722.	12.8	74
10	Rare Germline Variants in ATM Predispose to Prostate Cancer: A PRACTICAL Consortium Study. European Urology Oncology, 2021, 4, 570-579.	5.4	38
11	Pan cancer patterns of allelic imbalance from chromosomal alterations in 33 tumor types. Genetics, 2021, 217, 1-12.	2.9	5
12	Integrated case-control and somatic-germline interaction analyses of soft-tissue sarcoma. Journal of Medical Genetics, 2021, 58, 145-153.	3.2	2
13	Baseline Oral Microbiome and All-cancer Incidence in a Cohort of Nonsmoking Mexican American Women. Cancer Prevention Research, 2021, 14, 383-392.	1.5	3
14	Embracing study heterogeneity for finding genetic interactions in largeâ€scale research consortia. Genetic Epidemiology, 2020, 44, 52-66.	1.3	4
15	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
16	Multiomics profiling of primary lung cancers and distant metastases reveals immunosuppression as a common characteristic of tumor cells with metastatic plasticity. Genome Biology, 2020, 21, 271.	8.8	36
17	Back Cover Image. Genetic Epidemiology, 2020, 44, ii.	1.3	0
18	Comprehensive T cell repertoire characterization of non-small cell lung cancer. Nature Communications, 2020, 11, 603.	12.8	140

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19	Tumor Microbiome Diversity and Composition Influence Pancreatic Cancer Outcomes. Cell, 2019, 178, 795-806.e12.	28.9	830
20	Multi-region exome sequencing reveals genomic evolution from preneoplasia to lung adenocarcinoma. Nature Communications, 2019, 10, 2978.	12.8	91
21	Driver Mutations in Normal Airway Epithelium Elucidate Spatiotemporal Resolution of Lung Cancer. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 742-750.	5.6	20
22	Genomic landscape of allelic imbalance in premalignant atypical adenomatous hyperplasias of the lung. EBioMedicine, 2019, 42, 296-303.	6.1	15
23	The BE GONE trial study protocol: a randomized crossover dietary intervention of dry beans targeting the gut microbiome of overweight and obese patients with a history of colorectal polyps or cancer. BMC Cancer, 2019, 19, 1233.	2.6	12
24	System for Qualityâ€Assured Data Analysis: Flexible, reproducible scientific workflows. Genetic Epidemiology, 2019, 43, 227-237.	1.3	6
25	Directional allelic imbalance profiling and visualization from multi-sample data with RECUR. Bioinformatics, 2019, 35, 2300-2302.	4.1	9
26	DNA Sequencing of Small Bowel Adenocarcinomas Identifies Targetable Recurrent Mutations in the ERBB2 Signaling Pathway. Clinical Cancer Research, 2019, 25, 641-651.	7.0	21
27	Immune Profiling of Premalignant Lesions in Patients With Lynch Syndrome. JAMA Oncology, 2018, 4, 1085.	7.1	62
28	Genome-Wide Gene Expression Changes in the Normal-Appearing Airway during the Evolution of Smoking-Associated Lung Adenocarcinoma. Cancer Prevention Research, 2018, 11, 237-248.	1.5	23
29	Integrated case-control and somatic-germline interaction analyses of melanoma susceptibility genes. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 2247-2254.	3.8	13
30	XPAT: a toolkit to conduct cross-platform association studies with heterogeneous sequencing datasets. Nucleic Acids Research, 2018, 46, e32-e32.	14.5	6
31	Assessing inter-component heterogeneity of biphasic uterine carcinosarcomas. Gynecologic Oncology, 2018, 151, 243-249.	1.4	11
32	Molecular mechanisms of the preventable causes of cancer in the United States. Genes and Development, 2018, 32, 868-902.	5.9	105
33	Oral microbiota reveals signs of acculturation in Mexican American women. PLoS ONE, 2018, 13, e0194100.	2.5	21
34	Strategies for identification of somatic variants using the Ion Torrent deep targeted sequencing platform. BMC Bioinformatics, 2018, 19, 5.	2.6	24
35	Can Microsatellite Status of Colorectal Cancer Be Reliably Assessed after Neoadjuvant Therapy?. Clinical Cancer Research, 2017, 23, 5246-5254.	7.0	34
36	NFAT5 and SLC4A10 Loci Associate with Plasma Osmolality. Journal of the American Society of Nephrology: JASN, 2017, 28, 2311-2321.	6.1	24

