Graham Casey

List of Publications by Citations

Source: https://exaly.com/author-pdf/7939702/graham-casey-publications-by-citations.pdf

Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

124
papers5,926
citations38
h-index75
g-index134
ext. papers7,629
ext. citations8.9
avg, IF4.21
L-index

#	Paper	IF	Citations
124	Convergence of genes and cellular pathways dysregulated in autism spectrum disorders. <i>American Journal of Human Genetics</i> , 2014 , 94, 677-94	11	635
123	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015 , 47, 373-80	36.3	406
122	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , 2014 , 46, 1103-9	36.3	331
121	Principles for the post-GWAS functional characterization of cancer risk loci. <i>Nature Genetics</i> , 2011 , 43, 513-8	36.3	326
120	Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-Wide Meta-analysis. <i>Gastroenterology</i> , 2013 , 144, 799-807.e24	13.3	250
119	Prevalence and Penetrance of Major Genes and Polygenes for Colorectal Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 404-412	4	185
118	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. <i>Nature Genetics</i> , 2012 , 44, 770-6	36.3	184
117	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 126-135	4	183
116	Discovery of common and rare genetic risk variants for colorectal cancer. <i>Nature Genetics</i> , 2019 , 51, 76-	83 6.3	177
115	Large-scale genetic study in East Asians identifies six new loci associated with colorectal cancer risk. <i>Nature Genetics</i> , 2014 , 46, 533-42	36.3	175
114	Meta-analysis of new genome-wide association studies of colorectal cancer risk. <i>Human Genetics</i> , 2012 , 131, 217-34	6.3	173
113	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	6	169
112	Genome-wide association analyses in East Asians identify new susceptibility loci for colorectal cancer. <i>Nature Genetics</i> , 2013 , 45, 191-6	36.3	155
111	Association of aspirin and NSAID use with risk of colorectal cancer according to genetic variants. JAMA - Journal of the American Medical Association, 2015, 313, 1133-42	27.4	135
110	Identification of susceptibility loci for colorectal cancer in a genome-wide meta-analysis. <i>Human Molecular Genetics</i> , 2014 , 23, 4729-37	5.6	107
109	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. <i>Nature Communications</i> , 2015 , 6, 7138	17.4	106
108	A new GWAS and meta-analysis with 1000Genomes imputation identifies novel risk variants for colorectal cancer. <i>Scientific Reports</i> , 2015 , 5, 10442	4.9	94

(2014-2019)

107	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. <i>Nature Communications</i> , 2019 , 10, 2154	17.4	81
106	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. <i>PLoS Medicine</i> , 2016 , 13, e1002105	11.6	8o
105	Prostate Cancer Susceptibility in Men of African Ancestry at 8q24. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	72
104	Risk of extracolonic cancers for people with biallelic and monoallelic mutations in MUTYH. <i>International Journal of Cancer</i> , 2016 , 139, 1557-63	7.5	67
103	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2019 , 111, 146-157	9.7	67
102	Genome-wide diet-gene interaction analyses for risk of colorectal cancer. <i>PLoS Genetics</i> , 2014 , 10, e100	4228	66
101	Trans-ethnic genome-wide association study of colorectal cancer identifies a new susceptibility locus in VTI1A. <i>Nature Communications</i> , 2014 , 5, 4613	17.4	62
100	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. <i>Nature Genetics</i> , 2021 , 53, 65-75	36.3	62
99	Association of the colorectal CpG island methylator phenotype with molecular features, risk factors, and family history. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 512-519	4	59
98	Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. <i>European Journal of Cancer</i> , 2017 , 84, 228-238	7.5	56
97	Large-Scale Genome-Wide Association Study of East Asians Identifies Loci Associated With Risk for Colorectal Cancer. <i>Gastroenterology</i> , 2019 , 156, 1455-1466	13.3	55
96	Female Hormonal Factors and the Risk of Endometrial Cancer in Lynch Syndrome. <i>JAMA - Journal of the American Medical Association</i> , 2015 , 314, 61-71	27.4	53
95	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. <i>International Journal of Cancer</i> , 2017 , 140, 2701-2708	7.5	50
94	Cumulative Burden of Colorectal Cancer-Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. <i>Gastroenterology</i> , 2020 , 158, 1274-1286.e12	13.3	47
93	Genome-wide scan of 29,141 African Americans finds no evidence of directional selection since admixture. <i>American Journal of Human Genetics</i> , 2014 , 95, 437-44	11	46
92	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019 , 10, 431	17.4	45
91	Circulating Levels of Insulin-like Growth Factor 1 and Insulin-like Growth Factor Binding Protein 3 Associate With Risk of Colorectal Cancer Based on Serologic and Mendelian Randomization Analyses. <i>Gastroenterology</i> , 2020 , 158, 1300-1312.e20	13.3	45
90	Gene-environment interaction involving recently identified colorectal cancer susceptibility Loci. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 1824-33	4	40

