Peter Broderick

List of Publications by Year
in descending order

106	13,124	38742 50	24982 109
papers	citations	h-index	g-index

112	112	112	16136
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetically predicted physical activity levels are associated with lower colorectal cancer risk: a Mendelian randomisation study. British Journal of Cancer, 2021, 124, 1330-1338.	6.4	17
2	Genomic landscape of platinum resistant and sensitive testicular cancers. Nature Communications, 2020, 11, 2189.	12.8	43
3	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	12.8	172
4	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
5	Identification of four novel associations for B-cell acute lymphoblastic leukaemia risk. Nature Communications, 2019, 10, 5348.	12.8	58
6	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. Blood Cancer Journal, 2019, 9, 1.	6.2	40
7	Identification of New Risk Loci and Regulatory Mechanisms Influencing Genetic Susceptibility to Acute Lymphoblastic Leukaemia. Blood, 2019, 134, 650-650.	1.4	0
8	Genome-wide association study identifies susceptibility loci for B-cell childhood acute lymphoblastic leukemia. Nature Communications, 2018, 9, 1340.	12.8	58
9	Large-scale Sequencing of Testicular Germ Cell Tumour (TGCT) Cases Excludes Major TGCT Predisposition Gene. European Urology, 2018, 73, 828-831.	1.9	54
10	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707.	12.8	86
11	Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. Blood, 2018, 132, 2040-2052.	1.4	17
12	Promoter capture Hi-C-based identification of recurrent noncoding mutations in colorectal cancer. Nature Genetics, 2018, 50, 1375-1380.	21.4	49
13	Genome-wide association analysis identifies a meningioma risk locus at 11p15.5. Neuro-Oncology, 2018, 20, 1485-1493.	1.2	23
14	Large-scale Analysis Demonstrates Familial Testicular Cancer to have Polygenic Aetiology. European Urology, 2018, 74, 248-252.	1.9	20
15	Validation of loci at 2q14.2 and 15q21.3 as risk factors for testicular cancer. Oncotarget, 2018, 9, 12630-12638.	1.8	8
16	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
17	Identification of 19 new risk loci and potential regulatory mechanisms influencing susceptibility to testicular germ cell tumor. Nature Genetics, 2017, 49, 1133-1140.	21.4	120
18	Genome-wide association study of glioma subtypes identifies specific differences in genetic susceptibility to glioblastoma and non-glioblastoma tumors. Nature Genetics, 2017, 49, 789-794.	21.4	259

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19	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. Nature Communications, 2017, 8, 1892.	12.8	40
20	Validation of Recently Proposed Colorectal Cancer Susceptibility Gene Variants in an Analysis of Families and Patientsâ€"a Systematic Review. Gastroenterology, 2017, 152, 75-77.e4.	1.3	80
21	Undefined familial colorectal cancer and the role of pleiotropism in cancer susceptibility genes. Familial Cancer, 2016, 15, 593-599.	1.9	12
22	Rare disruptive mutations in ciliary function genes contribute to testicular cancer susceptibility. Nature Communications, 2016, 7, 13840.	12.8	32
23	Germ line mutations in shelterin complex genes are associated with familial chronic lymphocytic leukemia. Blood, 2016, 128, 2319-2326.	1.4	90
24	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. Nature Communications, 2016, 7, 12050.	12.8	146
25	Rare disruptive mutations and their contribution to the heritable risk of colorectal cancer. Nature Communications, 2016, 7, 11883.	12.8	122
26	Cytochrome P450 Allele CYP3A7*1C Associates with Adverse Outcomes in Chronic Lymphocytic Leukemia, Breast, and Lung Cancer. Cancer Research, 2016, 76, 1485-1493.	0.9	28
27	CanVar: A resource for sharing germline variation in cancer patients. F1000Research, 2016, 5, 2813.	1.6	10
28	Implementation of genome-wide complex trait analysis to quantify the heritability in multiple myeloma. Scientific Reports, 2015, 5, 12473.	3.3	16
29	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. Scientific Reports, 2015, 5, 16286.	3.3	24
30	A Retrospective Observational Study of the Relationship between Single Nucleotide Polymorphisms Associated with the Risk of Developing Colorectal Cancer and Survival. PLoS ONE, 2015, 10, e0117816.	2.5	10
31	Whole-exome sequencing reveals the mutational spectrum of testicular germ cell tumours. Nature Communications, 2015, 6, 5973.	12.8	161
32	Genetic Diagnosis of High-Penetrance Susceptibility for Colorectal Cancer (CRC) Is Achievable for a High Proportion of Familial CRC by Exome Sequencing. Journal of Clinical Oncology, 2015, 33, 426-432.	1.6	80
33	The association of rs1051730 genotype on adherence to and consumption of prescribed nicotine replacement therapy dose during a smoking cessation attempt. Drug and Alcohol Dependence, 2015, 151, 236-240.	3.2	7
34	Genome-wide association study identifies multiple susceptibility loci for glioma. Nature Communications, 2015, 6, 8559.	12.8	112
35	Identification of lung cancer histology-specific variants applying Bayesian framework variant prioritization approaches within the TRICL and ILCCO consortia. Carcinogenesis, 2015, 36, 1314-1326.	2.8	15
36	Identification of four new susceptibility loci for testicular germ cell tumour. Nature Communications, 2015, 6, 8690.	12.8	36

