Claire Palles

List of Publications by Year
in descending order

70 papers	7,590 citations	101543 36 h-index	95266 68 g-index
73 all docs	73 docs citations	73 times ranked	14289 citing authors

#	Article	IF	Citations
1	COVID-19 mortality in patients with cancer on chemotherapy or other anticancer treatments: a prospective cohort study. Lancet, The, 2020, 395, 1919-1926.	13.7	908
2	Germline mutations affecting the proofreading domains of POLE and POLD1 predispose to colorectal adenomas and carcinomas. Nature Genetics, 2013, 45, 136-144.	21.4	851
3	COVID-19 prevalence and mortality in patients with cancer and the effect of primary tumour subtype and patient demographics: a prospective cohort study. Lancet Oncology, The, 2020, 21, 1309-1316.	10.7	473
4	100,000 Genomes Pilot on Rare-Disease Diagnosis in Health Care â€" Preliminary Report. New England Journal of Medicine, 2021, 385, 1868-1880.	27.0	352
5	DNA polymerase É› and Î´ exonuclease domain mutations in endometrial cancer. Human Molecular Genetics, 2013, 22, 2820-2828.	2.9	319
6	A panoply of errors: polymerase proofreading domain mutations in cancer. Nature Reviews Cancer, 2016, 16, 71-81.	28.4	292
7	Clinical relevance of DPYD variants c.1679T>G, c.1236G>A/HapB3, and c.1601G>A as predictors of severe fluoropyrimidine-associated toxicity: a systematic review and meta-analysis of individual patient data. Lancet Oncology, The, 2015, 16, 1639-1650.	10.7	277
8	POLE Proofreading Mutations Elicit an Antitumor Immune Response in Endometrial Cancer. Clinical Cancer Research, 2015, 21, 3347-3355.	7.0	249
9	Novel Breast Cancer Susceptibility Locus at 9q31.2: Results of a Genome-Wide Association Study. Journal of the National Cancer Institute, 2011, 103, 425-435.	6.3	225
10	Genetic Markers of Toxicity From Capecitabine and Other Fluorouracil-Based Regimens: Investigation in the QUASAR2 Study, Systematic Review, and Meta-Analysis. Journal of Clinical Oncology, 2014, 32, 1031-1039.	1.6	216
11	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. Nature Genetics, 2012, 44, 770-776.	21.4	210
12	Multiple Common Susceptibility Variants near BMP Pathway Loci GREM1, BMP4, and BMP2 Explain Part of the Missing Heritability of Colorectal Cancer. PLoS Genetics, 2011, 7, e1002105.	3.5	188
13	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	12.8	178
14	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	12.8	172
15	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrett's esophagus. Nature Genetics, 2012, 44, 1131-1136.	21.4	162
16	Genome-wide association studies in oesophageal adenocarcinoma and Barrett's oesophagus: a large-scale meta-analysis. Lancet Oncology, The, 2016, 17, 1363-1373.	10.7	133
17	Identification of susceptibility loci for colorectal cancer in a genome-wide meta-analysis. Human Molecular Genetics, 2014, 23, 4729-4737.	2.9	128
18	Mutational Signature Analysis Reveals NTHL1 Deficiency to Cause a Multi-tumor Phenotype. Cancer Cell, 2019, 35, 256-266.e5.	16.8	123

