Nicola J Waddell

List of Publications by Year
in descending order

158	32,383	23500 58	6454 157
papers	citations	h-index	g-index

176	176	176	47214
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomic and Molecular Analyses Identify Molecular Subtypes of Pancreatic Cancer Recurrence. Gastroenterology, 2022, 162, 320-324.e4.	0.6	26
2	Patient-derived xenograft models capture genomic heterogeneity in endometrial cancer. Genome Medicine, 2022, 14, 3.	3.6	16
3	Re-analysis of genomic data: An overview of the mechanisms and complexities of clinical adoption. Genetics in Medicine, 2022, 24, 798-810.	1.1	26
4	Multiomic profiling of checkpoint inhibitor-treated melanoma: Identifying predictors of response and resistance, and markers of biological discordance. Cancer Cell, 2022, 40, 88-102.e7.	7.7	64
5	qmotif: determination of telomere content from whole-genome sequence data. Bioinformatics Advances, 2022, 2, .	0.9	5
6	Combined Inhibition of G9a and EZH2 Suppresses Tumor Growth via Synergistic Induction of IL24-Mediated Apoptosis. Cancer Research, 2022, 82, 1208-1221.	0.4	8
7	Anatomic position determines oncogenic specificity in melanoma. Nature, 2022, 604, 354-361.	13.7	44
8	Comprehensive genomic and tumour immune profiling reveals potential therapeutic targets in malignant pleural mesothelioma. Genome Medicine, 2022, 14, .	3.6	24
9	Targeting DNA Damage Response and Replication Stress in Pancreatic Cancer. Gastroenterology, 2021, 160, 362-377.e13.	0.6	90
10	CRISPR/Cas9â€mediated genome editing of Schistosoma mansoni acetylcholinesterase. FASEB Journal, 2021, 35, e21205.	0.2	21
11	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. Communications Biology, 2021, 4, 155.	2.0	26
12	ERK and mTORC1 Inhibitors Enhance the Anti-Cancer Capacity of the Octpep-1 Venom-Derived Peptide in Melanoma BRAF(V600E) Mutations. Toxins, 2021, 13, 146.	1.5	7
13	Histone Modifying Enzymes in Gynaecological Cancers. Cancers, 2021, 13, 816.	1.7	10
14	Developing a gene panel for pharmacoresistant epilepsy: a review of epilepsy pharmacogenetics. Pharmacogenomics, 2021, 22, 225-234.	0.6	12
15	Considerations for using population frequency data in germline variant interpretation: Cancer syndrome genes as a model. Human Mutation, 2021, 42, 530-536.	1.1	8
16	The Genomic Landscape of Lobular Breast Cancer. Cancers, 2021, 13, 1950.	1.7	13
17	Radiomics Biomarkers Correlate with CD8 Expression and Predict Immune Signatures in Melanoma Patients. Molecular Cancer Research, 2021, 19, 950-956.	1.5	19
18	Tumor Signature Analysis Implicates Hereditary Cancer Genes in Endometrial Cancer Development. Cancers, 2021, 13, 1762.	1.7	5

#	Article	IF	Citations
19	Targeting novel LSD1-dependent ACE2 demethylation domains inhibits SARS-CoV-2 replication. Cell Discovery, 2021, 7, 37.	3.1	11
20	Evaluation of Crizotinib Treatment in a Patient With Unresectable GOPC-ROS1 Fusion Agminated Spitz Nevi. JAMA Dermatology, 2021, 157, 836-841.	2.0	9
21	Acquired RAD51C Promoter Methylation Loss Causes PARP Inhibitor Resistance in High-Grade Serous Ovarian Carcinoma. Cancer Research, 2021, 81, 4709-4722.	0.4	42
22	Queensland Genomics: an adaptive approach for integrating genomics into a public healthcare system. Npj Genomic Medicine, 2021, 6, 71.	1.7	13
23	Deep learning in cancer diagnosis, prognosis and treatment selection. Genome Medicine, 2021, 13, 152.	3.6	274
24	Verifying explainability of a deep learning tissue classifier trained on RNA-seq data. Scientific Reports, 2021, 11, 2641.	1.6	32
25	Precision diagnostics: Integration of tissue pathology and genomics in cancer. Pathology, 2021, 53, 809-817.	0.3	2
26	Ask the people: developing guidelines for genomic research with Aboriginal and Torres Strait Islander peoples. BMJ Global Health, 2021, 6, e007259.	2.0	8
27	ROR1 and ROR2 expression in pancreatic cancer. BMC Cancer, 2021, 21, 1199.	1.1	4
28	Evaluation of a Genetics Education Program for Health Interpreters: A Pilot Study. Frontiers in Genetics, 2021, 12, 771892.	1.1	2
29	Chromatin interactome mapping at 139 independent breast cancer risk signals. Genome Biology, 2020, 21, 8.	3.8	27
30	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. Nature Communications, 2020, 11, 5259.	5.8	102
31	Pathogenic germline variants are associated with poor survival in stage III/IV melanoma patients. Scientific Reports, 2020, 10, 17687.	1.6	14
32	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.	1.0	13
33	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.	1.6	13
34	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. Npj Breast Cancer, 2020, 6, 33.	2.3	19
35	Queensland Consumersâ€™ Awareness and Understanding of Clinical Genetics Services. Frontiers in Genetics, 2020, 11, 537743.	1.1	4
36	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. Nature Communications, 2020, 11, 2408.	5.8	86

