

Claire Palles

List of Publications by Year in descending order

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Version: 2024-02-01

70
papers

7,590
citations

101384

36
h-index

95083

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. <i>Lancet, The</i> , 2020, 395, 1919-1926.	6.3	908
2	Germline mutations affecting the proofreading domains of POLE and POLD1 predispose to colorectal adenomas and carcinomas. <i>Nature Genetics</i> , 2013, 45, 136-144.	9.4	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. <i>Lancet Oncology, The</i> , 2020, 21, 1309-1316.	5.1	473
4	100,000 Genomes Pilot on Rare-Disease Diagnosis in Health Care – Preliminary Report. <i>New England Journal of Medicine</i> , 2021, 385, 1868-1880.	13.9	352
5	DNA polymerase ϵ and δ exonuclease domain mutations in endometrial cancer. <i>Human Molecular Genetics</i> , 2013, 22, 2820-2828.	1.4	319
6	A panoply of errors: polymerase proofreading domain mutations in cancer. <i>Nature Reviews Cancer</i> , 2016, 16, 71-81.	12.8	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. <i>Lancet Oncology, The</i> , 2015, 16, 1639-1650.	5.1	277
8	<i>POLE</i> Proofreading Mutations Elicit an Antitumor Immune Response in Endometrial Cancer. <i>Clinical Cancer Research</i> , 2015, 21, 3347-3355.	3.2	249
9	Novel Breast Cancer Susceptibility Locus at 9q31.2: Results of a Genome-Wide Association Study. <i>Journal of the National Cancer Institute</i> , 2011, 103, 425-435.	3.0	225
10	Genetic Markers of Toxicity From Capecitabine and Other Fluorouracil-Based Regimens: Investigation in the QUASAR2 Study, Systematic Review, and Meta-Analysis. <i>Journal of Clinical Oncology</i> , 2014, 32, 1031-1039.	0.8	216
11	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. <i>Nature Genetics</i> , 2012, 44, 770-776.	9.4	210
12	Multiple Common Susceptibility Variants near BMP Pathway Loci GREM1, BMP4, and BMP2 Explain Part of the Missing Heritability of Colorectal Cancer. <i>PLoS Genetics</i> , 2011, 7, e1002105.	1.5	188
13	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018, 9, 3166.	5.8	178
14	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. <i>Nature Communications</i> , 2019, 10, 2154.	5.8	172
15	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrett's esophagus. <i>Nature Genetics</i> , 2012, 44, 1131-1136.	9.4	162
16	Genome-wide association studies in oesophageal adenocarcinoma and Barrett's oesophagus: a large-scale meta-analysis. <i>Lancet Oncology, The</i> , 2016, 17, 1363-1373.	5.1	133
17	Identification of susceptibility loci for colorectal cancer in a genome-wide meta-analysis. <i>Human Molecular Genetics</i> , 2014, 23, 4729-4737.	1.4	128
18	Mutational Signature Analysis Reveals NTHL1 Deficiency to Cause a Multi-tumor Phenotype. <i>Cancer Cell</i> , 2019, 35, 256-266.e5.	7.7	123

