Nicola J Waddell

List of Publications by Year in Descending Order

154 papers	22,029 citations	49 h-index	148 g-index
176 ext. papers	28,311 ext. citations	12.2 avg, IF	7.19 L-index

#	Paper	IF	Citations
154	Patient-derived xenograft models capture genomic heterogeneity in endometrial cancer.. *Genome Medicine*, **2022**, 14, 3	14.4	2
153	Anatomic position determines oncogenic specificity in melanoma.. *Nature*, **2022**,	50.4	3
152	Multiomic profiling of checkpoint inhibitor-treated melanoma: Identifying predictors of response and resistance, and markers of biological discordance.. *Cancer Cell*, **2021**,	24.3	6
151	Evaluation of a Genetics Education Program for Health Interpreters: A Pilot Study.. *Frontiers in Genetics*, **2021**, 12, 771892	4.5	0
150	ROR1 and ROR2 expression in pancreatic cancer. *BMC Cancer*, **2021**, 21, 1199	4.8	0
149	Precision diagnostics: integration of tissue pathology and genomics in cancer. *Pathology*, **2021**, 53, 809-817	8.1	0
148	Developing a gene panel for pharmacoresistant epilepsy: a review of epilepsy pharmacogenetics. *Pharmacogenomics*, **2021**, 22, 225-234	2.6	3
147	Considerations for using population frequency data in germline variant interpretation: Cancer syndrome genes as a model. *Human Mutation*, **2021**, 42, 530-536	4.7	1
146	The Genomic Landscape of Lobular Breast Cancer. *Cancers*, **2021**, 13,	6.6	3
145	Radiomics Biomarkers Correlate with CD8 Expression and Predict Immune Signatures in Melanoma Patients. *Molecular Cancer Research*, **2021**, 19, 950-956	6.6	1
144	Tumor Signature Analysis Implicates Hereditary Cancer Genes in Endometrial Cancer Development. *Cancers*, **2021**, 13,	6.6	2
143	Targeting novel LSD1-dependent ACE2 demethylation domains inhibits SARS-CoV-2 replication. *Cell Discovery*, **2021**, 7, 37	22.3	3
142	Evaluation of Crizotinib Treatment in a Patient With Unresectable GOPC-ROS1 Fusion Agminated Spitz Nevi. *JAMA Dermatology*, **2021**, 157, 836-841	5.1	2
141	Targeting DNA Damage Response and Replication Stress in Pancreatic Cancer. *Gastroenterology*, **2021**, 160, 362-377.e13	13.3	32
140	CRISPR/Cas9-mediated genome editing of Schistosoma mansoni acetylcholinesterase. *FASEB Journal*, **2021**, 35, e21205	0.9	9
139	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. *Communications Biology*, **2021**, 4, 155	6.7	11
138	ERK and mTORC1 Inhibitors Enhance the Anti-Cancer Capacity of the Octpep-1 Venom-Derived Peptide in Melanoma BRAF(V600E) Mutations. *Toxins*, **2021**, 13,	4.9	2