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37	Common Variation at 1q24.1 (ALDH9A1) Is a Potential Risk Factor for Renal Cancer. PLoS ONE, 2015, 10, e0122589.	2.5	19
38	Identification of susceptibility loci for colorectal cancer in a genome-wide meta-analysis. Human Molecular Genetics, 2014, 23, 4729-4737.	2.9	128
39	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. Nature Genetics, 2014, 46, 736-741.	21.4	360
40	Inherited genetic susceptibility to monoclonal gammopathy of unknown significance. Blood, 2014, 123, 2513-2517.	1.4	32
41	Cumulative impact of common genetic variants and other risk factors on colorectal cancer risk in 42â€ˆ103 individuals. Gut, 2013, 62, 871-881.	12.1	117
42	Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk. Nature Genetics, 2013, 45, 1221-1225.	21.4	143
43	The CCND1 c.870G>A polymorphism is a risk factor for t(11;14)(q13;q32) multiple myeloma. Nature Genetics, 2013, 45, 522-525.	21.4	91
44	Deciphering the genetic architecture of low-penetrance susceptibility to colorectal cancer. Human Molecular Genetics, 2013, 22, 5075-5082.	2.9	19
45	Genome-Wide Association Study on Differentiated Thyroid Cancer. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E1674-E1681.	3.6	101
46	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
47	Risk of developing chronic lymphocytic leukemia is influenced by HLA-A class I variation. Leukemia, 2013, 27, 255-258.	7.2	17
48	Low penetrance susceptibility to glioma is caused by the TP53 variant rs78378222. British Journal of Cancer, 2013, 108, 2178-2185.	6.4	51
49	Variation at 3p24.1 and 6q23.3 influences the risk of Hodgkinâ€™s lymphoma. Nature Communications, 2013, 4, 2549.	12.8	62
50	Common variation at 2q22.3 (ZEB2) influences the risk of renal cancer. Human Molecular Genetics, 2013, 22, 825-831.	2.9	54
51	Deciphering the 8q24.21 association for glioma. Human Molecular Genetics, 2013, 22, 2293-2302.	2.9	50
52	Common genetic variation contributes significantly to the risk of developing chronic lymphocytic leukemia. Haematologica, 2013, 98, e23-e24.	3.5	10
53	Comprehensive Evaluation of the Impact of 14 Genetic Variants on Colorectal Cancer Phenotype and Risk. American Journal of Epidemiology, 2012, 175, 1-10.	3.4	33
54	Inherited Variation at Chromosome 12p13.33, Including RAD52, Influences the Risk of Squamous Cell Lung Carcinoma. Cancer Discovery, 2012, 2, 131-139.	9.4	54

