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	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	13.7	8,060
2	Genomic analyses identify molecular subtypes of pancreatic cancer. Nature, 2016, 531, 47-52.	13.7	2,700
3	Whole genomes redefine the mutational landscape of pancreatic cancer. Nature, 2015, 518, 495-501.	13.7	2,132
4	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
5	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
6	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	13.7	1,741
7	Wholeâ€“genome characterization of chemoresistant ovarian cancer. Nature, 2015, 521, 489-494.	13.7	1,206
8	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	13.7	1,068
9	Whole-genome landscape of pancreatic neuroendocrine tumours. Nature, 2017, 543, 65-71.	13.7	716
10	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	13.7	560
11	Tumor immunoevasion by the conversion of effector NK cells into type 1 innate lymphoid cells. Nature Immunology, 2017, 18, 1004-1015.	7.0	504
12	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	9.4	431
13	Mutational signatures in esophageal adenocarcinoma define etiologically distinct subgroups with therapeutic relevance. Nature Genetics, 2016, 48, 1131-1141.	9.4	332
14	PINA v2.0: mining interactome modules. Nucleic Acids Research, 2012, 40, D862-D865.	6.5	321
15	MicroRNAs and their isomiRs function cooperatively to target common biological pathways. Genome Biology, 2011, 12, R126.	13.9	297
16	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. Nature, 2012, 486, 266-270.	13.7	297
17	Deep learning in cancer diagnosis, prognosis and treatment selection. Genome Medicine, 2021, 13, 152.	3.6	274
18	A2AR Adenosine Signaling Suppresses Natural Killer Cell Maturation in the Tumor Microenvironment. Cancer Research, 2018, 78, 1003-1016.	0.4	269

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19	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	5.8	266
20	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. Nature Communications, 2014, 5, 5224.	5.8	236
21	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
22	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature Communications, 2019, 10, 3163.	5.8	205
23	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
24	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
25	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
26	Hypermutation In Pancreatic Cancer. Gastroenterology, 2017, 152, 68-74.e2.	0.6	174
27	Targeting CD39 in Cancer Reveals an Extracellular ATP- and Inflammasome-Driven Tumor Immunity. Cancer Discovery, 2019, 9, 1754-1773.	7.7	173
28	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
29	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
30	Aberrant Expression of E-cadherin in Lobular Carcinomas of the Breast. American Journal of Surgical Pathology, 2008, 32, 773-783.	2.1	160
31	miR-139-5p is a regulator of metastatic pathways in breast cancer. Rna, 2013, 19, 1767-1780.	1.6	137
32	HER3 and downstream pathways are involved in colonization of brain metastases from breast cancer. Breast Cancer Research, 2010, 12, R46.	2.2	122
33	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
34	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
35	MicroRNA-182-5p targets a network of genes involved in DNA repair. Rna, 2013, 19, 230-242.	1.6	108
36	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. Cell Reports, 2016, 14, 907-919.	2.9	107

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37	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. Nature Communications, 2020, 11, 5259.	5.8	102
38	Tailored first-line and second-line CDK4-targeting treatment combinations in mouse models of pancreatic cancer. Gut, 2018, 67, 2142-2155.	6.1	100
39	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
40	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
41	Clinical and molecular characterization of HER2 amplified-pancreatic cancer. Genome Medicine, 2013, 5, 78.	3.6	97
42	Neuropilin-2 Promotes Extravasation and Metastasis by Interacting with Endothelial Î±5 Integrin. Cancer Research, 2013, 73, 4579-4590.	0.4	97
43	qpure: A Tool to Estimate Tumor Cellularity from Genome-Wide Single-Nucleotide Polymorphism Profiles. PLoS ONE, 2012, 7, e45835.	1.1	92
44	Recurrent inactivating RASA2 mutations in melanoma. Nature Genetics, 2015, 47, 1408-1410.	9.4	90
45	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
46	Targeting DNA Damage Response and Replication Stress in Pancreatic Cancer. Gastroenterology, 2021, 160, 362-377.e13.	0.6	90
47	Subtypes of familial breast tumours revealed by expression and copy number profiling. Breast Cancer Research and Treatment, 2010, 123, 661-677.	1.1	86
48	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. Nature Communications, 2020, 11, 2408.	5.8	86
49	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
50	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
51	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. Cell Reports, 2020, 31, 107625.	2.9	78
52	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
53	Phenotypic and molecular dissection of metaplastic breast cancer and the prognostic implications. Journal of Pathology, 2019, 247, 214-227.	2.1	73
54	SOX9 regulates ERBB signalling in pancreatic cancer development. Gut, 2015, 64, 1790-1799.	6.1	71