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19	Rare disruptive mutations and their contribution to the heritable risk of colorectal cancer. <i>Nature Communications</i> , 2016, 7, 11883.	5.8	122
20	Counting potentially functional variants in BRCA1, BRCA2 and ATM predicts breast cancer susceptibility. <i>Human Molecular Genetics</i> , 2007, 16, 1051-1057.	1.4	109
21	A new GWAS and meta-analysis with 1000Genomes imputation identifies novel risk variants for colorectal cancer. <i>Scientific Reports</i> , 2015, 5, 10442.	1.6	109
22	The evolutionary landscape of colorectal tumorigenesis. <i>Nature Ecology and Evolution</i> , 2018, 2, 1661-1672.	3.4	99
23	Polymorphisms Near TBX5 and GDF7 Are Associated With Increased Risk for Barrett's Esophagus. <i>Gastroenterology</i> , 2015, 148, 367-378.	0.6	93
24	A candidate gene study of capecitabine-related toxicity in colorectal cancer identifies new toxicity variants at DPYD and a putative role for ENOSF1 rather than TYMS. <i>Gut</i> , 2015, 64, 111-120.	6.1	93
25	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. <i>Nature Genetics</i> , 2021, 53, 1434-1442.	9.4	85
26	Differential clonal evolution in oesophageal cancers in response to neo-adjuvant chemotherapy. <i>Nature Communications</i> , 2016, 7, 11111.	5.8	83
27	Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. <i>European Journal of Cancer</i> , 2017, 84, 228-238.	1.3	81
28	Modifiable pathways for colorectal cancer: a mendelian randomisation analysis. <i>The Lancet Gastroenterology and Hepatology</i> , 2020, 5, 55-62.	3.7	79
29	Five endometrial cancer risk loci identified through genome-wide association analysis. <i>Nature Genetics</i> , 2016, 48, 667-674.	9.4	77
30	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. <i>International Journal of Cancer</i> , 2017, 140, 2701-2708.	2.3	76
31	Somatic <i>POLE</i> exonuclease domain mutations are early events in sporadic endometrial and colorectal carcinogenesis, determining driver mutational landscape, clonal neoantigen burden and immune response. <i>Journal of Pathology</i> , 2018, 245, 283-296.	2.1	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. <i>The Lancet Gastroenterology and Hepatology</i> , 2018, 3, 635-643.	3.7	60
33	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. <i>British Journal of Cancer</i> , 2016, 115, 266-272.	2.9	57
34	The UK Coronavirus Cancer Monitoring Project: protecting patients with cancer in the era of COVID-19. <i>Lancet Oncology</i> , 2020, 21, 622-624.	5.1	53
35	Inconsistent Association Between the STK15 F31I Genetic Polymorphism and Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , 2006, 98, 1014-1018.	3.0	48
36	Identification of genetic variants that influence circulating IGF1 levels: a targeted search strategy. <i>Human Molecular Genetics</i> , 2008, 17, 1457-1464.	1.4	42

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37	A comprehensive re-assessment of the association between vitamin D and cancer susceptibility using Mendelian randomization. <i>Nature Communications</i> , 2021, 12, 246.	5.8	39
38	Germline variation in inflammation-related pathways and risk of Barrett's oesophagus and oesophageal adenocarcinoma. <i>Gut</i> , 2017, 66, 1739-1747.	6.1	38
39	Signatures of TOP1 transcription-associated mutagenesis in cancer and germline. <i>Nature</i> , 2022, 602, 623-631.	13.7	38
40	Variation at 2q35 (<i>PNKD</i> and <i>TMBIM1</i>) influences colorectal cancer risk and identifies a pleiotropic effect with inflammatory bowel disease. <i>Human Molecular Genetics</i> , 2016, 25, 2349-2359.	1.4	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. <i>BMC Genomics</i> , 2013, 14, 55.	1.2	36
42	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. <i>Scientific Reports</i> , 2015, 5, 17369.	1.6	35
43	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. <i>International Journal of Cancer</i> , 2021, 148, 307-319.	2.3	35
44	Mortality Among Adults With Cancer Undergoing Chemotherapy or Immunotherapy and Infected With COVID-19. <i>JAMA Network Open</i> , 2022, 5, e220130.	2.8	34
45	The HAP2 G534E Variant Is an Unlikely Cause of Familial Nonmedullary Thyroid Cancer. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2016, 101, 1098-1103.	1.8	32
46	Germline and Somatic Genetic Variants in the p53 Pathway Interact to Affect Cancer Risk, Progression, and Drug Response. <i>Cancer Research</i> , 2021, 81, 1667-1680.	0.4	32
47	The clinical features of polymerase proof-reading associated polyposis (PPAP) and recommendations for patient management. <i>Familial Cancer</i> , 2022, 21, 197-209.	0.9	31
48	CYP3A Variation, Premenopausal Estrone Levels, and Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , 2012, 104, 657-669.	3.0	30
49	'Toxgnostics': an unmet need in cancer medicine. <i>Nature Reviews Cancer</i> , 2014, 14, 440-445.	12.8	29
50	Genome-wide association study and meta-analysis in Northern European populations replicate multiple colorectal cancer risk loci. <i>International Journal of Cancer</i> , 2018, 142, 540-546.	2.3	26
51	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. <i>Scientific Reports</i> , 2015, 5, 16286.	1.6	24
52	Key findings from the UKCCMP cohort of 877 patients with haematological malignancy and COVID-19: disease control as an important factor relative to recent chemotherapy or anti-CD20 therapy. <i>British Journal of Haematology</i> , 2022, 196, 892-901.	1.2	23
53	Germline MBD4 deficiency causes a multi-tumor predisposition syndrome. <i>American Journal of Human Genetics</i> , 2022, 109, 953-960.	2.6	23
54	Deciphering the genetic architecture of low-penetrance susceptibility to colorectal cancer. <i>Human Molecular Genetics</i> , 2013, 22, 5075-5082.	1.4	19