137	Histone Modifying Enzymes in Gynaecological Cancers. *Cancers*, **2021**, 13,	6.6	3
136	Acquired Promoter Methylation Loss Causes PARP Inhibitor Resistance in High-Grade Serous Ovarian Carcinoma. *Cancer Research*, **2021**, 81, 4709-4722	10.1	11
135	Queensland Genomics: an adaptive approach for integrating genomics into a public healthcare system. *Npj Genomic Medicine*, **2021**, 6, 71	6.2	2
134	Genomic and Molecular Analyses Identify Molecular Subtypes of Pancreatic Cancer Recurrence. *Gastroenterology*, **2021**,	13.3	1
133	Deep learning in cancer diagnosis, prognosis and treatment selection. *Genome Medicine*, **2021**, 13, 152	14.4	24
132	Verifying explainability of a deep learning tissue classifier trained on RNA-seq data. *Scientific Reports*, **2021**, 11, 2641	4.9	6
131	Queensland ConsumersQAwareness and Understanding of Clinical Genetics Services. *Frontiers in Genetics*, **2020**, 11, 537743	4.5	3
130	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. *Nature Communications*, **2020**, 11, 2408	17.4	42
129	Mutation Marks an Aggressive Subtype of Mutant Colorectal Cancers. *Cancers*, **2020**, 12,	6.6	11
128	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. *Cell Reports*, **2020**, 31, 107625	10.6	34
127	Alterations in signaling pathways that accompany spontaneous transition to malignancy in a mouse model of BRAF mutant microsatellite stable colorectal cancer. *Neoplasia*, **2020**, 22, 120-128	6.4	7
126	Non-coding RNAs underlie genetic predisposition to breast cancer. *Genome Biology*, **2020**, 21, 7	18.3	11
125	Patterns of somatic structural variation in human cancer genomes. *Nature*, **2020**, 578, 112-121	50.4	232
124	Pan-cancer analysis of whole genomes. *Nature*, **2020**, 578, 82-93	50.4	840
123	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. *Nature Genetics*, **2020**, 52, 331-341	36.3	168
122	Tumor CD155 Expression Is Associated with Resistance to Anti-PD1 Immunotherapy in Metastatic Melanoma. *Clinical Cancer Research*, **2020**, 26, 3671-3681	12.9	27
121	Chromatin interactome mapping at 139 independent breast cancer risk signals. *Genome Biology*, **2020**, 21, 8	18.3	12
120	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. *Nature Communications*, **2020**, 11, 5259	17.4	28

119	Pathogenic germline variants are associated with poor survival in stage III/IV melanoma patients. *Scientific Reports*, **2020**, 10, 17687	4.9	6
118	Sharing genomic data from clinical testing with researchers: public survey of expectations of clinical genomic data management in Queensland, Australia. *BMC Medical Ethics*, **2020**, 21, 119	2.9	4
117	Tumor Mutation Burden and Structural Chromosomal Aberrations Are Not Associated with T-cell Density or Patient Survival in Acral, Mucosal, and Cutaneous Melanomas. *Cancer Immunology Research*, **2020**, 8, 1346-1353	12.5	4
116	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. *Npj Breast Cancer*, **2020**, 6, 33	7.8	6
115	MHC Class II Antigen Presentation by the Intestinal Epithelium Initiates Graft-versus-Host Disease and Is Influenced by the Microbiota. *Immunity*, **2019**, 51, 885-898.e7	32.3	84
114	Whole-genome sequencing reveals clinically relevant insights into the aetiology of familial breast cancers. *Annals of Oncology*, **2019**, 30, 1071-1079	10.3	35
113	Integrative Genome-Scale DNA Methylation Analysis of a Large and Unselected Cohort Reveals 5 Distinct Subtypes of Colorectal Adenocarcinomas. *Cellular and Molecular Gastroenterology and Hepatology*, **2019**, 8, 269-290	7.9	23
112	Molecular Genomic Profiling of Melanocytic Nevi. *Journal of Investigative Dermatology*, **2019**, 139, 1762-1768	4.8	36
111	What does Australia's investment in genomics mean for public health?. *Australian and New Zealand Journal of Public Health*, **2019**, 43, 204-206	2.3	1
110	Diff-Quik Cytology Smears from Endobronchial Ultrasound Transbronchial Needle Aspiration Lymph Node Specimens as a Source of DNA for Next-Generation Sequencing Instead of Cell Blocks. *Respiration*, **2019**, 97, 525-539	3.7	13
109	Patterns of Genomic Instability in Breast Cancer. *Trends in Pharmacological Sciences*, **2019**, 40, 198-211	13.2	38
108	Complex structural rearrangements are present in high-grade dysplastic Barrett's oesophagus samples. *BMC Medical Genomics*, **2019**, 12, 31	3.7	10
107	Intratumoural Heterogeneity Underlies Distinct Therapy Responses and Treatment Resistance in Glioblastoma. *Cancers*, **2019**, 11,	6.6	25
106	CAF hierarchy driven by pancreatic cancer cell p53-status creates a pro-metastatic and chemoresistant environment via perlecan. *Nature Communications*, **2019**, 10, 3637	17.4	100
105	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. *Nature Communications*, **2019**, 10, 3163	17.4	113
104	Targeting CD39 in Cancer Reveals an Extracellular ATP- and Inflammasome-Driven Tumor Immunity. *Cancer Discovery*, **2019**, 9, 1754-1773	24.4	86
103	Bone marrow transplantation generates T cell-dependent control of myeloma in mice. *Journal of Clinical Investigation*, **2019**, 129, 106-121	15.9	33
102	The immune checkpoint CD96 defines a distinct lymphocyte phenotype and is highly expressed on tumor-infiltrating T cells. *Immunology and Cell Biology*, **2019**, 97, 152-164	5	16