#	Article	IF	Citations
37	APC Mutation Marks an Aggressive Subtype of BRAF Mutant Colorectal Cancers. Cancers, 2020, 12, 1171.	1.7	28
38	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. Cell Reports, 2020, 31, 107625.	2.9	78
39	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.	2.3	14
40	Non-coding RNAs underlie genetic predisposition to breast cancer. Genome Biology, 2020, 21, 7.	3.8	21
41	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	13.7	560
42	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
43	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	9.4	431
44	Tumor CD155 Expression Is Associated with Resistance to Anti-PD1 Immunotherapy in Metastatic Melanoma. Clinical Cancer Research, 2020, 26, 3671-3681.	3.2	53
45	CAF hierarchy driven by pancreatic cancer cell p53-status creates a pro-metastatic and chemoresistant environment via perlecan. Nature Communications, 2019, 10, 3637.	5.8	170
46	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature Communications, 2019, 10, 3163.	5.8	205
47	Targeting CD39 in Cancer Reveals an Extracellular ATP- and Inflammasome-Driven Tumor Immunity. Cancer Discovery, 2019, 9, 1754-1773.	7.7	173
48	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.	6.6	164
49	Whole-genome sequencing reveals clinically relevant insights into the aetiology of familial breast cancers. Annals of Oncology, 2019, 30, 1071-1079.	0.6	64
50	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.	2.3	42
51	Molecular Genomic Profiling of MelanocyticÂNevi. Journal of Investigative Dermatology, 2019, 139, 1762-1768.	0.3	55
52	What does Australiaâ€™s investment in genomics mean for public health?. Australian and New Zealand Journal of Public Health, 2019, 43, 204-206.	0.8	2
53	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.	1.2	25
54	Patterns of Genomic Instability in Breast Cancer. Trends in Pharmacological Sciences, 2019, 40, 198-211.	4.0	68