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37	Genomic Landscape of Atypical Adenomatous Hyperplasia Reveals Divergent Modes to Lung Adenocarcinoma. Cancer Research, 2017, 77, 6119-6130.	0.9	92
38	On metaâ€•and megaâ€analyses for geneâ€“environment interactions. Genetic Epidemiology, 2017, 41, 876-886.	1.3	2
39	Development of Kras mutant lung adenocarcinoma in mice with knockout of the airway lineageâ€specific gene <scp>G</scp>prc5a. International Journal of Cancer, 2017, 141, 1589-1599.	5.1	33
40	TBX2subfamily suppression in lung cancer pathogenesis: a high-potential marker for early detection. Oncotarget, 2017, 8, 68230-68241.	1.8	25
41	Genomic Landscape Established by Allelic Imbalance in the Cancerization Field of a Normal Appearing Airway. Cancer Research, 2016, 76, 3676-3683.	0.9	35
42	Genomic Landscape of Colorectal Mucosa and Adenomas. Cancer Prevention Research, 2016, 9, 417-427.	1.5	65
43	Extensive Hidden Genomic Mosaicism Revealed in Normal Tissue. American Journal of Human Genetics, 2016, 98, 571-578.	6.2	59
44	Early Events in the Molecular Pathogenesis of Lung Cancer. Cancer Prevention Research, 2016, 9, 518-527.	1.5	82
45	Genetic risk factors for the development of osteonecrosis in children under age 10 treated for acute lymphoblastic leukemia. Blood, 2016, 127, 558-564.	1.4	56
46	A metaâ€analytic framework for detection of genetic interactions. Genetic Epidemiology, 2016, 40, 534-543.	1.3	2
47	Role of CDKN2C Copy Number in Sporadic Medullary Thyroid Carcinoma. Thyroid, 2016, 26, 1553-1562.	4.5	38
48	Rapid and powerful detection of subtle allelic imbalance from exome sequencing data with hapLOHseq. Bioinformatics, 2016, 32, 3015-3017.	4.1	17
49	Genetics of glucocorticoid-associated osteonecrosis in children with acute lymphoblastic leukemia. Blood, 2015, 126, 1770-1776.	1.4	102
50	Genetic Risk Factors for the Development of Osteonecrosis in Children Under Age 10 Treated for Acute Lymphoblastic Leukemia. Blood, 2015, 126, 250-250.	1.4	0
51	Cancer In Silico Drug Discovery: A Systems Biology Tool for Identifying Candidate Drugs to Target Specific Molecular Tumor Subtypes. Molecular Cancer Therapeutics, 2014, 13, 3230-3240.	4.1	21
52	Identification of Allelic Imbalance with a Statistical Model for Subtle Genomic Mosaicism. PLoS Computational Biology, 2014, 10, e1003765.	3.2	6
53	The Dopaminergic Reward System and Leisure Time Exercise Behavior: A Candidate Allele Study. BioMed Research International, 2014, 2014, 1-9.	1.9	20
54	A unified test of linkage analysis and rare-variant association for analysis of pedigree sequence data. Nature Biotechnology, 2014, 32, 663-669.	17.5	93

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55	Preliminary whole-exome sequencing reveals mutations that imply common tumorigenicity pathways in multiple endocrine neoplasia type 1 patients. Surgery, 2014, 156, 1351-1358.	1.9	8
56	MICA, a gene contributing strong susceptibility to ankylosing spondylitis. Annals of the Rheumatic Diseases, 2014, 73, 1552-1557.	0.9	47
57	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. American Journal of Human Genetics, 2014, 95, 49-65.	6.2	73
58	Clonal evolution in breast cancer revealed by single nucleus genome sequencing. Nature, 2014, 512, 155-160.	27.8	911
59	Somatic mutation load of estrogen receptor-positive breast tumors predicts overall survival: an analysis of genome sequence data. Breast Cancer Research and Treatment, 2014, 146, 211-220.	2.5	90
60	HLA-DRB1*07:01 is associated with a higher risk of asparaginase allergies. Blood, 2014, 124, 1266-1276.	1.4	84
61	Association Between Autozygosity and Major Depression: Stratification Due to Religious Assortment. Behavior Genetics, 2013, 43, 455-467.	2.1	34
62	Population structure, migration, and diversifying selection in the Netherlands. European Journal of Human Genetics, 2013, 21, 1277-1285.	2.8	137
63	Genome-wide analysis of BMI in adolescents and young adults reveals additional insight into the effects of genetic loci over the life course. Human Molecular Genetics, 2013, 22, 3597-3607.	2.9	116
64	Novel Susceptibility Variants at 10p12.31-12.2 for Childhood Acute Lymphoblastic Leukemia in Ethnically Diverse Populations. Journal of the National Cancer Institute, 2013, 105, 733-742.	6.3	208
65	Haplotype-based profiling of subtle allelic imbalance with SNP arrays. Genome Research, 2013, 23, 152-158.	5.5	47
66	The Molecular Genetic Architecture of Self-Employment. PLoS ONE, 2013, 8, e60542.	2.5	41
67	HLA-DRB1*07:01 Is Associated With Asparaginase Allergies In Children With Acute Lymphoblastic Leukemia. Blood, 2013, 122, 60-60.	1.4	1
68	A Genome-Wide Association Scan on the Levels of Markers of Inflammation in Sardinians Reveals Associations That Underpin Its Complex Regulation. PLoS Genetics, 2012, 8, e1002480.	3.5	141
69	ARID5B Genetic Polymorphisms Contribute to Racial Disparities in the Incidence and Treatment Outcome of Childhood Acute Lymphoblastic Leukemia. Journal of Clinical Oncology, 2012, 30, 751-757.	1.6	165
70	De novo and inherited CNVs in MZ twin pairs selected for discordance and concordance on Attention Problems. European Journal of Human Genetics, 2012, 20, 1037-1043.	2.8	52
71	Twins, Tissue, and Time: An Assessment of SNPs and CNVs. Twin Research and Human Genetics, 2012, 15, 737-745.	0.6	16
72	Rare versus common variants in pharmacogenetics: SLCO1B1 variation and methotrexate disposition. Genome Research, 2012, 22, 1-8.	5.5	232

