D Timothy Bishop

List of Publications by Year
in descending order

304 papers	32,854 citations	4641 85 h-index	4419 172 g-index
319 all docs	319 docs citations	319 times ranked	26921 citing authors

#	Article	IF	Citations
1	Multi-Trait Genetic Analysis Identifies Autoimmune Loci Associated with Cutaneous Melanoma. Journal of Investigative Dermatology, 2022, 142, 1607-1616.	0.3	11
2	Ulcerated melanoma: Systems biology evidence of inflammatory imbalance towards proâ€tumourigenicity. Pigment Cell and Melanoma Research, 2022, 35, 252-267.	1.5	4
3	The Different Immune Profiles of Normal Colonic Mucosa in Cancer-Free Lynch Syndrome Carriers and Lynch Syndrome Colorectal Cancer Patients. Gastroenterology, 2022, 162, 907-919.e10.	0.6	27
4	Risk Stratification for Early-Onset Colorectal Cancer Using a Combination of Genetic and Environmental Risk Scores: An International Multi-Center Study. Journal of the National Cancer Institute, 2022, , .	3.0	15
5	Dual modality of vertebral body tethering. Bone & Joint Open, 2022, 3, 123-129.	1.1	12
6	Independent evaluation of melanoma polygenic risk scores in <scp>UK</scp> and Australian prospective cohorts*. British Journal of Dermatology, 2022, 186, 823-834.	1.4	10
7	Defining novel causal SNPs and linked phenotypes at melanoma-associated loci. Human Molecular Genetics, 2022, 31, 2845-2856.	1.4	3
8	Beyond GWAS of Colorectal Cancer: Evidence of Interaction with Alcohol Consumption and Putative Causal Variant for the 10q24.2 Region. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1077-1089.	1.1	6
9	OUP accepted manuscript. Journal of the National Cancer Institute, 2022, , .	3.0	0
10	Association Study between Polymorphisms in DNA Methylationâ€“Related Genes and Testicular Germ Cell Tumor Risk. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1769-1779.	1.1	4
11	Common Susceptibility Loci for Male Breast Cancer. Journal of the National Cancer Institute, 2021, 113, 453-461.	3.0	12
12	Circulating adipokine concentrations and risk of five obesityâ€related cancers: A Mendelian randomization study. International Journal of Cancer, 2021, 148, 1625-1636.	2.3	29
13	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. Gastroenterology, 2021, 160, 1164-1178.e6.	0.6	36
14	Genetically predicted circulating concentrations of micronutrients and risk of colorectal cancer among individuals of European descent: a Mendelian randomization study. American Journal of Clinical Nutrition, 2021, 113, 1490-1502.	2.2	27
15	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334.	6.1	44
16	Response to Li and Hopper. American Journal of Human Genetics, 2021, 108, 527-529.	2.6	5
17	Circulating Levels of Testosterone, Sex Hormone Binding Globulin and Colorectal Cancer Risk: Observational and Mendelian Randomization Analyses. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1336-1348.	1.1	15
18	Birth cohort-specific trends of sun-related behaviors among individuals from an international consortium of melanoma-prone families. BMC Public Health, 2021, 21, 692.	1.2	4

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19	Nongenetic Determinants of Risk forÂEarly-Onset Colorectal Cancer. JNCI Cancer Spectrum, 2021, 5, pkab029.	1.4	39
20	Identification of 22 susceptibility loci associated with testicular germ cell tumors. Nature Communications, 2021, 12, 4487.	5.8	27
21	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. Human Genetics and Genomics Advances, 2021, 2, 100041.	1.0	6
22	Cell-type-specific meQTLs extend melanoma GWAS annotation beyond eQTLs and inform melanocyte gene-regulatory mechanisms. American Journal of Human Genetics, 2021, 108, 1631-1646.	2.6	12
23	Tumour gene expression signature in primary melanoma predicts long-term outcomes. Nature Communications, 2021, 12, 1137.	5.8	33