89	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. <i>British Journal of Cancer</i> , 2016 , 115, 266-72	8.7	39
88	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. <i>Journal of the National Cancer Institute</i> , 2017 , 109,	9.7	38
87	Association between body mass index and mortality for colorectal cancer survivors: overall and by tumor molecular phenotype. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 1229-38	4	38
86	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. <i>Nature Communications</i> , 2016 , 7, 10979	17.4	37
85	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. <i>Human Molecular Genetics</i> , 2015 , 24, 5603-18	5.6	35
84	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020 , 11, 3353	17.4	32
83	Identification and characterization of functional risk variants for colorectal cancer mapping to chromosome 11q23.1. <i>Human Molecular Genetics</i> , 2014 , 23, 2198-209	5.6	31
82	Modifiable pathways for colorectal cancer: a mendelian randomisation analysis. <i>The Lancet Gastroenterology and Hepatology</i> , 2020 , 5, 55-62	18.8	31
81	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. <i>American Journal of Human Genetics</i> , 2020 , 107, 432-444	11	31
80	Genome-Wide Interaction Analyses between Genetic Variants and Alcohol Consumption and Smoking for Risk of Colorectal Cancer. <i>PLoS Genetics</i> , 2016 , 12, e1006296	6	30
79	Telomere structure and maintenance gene variants and risk of five cancer types. <i>International Journal of Cancer</i> , 2016 , 139, 2655-2670	7.5	30
78	Alcohol Consumption and the Risk of Colorectal Cancer for Mismatch Repair Gene Mutation Carriers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 366-375	4	28
77	Variation at 2q35 (PNKD and TMBIM1) influences colorectal cancer risk and identifies a pleiotropic effect with inflammatory bowel disease. <i>Human Molecular Genetics</i> , 2016 , 25, 2349-2359	5.6	27
76	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	4.9	27
75	A genome-wide association study for colorectal cancer identifies a risk locus in 14q23.1. <i>Human Genetics</i> , 2015 , 134, 1249-1262	6.3	25
74	A novel colorectal cancer risk locus at 4q32.2 identified from an international genome-wide association study. <i>Carcinogenesis</i> , 2014 , 35, 2512-9	4.6	25
73	Germline mutations in PMS2 and MLH1 in individuals with solitary loss of PMS2 expression in colorectal carcinomas from the Colon Cancer Family Registry Cohort. <i>BMJ Open</i> , 2016 , 6, e010293	3	24
72	Multiple functional risk variants in a SMAD7 enhancer implicate a colorectal cancer risk haplotype. <i>PLoS ONE</i> , 2014 , 9, e111914	3.7	24

(2020-2018)

