Ian Tomlinson

List of Publications by Year
in descending order

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Version: 2024-02-01

208 papers	25,445 citations	8181 76 h-index	7518 151 g-index
219 all docs	219 docs citations	219 times ranked	28658 citing authors

#	Article	IF	Citations
1	A serine/threonine kinase gene defective in Peutzâ€“Jeghers syndrome. Nature, 1998, 391, 184-187.	27.8	1,451
2	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
3	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
4	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
5	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
6	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
7	Genetic prognostic and predictive markers in colorectal cancer. Nature Reviews Cancer, 2009, 9, 489-499.	28.4	602
8	CCAT2, a novel noncoding RNA mapping to 8q24, underlies metastatic progression and chromosomal instability in colon cancer. Genome Research, 2013, 23, 1446-1461.	5.5	526
9	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	21.4	513
10	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	21.4	493
11	A genome-wide association study shows that common alleles of SMAD7 influence colorectal cancer risk. Nature Genetics, 2007, 39, 1315-1317.	21.4	463
12	The common colorectal cancer predisposition SNP rs6983267 at chromosome 8q24 confers potential to enhanced Wnt signaling. Nature Genetics, 2009, 41, 885-890.	21.4	463
13	Localization of a susceptibility locus for Peutz-Jeghers syndrome to 19p using comparative genomic hybridization and targeted linkage analysis. Nature Genetics, 1997, 15, 87-90.	21.4	444
14	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
15	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
16	Deep learning for prediction of colorectal cancer outcome: a discovery and validation study. Lancet, The, 2020, 395, 350-360.	13.7	364
17	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
18	The type of somatic mutation at APC in familial adenomatous polyposis is determined by the site of the germline mutation: a new facet to Knudson's 'two-hit' hypothesis. Nature Medicine, 1999, 5, 1071-1075.	30.7	339

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19	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	21.4	321
20	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726.	21.4	310
21	A panoply of errors: polymerase proofreading domain mutations in cancer. Nature Reviews Cancer, 2016, 16, 71-81.	28.4	292
22	Selection, the mutation rate and cancer: Ensuring that the tail does not wag the dog. Nature Medicine, 1999, 5, 11-12.	30.7	289
23	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
24	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptorâ€“negative breast cancer. Nature Genetics, 2011, 43, 1210-1214.	21.4	279
25	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
26	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.	10.7	277
27	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	21.4	276
28	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	21.4	265
29	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.	12.1	263
30	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	256
31	British Society of Gastroenterology position statement on serrated polyps in the colon and rectum. Gut, 2017, 66, 1181-1196.	12.1	250
32	Germline and somatic polymerase Ïµ and Î´ mutations define a new class of hypermutated colorectal and endometrial cancers. Journal of Pathology, 2013, 230, 148-153.	4.5	242
33	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	21.4	235
34	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.	8.1	227
35	Hereditary mixed polyposis syndrome is caused by a 40-kb upstream duplication that leads to increased and ectopic expression of the BMP antagonist GREM1. Nature Genetics, 2012, 44, 699-703.	21.4	222
36	Multiple ways of silencing E-cadherin gene expression in lobular carcinoma of the breast. International Journal of Cancer, 2001, 92, 404-408.	5.1	217

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37	Genetic Markers of Toxicity From Capecitabine and Other Fluorouracil-Based Regimens: Investigation in the QUASAR2 Study, Systematic Review, and Meta-Analysis. Journal of Clinical Oncology, 2014, 32, 1031-1039.	1.6	216
38	Aberrant epithelial GREM1 expression initiates colonic tumorigenesis from cells outside the stem cell niche. Nature Medicine, 2015, 21, 62-70.	30.7	213
39	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	6.2	201
40	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	27.8	198
41	Cancer: Evolution Within a Lifetime. Annual Review of Genetics, 2014, 48, 215-236.	7.6	196
42	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	12.8	178
43	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
44	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	12.8	172
45	Prognostic and Predictive Biomarkers in Resected Colon Cancer: Current Status and Future Perspectives for Integrating Genomics into Biomarker Discovery. Oncologist, 2010, 15, 390-404.	3.7	155
46	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152
47	Mutations in DPC4 (SMAD4) cause juvenile polyposis syndrome, but only account for a minority of cases. Human Molecular Genetics, 1998, 7, 1907-1912.	2.9	142
48	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. Nature Genetics, 2011, 43, 451-454.	21.4	141
49	Relationship of Extreme Chromosomal Instability with Long-term Survival in a Retrospective Analysis of Primary Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 2183-2194.	2.5	141
50	Proportion and Phenotype of MYH-Associated Colorectal Neoplasia in a Population-Based Series of Finnish Colorectal Cancer Patients. American Journal of Pathology, 2003, 163, 827-832.	3.8	129
51	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.	10.7	129
52	Germline APC variants in patients with multiple colorectal adenomas, with evidence for the particular importance of E1317Q. Human Molecular Genetics, 2000, 9, 2215-2221.	2.9	125
53	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	21.4	125
54	Rare disruptive mutations and their contribution to the heritable risk of colorectal cancer. Nature Communications, 2016, 7, 11883.	12.8	122

