Lauri A Aaltonen

List of Publications by Year
in descending order

338	41,972	2975	2448
papers	citations	93 h-index	197 g-index

349	349	349	31157
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Comparison of 2SC, AKR1B10, and FH Antibodies as Potential Biomarkers for FH-deficient Uterine Leiomyomas. American Journal of Surgical Pathology, 2022, 46, 537-546.	3.7	8
2	Histopathologic and Molecular Characterization of Uterine Leiomyomaâ€“like Inflammatory Myofibroblastic Tumor. American Journal of Surgical Pathology, 2022, 46, 1126-1136.	3.7	8
3	Lack of an association between gallstone disease and bilirubin levels with risk of colorectal cancer: a Mendelian randomisation analysis. British Journal of Cancer, 2021, 124, 1169-1174.	6.4	6
4	No evidence of EMAST in whole genome sequencing data from 248 colorectal cancers. Genes Chromosomes and Cancer, 2021, 60, 463-473.	2.8	5
5	Identification of ZBTB18 as a novel colorectal tumor suppressor gene through genome-wide promoter hypermethylation analysis. Clinical Epigenetics, 2021, 13, 88.	4.1	5
6	From APC to the genetics of hereditary and familial colon cancer syndromes. Human Molecular Genetics, 2021, 30, R206-R224.	2.9	15
7	Novel germline variant in the histone demethylase and transcription regulator KDM4C induces a multi-cancer phenotype. Journal of Medical Genetics, 2021, , jmedgenet-2021-107747.	3.2	2
8	Next-generation sequencing in a large pedigree segregating visceral artery aneurysms suggests potential role of COL4A1/COL4A2 in disease etiology. Vascular, 2021, , 170853812110331.	0.9	2
9	WNT2 activation through proximal germline deletion predisposes to small intestinal neuroendocrine tumors and intestinal adenocarcinomas. Human Molecular Genetics, 2021, 30, 2429-2440.	2.9	6
10	Human cell transformation by combined lineage conversion and oncogene expression. Oncogene, 2021, 40, 5533-5547.	5.9	12
11	Genetic and Epigenetic Characteristics of Inflammatory Bowel Diseaseâ€“Associated Colorectal Cancer. Gastroenterology, 2021, 161, 592-607.	1.3	81
12	Deficient H2A.Z deposition is associated with genesis of uterine leiomyoma. Nature, 2021, 596, 398-403.	27.8	53
13	Uterine leiomyomas in hereditary leiomyomatosis and renal cell cancer (HLRCC) syndrome can be identified through distinct clinical characteristics and typical morphology. Acta Obstetricia Et Gynecologica Scandinavica, 2021, 100, 2066-2075.	2.8	5
14	Parity associates with chromosomal damage in uterine leiomyomas. Nature Communications, 2021, 12, 5448.	12.8	2
15	Modifiable pathways for colorectal cancer: a mendelian randomisation analysis. The Lancet Gastroenterology and Hepatology, 2020, 5, 55-62.	8.1	79
16	Prognostic Value of Immune Environment Analysis in Small Bowel Adenocarcinomas with Verified Mutational Landscape and Predisposing Conditions. Cancers, 2020, 12, 2018.	3.7	5
17	Colibactin DNA-damage signature indicates mutational impact in colorectal cancer. Nature Medicine, 2020, 26, 1063-1069.	30.7	149
18	Mutational processes of distinct POLE exonuclease domain mutants drive an enrichment of a specific TP53 mutation in colorectal cancer. PLoS Genetics, 2020, 16, e1008572.	3.5	27

