Ian Tomlinson

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/11103583/publications.pdf

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	The clinical features of polymerase proof-reading associated polyposis (PPAP) and recommendations for patient management. Familial Cancer, 2022, 21, 197-209.	1.9	31
2	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	4.4	6
3	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.	6.4	5
4	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
5	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.	3.7	12
6	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.	3.5	8
7	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.	6.2	6
8	Non-Lynch Familial and Early-Onset Colorectal Cancer Explained by Accumulation of Low-Risk Genetic Variants. Cancers, 2021, 13, 3857.	3.7	8
9	Genetic mapping of novel modifiers for ApcMin induced intestinal polypsâ€™ development using the genetic architecture power of the collaborative cross mice. BMC Genomics, 2021, 22, 566.	2.8	8
10	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.	5.0	7
11	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	6.4	9
12	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. Nature Genetics, 2021, 53, 1434-1442.	21.4	85
13	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	3.3	2
14	Exploiting differential Wnt target gene expression to generate a molecular biomarker for colorectal cancer stratification. Gut, 2020, 69, 1092-1103.	12.1	52
15	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
16	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.	2.3	4
17	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
18	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

#	Article	IF	Citations
19	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	12.8	75
20	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
21	Deep learning for prediction of colorectal cancer outcome: a discovery and validation study. Lancet, The, 2020, 395, 350-360.	13.7	364
22	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
23	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
24	Tumour-infiltrating CD8+ lymphocytes and colorectal cancer recurrence by tumour and nodal stage. British Journal of Cancer, 2019, 121, 474-482.	6.4	41
25	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.	3.3	6
26	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	12.8	172
27	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
28	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	27.8	198
29	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
30	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
31	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
32	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
33	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
34	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.	6.4	11
35	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
36	Hereditary Mixed Polyposis Syndrome. , 2018, , 185-192.		1

#	Article	IF	Citations
37	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	12.8	178
38	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
39	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
40	British Society of Gastroenterology position statement on serrated polyps in the colon and rectum. Gut, 2017, 66, 1181-1196.	12.1	250
41	Bone morphogenetic protein and Notch signalling crosstalk in poorâ€prognosis, mesenchymalâ€subtype colorectal cancer. Journal of Pathology, 2017, 242, 178-192.	4.5	36
42	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
43	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
44	Evidence for genetic association between chromosome 1q loci and predisposition to colorectal neoplasia. British Journal of Cancer, 2017, 117, 1215-1223.	6.4	10
45	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
46	Cancer predisposition syndromes: lessons for truly precision medicine. Journal of Pathology, 2017, 241, 226-235.	4.5	13
47	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
48	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
49	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
50	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	2.5	12
51	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
52	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
53	Correspondence: SEMA4A variation and risk of colorectal cancer. Nature Communications, 2016, 7, 10611.	12.8	7
54	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43

#	Article	IF	Citations
55	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
56	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	21.4	77
57	The Hunting of the Snark: Whither Genome-Wide Association Studies for Colorectal Cancer?. Gastroenterology, 2016, 150, 1528-1530.	1.3	4
58	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
59	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
60	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
61	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
62	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.	1.6	7
63	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.	3.3	2
64	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
65	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
66	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
67	Rare disruptive mutations and their contribution to the heritable risk of colorectal cancer. Nature Communications, 2016, 7, 11883.	12.8	122
68	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
69	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
70	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152
71	A panoply of errors: polymerase proofreading domain mutations in cancer. Nature Reviews Cancer, 2016, 16, 71-81.	28.4	292
72	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	3.1	62

#	Article	IF	Citations
73	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
74	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
75	Hereditary Mixed Polyposis Syndrome. , 2016, , 165-171.		2
76	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.	3.8	8
77	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
78	Systematic meta-analyses and field synopsis of genetic association studies in colorectal adenomas. International Journal of Epidemiology, 2016, 45, 186-205.	1.9	21
79	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
80	GREM1 germline mutation screening in Ashkenazi Jewish patients with familial colorectal cancer. Genetical Research, 2015, 97, e11.	0.9	17
81	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
82	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
83	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.4	0
84	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
85	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
86	Polymorphisms Near TBX5 and GDF7 Are Associated With Increased Risk for Barrettâ€™s Esophagus. Gastroenterology, 2015, 148, 367-378.	1.3	93
87	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
88	Clinical management of hereditary colorectal cancer syndromes. Nature Reviews Gastroenterology and Hepatology, 2015, 12, 88-97.	17.8	99
89	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
90	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