71	Cohort Profile: The Colon Cancer Family Registry Cohort (CCFRC). <i>International Journal of Epidemiology</i> , 2018 , 47, 387-388i	7.8	23
70	Identification of a common variant with potential pleiotropic effect on risk of inflammatory bowel disease and colorectal cancer. <i>Carcinogenesis</i> , 2015 , 36, 999-1007	4.6	21
69	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	7.5	21
68	A Mixed-Effects Model for Powerful Association Tests in Integrative Functional Genomics. <i>American Journal of Human Genetics</i> , 2018 , 102, 904-919	11	20
67	Next generation sequencing and a new era of medicine. <i>Gut</i> , 2013 , 62, 920-32	19.2	19
66	Risk factors for metachronous colorectal cancer following a primary colorectal cancer: A prospective cohort study. <i>International Journal of Cancer</i> , 2016 , 139, 1081-90	7.5	19
65	Mendelian randomization analysis of C-reactive protein on colorectal cancer risk. <i>International Journal of Epidemiology</i> , 2019 , 48, 767-780	7.8	18
64	Ability of known susceptibility SNPs to predict colorectal cancer risk for persons with and without a family history. <i>Familial Cancer</i> , 2019 , 18, 389-397	3	17
63	Deciphering the genetic architecture of low-penetrance susceptibility to colorectal cancer. <i>Human Molecular Genetics</i> , 2013 , 22, 5075-82	5.6	17
62	Adiposity, metabolites, and colorectal cancer risk: Mendelian randomization study. <i>BMC Medicine</i> , 2020 , 18, 396	11.4	17
61	CYP24A1 variant modifies the association between use of oestrogen plus progestogen therapy and colorectal cancer risk. <i>British Journal of Cancer</i> , 2016 , 114, 221-9	8.7	16
60	Nongenetic Determinants of Risk for Early-Onset Colorectal Cancer. JNCI Cancer Spectrum, 2021, 5, pkal	ьрё9	15
59	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. <i>Cancer Causes and Control</i> , 2016 , 27, 679-93	2.8	15
58	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. <i>Gastroenterology</i> , 2021 , 160, 1164-1178.e6	13.3	15
57	Common colorectal cancer risk alleles contribute to the multiple colorectal adenoma phenotype, but do not influence colonic polyposis in FAP. <i>European Journal of Human Genetics</i> , 2015 , 23, 260-3	5.3	14
56	A Germline Variant at 8q24 Contributes to Familial Clustering of Prostate Cancer in Men of African Ancestry. <i>European Urology</i> , 2020 , 78, 316-320	10.2	13
55	A Meta-analysis of Multiple Myeloma Risk Regions in African and European Ancestry Populations Identifies Putatively Functional Loci. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016 , 25, 1609-161	18	13
54	DNA repair and cancer in colon and rectum: Novel players in genetic susceptibility. <i>International Journal of Cancer</i> , 2020 , 146, 363-372	7.5	13

53	Mendelian Randomization of Circulating Polyunsaturated Fatty Acids and Colorectal Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 860-870	4	12
52	Modeling the effect of prolonged ethanol exposure on global gene expression and chromatin accessibility in normal 3D colon organoids. <i>PLoS ONE</i> , 2020 , 15, e0227116	3.7	12
51	Circulating bilirubin levels and risk of colorectal cancer: serological and Mendelian randomization analyses. <i>BMC Medicine</i> , 2020 , 18, 229	11.4	11
50	Common variants in the obesity-associated genes FTO and MC4R are not associated with risk of colorectal cancer. <i>Cancer Epidemiology</i> , 2016 , 44, 1-4	2.8	9
49	No evidence of gene-calcium interactions from genome-wide analysis of colorectal cancer risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 2971-6	4	9
48	Racial Disparities in Epigenetic Aging of the Right vs Left Colon. <i>Journal of the National Cancer Institute</i> , 2020 ,	9.7	9
47	A latent unknown clustering integrating multi-omics data (LUCID) with phenotypic traits. <i>Bioinformatics</i> , 2020 , 36, 842-850	7.2	9
46	Risk of colorectal cancer for people with a mutation in both a MUTYH and a DNA mismatch repair gene. <i>Familial Cancer</i> , 2015 , 14, 575-83	3	8
45	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. <i>American Journal of Human Genetics</i> , 2021 , 108, 564-582	11	7
44	Ethanol exposure drives colon location specific cell composition changes in a normal colon crypt 3D organoid model. <i>Scientific Reports</i> , 2021 , 11, 432	4.9	7
43	Genetic architectures of proximal and distal colorectal cancer are partly distinct. <i>Gut</i> , 2021 , 70, 1325-13	34 9.2	7
42	Mendelian randomisation study of age at menarche and age at menopause and the risk of colorectal cancer. <i>British Journal of Cancer</i> , 2018 , 118, 1639-1647	8.7	7
41	Germline miRNA DNA variants and the risk of colorectal cancer by subtype. <i>Genes Chromosomes and Cancer</i> , 2017 , 56, 177-184	5	6
40	Association of Body Mass Index With Colorectal Cancer Risk by Genome-Wide Variants. <i>Journal of the National Cancer Institute</i> , 2021 , 113, 38-47	9.7	6
39	A functional variant on 20q13.33 related to glioma risk alters enhancer activity and modulates expression of multiple genes. <i>Human Mutation</i> , 2021 , 42, 77-88	4.7	6
38	Determining the familial risk distribution of colorectal cancer: a data mining approach. <i>Familial Cancer</i> , 2016 , 15, 241-51	3	5
37	A meta-analysis of genome-wide association studies of multiple myeloma among men and women of African ancestry. <i>Blood Advances</i> , 2020 , 4, 181-190	7.8	5
36	Oncogenic Features in Histologically Normal Mucosa: Novel Insights Into Field Effect From a Mega-Analysis of Colorectal Transcriptomes. <i>Clinical and Translational Gastroenterology</i> , 2020 , 11, e002	10 ²	5