24	A Combined Proteomics and Mendelian Randomization Approach to Investigate the Effects of Aspirin-Targeted Proteins on Colorectal Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 564-575.	1.1	10
25	An Overview of Strategies for Detecting Genotype-Phenotype Associations Across Ancestrally Diverse Populations. Frontiers in Genetics, 2021, 12, 703901.	1.1	13
26	Salicylic Acid and Risk of Colorectal Cancer: A Two-Sample Mendelian Randomization Study. Nutrients, 2021, 13, 4164.	1.7	3
27	Environmental Exposures Such as Smoking and Low Vitamin D Are Predictive of Poor Outcome in Cutaneous Melanoma rather than Other Deprivation Measures. Journal of Investigative Dermatology, 2020, 140, 327-337.e2.	0.3	14
28	Chris Cannings: A Life in Games. Dynamic Games and Applications, 2020, 10, 591-617.	1.1	1
29	Cumulative Burden of Colorectal Cancerâ€“Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. Gastroenterology, 2020, 158, 1274-1286.e12.	0.6	110
30	Circulating Levels of Insulin-like Growth Factor 1 and Insulin-like Growth Factor Binding Protein 3 Associate With Risk of Colorectal Cancer Based on Serologic and Mendelian Randomization Analyses. Gastroenterology, 2020, 158, 1300-1312.e20.	0.6	90
31	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. American Journal of Human Genetics, 2020, 107, 432-444.	2.6	124
32	Adiposity, metabolites, and colorectal cancer risk: Mendelian randomization study. BMC Medicine, 2020, 18, 396.	2.3	76
33	Hemochromatosis risk genotype is not associated with colorectal cancer or age at its diagnosis. Human Genetics and Genomics Advances, 2020, 1, 100010.	1.0	3
34	Cancer prevention with aspirin in hereditary colorectal cancer (Lynch syndrome), 10-year follow-up and registry-based 20-year data in the CAPP2 study: a double-blind, randomised, placebo-controlled trial. Lancet, The, 2020, 395, 1855-1863.	6.3	220
35	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	5.8	75
36	Systematic meta-analyses, field synopsis and global assessment of the evidence of genetic association studies in colorectal cancer. Gut, 2020, 69, 1460-1471.	6.1	27

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37	Spinal-Pelvic Dissociation in Pregnancy: Surgical Fixation of Culture-Negative Extrapulmonary Tuberculosis. Case Reports in Orthopedics, 2020, 2020, 1-7.	0.1	0
38	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. Nature Genetics, 2020, 52, 494-504.	9.4	138
39	Physical activity and risks of breast and colorectal cancer: a Mendelian randomisation analysis. Nature Communications, 2020, 11, 597.	5.8	193
40	Melanoma Genomics. Acta Dermato-Venereologica, 2020, 100, adv00138.	0.6	11
41	Estimating CDKN2A mutation carrier probability among global familial melanoma cases using GenoMELPREDICT. Journal of the American Academy of Dermatology, 2019, 81, 386-394.	0.6	17
42	Transcriptomic Analysis Reveals Prognostic Molecular Signatures of Stage I Melanoma. Clinical Cancer Research, 2019, 25, 7424-7435.	3.2	27
43	High-Resolution Copy Number Patterns From Clinically Relevant FFPE Material. Scientific Reports, 2019, 9, 8908.	1.6	6
44	Genetic and Environmental Determinants of Immune Response to Cutaneous Melanoma. Cancer Research, 2019, 79, 2684-2696.	0.4	45
45	Vitamin Dâ€“VDR Signaling Inhibits Wnt/Î²-Cateninâ€“Mediated Melanoma Progression and Promotes Antitumor Immunity. Cancer Research, 2019, 79, 5986-5998.	0.4	65
46	Association of the POT1 Germline Missense Variant p.I78T With Familial Melanoma. JAMA Dermatology, 2019, 155, 604.	2.0	34
47	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377
48	The Feasibility of a Health Care Application in the Treatment of Patients Undergoing Radical Cystectomy. Journal of Urology, 2019, 201, 902-908.	0.2	25
49	Large-scale Sequencing of Testicular Germ Cell Tumour (TGCT) Cases Excludes Major TGCT Predisposition Gene. European Urology, 2018, 73, 828-831.	0.9	54