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55	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
56	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.	8.4	118
57	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
58	Mutation Cluster Region, Association Between Germline and Somatic Mutations and Genotype-Phenotype Correlation in Upper Gastrointestinal Familial Adenomatous Polyposis. American Journal of Pathology, 2002, 160, 2055-2061.	3.8	111
59	How Many Mutations in a Cancer?. American Journal of Pathology, 2002, 160, 755-758.	3.8	110
60	Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. Cancer Research, 2011, 71, 6240-6249.	0.9	109
61	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
62	The mini-driver model of polygenic cancer evolution. Nature Reviews Cancer, 2015, 15, 680-685.	28.4	104
63	19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.9	100
64	Clinical management of hereditary colorectal cancer syndromes. Nature Reviews Gastroenterology and Hepatology, 2015, 12, 88-97.	17.8	99
65	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
66	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	6.2	98
67	The genetics of FAP and FAP-like syndromes. Familial Cancer, 2006, 5, 221-226.	1.9	97
68	Thyroid cancer susceptibility polymorphisms: confirmation of loci on chromosomes 9q22 and 14q13, validation of a recessive 8q24 locus and failure to replicate a locus on 5q24. Journal of Medical Genetics, 2012, 49, 158-163.	3.2	95
69	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.	3.2	94
70	Somatic Mutations in the Peutz-Jegners (LKB1/STKII) Gene in Sporadic Malignant Melanomas. Journal of Investigative Dermatology, 1999, 112, 509-511.	0.7	93
71	Polymorphisms Near TBX5 and GDF7 Are Associated With Increased Risk for Barrettâ€™s Esophagus. Gastroenterology, 2015, 148, 367-378.	1.3	93
72	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93

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73	Inherited susceptibility to colorectal adenomas and carcinomas: Evidence for a new predisposition gene on 15q14-q22. Gastroenterology, 1999, 116, 789-795.	1.3	92
74	Replicative DNA polymerase mutations in cancer. Current Opinion in Genetics and Development, 2014, 24, 107-113.	3.3	92
75	Allelic imbalance at theLKB1 (STK11) locus in tumours from patients with Peutz-Jeghers' syndrome provides evidence for a hamartoma-(adenoma)-carcinoma sequence. , 1999, 188, 9-13.		85
76	CDC4 Mutations Occur in a Subset of Colorectal Cancers but Are Not Predicted to Cause Loss of Function and Are Not Associated with Chromosomal Instability. Cancer Research, 2005, 65, 11361-11366.	0.9	85
77	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. Nature Genetics, 2021, 53, 1434-1442.	21.4	85
78	Use of multivariate analysis to suggest a new molecular classification of colorectal cancer. Journal of Pathology, 2013, 229, 441-448.	4.5	80
79	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
80	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	21.4	77
81	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	6.3	77
82	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.	6.2	76
83	Genetic Pathways of Colorectal Carcinogenesis Rarely Involve thePTEN and LKB1 Genes Outside the Inherited Hamartoma Syndromes. American Journal of Pathology, 1998, 153, 363-366.	3.8	75
84	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
85	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	12.8	75
86	Chromosomal Instability, Colorectal Cancer and Taxane Resistance. Cell Cycle, 2006, 5, 818-823.	2.6	73
87	Putative direct and indirect Wnt targets identified through consistent gene expression changes in APC-mutant intestinal adenomas from humans and mice. Human Molecular Genetics, 2008, 17, 3864-3875.	2.9	73
88	Associations of common variants at 1p11.2 and 14q24.1 (RAD51L1) with breast cancer risk and heterogeneity by tumor subtype: findings from the Breast Cancer Association Consortiumâ€. Human Molecular Genetics, 2011, 20, 4693-4706.	2.9	71
89	Multilevel genomics of colorectal cancers with microsatellite instabilityâ€”clinical impact of JAK1 mutations and consensus molecular subtype 1. Genome Medicine, 2017, 9, 46.	8.2	71
90	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.	4.5	71