(2021-2016)

35	Fine-Mapping of Common Genetic Variants Associated with Colorectal Tumor Risk Identified Potential Functional Variants. <i>PLoS ONE</i> , 2016 , 11, e0157521	3.7	5
34	Cholecystectomy and the risk of colorectal cancer by tumor mismatch repair deficiency status. <i>International Journal of Colorectal Disease</i> , 2016 , 31, 1451-7	3	5
33	Genetically predicted circulating concentrations of micronutrients and risk of colorectal cancer among individuals of European descent: a Mendelian randomization study. <i>American Journal of Clinical Nutrition</i> , 2021 , 113, 1490-1502	7	5
32	SNPs associated with colorectal cancer at 15q13.3 affect risk enhancers that modulate GREM1 gene expression. <i>Human Mutation</i> , 2021 , 42, 237-245	4.7	5
31	Type 2 diabetes mellitus, blood cholesterol, triglyceride and colorectal cancer risk in Lynch syndrome. <i>British Journal of Cancer</i> , 2019 , 121, 869-876	8.7	4
30	Childhood cancers in families with and without Lynch syndrome. Familial Cancer, 2015, 14, 545-51	3	4
29	Functional informed genome-wide interaction analysis of body mass index, diabetes and colorectal cancer risk. <i>Cancer Medicine</i> , 2020 , 9, 3563-3573	4.8	4
28	Interaction between polymorphisms in aspirin metabolic pathways, regular aspirin use and colorectal cancer risk: A case-control study in unselected white European populations. <i>PLoS ONE</i> , 2018 , 13, e0192223	3.7	4
27	Genetic Effects on Transcriptome Profiles in Colon Epithelium Provide Functional Insights for Genetic Risk Loci. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021 , 12, 181-197	7.9	4
26	Circulating Levels of Testosterone, Sex Hormone Binding Globulin and Colorectal Cancer Risk: Observational and Mendelian Randomization Analyses. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 , 30, 1336-1348	4	3
25	Controlling for cellular heterogeneity using single-cell deconvolution of gene expression reveals novel markers of colorectal tumors exhibiting microsatellite instability. <i>Oncotarget</i> , 2021 , 12, 767-782	3.3	3
24	A Functional Variant on 9p21.3 Related to Glioma Risk Affects Enhancer Activity and Modulates Expression of CDKN2B-AS1. <i>Human Mutation</i> , 2021 , 42, 1208-1214	4.7	3
23	Transcriptome-wide Effects of Aspirin on Patient-derived Normal Colon Organoids. <i>Cancer Prevention Research</i> , 2021 , 14, 1089-1100	3.2	3
22	Methodological Considerations in Estimation of Phenotype Heritability Using Genome-Wide SNP Data, Illustrated by an Analysis of the Heritability of Height in a Large Sample of African Ancestry Adults. <i>PLoS ONE</i> , 2015 , 10, e0131106	3.7	2
21	Genetically proxied therapeutic inhibition of antihypertensive drug targets and risk of common cancers: A mendelian randomization analysis <i>PLoS Medicine</i> , 2022 , 19, e1003897	11.6	2
20	A Combined Proteomics and Mendelian Randomization Approach to Investigate the Effects of Aspirin-Targeted Proteins on Colorectal Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 , 30, 564-575	4	2
19	Assessment of a Polygenic Risk Score for Colorectal Cancer to Predict Risk of Lynch Syndrome Colorectal Cancer. <i>JNCI Cancer Spectrum</i> , 2021 , 5, pkab022	4.6	2
18	Genomic Analysis of Germline Variation Associated with Survival of Patients with Colorectal Cancer Treated with Chemotherapy Plus Biologics in CALGB/SWOG 80405 (Alliance). <i>Clinical Cancer Research</i> , 2021 , 27, 267-275	12.9	2