101	Whole genome sequencing of melanomas in adolescent and young adults reveals distinct mutation landscapes and the potential role of germline variants in disease susceptibility. *International Journal of Cancer*, **2019**, 144, 1049-1060	7.5	27
100	A plugin for the Ensembl Variant Effect Predictor that uses MaxEntScan to predict variant spliceogenicity. *Bioinformatics*, **2019**, 35, 2315-2317	7.2	19
99	IL23R-Protective Coding Variant Promotes Beneficial Bacteria and Diversity in the Ileal Microbiome in Healthy Individuals Without Inflammatory Bowel Disease. *Journal of Crohn's and Colitis*, **2019**, 13, 451-461	7.5	10
98	Phenotypic and molecular dissection of metaplastic breast cancer and the prognostic implications. *Journal of Pathology*, **2019**, 247, 214-227	9.4	42
97	The Prognostic Significance of Low-Frequency Somatic Mutations in Metastatic Cutaneous Melanoma. *Frontiers in Oncology*, **2018**, 8, 584	5.3	9
96	Characterization of a novel breast cancer cell line derived from a metastatic bone lesion of a breast cancer patient. *Breast Cancer Research and Treatment*, **2018**, 170, 179-188	4.4	2
95	The Landscape of Somatic Genetic Alterations in Breast Cancers From ATM Germline Mutation Carriers. *Journal of the National Cancer Institute*, **2018**, 110, 1030-1034	9.7	65
94	Mixed ductal-lobular carcinomas: evidence for progression from ductal to lobular morphology. *Journal of Pathology*, **2018**, 244, 460-468	9.4	18
93	Telomere sequence content can be used to determine ALT activity in tumours. *Nucleic Acids Research*, **2018**, 46, 4903-4918	20.1	26
92	Malignant cells from pleural fluids in malignant mesothelioma patients reveal novel mutations. *Lung Cancer*, **2018**, 119, 64-70	5.9	17
91	Homologous Recombination DNA Repair Pathway Disruption and Retinoblastoma Protein Loss Are Associated with Exceptional Survival in High-Grade Serous Ovarian Cancer. *Clinical Cancer Research*, **2018**, 24, 569-580	12.9	46
90	Tailored first-line and second-line CDK4-targeting treatment combinations in mouse models of pancreatic cancer. *Gut*, **2018**, 67, 2142-2155	19.2	71
89	Germline and somatic variant identification using BGISEQ-500 and HiSeq X Ten whole genome sequencing. *PLoS ONE*, **2018**, 13, e0190264	3.7	29
88	Copy number profiles of paired primary and metastatic colorectal cancers. *Oncotarget*, **2018**, 9, 3394-3405	5.3	10
87	A2AR Adenosine Signaling Suppresses Natural Killer Cell Maturation in the Tumor Microenvironment. *Cancer Research*, **2018**, 78, 1003-1016	10.1	159
86	Mutations in Low-Grade Serous Ovarian Cancer and Response to BRAF Inhibition.. *JCO Precision Oncology*, **2018**, 2, 1-14	3.6	9
85	Jak2V617F and Dnmt3a loss cooperate to induce myelofibrosis through activated enhancer-driven inflammation. *Blood*, **2018**, 132, 2707-2721	2.2	37
84	CEP55 is a determinant of cell fate during perturbed mitosis in breast cancer. *EMBO Molecular Medicine*, **2018**, 10,	12	43