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91	The multiple colorectal adenoma phenotype and MYH, a base excision repair gene. Clinical Gastroenterology and Hepatology, 2004, 2, 633-638.	4.4	69
92	An update on the genetics of colorectal cancer. Human Molecular Genetics, 2004, 13, R177-R185.	2.9	69
93	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
94	Genomic stability and tumorigenesis. Seminars in Cancer Biology, 2005, 15, 61-66.	9.6	64
95	Enrichment of Low Penetrance Susceptibility Loci in a Dutch Familial Colorectal Cancer Cohort. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 3062-3067.	2.5	64
96	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.	2.5	64
97	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	3.1	62
98	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	2.8	62
99	Severe polyposis in Apc^{1322T}mice is associated with submaximal Wnt signalling and increased expression of the stem cell markerLgr5. Gut, 2010, 59, 1680-1686.	12.1	60
100	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.	8.1	60
101	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.	6.2	59
102	In situ analysis ofLKB1/STK11 mRNA expression in human normal tissues and tumours. Journal of Pathology, 2000, 192, 203-206.	4.5	56
103	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
104	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
105	Refining Molecular Analysis in the Pathways of Colorectal Carcinogenesis. Clinical Gastroenterology and Hepatology, 2005, 3, 1115-1123.	4.4	55
106	The Apc1322T Mouse Develops Severe Polyposis Associated With Submaximal Nuclear Î²-Catenin Expression. Gastroenterology, 2009, 136, 2204-2213.e13.	1.3	55
107	APC mutations in FAP-associated desmoid tumours are non-random but not â€˜just rightâ€™. Human Molecular Genetics, 2007, 16, 78-82.	2.9	53
108	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	2.9	53

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109	Evidence for a colorectal cancer susceptibility locus on chromosome 3q21-q24 from a high-density SNP genome-wide linkage scan. Human Molecular Genetics, 2006, 15, 2903-2910.	2.9	52
110	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
111	Exploiting differential Wnt target gene expression to generate a molecular biomarker for colorectal cancer stratification. Gut, 2020, 69, 1092-1103.	12.1	52
112	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	5.1	51
113	Comparison of 6q25 Breast Cancer Hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). PLoS ONE, 2012, 7, e42380.	2.5	51
114	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	2.9	50
115	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
116	Rationale and design of the POLEM trial: avelumab plus fluoropyrimidine-based chemotherapy as adjuvant treatment for stage III mismatch repair deficient or POLE exonuclease domain mutant colon cancer: a phase III randomised study. ESMO Open, 2020, 5, e000638.	4.5	47
117	Oral rapamycin reduces tumour burden and vascularization in Lkb1^{+/â^'} mice. Journal of Pathology, 2009, 219, 35-40.	4.5	45
118	A Polymorphic Enhancer near GREM1 Influences Bowel Cancer Risk through Differential CDX2 and TCF7L2 Binding. Cell Reports, 2014, 8, 983-990.	6.4	45
119	POLE mutations in families predisposed to cutaneous melanoma. Familial Cancer, 2015, 14, 621-628.	1.9	43
120	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
121	Much of the Genetic Risk of Colorectal Cancer Is Likely to Be Mediated Through Susceptibility to Adenomas. Gastroenterology, 2013, 144, 53-55.	1.3	41
122	Tumour-infiltrating CD8+ lymphocytes and colorectal cancer recurrence by tumour and nodal stage. British Journal of Cancer, 2019, 121, 474-482.	6.4	41
123	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
124	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
125	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
126	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.	2.9	38