50	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	5.8	87
51	Cell-typeâ€specific eQTL of primary melanocytes facilitates identification of melanoma susceptibility genes. Genome Research, 2018, 28, 1621-1635.	2.4	67
52	Combining common genetic variants and non-genetic risk factors to predict risk of cutaneous melanoma. Human Molecular Genetics, 2018, 27, 4145-4156.	1.4	34
53	Assessing the Incremental Contribution of Common Genomic Variants to Melanoma Risk Prediction in Two Population-Based Studies. Journal of Investigative Dermatology, 2018, 138, 2617-2624.	0.3	52
54	Interaction between polymorphisms in aspirin metabolic pathways, regular aspirin use and colorectal cancer risk: A case-control study in unselected white European populations. PLoS ONE, 2018, 13, e0192223.	1.1	5

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55	Î²-Cateninâ€“mediated immune evasion pathway frequently operates in primary cutaneous melanomas. Journal of Clinical Investigation, 2018, 128, 2048-2063.	3.9	71
56	Abstract 5205: Primary melanoma expression of the vitamin D receptor (VDR) is protective for melanoma survival and is associated with increased tumor immune response, decreased Wnt/B-catenin signaling and tumor proliferation. , 2018, , .		0
57	A population-based analysis of germline BAP1 mutations in melanoma. Human Molecular Genetics, 2017, 26, ddw403.	1.4	31
58	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. Nature Communications, 2017, 8, 15034.	5.8	40
59	Meta-analysis of five genome-wide association studies identifies multiple new loci associated with testicular germ cell tumor. Nature Genetics, 2017, 49, 1141-1147.	9.4	105
60	Identification of 19 new risk loci and potential regulatory mechanisms influencing susceptibility to testicular germ cell tumor. Nature Genetics, 2017, 49, 1133-1140.	9.4	120
61	Rare Variant, Gene-Based Association Study of Hereditary Melanoma Using Whole-Exome Sequencing. Journal of the National Cancer Institute, 2017, 109, .	3.0	32
62	Design Considerations for Genetic Linkage and Association Studies. Methods in Molecular Biology, 2017, 1666, 257-281.	0.4	12
63	Germline Variation at CDKN2A and Associations with Nevus Phenotypes amongÂMembers of Melanoma Families. Journal of Investigative Dermatology, 2017, 137, 2606-2612.	0.3	18
64	A common intronic variant of PARP1 confers melanoma risk and mediates melanocyte growth via regulation of MITF. Nature Genetics, 2017, 49, 1326-1335.	9.4	51
65	Identification of a gene signature for discriminating metastatic from primary melanoma using a molecular interaction network approach. Scientific Reports, 2017, 7, 17314.	1.6	32
66	Constraints on the Progenitor of SN 2016gkg from Its Shock-cooling Light Curve. Astrophysical Journal Letters, 2017, 837, L2.	3.0	49
67	Abstract 1741: Whole-transcriptome characterisation ofNRASandBRAFmutated primary melanomas associated with immune cell infiltration signatures and differential survival benefit. , 2017, , .		0
68	Psychosocial, clinical and demographic features related to worry in patients with melanoma. Melanoma Research, 2016, 26, 497-504.	0.6	8
69	Germline MC1R status influences somatic mutation burden in melanoma. Nature Communications, 2016, 7, 12064.	5.8	103
70	Rare disruptive mutations in ciliary function genes contribute to testicular cancer susceptibility. Nature Communications, 2016, 7, 13840.	5.8	32
71	Correspondence: SEMA4A variation and risk of colorectal cancer. Nature Communications, 2016, 7, 10611.	5.8	7
72	Rare disruptive mutations and their contribution to the heritable risk of colorectal cancer. Nature Communications, 2016, 7, 11883.	5.8	122

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73	Development and External Validation of a Melanoma Risk Prediction Model Based on Self-assessed Risk Factors. JAMA Dermatology, 2016, 152, 889.	2.0	53