#	Article	IF	Citations
19	Defining eligible patients for allele-selective chemotherapies targeting NAT2 in colorectal cancer. Scientific Reports, 2020, 10, 22436.	3.3	5
20	Title is missing!. , 2020, 16, e1008572.		0
21	Title is missing!. , 2020, 16, e1008572.		0
22	Title is missing!. , 2020, 16, e1008572.		0
23	Title is missing!. , 2020, 16, e1008572.		0
24	Candidate susceptibility variants in angioimmunoblastic T-cell lymphoma. Familial Cancer, 2019, 18, 113-119.	1.9	8
25	Candidate Predisposition Variants in Kaposi Sarcoma as Detected by Whole-Genome Sequencing. Open Forum Infectious Diseases, 2019, 6, ofz337.	0.9	5
26	Retrotransposon insertions can initiate colorectal cancer and are associated with poor survival. Nature Communications, 2019, 10, 4022.	12.8	53
27	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	12.8	172
28	Impact of constitutional TET2 haploinsufficiency on molecular and clinical phenotype in humans. Nature Communications, 2019, 10, 1252.	12.8	67
29	Exome and immune cell score analyses reveal great variation within synchronous primary colorectal cancers. British Journal of Cancer, 2019, 120, 922-930.	6.4	4
30	Biallelic loss-of-function P4HTM gene variants cause hypotonia, hypoventilation, intellectual disability, dysautonomia, epilepsy, and eye abnormalities (HIDEA syndrome). Genetics in Medicine, 2019, 21, 2355-2363.	2.4	19
31	Genetic and Epigenetic Characterization of Growth Hormoneâ€“Secreting Pituitary Tumors. Molecular Cancer Research, 2019, 17, 2432-2443.	3.4	16
32	Oncogenic exon 2 mutations in Mediator subunit MED12 disrupt allosteric activation of cyclin C-CDK8/19. Journal of Biological Chemistry, 2018, 293, 4870-4882.	3.4	44
33	Genomeâ€wide association study and metaâ€analysis in Northern European populations replicate multiple colorectal cancer risk loci. International Journal of Cancer, 2018, 142, 540-546.	5.1	26
34	Discovery of potential causative mutations in human coding and noncoding genome with the interactive software BasePlayer. Nature Protocols, 2018, 13, 2580-2600.	12.0	27
35	Contribution of allelic imbalance to colorectal cancer. Nature Communications, 2018, 9, 3664.	12.8	25
36	Germline mutations in young non-smoking women with lung adenocarcinoma. Lung Cancer, 2018, 122, 76-82.	2.0	36

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37	Comprehensive evaluation of coding region point mutations in microsatelliteâ€unstable colorectal cancer. EMBO Molecular Medicine, 2018, 10, .	6.9	10
38	Exome-wide somatic mutation characterization of small bowel adenocarcinoma. PLoS Genetics, 2018, 14, e1007200.	3.5	62
39	Genetic predisposition to uterine leiomyoma is determined by loci for genitourinary development and genome stability. ELife, 2018, 7, .	6.0	58
40	Abstract 1159: Development of uterine leiomyoma 3D in vitro models for high-throughput drug and chemical compound screenings: Towards personalized medicine. , 2018, , .		0
41	Abstract LB-375: The landscape of somatic mutations in uterine adenomyomas. , 2018, , .		0
42	Abstract LB-382: Identification of predisposing genes for small bowel adenocarcinoma by exome sequencing. , 2018, , .		0
43	Candidate susceptibility variants for esophageal squamous cell carcinoma. Genes Chromosomes and Cancer, 2017, 56, 453-459.	2.8	23
44	Comprehensive Evaluation of Protein Coding Mononucleotide Microsatellites in Microsatellite-Unstable Colorectal Cancer. Cancer Research, 2017, 77, 4078-4088.	0.9	18
45	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. International Journal of Cancer, 2017, 140, 2701-2708.	5.1	76
46	Global metabolomic profiling of uterine leiomyomas. British Journal of Cancer, 2017, 117, 1855-1864.	6.4	29
47	Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. European Journal of Cancer, 2017, 84, 228-238.	2.8	81
48	Multiple clinical characteristics separate MED12-mutation-positive and -negative uterine leiomyomas. Scientific Reports, 2017, 7, 1015.	3.3	44
49	Germline MSH6 Mutation in a Patient With Two Independent Primary Glioblastomas. Journal of Neuropathology and Experimental Neurology, 2017, 76, 848-853.	1.7	4
50	Detection of subclonal L1 transductions in colorectal cancer by long-distance inverse-PCR and Nanopore sequencing. Scientific Reports, 2017, 7, 14521.	3.3	24
51	Whole-exome sequencing identifies novel candidate predisposition genes for familial polycythemia vera. Human Genomics, 2017, 11, 6.	2.9	11
52	Multiple components of PKA and TGF-Î² pathways are mutated in pseudomyxoma peritonei. PLoS ONE, 2017, 12, e0174898.	2.5	15
53	Abstract 4381: The mobile genome of colorectal cancer: Characterization of retrotransposon insertions in 202 colorectal cancer whole genomes. , 2017, , .		0
54	Abstract 4379: Somatic exomic landscape of small intestinal adenocarcinomas. , 2017, , .		0

