

# Jeremy P Cheadle

## List of Publications by Year in descending order

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Version: 2024-02-01

63  
papers

7,979  
citations

109321

35  
h-index

144013

57  
g-index

64  
all docs

64  
docs citations

64  
times ranked

9308  
citing authors

#	ARTICLE	IF	CITATIONS
1	Inherited variants of MYH associated with somatic G:C→T:A mutations in colorectal tumors. <i>Nature Genetics</i> , 2002, 30, 227-232.	21.4	1,239
2	Addition of cetuximab to oxaliplatin-based first-line combination chemotherapy for treatment of advanced colorectal cancer: results of the randomised phase 3 MRC COIN trial. <i>Lancet</i> , The, 2011, 377, 2103-2114.	13.7	876
3	Relationship between trinucleotide repeat expansion and phenotypic variation in Huntington's disease. <i>Nature Genetics</i> , 1993, 4, 393-397.	21.4	672
4	Mismatch Repair Status and BRAF Mutation Status in Metastatic Colorectal Cancer Patients: A Pooled Analysis of the CAIRO, CAIRO2, COIN, and FOCUS Studies. <i>Clinical Cancer Research</i> , 2014, 20, 5322-5330.	7.0	561
5	Comprehensive Mutation Analysis of TSC1 and TSC2 and Phenotypic Correlations in 150 Families with Tuberous Sclerosis. <i>American Journal of Human Genetics</i> , 1999, 64, 1305-1315.	6.2	453
6	Autosomal recessive colorectal adenomatous polyposis due to inherited mutations of MYH. <i>Lancet</i> , The, 2003, 362, 39-41.	13.7	421
7	Biallelic germline mutations in MYH predispose to multiple colorectal adenoma and somatic G:C→T:A mutations. <i>Human Molecular Genetics</i> , 2002, 11, 2961-2967.	2.9	365
8	Meta-analysis of three genome-wide association studies identifies susceptibility loci for colorectal cancer at 1q41, 3q26.2, 12q13.13 and 20q13.33. <i>Nature Genetics</i> , 2010, 42, 973-977.	21.4	335
9	Molecular genetic advances in tuberous sclerosis. <i>Human Genetics</i> , 2000, 107, 97-114.	3.8	323
10	The tuberous sclerosis-1 (TSC1) gene product hamartin suppresses cell growth and augments the expression of the TSC2 product tuberin by inhibiting its ubiquitination. <i>Oncogene</i> , 2000, 19, 6306-6316.	5.9	227
11	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. <i>Nature Genetics</i> , 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. <i>PLoS Genetics</i> , 2011, 7, e1002105.	3.5	188
13	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. <i>Nature Communications</i> , 2019, 10, 2154.	12.8	172
14	MUTYH-associated polyposis—From defect in base excision repair to clinical genetic testing. <i>DNA Repair</i> , 2007, 6, 274-279.	2.8	135
15	Germline APC variants in patients with multiple colorectal adenomas, with evidence for the particular importance of E1317Q. <i>Human Molecular Genetics</i> , 2000, 9, 2215-2221.	2.9	125
16	Comprehensive analysis of the contribution of germline MYH variation to early-onset colorectal cancer. <i>International Journal of Cancer</i> , 2004, 109, 554-558.	5.1	114
17	A new GWAS and meta-analysis with 1000Genomes imputation identifies novel risk variants for colorectal cancer. <i>Scientific Reports</i> , 2015, 5, 10442.	3.3	109
18	Somatic Profiling of the Epidermal Growth Factor Receptor Pathway in Tumors from Patients with Advanced Colorectal Cancer Treated with Chemotherapy ± Cetuximab. <i>Clinical Cancer Research</i> , 2013, 19, 4104-4113.	7.0	95

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19	Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. <i>European Journal of Cancer</i> , 2017, 84, 228-238.	2.8	81
20	Exposing the MYTH about base excision repair and human inherited disease. <i>Human Molecular Genetics</i> , 2003, 12, R159-R165.	2.9	80
21	Modifiable pathways for colorectal cancer: a mendelian randomisation analysis. <i>The Lancet Gastroenterology and Hepatology</i> , 2020, 5, 55-62.	8.1	79
22	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. <i>International Journal of Cancer</i> , 2017, 140, 2701-2708.	5.1	76
23	Comparative Analysis and Genomic Structure of the Tuberous Sclerosis 2 (TSC2) Gene in Human and Pufferfish. <i>Human Molecular Genetics</i> , 1996, 5, 131-137.	2.9	66
24	A mouse model of tuberous sclerosis 1 showing background specific early post-natal mortality and metastatic renal cell carcinoma. <i>Human Molecular Genetics</i> , 2005, 14, 1839-1850.	2.9	63
25	Common genetic variation and survival after colorectal cancer diagnosis: a genome-wide analysis. <i>Carcinogenesis</i> , 2016, 37, 87-95.	2.8	62
26	Functional characterization of two human MutY homolog (hMYH) missense mutations (R227W and Tj ETQq0 0 0 rgBT /Overlock 10 Tf). <i>Nucleic Acids Research</i> , 2005, 33, 597-604.	14.5	61
27	Application and evaluation of denaturing HPLC for molecular genetic analysis in tuberous sclerosis. <i>Human Genetics</i> , 2000, 106, 663-668.	3.8	58
28	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. <i>British Journal of Cancer</i> , 2016, 115, 266-272.	6.4	57
29	Low level mosaicism detectable by DHPLC but not by direct sequencing. <i>Human Mutation</i> , 2001, 17, 233-234.	2.5	53
30	Exome Resequencing Identifies Potential Tumor-Suppressor Genes that Predispose to Colorectal Cancer. <i>Human Mutation</i> , 2013, 34, 1026-1034.	2.5	48
31	Characterizing mutations in samples with low-level mosaicism by collection and analysis of DHPLC fractionated heteroduplexes. <i>Human Mutation</i> , 2003, 21, 112-115.	2.5	43
32	Direct sequencing of the complete CFTR gene: the molecular characterisation of 99.5% of CF chromosomes in Wales. <i>Human Molecular Genetics</i> , 1993, 2, 1551-1556.	2.9	41
33	Molecular analysis of the TSC1 and TSC2 tumour suppressor genes in sporadic glial and glioneuronal tumours. <i>Human Genetics</i> , 2000, 107, 350-356.	3.8	41
34	Inherited variants in MYH are unlikely to contribute to the risk of lung carcinoma. <i>Human Genetics</i> , 2004, 114, 207-210.	3.8	39
35	Cystic fibrosis mutation analysis: Report from 22 U.K. regional genetics laboratories. <i>Human Mutation</i> , 1995, 6, 326-333.	2.5	38
36	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.	2.9	37

