Amit Sud

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5330913/publications.pdf

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53	2,212	304701	243610
papers	citations	22 h-index	44 g-index

59	59	59	5392
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Polygenic risk scores to stratify cancer screening should predict mortality not incidence. Npj Precision Oncology, 2022, 6, .	5.4	5
2	Prioritisation by FIT to mitigate the impact of delays in the 2-week wait colorectal cancer referral pathway during the COVID-19 pandemic: a UK modelling study. Gut, 2021, 70, 1053-1060.	12.1	57
3	Will polygenic risk scores for cancer ever be clinically useful?. Npj Precision Oncology, 2021, 5, 40.	5.4	37
4	Response to first vaccination against SARS-CoV-2 in patients with multiple myeloma. Lancet Haematology,the, 2021, 8, e389-e392.	4.6	121
5	Epidemiology, genetics and treatment of multiple myeloma and precursor diseases. International Journal of Cancer, 2021, 149, 1980-1996.	5.1	25
6	The clinical utility of polygenic risk scores for chronic lymphocytic leukemia. Leukemia, 2021, 35, 3608-3610.	7.2	0
7	Avenue - Avelumab in the Frontline Treatment of Advanced Classic Hodgkin Lymphoma - a Window Study. Blood, 2021, 138, 2470-2470.	1.4	0
8	P-144: Response to SARS-CoV-2 vaccination in patients with Multiple Myeloma using a 12-week spaced dosing strategy. Clinical Lymphoma, Myeloma and Leukemia, 2021, 21, S114.	0.4	2
9	Second primary cancers in nonâ€Hodgkin lymphoma: Family history and survival. International Journal of Cancer, 2020, 146, 970-976.	5.1	15
10	Effect of delays in the 2-week-wait cancer referral pathway during the COVID-19 pandemic on cancer survival in the UK: a modelling study. Lancet Oncology, The, 2020, 21, 1035-1044.	10.7	359
11	Analysis of 153â€‰115 patients with hematological malignancies refines the spectrum of familial risk. Blood, 2019, 134, 960-969.	1.4	51
12	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	1.7	22
13	Transcriptome-wide association study of multiple myeloma identifies candidate susceptibility genes. Human Genomics, 2019, 13, 37.	2.9	14
14	Mendelian randomization provides support for obesity as a risk factor for meningioma. Scientific Reports, 2019, 9, 309.	3.3	21
15	Second primary cancers in patients with acute lymphoblastic, chronic lymphocytic and hairy cell leukaemia. British Journal of Haematology, 2019, 185, 232-239.	2.5	34
16	Types of second primary cancers influence survival in chronic lymphocytic and hairy cell leukemia patients. Blood Cancer Journal, 2019, 9, 40.	6.2	7
17	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	12.8	172
18	A genome-wide association study identifies susceptibility loci for primary central nervous system lymphoma at 6p25.3 and 3p22.1: a LOC Network study. Neuro-Oncology, 2019, 21, 1039-1048.	1.2	13