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55	Abstract 1440: Germline loss-of-function alleles in Finnish colorectal cancer patients. , 2017, , .		0
56	Abstract 2461: Molecular classification and clinical characterization of a large uterine leiomyoma patient cohort. , 2017, , .		0
57	Abstract 1457: Somatic biallelic inactivation offumarate hydratase(FH) in uterine leiomyomas. , 2017, , .		0
58	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. British Journal of Cancer, 2016, 115, 266-272.	6.4	57
59	MED12 mutations and FH inactivation are mutually exclusive in uterine leiomyomas. British Journal of Cancer, 2016, 114, 1405-1411.	6.4	43
60	Integrated data analysis reveals uterine leiomyoma subtypes with distinct driver pathways and biomarkers. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1315-1320.	7.1	166
61	Variation at 2q35 (PNKDandTMBIM1) influences colorectal cancer risk and identifies a pleiotropic effect with inflammatory bowel disease. Human Molecular Genetics, 2016, 25, 2349-2359.	2.9	37
62	Abstract 4435: Genome-scale DNA methylation changes delineate uterine leiomyoma subgroups. , 2016, , .		1
63	Abstract 171: Comparative genomic analyses of synchronous colorectal cancers by exome sequencing. , 2016, , .		0
64	Abstract 5281: Fast and scalable software for comparative variant analysis and visualization of massive next-generation sequencing data. , 2016, , .		0
65	Abstract 120: Estrogen and progesterone receptor expression in different molecular uterine leiomyoma subclasses. , 2016, , .		0
66	CTCF/cohesin-binding sites are frequently mutated in cancer. Nature Genetics, 2015, 47, 818-821.	21.4	383
67	3â€²-UTR poly(T/U) repeat of EWSR1 is altered in microsatellite unstable colorectal cancer with nearly perfect sensitivity. Familial Cancer, 2015, 14, 449-453.	1.9	2
68	Clonally related uterine leiomyomas are common and display branched tumor evolution. Human Molecular Genetics, 2015, 24, 4407-4416.	2.9	19
69	Exome sequencing reveals three novel candidate predisposition genes for diffuse gastric cancer. Familial Cancer, 2015, 14, 241-246.	1.9	50
70	Identification of homozygous deletion in ACAN and other candidate variants in familial classical Hodgkin lymphoma by exome sequencing. British Journal of Haematology, 2015, 170, 428-431.	2.5	25
71	Systematic search for rare variants in Finnish early-onset colorectal cancer patients. Cancer Genetics, 2015, 208, 35-40.	0.4	24
72	Whole-Genome Sequencing of Growth Hormone (GH)-Secreting Pituitary Adenomas. Journal of Clinical Endocrinology and Metabolism, 2015, 100, 3918-3927.	3.6	96

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73	Whole-Genome Sequencing IdentifiesSTAT4as a Putative Susceptibility Gene in Classic Kaposi Sarcoma. Journal of Infectious Diseases, 2015, 211, 1842-1851.	4.0	25
74	Genomic profile of pseudomyxoma peritonei analyzed using nextâ€generation sequencing and immunohistochemistry. International Journal of Cancer, 2015, 136, E282-9.	5.1	66
75	Abstract 2744: Familial multiple metastatic small intestine neuroendocrine tumors: searching for genetic susceptibility. , 2015, , .		0
76	Abstract 4800: Identification of candidate predisposition genes for familial uterine leiomyomas. , 2015, , .		0
77	Abstract 2176: Joint structural variant analysis of colorectal cancer whole genome sequencing data. , 2015, , .		0
78	Abstract 1079: Transcriptional profiling reveals uterine leiomyoma subtypes with distinct pathways and biomarkers of tumorigenesis. , 2015, , .		0
79	New Target Genes in Endometrial Tumors Show a Role for the Estrogen-Receptor Pathway in Microsatellite-Unstable Cancers. Human Mutation, 2014, 35, 1514-1523.	2.5	10
80	Exomic landscape of MED12 mutationâ€negative and â€positive uterine leiomyomas. International Journal of Cancer, 2014, 134, 1008-1012.	5.1	36
81	High Frequency ofRPL22Mutations in Microsatellite-Unstable Colorectal and Endometrial Tumors. Human Mutation, 2014, 35, 1442-1445.	2.5	38
82	Clinical characterization, genetic mapping and whole-genome sequence analysis of a novel autosomal recessive intellectual disability syndrome. European Journal of Medical Genetics, 2014, 57, 543-551.	1.3	19
83	Genomics of uterine leiomyomas:Âinsights from high-throughput sequencing. Fertility and Sterility, 2014, 102, 621-629.	1.0	164
84	MED12 mutation frequency in unselected sporadic uterine leiomyomas. Fertility and Sterility, 2014, 102, 1137-1142.	1.0	62
85	Mutation analysis of components of the Mediator kinase module in MED12 mutation-negative uterine leiomyomas. British Journal of Cancer, 2014, 110, 2246-2249.	6.4	19
86	Identification of 33 candidate oncogenes by screening for base-specific mutations. British Journal of Cancer, 2014, 111, 1657-1662.	6.4	30
87	Uterine Leiomyoma-Linked MED12 Mutations Disrupt Mediator-Associated CDK Activity. Cell Reports, 2014, 7, 654-660.	6.4	125
88	Frequent L1 retrotranspositions originating fromTTC28in colorectal cancer. Oncotarget, 2014, 5, 853-859.	1.8	60
89	Population distribution and ancestry of the cancer protective MDM2 SNP285 (rs117039649). Oncotarget, 2014, 5, 8223-8234.	1.8	22
90	Abstract 3514: MED12 and FH mutations in HLRCC associated uterine leiomyomas. , 2014, , .		0