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127	Low penetrance breast cancer predisposition SNPs are site specific. Breast Cancer Research and Treatment, 2009, 117, 151-159.	2.5	37
128	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.	6.2	37
129	Colorectal Cancer Risk Is Not Associated with Increased Levels of Homozygosity in a Population from the United Kingdom. Cancer Research, 2009, 69, 7422-7429.	0.9	36
130	Bone morphogenetic protein and Notch signalling crosstalk in poorâ€prognosis, mesenchymalâ€subtype colorectal cancer. Journal of Pathology, 2017, 242, 178-192.	4.5	36
131	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	2.5	35
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.	3.3	35
133	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.	3.8	34
134	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.	1.3	34
135	The role of E-cadherin in low-grade ductal breast tumourigenesis. Journal of Pathology, 2003, 200, 53-58.	4.5	33
136	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.	2.9	33
137	A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46 450 cases and 42 461 controls from the breast cancer association consortium. Human Molecular Genetics, 2014, 23, 1934-1946.	2.9	32
138	A Common Variant at the 14q32 Endometrial Cancer Risk Locus Activates AKT1 through YY1 Binding. American Journal of Human Genetics, 2016, 98, 1159-1169.	6.2	32
139	Germline and Somatic Genetic Variants in the p53 Pathway Interact to Affect Cancer Risk, Progression, and Drug Response. Cancer Research, 2021, 81, 1667-1680.	0.9	32
140	Deciphering the genetics of hereditary non-syndromic colorectal cancer. European Journal of Human Genetics, 2008, 16, 1477-1486.	2.8	31
141	Common variation at the adiponectin locus is not associated with colorectal cancer risk in the UK. Human Molecular Genetics, 2009, 18, 1889-1892.	2.9	31
142	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.	1.8	31
143	The clinical features of polymerase proof-reading associated polyposis (PPAP) and recommendations for patient management. Familial Cancer, 2022, 21, 197-209.	1.9	31
144	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30

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145	'Toxgnostics': an unmet need in cancer medicine. Nature Reviews Cancer, 2014, 14, 440-445.	28.4	29
146	Serum- and Glucocorticoid-induced Kinase Sgk1 Directly Promotes the Differentiation of Colorectal Cancer Cells and Restrains Metastasis. Clinical Cancer Research, 2019, 25, 629-640.	7.0	28
147	General lessons from largeâ€scale studies to identify human cancer predisposition genes. Journal of Pathology, 2010, 220, 255-262.	4.5	27
148	Comprehensive assessment of variation at the transforming growth factor Î² type 1 receptor locus and colorectal cancer predisposition. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7858-7862.	7.1	26
149	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
150	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
151	FBXW7 mutations typically found in human cancers are distinct from null alleles and disrupt lung development. Journal of Pathology, 2011, 224, 180-189.	4.5	24
152	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.	7.0	24
153	CDC4/FBXW7 and the â€˜just enoughâ€™ model of tumourigenesis. Journal of Pathology, 2012, 227, 131-135.	4.5	21
154	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.	1.8	21
155	Systematic meta-analyses and field synopsis of genetic association studies in colorectal adenomas. International Journal of Epidemiology, 2016, 45, 186-205.	1.9	21
156	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.	3.3	19
157	The BRCA2 c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	2.5	19
158	A mitotic recombination map proximal to the APC locus on chromosome 5q and assessment of influences on colorectal cancer risk. BMC Medical Genetics, 2009, 10, 54.	2.1	18
159	9q31.2-rs865686 as a Susceptibility Locus for Estrogen Receptor-Positive Breast Cancer: Evidence from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1783-1791.	2.5	17
160	GREM1 germline mutation screening in Ashkenazi Jewish patients with familial colorectal cancer. Genetical Research, 2015, 97, e11.	0.9	17
161	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.	2.8	17
162	Genome-wide allelotyping of 104 Finnish colorectal cancers reveals an excess of allelic imbalance in chromosome 20q in familial cases. Oncogene, 2003, 22, 2206-2214.	5.9	16

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163	The Câ€terminus of Apc does not influence intestinal adenoma development or progression. Journal of Pathology, 2012, 226, 73-83.	4.5	16
164	The Mendelian colorectal cancer syndromes. Annals of Clinical Biochemistry, 2015, 52, 690-692.	1.6	16
165	The 8q24 rs6983267G variant is associated with increased thyroid cancer risk. Endocrine-Related Cancer, 2015, 22, 841-849.	3.1	16
166	The in Vivo Rate of Somatic Adenomatous Polyposis Coli Mutation. American Journal of Pathology, 2008, 172, 1062-1068.	3.8	14
167	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	5.0	14
168	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.	2.8	14
169	Cancer predisposition syndromes: lessons for truly precision medicine. Journal of Pathology, 2017, 241, 226-235.	4.5	13
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