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73	Integrated annotation and analysis of genetic variants from next-generation sequencing studies with variant tools. Bioinformatics, 2012, 28, 421-422.	4.1	121
74	Haploscope: a tool for the graphical display of haplotype structure in populations. Genetic Epidemiology, 2012, 36, 17-21.	1.3	10
75	Genome-Wide Association Study Identifies Germline Polymorphisms Associated with Relapse of Childhood Acute Lymphoblastic Leukemia. Blood, 2012, 120, 878-878.	1.4	0
76	Genome-Wide Association Study Identifies a Novel Susceptibility Locus At 10p12.31-12.2 for Childhood Acute Lymphoblastic Leukemia in Ethinically Diverse Populations. Blood, 2012, 120, 877-877.	1.4	2
77	Meta-Analysis of Genome-Wide Association Studies in >80 000 Subjects Identifies Multiple Loci for C-Reactive Protein Levels. Circulation, 2011, 123, 731-738.	1.6	461
78	Ancestry and pharmacogenomics of relapse in acute lymphoblastic leukemia. Nature Genetics, 2011, 43, 237-241.	21.4	239
79	A comparison of approaches to account for uncertainty in analysis of imputed genotypes. Genetic Epidemiology, 2011, 35, 102-110.	1.3	98
80	MaCH: using sequence and genotype data to estimate haplotypes and unobserved genotypes. Genetic Epidemiology, 2010, 34, 816-834.	1.3	1,718
81	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. Nature Genetics, 2010, 42, 436-440.	21.4	581
82	Nicotinic Acetylcholine Receptor Region on Chromosome 15q25 and Lung Cancer Risk Among African Americans: A Caseâ€“Control Study. Journal of the National Cancer Institute, 2010, 102, 1199-1205.	6.3	62
83	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
84	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	3.5	453
85	STrengthening the REporting of Genetic Association Studies (STREGA)â€” An Extension of the STROBE Statement. PLoS Medicine, 2009, 6, e1000022.	8.4	411
86	STrengthening the REporting of Genetic Association Studies (STREGA)â€”an extension of the STROBE statement. Genetic Epidemiology, 2009, 33, 581-598.	1.3	211
87	Strengthening the reporting of genetic association studies (STREGA): an extension of the STROBE Statement. Human Genetics, 2009, 125, 131-151.	3.8	167
88	Strengthening the reporting of genetic association studies (STREGA): an extension of the STROBE statement. European Journal of Epidemiology, 2009, 24, 37-55.	5.7	41
89	STrengthening the REporting of Genetic Association studies (STREGA) â€“ an extension of the STROBE statement. European Journal of Clinical Investigation, 2009, 39, 247-266.	3.4	216
90	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	21.4	1,572

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91	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	21.4	662
92	Common variants at 30 loci contribute to polygenic dyslipidemia. Nature Genetics, 2009, 41, 56-65.	21.4	1,234
93	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	21.4	1,104
94	Genome-wide Association Study of Vitamin B6, Vitamin B12, Folate, and Homocysteine Blood Concentrations. American Journal of Human Genetics, 2009, 84, 477-482.	6.2	225
95	Genotype-Imputation Accuracy across Worldwide Human Populations. American Journal of Human Genetics, 2009, 84, 235-250.	6.2	231
96	Strengthening the reporting of genetic association studies (STREGA)â€"an extension of the strengthening the reporting of observational studies in epidemiology (STROBE) statement. Journal of Clinical Epidemiology, 2009, 62, 597-608.e4.	5.0	98
97	STrengthening the REporting of Genetic Association Studies (STREGA): An Extension of the STROBE Statement. Annals of Internal Medicine, 2009, 150, 206.	3.9	105
98	Genotype, haplotype and copy-number variation in worldwide human populations. Nature, 2008, 451, 998-1003.	27.8	780
99	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	21.4	1,179
100	Linkage Disequilibrium-Based Quality Control for Large-Scale Genetic Studies. PLoS Genetics, 2008, 4, e1000147.	3.5	15
101	A Fast and Flexible Statistical Model for Large-Scale Population Genotype Data: Applications to Inferring Missing Genotypes and Haplotypic Phase. American Journal of Human Genetics, 2006, 78, 629-644.	6.2	1,748
102	Automating sequence-based detection and genotyping of SNPs from diploid samples. Nature Genetics, 2006, 38, 375-381.	21.4	145
103	Accounting for Decay of Linkage Disequilibrium in Haplotype Inference and Missing-Data Imputation. American Journal of Human Genetics, 2005, 76, 449-462.	6.2	1,230