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37	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.	3.3	35
38	<i>BRAF</i> and <i>NRAS</i> Locus-Specific Variants Have Different Outcomes on Survival to Colorectal Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 2742-2749.	7.0	32
39	Different combinations of biallelic APC mutation confer different growth advantages in colorectal tumours. <i>Cancer Research</i> , 2002, 62, 363-6.	0.9	32
40	Identification of a leader exon and a core promoter for the rat tuberous sclerosis 2 (Tsc2) gene and structural comparison with the human homolog. <i>Mammalian Genome</i> , 1997, 8, 554-558.	2.2	30
41	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.	5.1	26
42	Pharmacogenetic analyses of 2183 patients with advanced colorectal cancer; potential role for common dihydropyrimidine dehydrogenase variants in toxicity to chemotherapy. <i>European Journal of Cancer</i> , 2018, 102, 31-39.	2.8	25
43	Analyses of 7,635 Patients with Colorectal Cancer Using Independent Training and Validation Cohorts Show That rs9929218 in <i>CDH1</i> Is a Prognostic Marker of Survival. <i>Clinical Cancer Research</i> , 2015, 21, 3453-3461.	7.0	24
44	Germline MBD4 deficiency causes a multi-tumor predisposition syndrome. <i>American Journal of Human Genetics</i> , 2022, 109, 953-960.	6.2	23
45	Role of the Oxidative DNA Damage Repair Gene OGG1 in Colorectal Tumorigenesis. <i>Journal of the National Cancer Institute</i> , 2013, 105, 1249-1253.	6.3	22
46	Temperature modulation of DHPLC analysis for detection of coexisting constitutional and mosaic sequence variants in TSC2. <i>Journal of Proteomics</i> , 2002, 51, 161-164.	2.4	15
47	Application and evaluation of denaturing HPLC for molecular genetic analysis in tuberous sclerosis. <i>Human Genetics</i> , 2000, 106, 663-668.	3.8	15
48	Pattern Recognition Receptor Polymorphisms as Predictors of Oxaliplatin Benefit in Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2019, 111, 828-836.	6.3	10
49	Comprehensive analysis of colorectal cancer-risk loci and survival outcome: A prognostic role for CDH1 variants. <i>European Journal of Cancer</i> , 2020, 124, 56-63.	2.8	10
50	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.	5.1	7
51	Lack of an association between gallstone disease and bilirubin levels with risk of colorectal cancer: a Mendelian randomisation analysis. <i>British Journal of Cancer</i> , 2021, 124, 1169-1174.	6.4	6
52	A genome-wide search for determinants of survival in 1926 patients with advanced colorectal cancer with follow-up in over 22,000 patients. <i>European Journal of Cancer</i> , 2021, 159, 247-258.	2.8	6
53	Genomic organization and comparative analysis of the mouse tuberous sclerosis 1 (Tsc1) locus. <i>Mammalian Genome</i> , 2000, 11, 1135-1138.	2.2	5
54	Rapid recognition of aberrant dHPLC elution profiles using the Transgenomic Navigator™ software. <i>Human Mutation</i> , 2005, 26, 165-165.	2.5	5

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55	Comprehensive pharmacogenetic profiling of the epidermal growth factor receptor pathway for biomarkers of response to, and toxicity from, cetuximab. <i>Journal of Medical Genetics</i> , 2017, 54, 567-571.	3.2	4
56	Genetic variation in <i>ST6GAL1</i> is a determinant of capecitabine and oxaliplatin induced hand-foot syndrome. <i>International Journal of Cancer</i> , 2022, , .	5.1	3
57	Role for Nucleotide Excision Repair Gene Variants in Oxaliplatin-Induced Peripheral Neuropathy. <i>JCO Precision Oncology</i> , 2018, 2, 1-18.	3.0	1
58	LD-PCR coupled to long-read direct sequencing: an approach for mutation detection in genes with compact genomic structures. <i>Journal of Proteomics</i> , 2001, 47, 131-136.	2.4	0
59	Response. <i>Journal of the National Cancer Institute</i> , 2014, 106, .	6.3	0
60	MUTYH-Associated Polyposis. , 2010, , 133-146.		0
61	MUTYH-Associated Colorectal Polyposis. , 2011, , 2420-2423.		0
62	MUTYH-Associated Colorectal Polyposis. , 2015, , 2969-2973.		0
63	MUTYH-Associated Colorectal Polyposis. , 2015, , 1-4.		0