74	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
75	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. Human Molecular Genetics, 2016, 25, 1203-1214.	1.4	38
76	Phenotypic and Histopathological Tumor Characteristics According to CDKN2A Mutation Status among Affected Members ofÂMelanoma Families. Journal of Investigative Dermatology, 2016, 136, 1066-1069.	0.3	13
77	Loss-of-Function Mutations in the Cell-Cycle Control Gene CDKN2A Impact on Glucose Homeostasis in Humans. Diabetes, 2016, 65, 527-533.	0.3	38
78	Germline TERT promoter mutations are rare in familial melanoma. Familial Cancer, 2016, 15, 139-144.	0.9	51
79	25â€Hydroxyvitamin D₂/D₃ levels and factors associated with systemic inflammation and melanoma survival in the Leeds Melanoma Cohort. International Journal of Cancer, 2015, 136, 2890-2899.	2.3	61
80	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. Scientific Reports, 2015, 5, 16286.	1.6	24
81	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.	1.1	10
82	Response. Journal of the National Cancer Institute, 2015, 107, djv238.	3.0	0
83	Development and Validation of a Melanoma Risk Score Based on Pooled Data from 16 Caseâ€“Control Studies. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 817-824.	1.1	25
84	Nonsense Mutations in the Shelterin Complex Genes ACD and TERF2IP in Familial Melanoma. Journal of the National Cancer Institute, 2015, 107, .	3.0	134
85	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	9.4	218
86	Multi-stage genome-wide association study identifies new susceptibility locus for testicular germ cell tumour on chromosome 3q25. Human Molecular Genetics, 2015, 24, 1169-1176.	1.4	31
87	Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. Lancet Diabetes and Endocrinology,the, 2015, 3, 243-253.	5.5	115
88	Fine mapping of genetic susceptibility loci for melanoma reveals a mixture of single variant and multiple variant regions. International Journal of Cancer, 2015, 136, 1351-1360.	2.3	30
89	Identification of four new susceptibility loci for testicular germ cell tumour. Nature Communications, 2015, 6, 8690.	5.8	36
90	Obesity, Aspirin, and Risk of Colorectal Cancer in Carriers of Hereditary Colorectal Cancer: A Prospective Investigation in the CAPP2 Study. Journal of Clinical Oncology, 2015, 33, 3591-3597.	0.8	91

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91	Independent replication of a melanoma subtype gene signature and evaluation of its prognostic value and biological correlates in a population cohort. Oncotarget, 2015, 6, 11683-11693.	0.8	44
92	Colorectal Tumors from APC*I1307K Carriers Principally Harbor Somatic APC Mutations outside the A8 Tract. PLoS ONE, 2014, 9, e84498.	1.1	9
93	Identification of a melanoma susceptibility locus and somatic mutation inTET2. Carcinogenesis, 2014, 35, 2097-2101.	1.3	41
94	Inherited variation in the PARP1 gene and survival from melanoma. International Journal of Cancer, 2014, 135, 1625-1633.	2.3	24
95	Next-generation sequencing identifies germline MRE11A variants as markers of radiotherapy outcomes in muscle-invasive bladder cancer. Annals of Oncology, 2014, 25, 877-883.	0.6	41
96	An inherited variant in the gene coding for vitamin <scp>D</scp>â€binding protein and survival from cutaneous melanoma: a <scp>B</scp>io<scp>G</scp>eno<scp>MEL</scp> study. Pigment Cell and Melanoma Research, 2014, 27, 234-243.	1.5	25
97	Prevalence and predictors of germline CDKN2A mutations for melanoma cases from Australia, Spain and the United Kingdom. Hereditary Cancer in Clinical Practice, 2014, 12, 20.	0.6	45
98	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	3.0	109
99	POT1 loss-of-function variants predispose to familial melanoma. Nature Genetics, 2014, 46, 478-481.	9.4	319
100	Genome-wide association study yields variants at 20p12.2 that associate with urinary bladder cancer. Human Molecular Genetics, 2014, 23, 5545-5557.	1.4	46