17	Genetic susceptibility markers for a breast-colorectal cancer phenotype: Exploratory results from genome-wide association studies. <i>PLoS ONE</i> , 2018 , 13, e0196245	3.7	2
16	Prioritization and functional analysis of GWAS risk loci for Barrett's esophagus and esophageal adenocarcinoma. <i>Human Molecular Genetics</i> , 2021 ,	5.6	2
15	Cross-Cancer Analysis Reveals Novel Pleiotropic Associations-Response. Cancer Research, 2017 , 77, 60)45 <u>160</u> 4	6 1
14	Genome-wide association study of circulating folate one-carbon metabolites. <i>Genetic Epidemiology</i> , 2019 , 43, 1030-1045	2.6	1
13	Principles for the post-GWAS functional characterisation of risk loci. <i>Nature Precedings</i> , 2010 ,		1
12	Salicylic Acid and Risk of Colorectal Cancer: A Two-Sample Mendelian Randomization Study. <i>Nutrients</i> , 2021 , 13,	6.7	1
11	A RecQ Protein-like 5 Haplotype is Associated With Colon Cancer. <i>Gastroenterology Research</i> , 2010 , 3, 101-105	1.8	1
10	Exploratory Genome-Wide Interaction Analysis of Nonsteroidal Anti-inflammatory Drugs and Predicted Gene Expression on Colorectal Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 1800-1808	4	1
9	Response to Li and Hopper. American Journal of Human Genetics, 2021, 108, 527-529	11	1
8	Genetically Predicted Circulating C-Reactive Protein Concentration and Colorectal Cancer Survival: A Mendelian Randomization Consortium Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 , 30, 1349-1358	4	1
7	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	8.7	1
6	Rare Variants in the DNA Repair Pathway and the Risk of Colorectal Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 , 30, 895-903	4	1
5	Novel insights into the molecular mechanisms underlying risk of colorectal cancer from smoking and red/processed meat carcinogens by modeling exposure in normal colon organoids. <i>Oncotarget</i> , 2021 , 12, 1863-1877	3.3	1
4	Colon Crypts of Subjects With Familial Adenomatous Polyposis Show an Increased Number of LGR5+ Ectopic Stem Cells. <i>Clinical and Translational Gastroenterology</i> , 2021 , 12, e00353	4.2	O
3	Beyond GWAS of Colorectal Cancer: Evidence of Interaction with Alcohol Consumption and Putative Causal Variant for the 10q24.2 Region <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022 , OF1-OF13	4	O
2	No Association of Obesity and Type 2 Diabetes Mellitus Related Genetic Variants With Colon Cancer. <i>Gastroenterology Research</i> , 2009 , 2, 311-316	1.8	
1	DCC and RET pathway analysis to identify factors associated with advanced colorectal cancer <i>Journal of Clinical Oncology</i> , 2014 , 32, 457-457	2.2	