Ian P M Tomlinson

List of Publications by Year
in descending order

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232 papers	26,286 citations	8755 77 h-index	8627 151 g-index
260 all docs	260 docs citations	260 times ranked	33423 citing authors

#	Article	IF	Citations
1	The clinical features of polymerase proof-reading associated polyposis (PPAP) and recommendations for patient management. Familial Cancer, 2022, 21, 197-209.	0.9	31
2	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	2.0	6
3	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	3.4	51
4	Phenome-wide association study (PheWAS) of colorectal cancer risk SNP effects on health outcomes in UK Biobank. British Journal of Cancer, 2022, 126, 822-830.	2.9	4
5	Germline MBD4 deficiency causes a multi-tumor predisposition syndrome. American Journal of Human Genetics, 2022, 109, 953-960.	2.6	23
6	Germline RET variants underlie a subset of paediatric osteosarcoma. Journal of Medical Genetics, 2021, 58, 20-24.	1.5	7
7	Image-based consensus molecular subtype (imCMS) classification of colorectal cancer using deep learning. Gut, 2021, 70, 544-554.	6.1	148
8	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. International Journal of Cancer, 2021, 148, 307-319.	2.3	35
9	In-depth Clinical and Biological Exploration of DNA Damage Immune Response as a Biomarker for Oxaliplatin Use in Colorectal Cancer. Clinical Cancer Research, 2021, 27, 288-300.	3.2	13
10	The Glasgow Microenvironment Score associates with prognosis and adjuvant chemotherapy response in colorectal cancer. British Journal of Cancer, 2021, 124, 786-796.	2.9	11
11	Germline variation in the insulin-like growth factor pathway and risk of Barrettâ€™s esophagus and esophageal adenocarcinoma. Carcinogenesis, 2021, 42, 369-377.	1.3	11
12	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. British Journal of Cancer, 2021, 124, 842-854.	2.9	5
13	Genetically predicted physical activity levels are associated with lower colorectal cancer risk: a Mendelian randomisation study. British Journal of Cancer, 2021, 124, 1330-1338.	2.9	17
14	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	13.9	532
15	Germline and Somatic Genetic Variants in the p53 Pathway Interact to Affect Cancer Risk, Progression, and Drug Response. Cancer Research, 2021, 81, 1667-1680.	0.4	32
16	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.	1.7	12
17	Oncogenic BRAF, unrestrained by TGFÎ²-receptor signalling, drives right-sided colonic tumorigenesis. Nature Communications, 2021, 12, 3464.	5.8	33
18	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.	1.5	8

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19	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	2.6	6
20	Non-Lynch Familial and Early-Onset Colorectal Cancer Explained by Accumulation of Low-Risk Genetic Variants. Cancers, 2021, 13, 3857.	1.7	8
21	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. Human Genetics, 2021, 140, 1353-1365.	1.8	18
22	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. Breast Cancer Research, 2021, 23, 86.	2.2	7
23	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	2.9	9
24	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. Nature Genetics, 2021, 53, 1434-1442.	9.4	85
25	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 623-642.	1.1	19
26	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	1.6	2
27	Exploiting differential Wnt target gene expression to generate a molecular biomarker for colorectal cancer stratification. Gut, 2020, 69, 1092-1103.	6.1	52
28	Modifiable pathways for colorectal cancer: a mendelian randomisation analysis. The Lancet Gastroenterology and Hepatology, 2020, 5, 55-62.	3.7	79
29	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
30	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.	1.1	4
31	Prediction of relapse-free survival according to adjuvant chemotherapy and regulator of chromosome condensation 2 (RCC2) expression in colorectal cancer. ESMO Open, 2020, 5, e001040.	2.0	6
32	Why is cancer not more common? A changing microenvironment may help to explain why, and suggests strategies for anti-cancer therapy. Open Biology, 2020, 10, 190297.	1.5	4
33	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	2.6	39
34	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	9.4	265
35	Histological phenotypic subtypes predict recurrence risk and response to adjuvant chemotherapy in patients with stage III colorectal cancer. Journal of Pathology: Clinical Research, 2020, 6, 283-296.	1.3	17
36	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.	1.1	7