#	Article	IF	Citations
55	Complex structural rearrangements are present in high-grade dysplastic Barrettâ€™s oesophagus samples. BMC Medical Genomics, 2019, 12, 31.	0.7	19
56	Intratumoural Heterogeneity Underlies Distinct Therapy Responses and Treatment Resistance in Glioblastoma. Cancers, 2019, 11, 190.	1.7	39
57	The immune checkpoint CD96 defines a distinct lymphocyte phenotype and is highly expressed on tumorâ€infiltrating TÂcells. Immunology and Cell Biology, 2019, 97, 152-164.	1.0	29
58	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.	2.3	54
59	A plugin for the Ensembl Variant Effect Predictor that uses MaxEntScan to predict variant spliceogenicity. Bioinformatics, 2019, 35, 2315-2317.	1.8	52
60	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.	0.6	23
61	Phenotypic and molecular dissection of metaplastic breast cancer and the prognostic implications. Journal of Pathology, 2019, 247, 214-227.	2.1	73
62	Abstract 479:BRAFandKRAS mutation define distinct subtypes of the CpG island methylator phenotype in colorectal cancers. , 2019, , .		0
63	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.	1.1	5
64	The Landscape of Somatic Genetic Alterations in Breast Cancers From ATM Germline Mutation Carriers. Journal of the National Cancer Institute, 2018, 110, 1030-1034.	3.0	90
65	Mixed ductalâ€lobular carcinomas: evidence for progression from ductal to lobular morphology. Journal of Pathology, 2018, 244, 460-468.	2.1	31
66	Telomere sequence content can be used to determine ALT activity in tumours. Nucleic Acids Research, 2018, 46, 4903-4918.	6.5	40
67	Malignant cells from pleural fluids in malignant mesothelioma patients reveal novel mutations. Lung Cancer, 2018, 119, 64-70.	0.9	23
68	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.	3.2	79
69	Tailored first-line and second-line CDK4-targeting treatment combinations in mouse models of pancreatic cancer. Gut, 2018, 67, 2142-2155.	6.1	100
70	A2AR Adenosine Signaling Suppresses Natural Killer Cell Maturation in the Tumor Microenvironment. Cancer Research, 2018, 78, 1003-1016.	0.4	269
71	BRAF Mutations in Low-Grade Serous Ovarian Cancer and Response to BRAF Inhibition. JCO Precision Oncology, 2018, 2, 1-14.	1.5	19
72	Jak2V617F and Dnmt3a loss cooperate to induce myelofibrosis through activated enhancer-driven inflammation. Blood, 2018, 132, 2707-2721.	0.6	56

#	Article	IF	Citations
73	<scp>CEP</scp> 55 is a determinant of cell fate during perturbed mitosis in breast cancer. EMBO Molecular Medicine, 2018, 10, .	3.3	59
74	Early Changes in CD4+ T-Cell Activation During Blood-Stage Plasmodium falciparum Infection. Journal of Infectious Diseases, 2018, 218, 1119-1129.	1.9	17
75	Germline and somatic variant identification using BGISEQ-500 and HiSeq X Ten whole genome sequencing. PLoS ONE, 2018, 13, e0190264.	1.1	57
76	The Prognostic Significance of Low-Frequency Somatic Mutations in Metastatic Cutaneous Melanoma. Frontiers in Oncology, 2018, 8, 584.	1.3	14
77	Bone marrow transplantation generates T cellâ€“dependent control of myeloma in mice. Journal of Clinical Investigation, 2018, 129, 106-121.	3.9	49
78	Copy number profiles of paired primary and metastatic colorectal cancers. Oncotarget, 2018, 9, 3394-3405.	0.8	14
79	Whole-genome landscape of pancreatic neuroendocrine tumours. Nature, 2017, 543, 65-71.	13.7	716
80	Unexpected UVR and non-UVR mutation burden in some acral and cutaneous melanomas. Laboratory Investigation, 2017, 97, 130-145.	1.7	40
81	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. Nature Genetics, 2017, 49, 825-833.	9.4	55
82	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	13.7	1,068
83	Mitochondrial mutations and metabolic adaptation in pancreatic cancer. Cancer & Metabolism, 2017, 5, 2.	2.4	51
84	Mutation load in melanoma is affected by <scp>MC</scp>1R genotype. Pigment Cell and Melanoma Research, 2017, 30, 255-258.	1.5	19
85	Interleukin-12 from CD103+ Batf3-Dependent Dendritic Cells Required for NK-Cell Suppression of Metastasis. Cancer Immunology Research, 2017, 5, 1098-1108.	1.6	98
86	Tumor immunoevasion by the conversion of effector NK cells into type 1 innate lymphoid cells. Nature Immunology, 2017, 18, 1004-1015.	7.0	504
87	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.	2.5	14
88	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.	2.6	77
89	EIF1AX and NRAS Mutations Co-occur and Cooperate in Low-Grade Serous Ovarian Carcinomas. Cancer Research, 2017, 77, 4268-4278.	0.4	56
90	Whole exome sequencing of an asbestos-induced wild-type murine model of malignant mesothelioma. BMC Cancer, 2017, 17, 396.	1.1	30