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19	Regions of homozygosity as risk factors for multiple myeloma. Annals of Human Genetics, 2019, 83, 231-238.	0.8	2
20	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. Blood Cancer Journal, 2019, 9, 1.	6.2	40
21	Mendelian randomisation study of the relationship between vitamin D and risk of glioma. Scientific Reports, 2018, 8, 2339.	3.3	23
22	Impact of atopy on risk of glioma: a Mendelian randomisation study. BMC Medicine, 2018, 16, 42.	5.5	38
23	Influence of obesity-related risk factors in the aetiology of glioma. British Journal of Cancer, 2018, 118, 1020-1027.	6.4	32
24	Leveraging Human Genetics to Guide Cancer Drug Development. JCO Clinical Cancer Informatics, 2018, 2, 1-11.	2.1	3
25	Second primary cancers in nonâ€Hodgkin lymphoma: Bidirectional analyses suggesting role for immune dysfunction. International Journal of Cancer, 2018, 143, 2449-2457.	5.1	22
26	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707.	12.8	86
27	Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. Blood, 2018, 132, 2040-2052.	1.4	17
28	Cancer genetics, precision prevention and a call to action. Nature Genetics, 2018, 50, 1212-1218.	21.4	94
29	Risk of second primary cancer following myeloid neoplasia and risk of myeloid neoplasia as second primary cancer: a nationwide, observational follow up study in Sweden. Lancet Haematology,the, 2018, 5, e368-e377.	4.6	14
30	Familial risks of acute myeloid leukemia, myelodysplastic syndromes, and myeloproliferative neoplasms. Blood, 2018, 132, 973-976.	1.4	35
31	Multiple myeloma: family history and mortality in second primary cancers. Blood Cancer Journal, 2018, 8, 75.	6.2	5
32	Combined linkage and association analysis of classical Hodgkin lymphoma. Oncotarget, 2018, 9, 20377-20385.	1.8	8
33	Abstract 776: Utilising genetic susceptibility and big data to inform novel cancer therapies. , 2018, , .		0
34	Candidate gene association studies and risk of Hodgkin lymphoma: a systematic review and metaâ€analysis. Hematological Oncology, 2017, 35, 34-50.	1.7	14
35	Genome-wide association analysis of chronic lymphocytic leukaemia, Hodgkin lymphoma and multiple myeloma identifies pleiotropic risk loci. Scientific Reports, 2017, 7, 41071.	3.3	31
36	Assessing the effect of obesity-related traits on multiple myeloma using a Mendelian randomisation approach. Blood Cancer Journal, 2017, 7, e573-e573.	6.2	12

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37	T-cell Prolymphocytic Leukemia. Hematology/Oncology Clinics of North America, 2017, 31, 273-283.	2.2	17
38	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. International Journal of Cancer, 2017, 140, 2701-2708.	5.1	76
39	Genome-wide association studies of cancer: current insights and future perspectives. Nature Reviews Cancer, 2017, 17, 692-704.	28.4	285
40	Mendelian randomisation analysis provides no evidence for a relationship between adult height and testicular cancer risk. Andrology, 2017, 5, 914-922.	3.5	4
41	Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. European Journal of Cancer, 2017, 84, 228-238.	2.8	81
42	Genetic Predisposition to Multiple Myeloma at 5q15 Is Mediated by an ELL2 Enhancer Polymorphism. Cell Reports, 2017, 20, 2556-2564.	6.4	17
43	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. Nature Communications, 2017, 8, 1892.	12.8	40
44	Survivors at risk: Hodgkin lymphoma survivors at high risk of second cancers. International Journal of Hematologic Oncology, 2017, 6, 5-8.	1.6	0
45	Risk of Second Cancer in Hodgkin Lymphoma Survivors and Influence of Family History. Journal of Clinical Oncology, 2017, 35, 1584-1590.	1.6	61
46	Second cancer risk following Hodgkin lymphoma. Oncotarget, 2017, 8, 78261-78262.	1.8	5
47	Genome-wide homozygosity signature and risk of Hodgkin lymphoma. Scientific Reports, 2015, 5, 14315.	3.3	13
48	Greenâ€grey crystals in acute myeloid leukaemia. British Journal of Haematology, 2015, 168, 618-618.	2.5	2
49	A genomic approach to estimating the heritability of Hodgkin lymphoma. Clinical Lymphoma, Myeloma and Leukemia, 2015, 15, S39-S40.	0.4	1
50	Mutations in CUL7, OBSL1 and CCDC8 in 3-M syndrome lead to disordered growth factor signalling. Journal of Molecular Endocrinology, 2012, 49, 267-275.	2.5	49
51	The Primordial Growth Disorder 3-M Syndrome Connects Ubiquitination to the Cytoskeletal Adaptor OBSL1. American Journal of Human Genetics, 2009, 84, 801-806.	6.2	93
52	Collateral Damage: The Impact on Cancer Outcomes of the COVID-19 Pandemic. SSRN Electronic Journal, 0, , .	0.4	4
53	Quantifying and Mitigating the Impact of the COVID-19 Pandemic on Outcomes in Colorectal Cancer. SSRN Electronic Journal, 0, , .	0.4	0