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37	The use of Mendelian randomisation to identify causal cancer risk factors: promise and limitations. Journal of Pathology, 2020, 250, 541-554.	2.1	28
38	Prediction of colorectal cancer risk based on profiling with common genetic variants. International Journal of Cancer, 2020, 147, 3431-3437.	2.3	17
39	The MLH1 polymorphism rs1800734 and risk of endometrial cancer with microsatellite instability. Clinical Epigenetics, 2020, 12, 102.	1.8	8
40	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	5.8	75
41	Measuring single cell divisions in human tissues from multi-region sequencing data. Nature Communications, 2020, 11, 1035.	5.8	41
42	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
43	Deep learning for prediction of colorectal cancer outcome: a discovery and validation study. Lancet, The, 2020, 395, 350-360.	6.3	364
44	Guidelines for the management of hereditary colorectal cancer from the British Society of Gastroenterology (BSG)/Association of Coloproctology of Great Britain and Ireland (ACPGBI)/United Kingdom Cancer Genetics Group (UKCGG). Gut, 2020, 69, 411-444.	6.1	263
45	A sensitive and affordable multiplex RT-qPCR assay for SARS-CoV-2 detection. PLoS Biology, 2020, 18, e3001030.	2.6	32
46	Evolutionary history of human colitis-associated colorectal cancer. Gut, 2019, 68, 985-995.	6.1	97
47	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.	1.6	6
48	Mendelian randomisation: A powerful and inexpensive method for identifying and excluding non-genetic risk factors for colorectal cancer. Molecular Aspects of Medicine, 2019, 69, 41-47.	2.7	39
49	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	5.8	172
50	An FBXW7-ZEB2 axis links EMT and tumour microenvironment to promote colorectal cancer stem cells and chemoresistance. Oncogenesis, 2019, 8, 13.	2.1	99
51	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
52	CRISPR-Cas9 Causes Chromosomal Instability and Rearrangements in Cancer Cell Lines, Detectable by Cytogenetic Methods. CRISPR Journal, 2019, 2, 406-416.	1.4	51
53	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	13.7	198
54	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711

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55	Serum- and Glucocorticoid-induced Kinase Sgk1 Directly Promotes the Differentiation of Colorectal Cancer Cells and Restrains Metastasis. Clinical Cancer Research, 2019, 25, 629-640.	3.2	28
56	The BRCA2 c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	1.1	19
57	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	1.3	62
58	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.	2.1	71
59	Clinically actionable mutation profiles in patients with cancer identified by whole-genome sequencing. Journal of Physical Education and Sports Management, 2018, 4, a002279.	0.5	21
60	Chromatin organisation and cancer prognosis: a pan-cancer study. Lancet Oncology, The, 2018, 19, 356-369.	5.1	67
61	Telomere length and genetics are independent colorectal tumour risk factors in an evaluation of biomarkers in normal bowel. British Journal of Cancer, 2018, 118, 727-732.	2.9	11
62	Critical research gaps and recommendations to inform research prioritisation for more effective prevention and improved outcomes in colorectal cancer. Gut, 2018, 67, 179-193.	6.1	73
63	Prognostic markers for colorectal cancer: estimating ploidy and stroma. Annals of Oncology, 2018, 29, 616-623.	0.6	56
64	Adjuvant Treatment for POLE Proofreading Domainâ€“Mutant Cancers: Sensitivity to Radiotherapy, Chemotherapy, and Nucleoside Analogues. Clinical Cancer Research, 2018, 24, 3197-3203.	3.2	50
65	Heterogeneity of germline variants in high risk breast and ovarian cancer susceptibility genes in India. Precision Clinical Medicine, 2018, 1, 75-87.	1.3	5
66	The evolutionary landscape of colorectal tumorigenesis. Nature Ecology and Evolution, 2018, 2, 1661-1672.	3.4	99
67	Detecting repeated cancer evolution from multi-region tumor sequencing data. Nature Methods, 2018, 15, 707-714.	9.0	124
68	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.	3.7	60
69	Translational study identifies XPF and MUS81 as predictive biomarkers for oxaliplatin-based peri-operative chemotherapy in patients with esophageal adenocarcinoma. Scientific Reports, 2018, 8, 7265.	1.6	8
70	Hereditary Mixed Polyposis Syndrome. , 2018, , 185-192.		1
71	The effects of mutational processes and selection on driver mutations across cancer types. Nature Communications, 2018, 9, 1857.	5.8	91
72	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178