101	Re: Role of the Oxidative DNA Damage Repair Gene OGG1 in Colorectal Tumorigenesis. Journal of the National Cancer Institute, 2014, 106, .	3.0	9
102	Point of care testing for improving risk- benefit ratio of aspirin and warfarin. Molecular Cytogenetics, 2014, 7, I54.	0.4	0
103	Abstract 20: POT1 mutations predispose to familial melanoma. , 2014, , .		0
104	Chemoprevention in Lynch syndrome. Familial Cancer, 2013, 12, 707-718.	0.9	57
105	Testicular germ cell tumor susceptibility associated with the UCK2 locus on chromosome 1q23. Human Molecular Genetics, 2013, 22, 2748-2753.	1.4	59
106	MC1Rgenotype as a predictor of early-onset melanoma, compared with self-reported and physician-measured traditional risk factors: an Australian case-control-family study. BMC Cancer, 2013, 13, 406.	1.1	30
107	Do vitamin A serum levels moderate outcome or the protective effect of vitamin DÂon outcome from malignant melanoma?. Clinical Nutrition, 2013, 32, 1012-1016.	2.3	7
108	A variant in FTO shows association with melanoma risk not due to BMI. Nature Genetics, 2013, 45, 428-432.	9.4	111

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109	A retrospective observational study of the relationship between family history and survival from colorectal cancer. British Journal of Cancer, 2013, 108, 1502-1507.	2.9	27
110	Meta-analysis identifies four new loci associated with testicular germ cell tumor. Nature Genetics, 2013, 45, 680-685.	9.4	154
111	Association between putative functional variants in the <scp>PSMB</scp>9 gene and risk of melanoma â€“ reâ€analysis of published melanoma genomeâ€wide association studies. Pigment Cell and Melanoma Research, 2013, 26, 392-401.	1.5	5
112	Identification of nine new susceptibility loci for testicular cancer, including variants near DAZL and PRDM14. Nature Genetics, 2013, 45, 686-689.	9.4	149
113	Association between functional polymorphisms in genes involved in the MAPK signaling pathways and cutaneous melanoma risk. Carcinogenesis, 2013, 34, 885-892.	1.3	10
114	Reduced type II interleukin-4 receptor signalling drives initiation, but not progression, of colorectal carcinogenesis: evidence from transgenic mouse models and human caseâ€“control epidemiological observations. Carcinogenesis, 2013, 34, 2341-2349.	1.3	20
115	Response to P. Autier and M. Boniol regarding our article-Relationship between sunbed use and melanoma risk in a large case-control study in the United Kingdom. International Journal of Cancer, 2013, 132, 1960-1961.	2.3	1
116	Vitamin D and melanoma. Dermato-Endocrinology, 2013, 5, 121-129.	1.9	28
117	The role of microRNA-binding site polymorphisms in DNA repair genes as risk factors for bladder cancer and breast cancer and their impact on radiotherapy outcomes. Carcinogenesis, 2012, 33, 581-586.	1.3	103
118	People of the British Isles: preliminary analysis of genotypes and surnames in a UK-control population. European Journal of Human Genetics, 2012, 20, 203-210.	1.4	126
119	Genome-wide association study identifies a common variant in RAD51B associated with male breast cancer risk. Nature Genetics, 2012, 44, 1182-1184.	9.4	99
120	Inherited variants in the MC1R gene and survival from cutaneous melanoma: a BioGenoMEL study. Pigment Cell and Melanoma Research, 2012, 25, 384-394.	1.5	61
121	Design Considerations for Genetic Linkage and Association Studies. Methods in Molecular Biology, 2012, 850, 237-262.	0.4	21
122	Long-term effect of resistant starch on cancer risk in carriers of hereditary colorectal cancer: an analysis from the CAPP2 randomised controlled trial. Lancet Oncology, The, 2012, 13, 1242-1249.	5.1	95
123	Colorectal Cancer Linkage on Chromosomes 4q21, 8q13, 12q24, and 15q22. PLoS ONE, 2012, 7, e38175.	1.1	24
124	Relationship between sunbed use and melanoma risk in a large caseâ€control study in the United Kingdom. International Journal of Cancer, 2012, 130, 3011-3013.	2.3	17