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91	Abstract 2401: Identification of new target genes in microsatellite unstable colorectal cancer by exome sequencing. , 2014, , .		0
92	Abstract 5193: Novel candidate oncogenes with mutation hot spots in microsatellite unstable colorectal cancer. , 2014, , .		1
93	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
94	Characterization of Uterine Leiomyomas by Whole-Genome Sequencing. New England Journal of Medicine, 2013, 369, 43-53.	27.0	280
95	Familial Isolated Pituitary Adenomas (FIPA) and the Pituitary Adenoma Predisposition due to Mutations in the Aryl Hydrocarbon Receptor Interacting Protein (AIP) Gene. Endocrine Reviews, 2013, 34, 239-277.	20.1	289
96	Diagnostic Cancer Genome Sequencing and the Contribution of Germline Variants. Science, 2013, 339, 1559-1562.	12.6	57
97	Identification of Candidate Oncogenes in Human Colorectal Cancers With Microsatellite Instability. Gastroenterology, 2013, 145, 540-543.e22.	1.3	65
98	High Familial Risk in Nodular Lymphocyte-Predominant Hodgkin Lymphoma. Journal of Clinical Oncology, 2013, 31, 938-943.	1.6	51
99	Prevalence of Germline PTEN, BMPR1A, SMAD4, STK11, and ENG Mutations in Patients With Moderate-Load Colorectal Polyps. Gastroenterology, 2013, 144, 1402-1409.e5.	1.3	61
100	MED12 exon 2 mutations in histopathological uterine leiomyoma variants. European Journal of Human Genetics, 2013, 21, 1300-1303.	2.8	66
101	Trilateral Retinoblastoma in a Patient With Peutzâ€“<scp>J</scp>eghers Syndrome. American Journal of Medical Genetics, Part A, 2013, 161, 1096-1100.	1.2	4
102	Exome sequencing in diagnostic evaluation of colorectal cancer predisposition in young patients. Scandinavian Journal of Gastroenterology, 2013, 48, 672-678.	1.5	14
103	Chromothripsis in Uterine Leiomyomas. New England Journal of Medicine, 2013, 369, 2160-2161.	27.0	13
104	Lessons from Functional Analysis of Genome-Wide Association Studies. Cancer Research, 2013, 73, 4180-4184.	0.9	58
105	Eleven Candidate Susceptibility Genes for Common Familial Colorectal Cancer. PLoS Genetics, 2013, 9, e1003876.	3.5	69
106	HOXB13 G84E Mutation in Finland: Population-Based Analysis of Prostate, Breast, and Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 452-460.	2.5	75
107	Primary mediastinal large B-cell lymphoma segregating in a family: exome sequencing identifies MLL as a candidate predisposition gene. Blood, 2013, 121, 3428-3430.	1.4	21
108	Nationwide Registry-Based Analysis of Cancer Clustering Detects Strong Familial Occurrence of Kaposi Sarcoma. PLoS ONE, 2013, 8, e55209.	2.5	18