#	Article	IF	Citations
91	Lost in translation: returning germline genetic results in genome-scale cancer research. Genome Medicine, 2017, 9, 41.	3.6	27
92	Hypermutation In Pancreatic Cancer. Gastroenterology, 2017, 152, 68-74.e2.	0.6	174
93	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.	0.8	0
94	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.	2.6	201
95	Mutational signatures in esophageal adenocarcinoma define etiologically distinct subgroups with therapeutic relevance. Nature Genetics, 2016, 48, 1131-1141.	9.4	332
96	A Common Variant at the 14q32 Endometrial Cancer Risk Locus Activates AKT1 through YY1 Binding. American Journal of Human Genetics, 2016, 98, 1159-1169.	2.6	32
97	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, 356-365.	1.3	46
98	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. Cell Reports, 2016, 14, 907-919.	2.9	107
99	Genomic analyses identify molecular subtypes of pancreatic cancer. Nature, 2016, 531, 47-52.	13.7	2,700
100	Abstract A27: Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. , 2016, , .		1
101	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. Journal of Pathology, 2015, 237, 363-378.	2.1	98
102	Wholeâ€“genome characterization of chemoresistant ovarian cancer. Nature, 2015, 521, 489-494.	13.7	1,206
103	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	5.8	266
104	Whole genomes redefine the mutational landscape of pancreatic cancer. Nature, 2015, 518, 495-501.	13.7	2,132
105	PGTools: A Software Suite for Proteogenomic Data Analysis and Visualization. Journal of Proteome Research, 2015, 14, 2255-2266.	1.8	52
106	Recurrent inactivating RASA2 mutations in melanoma. Nature Genetics, 2015, 47, 1408-1410.	9.4	90
107	Comparative microRNA profiling of sporadic and BRCA1 associated basal-like breast cancers. BMC Cancer, 2015, 15, 506.	1.1	12
108	SOX9 regulates ERBB signalling in pancreatic cancer development. Gut, 2015, 64, 1790-1799.	6.1	71

#	Article	IF	Citations
109	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.	1.1	27
110	Abstract 3008: CEP55 is a determinant of genomic instability in aneuploid breast cancer cells and facilitates anti-mitotic drugs resistance by interacting directly with HSF1. , 2015, , .		1
111	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. BioTechniques, 2014, 57, 31-38.	0.8	0
112	Clinical and pathologic features of familial pancreatic cancer. Cancer, 2014, 120, 3669-3675.	2.0	53
113	Genomeâ€wide DNA methylation patterns in pancreatic ductal adenocarcinoma reveal epigenetic deregulation of SLITâ€ROBO, ITGA2 and MET signaling. International Journal of Cancer, 2014, 135, 1110-1118.	2.3	192
114	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. Nature Communications, 2014, 5, 5224.	5.8	236
115	Returning individual research results for genome sequences of pancreatic cancer. Genome Medicine, 2014, 6, 42.	3.6	25
116	Understanding pancreatic cancer genomes. Journal of Hepato-Biliary-Pancreatic Sciences, 2013, 20, 549-556.	1.4	31
117	Evaluating the repair of DNA derived from formalin-fixed paraffin-embedded tissues prior to genomic profiling by SNPâ€“CGH analysis. Laboratory Investigation, 2013, 93, 701-710.	1.7	26
118	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	13.7	8,060
119	Clinical and molecular characterization of HER2 amplified-pancreatic cancer. Genome Medicine, 2013, 5, 78.	3.6	97
120	Neuropilin-2 Promotes Extravasation and Metastasis by Interacting with Endothelial Î±5 Integrin. Cancer Research, 2013, 73, 4579-4590.	0.4	97
121	miR-139-5p is a regulator of metastatic pathways in breast cancer. Rna, 2013, 19, 1767-1780.	1.6	137
122	MicroRNA-182-5p targets a network of genes involved in DNA repair. Rna, 2013, 19, 230-242.	1.6	108
123	Somatic Point Mutation Calling in Low Cellularity Tumors. PLoS ONE, 2013, 8, e74380.	1.1	67
124	Abstract A75: The IMPaCT trial: Individualised Molecular Pancreatic Cancer Therapy. A pilot, randomized, open label Phase II trial assessing first line treatment with gemcitabine or personalized treatment based on tumour molecular signature in patients with metastatic pancreatic cancer.. , 2013, , .		0
125	PINA v2.0: mining interactome modules. Nucleic Acids Research, 2012, 40, D862-D865.	6.5	321
126	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. Nature, 2012, 486, 266-270.	13.7	297