125	RHBDF2 Mutations Are Associated with Tylosis, a Familial Esophageal Cancer Syndrome. American Journal of Human Genetics, 2012, 90, 340-346.	2.6	162
126	Ki-rasgene mutations are invariably present in low-grade mucinous tumors of the vermiform appendix. Scandinavian Journal of Gastroenterology, 2011, 46, 869-874.	0.6	47

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127	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	9.4	230
128	Relationship between sun exposure and melanoma risk for tumours in different body sites in a large case-control study in a temperate climate. European Journal of Cancer, 2011, 47, 732-741.	1.3	90
129	Long-term effect of aspirin on cancer risk in carriers of hereditary colorectal cancer: an analysis from the CAPP2 randomised controlled trial. Lancet, The, 2011, 378, 2081-2087.	6.3	849
130	Pathway-Based Analysis of a Melanoma Genome-Wide Association Study: Analysis of Genes Related to Tumour-Immunosuppression. PLoS ONE, 2011, 6, e29451.	1.1	18
131	The determinants of periorbital skin ageing in participants of a melanoma caseâ€“control study in the U.K.. British Journal of Dermatology, 2011, 165, 1011-1021.	1.4	17
132	The determinants of serum vitamin D levels in participants in a melanoma caseâ€“control study living in a temperate climate. Cancer Causes and Control, 2011, 22, 1471-1482.	0.8	32
133	Functional assays to determine the significance of two common XPC 3'UTR variants found in bladder cancer patients. BMC Medical Genetics, 2011, 12, 84.	2.1	3
134	Melanoma risk for CDKN2A mutation carriers who are relatives of population-based case carriers in Australia and the UK. Journal of Medical Genetics, 2011, 48, 266-272.	1.5	41
135	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. Nature, 2011, 480, 99-103.	13.7	413
136	A Randomized Placebo-Controlled Prevention Trial of Aspirin and/or Resistant Starch in Young People with Familial Adenomatous Polyposis. Cancer Prevention Research, 2011, 4, 655-665.	0.7	193
137	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	9.4	140
138	European genome-wide association study identifies SLC14A1 as a new urinary bladder cancer susceptibility gene. Human Molecular Genetics, 2011, 20, 4268-4281.	1.4	134
139	Polymorphisms in xenobiotic metabolizing enzymes and diet influence colorectal adenoma risk. Pharmacogenetics and Genomics, 2010, 20, 315-326.	0.7	42
140	IRF4 Variants Have Age-Specific Effects on Nevus Count and Predispose to Melanoma. American Journal of Human Genetics, 2010, 87, 6-16.	2.6	114
141	An evaluation of inflammatory gene polymorphisms in sibships discordant for premature coronary artery disease: the GRACE-IMMUNE study. BMC Medicine, 2010, 8, 5.	2.3	15
142	Deletion at chromosome arm 9p in relation to BRAF/NRAS mutations and prognostic significance for primary melanoma. Genes Chromosomes and Cancer, 2010, 49, 425-438.	1.5	46
143	MLH1 Differential Allelic Expression in Mutation Carriers and Controls. Annals of Human Genetics, 2010, 74, 479-488.	0.3	12
144	A sequence variant at 4p16.3 confers susceptibility to urinary bladder cancer. Nature Genetics, 2010, 42, 415-419.	9.4	169

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145	Variants near DMRT1, TERT and ATF7IP are associated with testicular germ cell cancer. Nature Genetics, 2010, 42, 604-607.	9.4	320
146	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. Nature Genetics, 2010, 42, 978-984.	9.4	493
147	Patterns of Expression of DNA Repair Genes and Relapse From Melanoma. Clinical Cancer Research, 2010, 16, 5211-5221.	3.2	53
148	MRE11 Expression Is Predictive of Cause-Specific Survival following Radical Radiotherapy for Muscle-Invasive Bladder Cancer. Cancer Research, 2010, 70, 7017-7026.	0.4	184