83	Early Changes in CD4+ T-Cell Activation During Blood-Stage Plasmodium falciparum Infection. *Journal of Infectious Diseases*, **2018**, 218, 1119-1129	7	10
82	Whole-genome landscape of pancreatic neuroendocrine tumours. *Nature*, **2017**, 543, 65-71	50.4	482
81	Unexpected UVR and non-UVR mutation burden in some acral and cutaneous melanomas. *Laboratory Investigation*, **2017**, 97, 130-145	5.9	25
80	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. *Nature Genetics*, **2017**, 49, 825-833	36.3	41
79	Whole-genome landscapes of major melanoma subtypes. *Nature*, **2017**, 545, 175-180	50.4	662
78	Mitochondrial mutations and metabolic adaptation in pancreatic cancer. *Cancer & Metabolism*, **2017** , 5, 2	5.4	40
77	Mutation load in melanoma is affected by MC1R genotype. *Pigment Cell and Melanoma Research*, **2017**, 30, 255-258	4.5	15
76	Interleukin-12 from CD103 Batf3-Dependent Dendritic Cells Required for NK-Cell Suppression of Metastasis. *Cancer Immunology Research*, **2017**, 5, 1098-1108	12.5	62
75	Tumor immunoevasion by the conversion of effector NK cells into type 1 innate lymphoid cells. *Nature Immunology*, **2017**, 18, 1004-1015	19.1	330
74	Next-Generation Sequencing of Endobronchial Ultrasound Transbronchial Needle Aspiration Specimens in Lung Cancer. *American Journal of Respiratory and Critical Care Medicine*, **2017**, 196, 388-391	10.2	12
73	Long Noncoding RNAs CUPID1 and CUPID2 Mediate Breast Cancer Risk at 11q13 by Modulating the Response to DNA Damage. *American Journal of Human Genetics*, **2017**, 101, 255-266	11	62
72	and Mutations Co-occur and Cooperate in Low-Grade Serous Ovarian Carcinomas. *Cancer Research*, **2017**, 77, 4268-4278	10.1	32
71	Whole exome sequencing of an asbestos-induced wild-type murine model of malignant mesothelioma. *BMC Cancer*, **2017**, 17, 396	4.8	20
70	Lost in translation: returning germline genetic results in genome-scale cancer research. *Genome Medicine*, **2017**, 9, 41	14.4	18
69	Hypermutation In Pancreatic Cancer. *Gastroenterology*, **2017**, 152, 68-74.e2	13.3	130
68	Clinical utilization of targetable molecular results in pancreatic cancer: Longer-term outcomes from the Individualized Molecular Pancreatic Cancer Therapy (IMPACT) trial.. *Journal of Clinical Oncology*, **2017**, 35, 314-314	2.2	
67	A Common Variant at the 14q32 Endometrial Cancer Risk Locus Activates AKT1 through YY1 Binding. *American Journal of Human Genetics*, **2016**, 98, 1159-1169	11	17
66	Identification of the CIMP-like subtype and aberrant methylation of members of the chromosomal segregation and spindle assembly pathways in esophageal adenocarcinoma. *Carcinogenesis*, **2016**, 37, 356-65	4.6	30

65	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. *Cell Reports*, **2016**, 14, 907-919	10.6	75
64	Genomic analyses identify molecular subtypes of pancreatic cancer. *Nature*, **2016**, 531, 47-52	50.4	1785
63	Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant. *American Journal of Human Genetics*, **2016**, 98, 830-842	11	153
62	Mutational signatures in esophageal adenocarcinoma define etiologically distinct subgroups with therapeutic relevance. *Nature Genetics*, **2016**, 48, 1131-41	36.3	233
61	Whole genomes redefine the mutational landscape of pancreatic cancer. *Nature*, **2015**, 518, 495-501	50.4	1579
60	PGTools: A Software Suite for Proteogenomic Data Analysis and Visualization. *Journal of Proteome Research*, **2015**, 14, 2255-66	5.6	47
59	Recurrent inactivating RASA2 mutations in melanoma. *Nature Genetics*, **2015**, 47, 1408-10	36.3	73
58	Comparative microRNA profiling of sporadic and BRCA1 associated basal-like breast cancers. *BMC Cancer*, **2015**, 15, 506	4.8	11
57	SOX9 regulates ERBB signalling in pancreatic cancer development. *Gut*, **2015**, 64, 1790-9	19.2	57
56	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. *Journal of Pathology*, **2015**, 237, 363-78	9.4	72
55	Whole-genome characterization of chemoresistant ovarian cancer. *Nature*, **2015**, 521, 489-94	50.4	890
54	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. *Nature Communications*, **2015**, 6, 10001	17.4	199
53	Using the MCF10A/MCF10CA1a Breast Cancer Progression Cell Line Model to Investigate the Effect of Active, Mutant Forms of EGFR in Breast Cancer Development and Treatment Using Gefitinib. *PLoS ONE*, **2015**, 10, e0125232	3.7	16
52	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. *Nature Communications*, **2014**, 5, 5224	17.4	176
51	Returning individual research results for genome sequences of pancreatic cancer. *Genome Medicine* , **2014**, 6, 42	14.4	18
50	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. *BioTechniques*, **2014**, 57, 31-8	2.5	
49	Clinical and pathologic features of familial pancreatic cancer. *Cancer*, **2014**, 120, 3669-75	6.4	38
48	Genome-wide DNA methylation patterns in pancreatic ductal adenocarcinoma reveal epigenetic deregulation of SLIT-ROBO, ITGA2 and MET signaling. *International Journal of Cancer*, **2014**, 135, 1110-8	7.5	149