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109	Brush border Myosin Ia has tumor suppressor activity in the intestine. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1530-1535.	7.1	60
110	A Finnish founder mutation inRAD51D: analysis in breast, ovarian, prostate, and colorectal cancer: Table 1. Journal of Medical Genetics, 2012, 49, 429-432.	3.2	41
111	Refinement of the associations between risk of colorectal cancer and polymorphisms on chromosomes 1q41 and 12q13.13. Human Molecular Genetics, 2012, 21, 934-946.	2.9	19
112	Strong family history of uterine leiomyomatosis warrants fumarate hydratase mutation screening. Human Reproduction, 2012, 27, 1865-1869.	0.9	28
113	COGENT (COlorectal cancer GENeTics) revisited. Mutagenesis, 2012, 27, 143-151.	2.6	27
114	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. Nature Genetics, 2012, 44, 770-776.	21.4	210
115	Analysis of a Finnish family confirms RHBDF2 mutations as the underlying factor in tylosis with esophageal cancer. Familial Cancer, 2012, 11, 525-528.	1.9	49
116	Villin Expression Is Frequently Lost in Poorly Differentiated Colon Cancer. American Journal of Pathology, 2012, 180, 1509-1521.	3.8	28
117	Characterization of the colorectal cancerâ€“associated enhancer MYC-335 at 8q24: the role of rs67491583. Cancer Genetics, 2012, 205, 25-33.	0.4	24
118	Identification of Lynch Syndrome Among Patients With Colorectal Cancer. JAMA - Journal of the American Medical Association, 2012, 308, 1555.	7.4	443
119	Screening of Finnish RAD51Cfounder mutations in prostate and colorectal cancer patients. BMC Cancer, 2012, 12, 552.	2.6	8
120	Somatic MED12 mutations in uterine leiomyosarcoma and colorectal cancer. British Journal of Cancer, 2012, 107, 1761-1765.	6.4	105
121	Segregation of a Missense Variant in Enteric Smooth Muscle Actin Î³-2 With Autosomal Dominant Familial Visceral Myopathy. Gastroenterology, 2012, 143, 1482-1491.e3.	1.3	89
122	Loss of SUFU Function in Familial Multiple Meningioma. American Journal of Human Genetics, 2012, 91, 520-526.	6.2	137
123	Mice Lacking a Myc Enhancer That Includes Human SNP rs6983267 Are Resistant to Intestinal Tumors. Science, 2012, 338, 1360-1363.	12.6	200
124	Rule-based induction method for haplotype comparison and identification of candidate disease loci. Genome Medicine, 2012, 4, 21.	8.2	0
125	Candidate driver genes in microsatelliteâ€unstable colorectal cancer. International Journal of Cancer, 2012, 130, 1558-1566.	5.1	99
126	Abstract 1161: The role of MED12 exon 2 mutations in histopathological variants of uterine leiomyoma. , 2012, , .		0