149	Melanocytic Nevi, Nevus Genes, and Melanoma Risk in a Large Case-Control Study in the United Kingdom. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2043-2054.	1.1	102
150	Reply to P.E. Hutchinson et al. Journal of Clinical Oncology, 2010, 28, e494-e495.	0.8	0
151	The International Testicular Cancer Linkage Consortium: A clinicopathologic descriptive analysis of 461 familial malignant testicular germ cell tumor kindred. Urologic Oncology: Seminars and Original Investigations, 2010, 28, 492-499.	0.8	42
152	Melanoma sentinel node biopsy and prediction models for relapse and overall survival. British Journal of Cancer, 2010, 103, 1229-1236.	2.9	54
153	The Association of Tumor Microsatellite Instability Phenotype with Family History of Colorectal Cancer. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 967-975.	1.1	26
154	Sun exposure and melanoma risk at different latitudes: a pooled analysis of 5700 cases and 7216 controls. International Journal of Epidemiology, 2009, 38, 814-830.	0.9	219
155	Polymorphisms in DNA Repair Genes, Smoking, and Bladder Cancer Risk: Findings from the International Consortium of Bladder Cancer. Cancer Research, 2009, 69, 6857-6864.	0.4	107
156	Genetic Variants inXRCC2: New Insights Into Colorectal Cancer Tumorigenesis. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2476-2484.	1.1	38
157	Gene Expression Profiling of Paraffin-Embedded Primary Melanoma Using the DASL Assay Identifies Increased Osteopontin Expression as Predictive of Reduced Relapse-Free Survival. Clinical Cancer Research, 2009, 15, 6939-6946.	3.2	93
158	Serum 25-Hydroxyvitamin D₃ Levels Are Associated With Breslow Thickness at Presentation and Survival From Melanoma. Journal of Clinical Oncology, 2009, 27, 5439-5444.	0.8	263
159	Meta Association of Colorectal Cancer Confirms Risk Alleles at 8q24 and 18q21. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 616-621.	1.1	71
160	Meta- and Pooled Analyses of the Methylenetetrahydrofolate Reductase (MTHFR) C677T Polymorphism and Colorectal Cancer: A HuGE-GSEC Review. American Journal of Epidemiology, 2009, 170, 1207-1221.	1.6	91
161	A pooled analysis of melanocytic nevus phenotype and the risk of cutaneous melanoma at different latitudes. International Journal of Cancer, 2009, 124, 420-428.	2.3	84
162	Younger age-at-diagnosis for familial malignant testicular germ cell tumor. Familial Cancer, 2009, 8, 451-456.	0.9	21

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163	Overseas Sun Exposure, Nevus Counts, and Premature Skin Aging in Young English Women: A Population-Based Survey. Journal of Investigative Dermatology, 2009, 129, 50-59.	0.3	40
164	Sequence variants at the TERT-CLPTM1L locus associate with many cancer types. Nature Genetics, 2009, 41, 221-227.	9.4	572
165	A genome-wide association study of testicular germ cell tumor. Nature Genetics, 2009, 41, 807-810.	9.4	317
166	Genome-wide association study identifies variants at 9p21 and 22q13 associated with development of cutaneous nevi. Nature Genetics, 2009, 41, 915-919.	9.4	204
167	Genome-wide association study identifies three loci associated with melanoma risk. Nature Genetics, 2009, 41, 920-925.	9.4	422
168	Genetic variation in the prostate stem cell antigen gene PSCA confers susceptibility to urinary bladder cancer. Nature Genetics, 2009, 41, 991-995.	9.4	321
169	Molecular Genetic Changes Associated With Colorectal Carcinogenesis Are Not Prognostic for Tumor Regression Following Preoperative Chemoradiation of Rectal Carcinoma. International Journal of Radiation Oncology Biology Physics, 2009, 74, 472-476.	0.4	28
170	Vitamin D receptor gene polymorphisms, serum 25-hydroxyvitamin D levels, and melanoma: UK caseâ€“control comparisons and a meta-analysis of published VDR data. European Journal of Cancer, 2009, 45, 3271-3281.	1.3	127
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