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55	The TERT variant rs2736100 is associated with colorectal cancer risk. British Journal of Cancer, 2012, 107, 1001-1008.	6.4	50
56	FGFR2 genotype and risk of radiation-associated breast cancer in Hodgkin lymphoma. Blood, 2012, 119, 1029-1031.	1.4	28
57	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. Nature Genetics, 2012, 44, 770-776.	21.4	210
58	Common variation at 3p22.1 and 7p15.3 influences multiple myeloma risk. Nature Genetics, 2012, 44, 58-61.	21.4	137
59	Relationship between 16 susceptibility loci and colorectal cancer phenotype in 3146 patients. Carcinogenesis, 2012, 33, 108-112.	2.8	22
60	Common variation at 6p21.31 (BAK1) influences the risk of chronic lymphocytic leukemia. Blood, 2012, 120, 843-846.	1.4	76
61	CYP3A Variation, Premenopausal Estrone Levels, and Breast Cancer Risk. Journal of the National Cancer Institute, 2012, 104, 657-669.	6.3	30
62	Common variation at 10p12.31 near MLLT10 influences meningioma risk. Nature Genetics, 2011, 43, 825-827.	21.4	49
63	Chromosome 15q25 (CHRNA3-CHRNA5) Variation Impacts Indirectly on Lung Cancer Risk. PLoS ONE, 2011, 6, e19085.	2.5	27
64	Exome sequencing reveals germline NPAT mutation as a candidate risk factor for Hodgkin lymphoma. Blood, 2011, 118, 493-498.	1.4	78
65	Multiple Hodgkin lymphomaâ€“associated loci within the HLA region at chromosome 6p21.3. Blood, 2011, 118, 670-674.	1.4	37
66	Common genetic variation at 15q25.2 impacts on chronic lymphocytic leukaemia risk. British Journal of Haematology, 2011, 154, 229-233.	2.5	19
67	Search for inherited susceptibility to radiation-associated meningioma by genomewide SNP linkage disequilibrium mapping. British Journal of Cancer, 2011, 104, 1049-1054.	6.4	29
68	Variation in TP63 is Associated with Lung Adenocarcinoma in the UK Population. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1453-1462.	2.5	25
69	MLH1-93G > A is a risk factor for MSI colorectal cancer. Carcinogenesis, 2011, 32, 1157-1161.	2.8	32
70	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
71	<emph type="ital">DICER1</emph> Mutations in Familial Multinodular Goiter With and Without Ovarian Sertoli-Leydig Cell Tumors. JAMA - Journal of the American Medical Association, 2011, 305, 68.	7.4	284
72	Genetic Variants at Chromosomes 2q35, 5p12, 6q25.1, 10q26.13, and 16q12.1 Influence the Risk of Breast Cancer in Men. PLoS Genetics, 2011, 7, e1002290.	3.5	43

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73	Fine-mapping of colorectal cancer susceptibility loci at 8q23.3, 16q22.1 and 19q13.11: refinement of association signals and use of in silico analysis to suggest functional variation and unexpected candidate target genes. Human Molecular Genetics, 2011, 20, 2879-2888.	2.9	56
74	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
75	IRF4 polymorphism rs872071 and risk of Hodgkin lymphoma. British Journal of Haematology, 2010, 148, 413-415.	2.5	17
76	COGENT (COlorectal cancer GENeTics): an international consortium to study the role of polymorphic variation on the risk of colorectal cancer. British Journal of Cancer, 2010, 102, 447-454.	6.4	43
77	A large-scale meta-analysis to refine colorectal cancer risk estimates associated with MUTYH variants. British Journal of Cancer, 2010, 103, 1875-1884.	6.4	107
78	Variant IRF4/MUM1 associates with CD38 status and treatment-free survival in chronic lymphocytic leukaemia. Leukemia, 2010, 24, 877-881.	7.2	18
79	Common variants at 2q37.3, 8q24.21, 15q21.3 and 16q24.1 influence chronic lymphocytic leukemia risk. Nature Genetics, 2010, 42, 132-136.	21.4	223
80	Meta-analysis of three genome-wide association studies identifies susceptibility loci for colorectal cancer at 1q41, 3q26.2, 12q13.13 and 20q13.33. Nature Genetics, 2010, 42, 973-977.	21.4	335
81	A genome-wide association study of Hodgkin's lymphoma identifies new susceptibility loci at 2p16.1 (REL), 8q24.21 and 10p14 (GATA3). Nature Genetics, 2010, 42, 1126-1130.	21.4	177
82	Fine-scale mapping of the 6p25.3 chronic lymphocytic leukaemia susceptibility locus. Human Molecular Genetics, 2010, 19, 1840-1845.	2.9	24
83	Role of 5p15.33 (TERT-CLPTM1L), 6p21.33 and 15q25.1 (CHRNA5-CHRNA3) variation and lung cancer risk in never-smokers. Carcinogenesis, 2010, 31, 234-238.	2.8	97
84	Multiple Independent Loci at Chromosome 15q25.1 Affect Smoking Quantity: a Meta-Analysis and Comparison with Lung Cancer and COPD. PLoS Genetics, 2010, 6, e1001053.	3.5	332
85	Allelic Variation at the 8q23.3 Colorectal Cancer Risk Locus Functions as a Cis-Acting Regulator of EIF3H. PLoS Genetics, 2010, 6, e1001126.	3.5	74
86	The colorectal cancer risk at 18q21 is caused by a novel variant altering SMAD7 expression. Genome Research, 2009, 19, 987-993.	5.5	85
87	Deciphering the Impact of Common Genetic Variation on Lung Cancer Risk: A Genome-Wide Association Study. Cancer Research, 2009, 69, 6633-6641.	0.9	206
88	The CDH1â€160C>A polymorphism is a risk factor for colorectal cancer. International Journal of Cancer, 2009, 125, 1622-1625.	5.1	26
89	A genome-wide scan of 10â€‰000 gene-centric variants and colorectal cancer risk. European Journal of Human Genetics, 2009, 17, 1507-1514.	2.8	12
90	Deciphering the genetics of hereditary non-syndromic colorectal cancer. European Journal of Human Genetics, 2008, 16, 1477-1486.	2.8	31