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127	Abstract 105: Characterizing the exomic profile of MSI colorectal cancer. , 2012, , .		0
128	Abstract 2976: KSHV-initiated Notch activation leads to membrane-type-1 matrix metalloproteinase-dependent lymphatic endothelial-to-mesenchymal transition. , 2012, , .		0
129	Abstract 4316: Villin expression is frequently lost in colon cancers with microsatellite instability.. , 2012, , .		0
130	Variants in the Netrin-1 Receptor UNC5C Prevent Apoptosis and Increase Risk of Familial Colorectal Cancer. Gastroenterology, 2011, 141, 2039-2046.	1.3	28
131	Mutations in BRIP1 confer high risk of ovarian cancer. Nature Genetics, 2011, 43, 1104-1107.	21.4	338
132	MED12 , the Mediator Complex Subunit 12 Gene, Is Mutated at High Frequency in Uterine Leiomyomas. Science, 2011, 334, 252-255.	12.6	547
133	Systematic search for enhancer elements and somatic allelic imbalance at seven low-penetrance colorectal cancer predisposition loci. BMC Medical Genetics, 2011, 12, 23.	2.1	16
134	KSHV-Initiated Notch Activation Leads to Membrane-Type-1 Matrix Metalloproteinase-Dependent Lymphatic Endothelial-to-Mesenchymal Transition. Cell Host and Microbe, 2011, 10, 577-590.	11.0	123
135	Exome sequencing reveals germline NPAT mutation as a candidate risk factor for Hodgkin lymphoma. Blood, 2011, 118, 493-498.	1.4	78
136	Analysis of KLHDC8B in familial nodular lymphocyte predominant Hodgkin lymphoma. British Journal of Haematology, 2011, 154, 413-415.	2.5	7
137	The MDM2 Promoter SNP285C/309G Haplotype Diminishes Sp1 Transcription Factor Binding and Reduces Risk for Breast and Ovarian Cancer in Caucasians. Cancer Cell, 2011, 19, 273-282.	16.8	104
138	Downregulation of the hedgehog receptor PTCH1 in colorectal serrated adenocarcinomas is not caused by PTCH1 mutations. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2011, 458, 213-219.	2.8	5
139	Aberrant succination of proteins in fumarate hydrataseâ€deficient mice and HLRCC patients is a robust biomarker of mutation status. Journal of Pathology, 2011, 225, 4-11.	4.5	225
140	No evidence of RET germline mutations in familial pituitary adenoma. Journal of Molecular Endocrinology, 2011, 46, 1-8.	2.5	35
141	High frequency of TTK mutations in microsatellite-unstable colorectal cancer and evaluation of their effect on spindle assembly checkpoint. Carcinogenesis, 2011, 32, 305-311.	2.8	14
142	Multiple Common Susceptibility Variants near BMP Pathway Loci GREM1, BMP4, and BMP2 Explain Part of the Missing Heritability of Colorectal Cancer. PLoS Genetics, 2011, 7, e1002105.	3.5	188
143	MED12 exon 2 mutations are common in uterine leiomyomas from South African patients. Oncotarget, 2011, 2, 966-969.	1.8	95
144	No evidence for a genetic modifier for renal cell cancer risk in HLRCC syndrome. Familial Cancer, 2010, 9, 245-251.	1.9	26

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145	Somatic mutations and germline sequence variants in patients with familial colorectal cancer. International Journal of Cancer, 2010, 127, 2974-2980.	5.1	26
146	COGENT (COlorectal cancer GENeTics): an international consortium to study the role of polymorphic variation on the risk of colorectal cancer. British Journal of Cancer, 2010, 102, 447-454.	6.4	43
147	A large-scale meta-analysis to refine colorectal cancer risk estimates associated with MUTYH variants. British Journal of Cancer, 2010, 103, 1875-1884.	6.4	107
148	Meta-analysis of three genome-wide association studies identifies susceptibility loci for colorectal cancer at 1q41, 3q26.2, 12q13.13 and 20q13.33. Nature Genetics, 2010, 42, 973-977.	21.4	335
149	Mutations in the Circadian Gene CLOCK in Colorectal Cancer. Molecular Cancer Research, 2010, 8, 952-960.	3.4	77
150	Correction: An A13 Repeat within the 3â€²-Untranslated Region of Epidermal Growth Factor Receptor (EGFR) Is Frequently Mutated in Microsatellite Instability Colon Cancers and Is Associated with Increased EGFR Expression. Cancer Research, 2010, 70, 1275-1275.	0.9	0
151	Clinical Characteristics and Therapeutic Responses in Patients with Germ-LineAIPMutations and Pituitary Adenomas: An International Collaborative Study. Journal of Clinical Endocrinology and Metabolism, 2010, 95, E373-E383.	3.6	323
152	Low-Penetrance Susceptibility Variants in Familial Colorectal Cancer. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 1478-1483.	2.5	22
153	Recessively inherited right atrial isomerism caused by mutations in growth/differentiation factor 1 (GDF1). Human Molecular Genetics, 2010, 19, 2747-2753.	2.9	48
154	Mixed lineage kinase 3 gene mutations in mismatch repair deficient gastrointestinal tumours. Human Molecular Genetics, 2010, 19, 697-706.	2.9	26
155	Expression Profiling in Progressive Stages of Fumarate-Hydratase Deficiency: The Contribution of Metabolic Changes to Tumorigenesis. Cancer Research, 2010, 70, 9153-9165.	0.9	63
156	Mice with Inactivation of Aryl Hydrocarbon Receptor-Interacting Protein (Aip) Display Complete Penetrance of Pituitary Adenomas with Aberrant ARNT Expression. American Journal of Pathology, 2010, 177, 1969-1976.	3.8	78
157	Allelic Variation at the 8q23.3 Colorectal Cancer Risk Locus Functions as a Cis-Acting Regulator of EIF3H. PLoS Genetics, 2010, 6, e1001126.	3.5	74
158	Abstract 5756: The receptor tyrosine kinase EPHB4 has tumor suppressor activities in intestinal tumorigenesis. , 2010, , .		0
159	Abstract 3864: Low-penetrance variants underlying familial colorectal cancer. , 2010, , .		0
160	Abstract 1844: No evidence for genetic factor increasing renal cell cancer risk in Hereditary Leiomyomatosis and Renal Cell Cancer syndrome. , 2010, , .		0
161	Abstract LB-121: Serrated colorectal adenocarcinoma: Specific copy number alterations. , 2010, , .		0
162	Ten Years After Mutation Testing for Lynch Syndrome: Cancer Incidence and Outcome in Mutation-Positive and Mutation-Negative Family Members. Journal of Clinical Oncology, 2009, 27, 4793-4797.	1.6	252