47	Understanding pancreatic cancer genomes. *Journal of Hepato-Biliary-Pancreatic Sciences*, **2013**, 20, 549-56	2.8	26
46	Evaluating the repair of DNA derived from formalin-fixed paraffin-embedded tissues prior to genomic profiling by SNP-CGH analysis. *Laboratory Investigation*, **2013**, 93, 701-10	5.9	21
45	Signatures of mutational processes in human cancer. *Nature*, **2013**, 500, 415-21	50.4	5895
44	Clinical and molecular characterization of HER2 amplified-pancreatic cancer. *Genome Medicine*, **2013**, 5, 78	14.4	82
43	Neuropilin-2 promotes extravasation and metastasis by interacting with endothelial 5 integrin. *Cancer Research*, **2013**, 73, 4579-4590	10.1	65
42	miR-139-5p is a regulator of metastatic pathways in breast cancer. *Rna*, **2013**, 19, 1767-80	5.8	121
41	MicroRNA-182-5p targets a network of genes involved in DNA repair. *Rna*, **2013**, 19, 230-42	5.8	95
40	Somatic point mutation calling in low cellularity tumors. *PLoS ONE*, **2013**, 8, e74380	3.7	49
39	Enhanced RAD21 cohesin expression confers poor prognosis in BRCA2 and BRCAX, but not BRCA1 familial breast cancers. *Breast Cancer Research*, **2012**, 14, R69	8.3	32
38	Germline copy number variants are not associated with globally acquired copy number changes in familial breast tumours. *Breast Cancer Research and Treatment*, **2012**, 134, 1005-11	4.4	5
37	Gene expression profiling of tumour epithelial and stromal compartments during breast cancer progression. *Breast Cancer Research and Treatment*, **2012**, 135, 153-65	4.4	92
36	The application of nonsense-mediated mRNA decay inhibition to the identification of breast cancer susceptibility genes. *BMC Cancer*, **2012**, 12, 246	4.8	4
35	RON is not a prognostic marker for resectable pancreatic cancer. *BMC Cancer*, **2012**, 12, 395	4.8	16
34	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. *Nature*, **2012**, 491, 399-405	50.4	1427
33	Morphological and molecular analysis of a breast cancer cluster at the ABC Studio in Toowong. *Pathology*, **2012**, 44, 469-72	1.6	
32	Identification of fifteen novel germline variants in the BRCA1 3QTR reveals a variant in a breast cancer case that introduces a functional miR-103 target site. *Human Mutation*, **2012**, 33, 1665-75	4.7	42
31	PINA v2.0: mining interactome modules. *Nucleic Acids Research*, **2012**, 40, D862-5	20.1	267
30	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. *Nature*, **2012**, 486, 266-70	50.4	253