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19	Rare disruptive mutations and their contribution to the heritable risk of colorectal cancer. Nature Communications, 2016, 7, 11883.	12.8	122
20	Counting potentially functional variants in BRCA1, BRCA2 and ATM predicts breast cancer susceptibility. Human Molecular Genetics, 2007, 16, 1051-1057.	2.9	109
21	A new GWAS and meta-analysis with 1000Genomes imputation identifies novel risk variants for colorectal cancer. Scientific Reports, 2015, 5, 10442.	3.3	109
22	The evolutionary landscape of colorectal tumorigenesis. Nature Ecology and Evolution, 2018, 2, 1661-1672.	7.8	99
23	Polymorphisms Near TBX5 and GDF7 Are Associated With Increased Risk for Barrettâ€™s Esophagus. Gastroenterology, 2015, 148, 367-378.	1.3	93
24	A candidate gene study of capecitabine-related toxicity in colorectal cancer identifies new toxicity variants atDPYDand a putative role forENOSF1rather thanTYMS. Gut, 2015, 64, 111-120.	12.1	93
25	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. Nature Genetics, 2021, 53, 1434-1442.	21.4	85
26	Differential clonal evolution in oesophageal cancers in response to neo-adjuvant chemotherapy. Nature Communications, 2016, 7, 11111.	12.8	83
27	Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. European Journal of Cancer, 2017, 84, 228-238.	2.8	81
28	Modifiable pathways for colorectal cancer: a mendelian randomisation analysis. The Lancet Gastroenterology and Hepatology, 2020, 5, 55-62.	8.1	79
29	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	21.4	77
30	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. International Journal of Cancer, 2017, 140, 2701-2708.	5.1	76
31	Somatic POLE exonuclease domain mutations are early events in sporadic endometrial and colorectal carcinogenesis, determining driver mutational landscape, clonal neoantigen burden and immune response. Journal of Pathology, 2018, 245, 283-296.	4.5	71
32	Mutation burden and other molecular markers of prognosis in colorectal cancer treated with curative intent: results from the QUASAR 2 clinical trial and an Australian community-based series. The Lancet Gastroenterology and Hepatology, 2018, 3, 635-643.	8.1	60
33	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. British Journal of Cancer, 2016, 115, 266-272.	6.4	57
34	The UK Coronavirus Cancer Monitoring Project: protecting patients with cancer in the era of COVID-19. Lancet Oncology, The, 2020, 21, 622-624.	10.7	53
35	Inconsistent Association Between the STK15 F31I Genetic Polymorphism and Breast Cancer Risk. Journal of the National Cancer Institute, 2006, 98, 1014-1018.	6.3	48
36	Identification of genetic variants that influence circulating IGF1 levels: a targeted search strategy. Human Molecular Genetics, 2008, 17, 1457-1464.	2.9	42

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37	A comprehensive re-assessment of the association between vitamin D and cancer susceptibility using Mendelian randomization. Nature Communications, 2021, 12, 246.	12.8	39
38	Germline variation in inflammation-related pathways and risk of Barrett's oesophagus and oesophageal adenocarcinoma. Gut, 2017, 66, 1739-1747.	12.1	38
39	Signatures of TOP1 transcription-associated mutagenesis in cancer and germline. Nature, 2022, 602, 623-631.	27.8	38
40	Variation at 2q35 (PNKDandTMBIM1) influences colorectal cancer risk and identifies a pleiotropic effect with inflammatory bowel disease. Human Molecular Genetics, 2016, 25, 2349-2359.	2.9	37
41	A colorectal cancer genome-wide association study in a Spanish cohort identifies two variants associated with colorectal cancer risk at 1p33 and 8p12. BMC Genomics, 2013, 14, 55.	2.8	36
42	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. Scientific Reports, 2015, 5, 17369.	3.3	35
43	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. International Journal of Cancer, 2021, 148, 307-319.	5.1	35
44	Mortality Among Adults With Cancer Undergoing Chemotherapy or Immunotherapy and Infected With COVID-19. JAMA Network Open, 2022, 5, e220130.	5.9	34
45	The HABP2 G534E Variant Is an Unlikely Cause of Familial Nonmedullary Thyroid Cancer. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 1098-1103.	3.6	32
46	Germline and Somatic Genetic Variants in the p53 Pathway Interact to Affect Cancer Risk, Progression, and Drug Response. Cancer Research, 2021, 81, 1667-1680.	0.9	32
47	The clinical features of polymerase proof-reading associated polyposis (PPAP) and recommendations for patient management. Familial Cancer, 2022, 21, 197-209.	1.9	31
48	CYP3A Variation, Premenopausal Estrone Levels, and Breast Cancer Risk. Journal of the National Cancer Institute, 2012, 104, 657-669.	6.3	30
49	'Toxgnostics': an unmet need in cancer medicine. Nature Reviews Cancer, 2014, 14, 440-445.	28.4	29
50	Genomeâ€wide association study and metaâ€analysis in Northern European populations replicate multiple colorectal cancer risk loci. International Journal of Cancer, 2018, 142, 540-546.	5.1	26
51	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. Scientific Reports, 2015, 5, 16286.	3.3	24
52	Key findings from the UKCCMP cohort of 877 patients with haematological malignancy and COVIDâ€19: disease control as an important factor relative to recent chemotherapy or antiâ€CD20 therapy. British Journal of Haematology, 2022, 196, 892-901.	2.5	23
53	Germline MBD4 deficiency causes a multi-tumor predisposition syndrome. American Journal of Human Genetics, 2022, 109, 953-960.	6.2	23
54	Deciphering the genetic architecture of low-penetrance susceptibility to colorectal cancer. Human Molecular Genetics, 2013, 22, 5075-5082.	2.9	19