#	Article	IF	Citations
91	An update on the molecular pathology of the intestinal polyposis syndromes. Diagnostic Histopathology, 2015, 21, 147-151.	0.4	1
92	POLE mutations in families predisposed to cutaneous melanoma. Familial Cancer, 2015, 14, 621-628.	1.9	43
93	The Mendelian colorectal cancer syndromes. Annals of Clinical Biochemistry, 2015, 52, 690-692.	1.6	16
94	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
95	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
96	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
97	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726.	21.4	310
98	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
99	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
100	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
101	The mini-driver model of polygenic cancer evolution. Nature Reviews Cancer, 2015, 15, 680-685.	28.4	104
102	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
103	The 8q24 rs6983267G variant is associated with increased thyroid cancer risk. Endocrine-Related Cancer, 2015, 22, 841-849.	3.1	16
104	Aberrant epithelial GREM1 expression initiates colonic tumorigenesis from cells outside the stem cell niche. Nature Medicine, 2015, 21, 62-70.	30.7	213
105	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
106	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
107	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
108	Colorectal Tumors from APC*I1307K Carriers Principally Harbor Somatic APC Mutations outside the A8 Tract. PLoS ONE, 2014, 9, e84498.	2.5	9

#	Article	IF	Citations
109	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
110	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
111	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
112	Replicative DNA polymerase mutations in cancer. Current Opinion in Genetics and Development, 2014, 24, 107-113.	3.3	92
113	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
114	'Toxgnostics': an unmet need in cancer medicine. Nature Reviews Cancer, 2014, 14, 440-445.	28.4	29
115	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
116	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
117	Cancer: Evolution Within a Lifetime. Annual Review of Genetics, 2014, 48, 215-236.	7.6	196
118	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
119	Re: Role of the Oxidative DNA Damage Repair Gene OGG1 in Colorectal Tumorigenesis. Journal of the National Cancer Institute, 2014, 106, .	6.3	9
120	A Polymorphic Enhancer near GREM1 Influences Bowel Cancer Risk through Differential CDX2 and TCF7L2 Binding. Cell Reports, 2014, 8, 983-990.	6.4	45
121	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
122	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
123	Reply to "The classification of intestinal polyposis". Nature Genetics, 2013, 45, 2-3.	21.4	8
124	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
125	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
126	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

#	Article	IF	Citations
127	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
128	Use of multivariate analysis to suggest a new molecular classification of colorectal cancer. Journal of Pathology, 2013, 229, 441-448.	4.5	80
129	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
130	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
131	Genome-wide association studies identify four ER negativeâ€"specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
132	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
133	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
134	Germline Variants and Advanced Colorectal Adenomas: Adenoma Prevention with Celecoxib Trial Genome-wide Association Study. Clinical Cancer Research, 2013, 19, 6430-6437.	7.0	9
135	Genome-Wide Association Studies in Colorectal Cancer. , 2013, , 289-302.		0
136	19p13.1 Is a Triple-Negativeâ€"Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.9	100
137	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
138	The Utility of Mouse Models in Post-GWAS Research. Science, 2012, 338, 1301-1302.	12.6	6
139	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
140	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	256
141	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
142	The Câ€terminus of Apc does not influence intestinal adenoma development or progression. Journal of Pathology, 2012, 226, 73-83.	4.5	16
143	CDC4/FBXW7 and the â€˜just enoughâ€™ model of tumourigenesis. Journal of Pathology, 2012, 227, 131-135.	4.5	21
144	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	2.5	35

#	Article	IF	Citations
145	The Continuum Model of Selection in Human Tumors: General Paradigm or Niche Product?. Cancer Research, 2012, 72, 3131-3134.	0.9	9
146	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
147	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
148	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. Nature Genetics, 2011, 43, 451-454.	21.4	141
149	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
150	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
151	Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. Cancer Research, 2011, 71, 6240-6249.	0.9	109
152	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
153	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
154	General lessons from largeâ€scale studies to identify human cancer predisposition genes. Journal of Pathology, 2010, 220, 255-262.	4.5	27
155	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	21.4	235
156	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	21.4	321
157	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
158	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
159	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
160	Cancer Genetics. , 2010, , 451-470.		0
161	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
162	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