29	Sleeping Beauty mutagenesis reveals cooperating mutations and pathways in pancreatic adenocarcinoma. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 5934-41	11.5	179
28	qpure: A tool to estimate tumor cellularity from genome-wide single-nucleotide polymorphism profiles. *PLoS ONE*, **2012**, 7, e45835	3.7	80
27	Sequencing transcriptomes in toto. *Integrative Biology (United Kingdom)*, **2011**, 3, 522-8	3.7	16
26	MicroRNAs and their isomiRs function cooperatively to target common biological pathways. *Genome Biology*, **2011**, 12, R126	18.3	246
25	The expression of the ubiquitin ligase SIAH2 (seven in absentia homolog 2) is mediated through gene copy number in breast cancer and is associated with a basal-like phenotype and p53 expression. *Breast Cancer Research*, **2011**, 13, R19	8.3	37
24	Analysis of Brca1-deficient mouse mammary glands reveals reciprocal regulation of Brca1 and c-kit. *Oncogene*, **2011**, 30, 1597-607	9.2	20
23	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613
22	Use of DNA-damaging agents and RNA pooling to assess expression profiles associated with BRCA1 and BRCA2 mutation status in familial breast cancer patients. *PLoS Genetics*, **2010**, 6, e1000850	6	7
21	HER3 and downstream pathways are involved in colonization of brain metastases from breast cancer. *Breast Cancer Research*, **2010**, 12, R46	8.3	87
20	DNA methylome of familial breast cancer identifies distinct profiles defined by mutation status. *Breast Cancer Research*, **2010**, 12,	8.3	2
19	DNA methylome of familial breast cancer identifies distinct profiles defined by mutation status. *American Journal of Human Genetics*, **2010**, 86, 420-33	11	73
18	Frequent somatic mutations of GATA3 in non-BRCA1/BRCA2 familial breast tumors, but not in BRCA1-, BRCA2- or sporadic breast tumors. *Breast Cancer Research and Treatment*, **2010**, 119, 491-6	4.4	26
17	Subtypes of familial breast tumours revealed by expression and copy number profiling. *Breast Cancer Research and Treatment*, **2010**, 123, 661-77	4.4	81
16	Gene expression profiling of formalin-fixed, paraffin-embedded familial breast tumours using the whole genome-DASL assay. *Journal of Pathology*, **2010**, 221, 452-61	9.4	57
15	Aberrant expression of E-cadherin in lobular carcinomas of the breast. *American Journal of Surgical Pathology*, **2008**, 32, 773-83	6.7	128
14	Mutation of ERBB2 provides a novel alternative mechanism for the ubiquitous activation of RAS-MAPK in ovarian serous low malignant potential tumors. *Molecular Cancer Research*, **2008**, 6, 1678-90	6.6	93
13	BRCA1 and BRCA2 missense variants of high and low clinical significance influence lymphoblastoid cell line post-irradiation gene expression. *PLoS Genetics*, **2008**, 4, e1000080	6	11
12	Use of expression data and the CGEMS genome-wide breast cancer association study to identify genes that may modify risk in BRCA1/2 mutation carriers. *Breast Cancer Research and Treatment*, **2008**, 112, 229-36	4.4	17

11	Microarray-based DNA profiling to study genomic aberrations. *IUBMB Life*, **2008**, 60, 437-40	4.7	10
10	RAD51 135G-->C modifies breast cancer risk among BRCA2 mutation carriers: results from a combined analysis of 19 studies. *American Journal of Human Genetics*, **2007**, 81, 1186-200	11	204
9	Evaluation of the role of Finnish ataxia-telangiectasia mutations in hereditary predisposition to breast cancer. *Carcinogenesis*, **2007**, 28, 1040-5	4.6	16
8	Characterization of the breast cancer associated ATM 7271T>G (V2424G) mutation by gene expression profiling. *Genes Chromosomes and Cancer*, **2006**, 45, 1169-81	5	14
7	Alternate transcription of the Toll-like receptor signaling cascade. *Genome Biology*, **2006**, 7, R10	18.3	63
6	Genome-wide review of transcriptional complexity in mouse protein kinases and phosphatases. *Genome Biology*, **2006**, 7, R5	18.3	41
5	Acquired RAD51C promoter methylation loss causes PARP inhibitor resistance in high grade serous ovarian carcinoma		1
4	Anatomic position determines oncogenic specificity in melanoma		2
3	Genome Scale Epigenetic Profiling Reveals Five Distinct Subtypes of Colorectal Cancer		1
2	Studying Genomic and Epigenetic Aberrations by Microarray Profiling1-7		
1	Genomic analysis of patient-derived xenograft models reveals intra-tumor heterogeneity in endometrial cancer and can predict tumor growth inhibition with talazoparib		2