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73	Management and 5-year outcomes in 9938 women with screen-detected ductal carcinoma in situ: the UK Sloane Project. European Journal of Cancer, 2018, 101, 210-219.	1.3	52
74	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.4	75
75	Features of Patients With Hereditary Mixed Polyposis Syndrome Caused by Duplication of GREM1 and Implications for Screening and Surveillance. Gastroenterology, 2017, 152, 1876-1880.e1.	0.6	34
76	British Society of Gastroenterology position statement on serrated polyps in the colon and rectum. Gut, 2017, 66, 1181-1196.	6.1	250
77	Urgent improvements needed to diagnose and manage Lynch syndrome. BMJ: British Medical Journal, 2017, 356, j1388.	2.4	20
78	Germline variation in inflammation-related pathways and risk of Barrett's oesophagus and oesophageal adenocarcinoma. Gut, 2017, 66, 1739-1747.	6.1	38
79	Bone morphogenetic protein and Notch signalling crosstalk in poorâ€prognosis, mesenchymalâ€subtype colorectal cancer. Journal of Pathology, 2017, 242, 178-192.	2.1	36
80	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
81	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
82	Evidence for genetic association between chromosome 1q loci and predisposition to colorectal neoplasia. British Journal of Cancer, 2017, 117, 1215-1223.	2.9	10
83	Robust RNA-based in situ mutation detection delineates colorectal cancer subclonal evolution. Nature Communications, 2017, 8, 1998.	5.8	57
84	Multilevel genomics of colorectal cancers with microsatellite instabilityâ€"clinical impact of JAK1 mutations and consensus molecular subtype 1. Genome Medicine, 2017, 9, 46.	3.6	71
85	Cancer predisposition syndromes: lessons for truly precision medicine. Journal of Pathology, 2017, 241, 226-235.	2.1	13
86	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67
87	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.	0.6	80
88	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45
89	Clinical applicability and cost of a 46-gene panel for genomic analysis of solid tumours: Retrospective validation and prospective audit in the UK National Health Service. PLoS Medicine, 2017, 14, e1002230.	3.9	60
90	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. Oncotarget, 2016, 7, 80140-80163.	0.8	31

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91	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. PLoS Medicine, 2016, 13, e1002105.	3.9	118
92	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	1.1	12
93	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	2.3	51
94	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
95	Correspondence: SEMA4A variation and risk of colorectal cancer. Nature Communications, 2016, 7, 10611.	5.8	7
96	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	2.2	43
97	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. Cancer Causes and Control, 2016, 27, 679-693.	0.8	21
98	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	9.4	77
99	The Hunting of the Snark: Whither Genome-Wide Association Studies for Colorectal Cancer?. Gastroenterology, 2016, 150, 1528-1530.	0.6	4
100	Somatic POLE proofreading domain mutation, immune response, and prognosis in colorectal cancer: a retrospective, pooled biomarker study. The Lancet Gastroenterology and Hepatology, 2016, 1, 207-216.	3.7	227
101	Expression of Idh1R132H in the Murine Subventricular Zone Stem Cell Niche Recapitulates Features of Early Gliomagenesis. Cancer Cell, 2016, 30, 578-594.	7.7	122
102	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	2.6	59
103	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. Human Molecular Genetics, 2016, 25, 3863-3876.	1.4	33
104	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1503-1510.	1.1	64
105	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.	0.8	7
106	Genome-wide association studies in oesophageal adenocarcinoma and Barrett's oesophagus: a large-scale meta-analysis. Lancet Oncology, The, 2016, 17, 1363-1373.	5.1	133
107	rs2735383, located at a microRNA binding site in the 3â€™UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874.	1.6	2
108	Adjuvant capecitabine plus bevacizumab versus capecitabine alone in patients with colorectal cancer (QUASAR 2): an open-label, randomised phase 3 trial. Lancet Oncology, The, 2016, 17, 1543-1557.	5.1	129