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91	Comprehensive analysis of common mitochondrial DNA variants and colorectal cancer risk. British Journal of Cancer, 2008, 99, 2088-2093.	6.4	36
92	Genome-wide association scan of tag SNPs identifies a susceptibility locus for lung cancer at 15q25.1. Nature Genetics, 2008, 40, 616-622.	21.4	1,189
93	A genome-wide association study identifies colorectal cancer susceptibility loci on chromosomes 10p14 and 8q23.3. Nature Genetics, 2008, 40, 623-630.	21.4	514
94	Genome-wide association scan identifies a colorectal cancer susceptibility locus on 11q23 and replicates risk loci at 8q24 and 18q21. Nature Genetics, 2008, 40, 631-637.	21.4	542
95	Common genetic variants at the CRAC1 (HMPS) locus on chromosome 15q13.3 influence colorectal cancer risk. Nature Genetics, 2008, 40, 26-28.	21.4	277
96	A genome-wide association study identifies six susceptibility loci for chronic lymphocytic leukemia. Nature Genetics, 2008, 40, 1204-1210.	21.4	329
97	Meta-analysis of genome-wide association data identifies four new susceptibility loci for colorectal cancer. Nature Genetics, 2008, 40, 1426-1435.	21.4	498
98	Common 5p15.33 and 6p21.33 variants influence lung cancer risk. Nature Genetics, 2008, 40, 1407-1409.	21.4	510
99	Lack of a relationship between the common 18q24 variant rs12953717 and risk of chronic lymphocytic leukemia. Leukemia and Lymphoma, 2008, 49, 271-272.	1.3	5
100	Refinement of the basis and impact of common 11q23.1 variation to the risk of developing colorectal cancer. Human Molecular Genetics, 2008, 17, 3720-3727.	2.9	61
101	CASP8 variants D302H and â˜652 6N ins/del do not influence the risk of colorectal cancer in the United Kingdom population. British Journal of Cancer, 2008, 98, 1434-1436.	6.4	49
102	A genome-wide association study shows that common alleles of SMAD7 influence colorectal cancer risk. Nature Genetics, 2007, 39, 1315-1317.	21.4	463
103	A genome-wide association scan of tag SNPs identifies a susceptibility variant for colorectal cancer at 8q24.21. Nature Genetics, 2007, 39, 984-988.	21.4	754
104	National study of colorectal cancer genetics. British Journal of Cancer, 2007, 97, 1305-1309.	6.4	63
105	Evaluation of NTHL1, NEIL1, NEIL2, MPG, TDG, UNG and SMUG1genes in familial colorectal cancer predisposition. BMC Cancer, 2006, 6, 243.	2.6	69
106	MiMiR: a comprehensive solution for storage, annotation and exchange of microarray data. BMC Bioinformatics, 2005, 6, 268.	2.6	16