#	Article	IF	Citations
127	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, 5934-5941.	3.3	201
128	Enhanced RAD21 cohesin expression confers poor prognosis in BRCA2 and BRCAX, but not BRCA1 familial breast cancers. Breast Cancer Research, 2012, 14, R69.	2.2	45
129	Germline copy number variants are not associated with globally acquired copy number changes in familial breast tumours. Breast Cancer Research and Treatment, 2012, 134, 1005-1011.	1.1	7
130	Gene expression profiling of tumour epithelial and stromal compartments during breast cancer progression. Breast Cancer Research and Treatment, 2012, 135, 153-165.	1.1	111
131	The application of nonsense-mediated mRNA decay inhibition to the identification of breast cancer susceptibility genes. BMC Cancer, 2012, 12, 246.	1.1	4
132	RON is not a prognostic marker for resectable pancreatic cancer. BMC Cancer, 2012, 12, 395.	1.1	17
133	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	13.7	1,741
134	Morphological and molecular analysis of a breast cancer cluster at the ABC Studio in Toowong. Pathology, 2012, 44, 469-472.	0.3	0
135	Identification of fifteen novel germline variants in theBRCA13â€²UTR reveals a variant in a breast cancer case that introduces a functionalmiR-103target site. Human Mutation, 2012, 33, 1665-1675.	1.1	49
136	qpure: A Tool to Estimate Tumor Cellularity from Genome-Wide Single-Nucleotide Polymorphism Profiles. PLoS ONE, 2012, 7, e45835.	1.1	92
137	Sequencing transcriptomes in toto. Integrative Biology (United Kingdom), 2011, 3, 522.	0.6	16
138	MicroRNAs and their isomiRs function cooperatively to target common biological pathways. Genome Biology, 2011, 12, R126.	13.9	297
139	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.	2.2	45
140	Analysis of Brca1-deficient mouse mammary glands reveals reciprocal regulation of Brca1 and c-kit. Oncogene, 2011, 30, 1597-1607.	2.6	26
141	DNA Methylome of Familial Breast Cancer Identifies Distinct Profiles Defined by Mutation Status. American Journal of Human Genetics, 2010, 86, 420-433.	2.6	80
142	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, 491-496.	1.1	30
143	Subtypes of familial breast tumours revealed by expression and copy number profiling. Breast Cancer Research and Treatment, 2010, 123, 661-677.	1.1	86
144	Gene expression profiling of formalinâ€fixed, paraffinâ€embedded familial breast tumours using the whole genomeâ€DASL assay. Journal of Pathology, 2010, 221, 452-461.	2.1	62

#	Article	IF	Citations
145	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
146	Use of DNAâ€"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.	1.5	9
147	HER3 and downstream pathways are involved in colonization of brain metastases from breast cancer. Breast Cancer Research, 2010, 12, R46.	2.2	122
148	DNA methylome of familial breast cancer identifies distinct profiles defined by mutation status. Breast Cancer Research, 2010, 12, .	2.2	3
149	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, 229-236.	1.1	20
150	Microarrayâ€based DNA profiling to study genomic aberrations. IUBMB Life, 2008, 60, 437-440.	1.5	11
151	Aberrant Expression of E-cadherin in Lobular Carcinomas of the Breast. American Journal of Surgical Pathology, 2008, 32, 773-783.	2.1	160
152	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, 1678-1690.	1.5	108
153	BRCA1 and BRCA2 Missense Variants of High and Low Clinical Significance Influence Lymphoblastoid Cell Line Post-Irradiation Gene Expression. PLoS Genetics, 2008, 4, e1000080.	1.5	12
154	RAD51 135Gâ†'C Modifies Breast Cancer Risk among BRCA2 Mutation Carriers: Results from a Combined Analysis of 19 Studies. American Journal of Human Genetics, 2007, 81, 1186-1200.	2.6	217
155	Alternate transcription of the Toll-like receptor signaling cascade. Genome Biology, 2006, 7, R10.	13.9	66
156	Genome-wide review of transcriptional complexity in mouse protein kinases and phosphatases. Genome Biology, 2006, 7, R5.	13.9	48
157	Evaluation of the role of Finnish ataxia-telangiectasia mutations in hereditary predisposition to breast cancer. Carcinogenesis, 2006, 28, 1040-1045.	1.3	21
158	Characterization of the breast cancer associatedATM7271T>G (V2424G) mutation by gene expression profiling. Genes Chromosomes and Cancer, 2006, 45, 1169-1181.	1.5	17