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109	Premalignant SOX2 overexpression in the fallopian tubes of ovarian cancer patients: Discovery and validation studies. EBioMedicine, 2016, 10, 137-149.	2.7	34
110	Differential clonal evolution in oesophageal cancers in response to neo-adjuvant chemotherapy. Nature Communications, 2016, 7, 11111.	5.8	83
111	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
112	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
113	Rare disruptive mutations and their contribution to the heritable risk of colorectal cancer. Nature Communications, 2016, 7, 11883.	5.8	122
114	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). Scientific Reports, 2016, 6, 32512.	1.6	19
115	A Common Variant at the 14q32 Endometrial Cancer Risk Locus Activates AKT1 through YY1 Binding. American Journal of Human Genetics, 2016, 98, 1159-1169.	2.6	32
116	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	0.8	152
117	RE: HABP2 G534E Mutation in Familial Nonmedullary Thyroid Cancer. Journal of the National Cancer Institute, 2016, 108, djw108.	3.0	4
118	Genetic susceptibility to Barrettâ€™s oesophagus: Lessons from early studies. United European Gastroenterology Journal, 2016, 4, 485-492.	1.6	5
119	The HABP2 G534E Variant Is an Unlikely Cause of Familial Nonmedullary Thyroid Cancer. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 1098-1103.	1.8	32
120	A panoply of errors: polymerase proofreading domain mutations in cancer. Nature Reviews Cancer, 2016, 16, 71-81.	12.8	292
121	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	1.6	62
122	GWAS meta-analysis of 16 852 women identifies new susceptibility locus for endometrial cancer. Human Molecular Genetics, 2016, 25, ddw092.	1.4	19
123	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	1.5	94
124	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	9.4	125
125	Genetic variation in the immunosuppression pathway genes and breast cancer susceptibility: a pooled analysis of 42,510 cases and 40,577 controls from the Breast Cancer Association Consortium. Human Genetics, 2016, 135, 137-154.	1.8	8
126	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	3.0	77

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127	Systematic meta-analyses and field synopsis of genetic association studies in colorectal adenomas. International Journal of Epidemiology, 2016, 45, 186-205.	0.9	21
128	Genetic Biomarkers of Barrettâ€™s Esophagus Susceptibility and Progression to Dysplasia and Cancer: A Systematic Review and Meta-Analysis. Digestive Diseases and Sciences, 2016, 61, 25-38.	1.1	27
129	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
130	GREM1 germline mutation screening in Ashkenazi Jewish patients with familial colorectal cancer. Genetical Research, 2015, 97, e11.	0.3	17
131	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. Scientific Reports, 2015, 5, 16286.	1.6	24
132	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.	1.6	35
133	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
134	HOT mutation screening in human glioblastomas. Future Science OA, 2015, 1, .	0.9	1
135	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
136	Exome sequencing of osteosarcoma reveals mutation signatures reminiscent of BRCA deficiency. Nature Communications, 2015, 6, 8940.	5.8	242
137	A systematic review and meta-analysis of somatic and germline DNA sequence biomarkers of esophageal cancer survival, therapy response and stage. Annals of Oncology, 2015, 26, 624-644.	0.6	58
138	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
139	Polymorphisms Near TBX5 and GDF7 Are Associated With Increased Risk for Barrettâ€™s Esophagus. Gastroenterology, 2015, 148, 367-378.	0.6	93
140	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. American Journal of Human Genetics, 2015, 96, 5-20.	2.6	76
141	Prognostic Significance of POLE Proofreading Mutations in Endometrial Cancer. Journal of the National Cancer Institute, 2015, 107, 402.	3.0	229
142	Clinical management of hereditary colorectal cancer syndromes. Nature Reviews Gastroenterology and Hepatology, 2015, 12, 88-97.	8.2	99
143	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. Carcinogenesis, 2015, 36, 256-271.	1.3	14
144	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	9.4	513