#	Article	IF	Citations
163	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
164	Low penetrance breast cancer predisposition SNPs are site specific. Breast Cancer Research and Treatment, 2009, 117, 151-159.	2.5	37
165	Oral rapamycin reduces tumour burden and vascularization in Lkb1^{+/â^'} mice. Journal of Pathology, 2009, 219, 35-40.	4.5	45
166	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
167	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
168	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
169	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	21.4	276
170	Genetic prognostic and predictive markers in colorectal cancer. Nature Reviews Cancer, 2009, 9, 489-499.	28.4	602
171	The Apc1322T Mouse Develops Severe Polyposis Associated With Submaximal Nuclear Î²-Catenin Expression. Gastroenterology, 2009, 136, 2204-2213.e13.	1.3	55
172	Deciphering the genetics of hereditary non-syndromic colorectal cancer. European Journal of Human Genetics, 2008, 16, 1477-1486.	2.8	31
173	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
174	The in Vivo Rate of Somatic Adenomatous Polyposis Coli Mutation. American Journal of Pathology, 2008, 172, 1062-1068.	3.8	14
175	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
176	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
177	Pregnancy does not influence colonic polyp multiplicity but may modulate upper gastrointestinal disease in patients with FAP. Journal of Medical Genetics, 2007, 44, 541-544.	3.2	1
178	A genome-wide association study shows that common alleles of SMAD7 influence colorectal cancer risk. Nature Genetics, 2007, 39, 1315-1317.	21.4	463
179	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
180	Chromosomal Instability, Colorectal Cancer and Taxane Resistance. Cell Cycle, 2006, 5, 818-823.	2.6	73

#	Article	IF	Citations
181	The genetics of FAP and FAP-like syndromes. Familial Cancer, 2006, 5, 221-226.	1.9	97
182	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
183	Genomic stability and tumorigenesis. Seminars in Cancer Biology, 2005, 15, 61-66.	9.6	64
184	Sequence changes in predicted promoter elements of STK11/LKB1 are unlikely to contribute to Peutz-Jeghers syndrome. BMC Genomics, 2005, 6, 38.	2.8	12
185	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
186	Refining Molecular Analysis in the Pathways of Colorectal Carcinogenesis. Clinical Gastroenterology and Hepatology, 2005, 3, 1115-1123.	4.4	55
187	The multiple colorectal adenoma phenotype and MYH, a base excision repair gene. Clinical Gastroenterology and Hepatology, 2004, 2, 633-638.	4.4	69
188	An update on the genetics of colorectal cancer. Human Molecular Genetics, 2004, 13, R177-R185.	2.9	69
189	Colorectal tumourigenesis in carriers of theAPC I1307K variant: lone gunman or conspiracy?. Journal of Pathology, 2003, 199, 137-139.	4.5	11
190	The role of E-cadherin in low-grade ductal breast tumourigenesis. Journal of Pathology, 2003, 200, 53-58.	4.5	33
191	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
192	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
193	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
194	How Many Mutations in a Cancer?. American Journal of Pathology, 2002, 160, 755-758.	3.8	110
195	Is EXO1 a colon cancer predisposition gene?. Gastroenterology, 2001, 120, 1860-1861.	1.3	5
196	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
197	In situ analysis ofLKB1/STK11 mRNA expression in human normal tissues and tumours. Journal of Pathology, 2000, 192, 203-206.	4.5	56
198	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

#	Article	IF	Citations
199	Different Pathways of Colorectal Carcinogenesis and Their Clinical Pictures. Annals of the New York Academy of Sciences, 2000, 910, 10-20.	3.8	3
200	Somatic Mutations in the Peutz-Jegners (LKB1/STKII) Gene in Sporadic Malignant Melanomas. Journal of Investigative Dermatology, 1999, 112, 509-511.	0.7	93
201	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
202	Selection, the mutation rate and cancer: Ensuring that the tail does not wag the dog. Nature Medicine, 1999, 5, 11-12.	30.7	289
203	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
204	Inherited susceptibility to colorectal adenomas and carcinomas: Evidence for a new predisposition gene on 15q14-q22. Gastroenterology, 1999, 116, 789-795.	1.3	92
205	A serine/threonine kinase gene defective in Peutzâ€"Jeghers syndrome. Nature, 1998, 391, 184-187.	27.8	1,451
206	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
207	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
208	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