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55	Evaluating the role of ENOSF1 and TYMS variants as predictors in fluoropyrimidine-related toxicities: An IPD meta-analysis. Pharmacological Research, 2020, 152, 104594.	7.1	17
56	No Association Between Vitamin D Status and Risk of Barrett's Esophagus or Esophageal Adenocarcinoma: A Mendelian Randomization Study. Clinical Gastroenterology and Hepatology, 2019, 17, 2227-2235.e1.	4.4	16
57	BMP2 / BMP4 colorectal cancer susceptibility loci in northern and southern European populations. Carcinogenesis, 2013, 34, 314-318.	2.8	14
58	An Evaluation of the Diagnostic Accuracy of a Panel of Variants in DPYD and a Single Variant in ENOSF1 for Predicting Common Capecitabine Related Toxicities. Cancers, 2021, 13, 1497.	3.7	12
59	Germline variation in the insulin-like growth factor pathway and risk of Barrettâ€™s esophagus and esophageal adenocarcinoma. Carcinogenesis, 2021, 42, 369-377.	2.8	11
60	Expression of the cancer-associated DNA polymerase Îµ P286R in fission yeast leads to translesion synthesis polymerase dependent hypermutation and defective DNA replication. PLoS Genetics, 2021, 17, e1009526.	3.5	8
61	Correspondence: SEMA4A variation and risk of colorectal cancer. Nature Communications, 2016, 7, 10611.	12.8	7
62	Common Variants Confer Susceptibility to Barrettâ€™s Esophagus: Insights from the First Genome-Wide Association Studies. Advances in Experimental Medicine and Biology, 2016, 908, 265-290.	1.6	7
63	Shared Genetic Etiology of Obesity-Related Traits and Barrett's Esophagus/Adenocarcinoma: Insights from Genome-Wide Association Studies. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 427-433.	2.5	7
64	Genomeâ€wide association studies of toxicity to oxaliplatin and fluoropyrimidine chemotherapy with or without cetuximab in 1800 patients with advanced colorectal cancer. International Journal of Cancer, 2021, 149, 1713-1722.	5.1	7
65	ToxNav germline genetic testing and PROMinet digital mobile application toxicity monitoring: Results of a prospective singleâ€center clinical utility studyâ€”PRECISE study. Cancer Medicine, 2019, 8, 6305-6314.	2.8	6
66	The polymorphic variant rs1800734 influences methylation acquisition and allele-specific TFAP4 binding in the MLH1 promoter leading to differential mRNA expression. Scientific Reports, 2019, 9, 13463.	3.3	6
67	Detailed Molecular and Immune Marker Profiling of Archival Prostate Cancer Samples Reveals an Inverse Association between TMPRSS2:ERG Fusion Status and Immune Cell Infiltration. Journal of Molecular Diagnostics, 2020, 22, 652-669.	2.8	6
68	Adenomatous Polyposis Syndromes: Polymerase Proofreading-Associated Polyposis. , 2018, , 113-134.		4
69	Reply to: â€œDevelopment of an MSI-positive colon tumor with aberrant DNA methylation in a PPAP patientâ€. Journal of Human Genetics, 2020, 65, 513-514.	2.3	4
70	eQTL set-based association analysis identifies novel susceptibility loci for Barrett's esophagus and esophageal adenocarcinoma. Cancer Epidemiology Biomarkers and Prevention, 0, , .	2.5	1