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145	An update on the molecular pathology of the intestinal polyposis syndromes. Diagnostic Histopathology, 2015, 21, 147-151.	0.2	1
146	POLE mutations in families predisposed to cutaneous melanoma. Familial Cancer, 2015, 14, 621-628.	0.9	43
147	The Mendelian colorectal cancer syndromes. Annals of Clinical Biochemistry, 2015, 52, 690-692.	0.8	16
148	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. American Journal of Human Genetics, 2015, 97, 22-34.	2.6	37
149	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56
150	Candidate locus analysis of the TERTâ€“CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. Human Genetics, 2015, 134, 231-245.	1.8	34
151	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726.	9.4	310
152	Recurrent chromosomal gains and heterogeneous driver mutations characterise papillary renal cancer evolution. Nature Communications, 2015, 6, 6336.	5.8	100
153	Analyses of 7,635 Patients with Colorectal Cancer Using Independent Training and Validation Cohorts Show That rs9929218 in CDH1 Is a Prognostic Marker of Survival. Clinical Cancer Research, 2015, 21, 3453-3461.	3.2	24
154	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
155	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.	5.1	277
156	Target gene mutational pattern in Lynch syndrome colorectal carcinomas according to tumour location and germline mutation. British Journal of Cancer, 2015, 113, 686-692.	2.9	30
157	The mini-driver model of polygenic cancer evolution. Nature Reviews Cancer, 2015, 15, 680-685.	12.8	104
158	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
159	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. Endocrine-Related Cancer, 2015, 22, 851-861.	1.6	25
160	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	1.1	24
161	Aberrant epithelial GREM1 expression initiates colonic tumorigenesis from cells outside the stem cell niche. Nature Medicine, 2015, 21, 62-70.	15.2	213
162	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.	6.1	93

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163	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	1.4	38
164	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	1.4	50
165	Common colorectal cancer risk alleles contribute to the multiple colorectal adenoma phenotype, but do not influence colonic polyposis in FAP. European Journal of Human Genetics, 2015, 23, 260-263.	1.4	17
166	Methylation changes in the TFAP2E promoter region are associated with BRAF mutation and poorer overall & disease free survival in colorectal cancer. Oncoscience, 2015, 2, 508-516.	0.9	11
167	FBXW7-mutated colorectal cancer cells exhibit aberrant expression of phosphorylated-p53 at Serine-15. Oncotarget, 2015, 6, 9240-9256.	0.8	38
168	Colorectal Tumors from APC*I1307K Carriers Principally Harbor Somatic APC Mutations outside the A8 Tract. PLoS ONE, 2014, 9, e84498.	1.1	9
169	Association between CASP8 â€“652 6N Del Polymorphism (rs3834129) and Colorectal Cancer Risk: Results from a Multi-Centric Study. PLoS ONE, 2014, 9, e85538.	1.1	8
170	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49
171	Association analysis using next-generation sequence data from publicly available control groups: the robust variance score statistic. Bioinformatics, 2014, 30, 2179-2188.	1.8	31
172	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	1.5	39
173	Investigation of the atypicalFBXW7mutation spectrum in human tumours by conditional expression of a heterozygous propellor tip missense allele in the mouse intestines. Gut, 2014, 63, 792-799.	6.1	50
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