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163	Dysregulation of the transcription factors SOX4, CBFB and SMARCC1 correlates with outcome of colorectal cancer. British Journal of Cancer, 2009, 100, 511-523.	6.4	94
164	Metastasis-Associated Gene Expression Changes Predict Poor Outcomes in Patients with Dukes Stage B and C Colorectal Cancer. Clinical Cancer Research, 2009, 15, 7642-7651.	7.0	395
165	Aggressive pituitary adenomas occurring in young patients in a large Polynesian kindred with a germline R271W mutation in the AIP gene. European Journal of Endocrinology, 2009, 161, 799-804.	3.7	45
166	An A13 Repeat within the 3â€²-Untranslated Region of Epidermal Growth Factor Receptor (EGFR) Is Frequently Mutated in Microsatellite Instability Colon Cancers and Is Associated with Increased EGFR Expression. Cancer Research, 2009, 69, 7811-7818.	0.9	34
167	Array comparative genomic hybridization identifies a distinct DNA copy number profile in renal cell cancer associated with hereditary leiomyomatosis and renal cell cancer. Genes Chromosomes and Cancer, 2009, 48, 544-551.	2.8	25
168	A TARBP2 mutation in human cancer impairs microRNA processing and DICER1 function. Nature Genetics, 2009, 41, 365-370.	21.4	355
169	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
170	Downregulation of SRFâ€“FOSâ€“JUNB pathway in fumarate hydratase deficiency and in uterine leiomyomas. Oncogene, 2009, 28, 1261-1273.	5.9	31
171	The Expression of AIP-Related Molecules in Elucidation of Cellular Pathways in Pituitary Adenomas. American Journal of Pathology, 2009, 175, 2501-2507.	3.8	61
172	ARLTS1 germline variants and the risk for breast, prostate, and colorectal cancer. European Journal of Human Genetics, 2008, 16, 983-991.	2.8	12
173	A genome-wide association study identifies colorectal cancer susceptibility loci on chromosomes 10p14 and 8q23.3. Nature Genetics, 2008, 40, 623-630.	21.4	514
174	Meta-analysis of genome-wide association data identifies four new susceptibility loci for colorectal cancer. Nature Genetics, 2008, 40, 1426-1435.	21.4	498
175	Aryl hydrocarbon receptor interacting protein (AIP) gene mutation analysis in children and adolescents with sporadic pituitary adenomas. Clinical Endocrinology, 2008, 69, 621-627.	2.4	80
176	Somatic mutation analysis of MYH11in breast and prostate cancer. BMC Cancer, 2008, 8, 263.	2.6	26
177	Mutation screening of fumarate hydratase by multiplex ligation-dependent probe amplification: detection of exonic deletion in a patient with leiomyomatosis and renal cell cancer. Cancer Genetics and Cytogenetics, 2008, 183, 83-88.	1.0	30
178	Transcription Factor PROX1 Induces Colon Cancer Progression by Promoting the Transition from Benign to Highly Dysplastic Phenotype. Cancer Cell, 2008, 13, 407-419.	16.8	166
179	DNA Copy-Number Alterations Underlie Gene Expression Differences between Microsatellite Stable and Unstable Colorectal Cancers. Clinical Cancer Research, 2008, 14, 8061-8069.	7.0	84
180	Refinement of the basis and impact of common 11q23.1 variation to the risk of developing colorectal cancer. Human Molecular Genetics, 2008, 17, 3720-3727.	2.9	61

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