## **Geoffrey S Tobias**

List of Publications by Year in descending order

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186209 360920 6,692 35 28 35 citations h-index g-index papers 36 36 36 12396 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Body-Mass Index and Mortality among 1.46 Million White Adults. New England Journal of Medicine, 2010, 363, 2211-2219.	13.9	1,926
2	Genome-wide association study identifies variants in the ABO locus associated with susceptibility to pancreatic cancer. Nature Genetics, 2009, 41, 986-990.	9.4	597
3	A genome-wide association study identifies pancreatic cancer susceptibility loci on chromosomes 13q22.1, 1q32.1 and 5p15.33. Nature Genetics, 2010, 42, 224-228.	9.4	539
4	Detectable clonal mosaicism and its relationship to aging and cancer. Nature Genetics, 2012, 44, 651-658.	9.4	519
5	Anthropometric Measures, Body Mass Index, and Pancreatic Cancer. Archives of Internal Medicine, 2010, 170, 791.	4.3	314
6	Cigarette Smoking and Pancreatic Cancer: A Pooled Analysis From the Pancreatic Cancer Cohort Consortium. American Journal of Epidemiology, 2009, 170, 403-413.	1.6	298
7	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. Nature Genetics, 2014, 46, 994-1000.	9.4	294
8	Rare missense variants in POT1 predispose to familial cutaneous malignant melanoma. Nature Genetics, 2014, 46, 482-486.	9.4	283
9	Pancreatic Cancer Risk and ABO Blood Group Alleles: Results from the Pancreatic Cancer Cohort Consortium. Cancer Research, 2010, 70, 1015-1023.	0.4	203
10	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nature Communications, 2018, 9, 556.	5.8	188
11	Family history of cancer and risk of pancreatic cancer: A pooled analysis from the Pancreatic Cancer Cohort Consortium (PanScan). International Journal of Cancer, 2010, 127, 1421-1428.	2.3	128
12	An Absolute Risk Model to Identify Individuals at Elevated Risk for Pancreatic Cancer in the General Population. PLoS ONE, 2013, 8, e72311.	1.1	120
13	Diabetes and risk of pancreatic cancer: a pooled analysis from the pancreatic cancer cohort consortium. Cancer Causes and Control, 2013, 24, 13-25.	0.8	114
14	Hoyeraal-Hreidarsson syndrome caused by a germline mutation in the TEL patch of the telomere protein TPP1. Genes and Development, 2014, 28, 2090-2102.	2.7	106
15	Pathway analysis of genome-wide association study data highlights pancreatic development genes as susceptibility factors for pancreatic cancer. Carcinogenesis, 2012, 33, 1384-1390.	1.3	102
16	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	2.6	101
17	Alcohol intake and pancreatic cancer: a pooled analysis from the pancreatic cancer cohort consortium (PanScan). Cancer Causes and Control, 2010, 21, 1213-1225.	0.8	93
18	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. Human Molecular Genetics, 2014, 23, 6616-6633.	1.4	90

#	Article	IF	Citations
19	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. Oncotarget, 2016, 7, 66328-66343.	0.8	88
20	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, $11843$ .	5.8	86
21	Variant ABO Blood Group Alleles, Secretor Status, and Risk of Pancreatic Cancer: Results from the Pancreatic Cancer Cohort Consortium. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 3140-3149.	1.1	78
22	Genome-wide association study of survival in patients with pancreatic adenocarcinoma. Gut, 2014, 63, 152-160.	6.1	59
23	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. Journal of the National Cancer Institute, 2020, 112, 1003-1012.	3.0	59
24	The dbGaP data browser: a new tool for browsing dbGaP controlled-access genomic data. Nucleic Acids Research, 2017, 45, D819-D826.	6.5	54
25	Whole exome sequencing reveals a C-terminal germline variant in CEBPA-associated acute myeloid leukemia: 45-year follow up of a large family. Haematologica, 2016, 101, 846-852.	1.7	42
26	Whole exome sequencing in families at high risk for Hodgkin lymphoma: identification of a predisposing mutation in the KDR gene. Haematologica, 2016, 101, 853-860.	1.7	40
27	Vitamin D Metabolic Pathway Genes and Pancreatic Cancer Risk. PLoS ONE, 2015, 10, e0117574.	1.1	29
28	Hoyeraal-Hreidarsson Syndrome due to PARN Mutations: Fourteen Years of Follow-Up. Pediatric Neurology, 2016, 56, 62-68.e1.	1.0	29
29	Evaluation of Association of HNF1B Variants with Diverse Cancers: Collaborative Analysis of Data from 19 Genome-Wide Association Studies. PLoS ONE, 2010, 5, e10858.	1.1	28
30	Novel <i>FANCI</i> mutations in Fanconi anemia with VACTERL association. American Journal of Medical Genetics, Part A, 2016, 170, 386-391.	0.7	25
31	Juvenile myelomonocytic leukemia due to a germline CBL Y371C mutation: 35-year follow-up of a large family. Human Genetics, 2015, 134, 775-787.	1.8	21
32	Agnostic Pathway/Gene Set Analysis of Genome-Wide Association Data Identifies Associations for Pancreatic Cancer. Journal of the National Cancer Institute, 2019, 111, 557-567.	3.0	21
33	Inferring Past Pesticide Exposures: A Matrix of Individual Active Ingredients in Home and Garden Pesticides Used in Past Decades. Environmental Health Perspectives, 2007, 115, 248-254.	2.8	12
34	Polymorphisms in genes related to one-carbon metabolism are not related to pancreatic cancer in PanScan and PanC4. Cancer Causes and Control, 2013, 24, 595-602.	0.8	4
35	AuthorArranger automates formatting title pages and author affiliations for manuscript submissions. Communications Biology, 2022, 5, .	2.0	0