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55	Evaluating the role of ENOSF1 and TYMS variants as predictors in fluoropyrimidine-related toxicities: An IPD meta-analysis. <i>Pharmacological Research</i> , 2020, 152, 104594.	3.1	17
56	No Association Between Vitamin D Status and Risk of Barrett's Esophagus or Esophageal Adenocarcinoma: A Mendelian Randomization Study. <i>Clinical Gastroenterology and Hepatology</i> , 2019, 17, 2227-2235.e1.	2.4	16
57	BMP2 / BMP4 colorectal cancer susceptibility loci in northern and southern European populations. <i>Carcinogenesis</i> , 2013, 34, 314-318.	1.3	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. <i>Cancers</i> , 2021, 13, 1497.	1.7	12
59	Germline variation in the insulin-like growth factor pathway and risk of Barrett's esophagus and esophageal adenocarcinoma. <i>Carcinogenesis</i> , 2021, 42, 369-377.	1.3	11
60	Expression of the cancer-associated DNA polymerase δ P286R in fission yeast leads to translesion synthesis polymerase dependent hypermutation and defective DNA replication. <i>PLoS Genetics</i> , 2021, 17, e1009526.	1.5	8
61	Correspondence: SEMA4A variation and risk of colorectal cancer. <i>Nature Communications</i> , 2016, 7, 10611.	5.8	7
62	Common Variants Confer Susceptibility to Barrett's Esophagus: Insights from the First Genome-Wide Association Studies. <i>Advances in Experimental Medicine and Biology</i> , 2016, 908, 265-290.	0.8	7
63	Shared Genetic Etiology of Obesity-Related Traits and Barrett's Esophagus/Adenocarcinoma: Insights from Genome-Wide Association Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 427-433.	1.1	7
64	Genome-wide association studies of toxicity to oxaliplatin and fluoropyrimidine chemotherapy with or without cetuximab in 1800 patients with advanced colorectal cancer. <i>International Journal of Cancer</i> , 2021, 149, 1713-1722.	2.3	7
65	ToxNav germline genetic testing and PROMinet digital mobile application toxicity monitoring: Results of a prospective single-center clinical utility studyâ€”PRECISE study. <i>Cancer Medicine</i> , 2019, 8, 6305-6314.	1.3	6
66	The polymorphic variant rs1800734 influences methylation acquisition and allele-specific TFAP4 binding in the MLH1 promoter leading to differential mRNA expression. <i>Scientific Reports</i> , 2019, 9, 13463.	1.6	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. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 652-669.	1.2	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€. <i>Journal of Human Genetics</i> , 2020, 65, 513-514.	1.1	4
70	eQTL set-based association analysis identifies novel susceptibility loci for Barrett's esophagus and esophageal adenocarcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 0, , .	1.1	1