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55	Patterns of Genomic Instability in Breast Cancer. Trends in Pharmacological Sciences, 2019, 40, 198-211.	4.0	68
56	Somatic Point Mutation Calling in Low Cellularity Tumors. PLoS ONE, 2013, 8, e74380.	1.1	67
57	Alternate transcription of the Toll-like receptor signaling cascade. Genome Biology, 2006, 7, R10.	13.9	66
58	Whole-genome sequencing reveals clinically relevant insights into the aetiology of familial breast cancers. Annals of Oncology, 2019, 30, 1071-1079.	0.6	64
59	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
60	Gene expression profiling of formalinâ€fixed, paraffinâ€embedded familial breast tumours using the whole genomeâ€ÐASL assay. Journal of Pathology, 2010, 221, 452-461.	2.1	62
61	<scp>CEP</scp> 55 is a determinant of cell fate during perturbed mitosis in breast cancer. EMBO Molecular Medicine, 2018, 10, .	3.3	59
62	Germline and somatic variant identification using BGISEQ-500 and HiSeq X Ten whole genome sequencing. PLoS ONE, 2018, 13, e0190264.	1.1	57
63	EIF1AX and NRAS Mutations Co-occur and Cooperate in Low-Grade Serous Ovarian Carcinomas. Cancer Research, 2017, 77, 4268-4278.	0.4	56
64	Jak2V617F and Dnmt3a loss cooperate to induce myelofibrosis through activated enhancer-driven inflammation. Blood, 2018, 132, 2707-2721.	0.6	56
65	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. Nature Genetics, 2017, 49, 825-833.	9.4	55
66	Molecular Genomic Profiling of MelanocyticÂNevi. Journal of Investigative Dermatology, 2019, 139, 1762-1768.	0.3	55
67	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
68	Clinical and pathologic features of familial pancreatic cancer. Cancer, 2014, 120, 3669-3675.	2.0	53
69	Tumor CD155 Expression Is Associated with Resistance to Anti-PD1 Immunotherapy in Metastatic Melanoma. Clinical Cancer Research, 2020, 26, 3671-3681.	3.2	53
70	PGTools: A Software Suite for Proteogenomic Data Analysis and Visualization. Journal of Proteome Research, 2015, 14, 2255-2266.	1.8	52
71	A plugin for the Ensembl Variant Effect Predictor that uses MaxEntScan to predict variant spliceogenicity. Bioinformatics, 2019, 35, 2315-2317.	1.8	52
72	Mitochondrial mutations and metabolic adaptation in pancreatic cancer. Cancer & Metabolism, 2017, 5, 2.	2.4	51

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73	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
74	Bone marrow transplantation generates T cellâ€“dependent control of myeloma in mice. Journal of Clinical Investigation, 2018, 129, 106-121.	3.9	49
75	Genome-wide review of transcriptional complexity in mouse protein kinases and phosphatases. Genome Biology, 2006, 7, R5.	13.9	48
76	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
77	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
78	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
79	Anatomic position determines oncogenic specificity in melanoma. Nature, 2022, 604, 354-361.	13.7	44
80	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
81	Acquired RAD51C Promoter Methylation Loss Causes PARP Inhibitor Resistance in High-Grade Serous Ovarian Carcinoma. Cancer Research, 2021, 81, 4709-4722.	0.4	42
82	Unexpected UVR and non-UVR mutation burden in some acral and cutaneous melanomas. Laboratory Investigation, 2017, 97, 130-145.	1.7	40
83	Telomere sequence content can be used to determine ALT activity in tumours. Nucleic Acids Research, 2018, 46, 4903-4918.	6.5	40
84	Intratumoural Heterogeneity Underlies Distinct Therapy Responses and Treatment Resistance in Glioblastoma. Cancers, 2019, 11, 190.	1.7	39
85	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
86	Verifying explainability of a deep learning tissue classifier trained on RNA-seq data. Scientific Reports, 2021, 11, 2641.	1.6	32
87	Understanding pancreatic cancer genomes. Journal of Hepato-Biliary-Pancreatic Sciences, 2013, 20, 549-556.	1.4	31
88	Mixed ductalâ€lobular carcinomas: evidence for progression from ductal to lobular morphology. Journal of Pathology, 2018, 244, 460-468.	2.1	31
89	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
90	Whole exome sequencing of an asbestos-induced wild-type murine model of malignant mesothelioma. BMC Cancer, 2017, 17, 396.	1.1	30

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91	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
92	APC Mutation Marks an Aggressive Subtype of BRAF Mutant Colorectal Cancers. Cancers, 2020, 12, 1171.	1.7	28
93	Lost in translation: returning germline genetic results in genome-scale cancer research. Genome Medicine, 2017, 9, 41.	3.6	27
94	Chromatin interactome mapping at 139 independent breast cancer risk signals. Genome Biology, 2020, 21, 8.	3.8	27
95	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
96	Analysis of Brca1-deficient mouse mammary glands reveals reciprocal regulation of Brca1 and c-kit. Oncogene, 2011, 30, 1597-1607.	2.6	26
97	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
98	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. Communications Biology, 2021, 4, 155.	2.0	26
99	Genomic and Molecular Analyses Identify Molecular Subtypes of Pancreatic Cancer Recurrence. Gastroenterology, 2022, 162, 320-324.e4.	0.6	26
100	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
101	Returning individual research results for genome sequences of pancreatic cancer. Genome Medicine, 2014, 6, 42.	3.6	25
102	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
103	Comprehensive genomic and tumour immune profiling reveals potential therapeutic targets in malignant pleural mesothelioma. Genome Medicine, 2022, 14, .	3.6	24
104	Malignant cells from pleural fluids in malignant mesothelioma patients reveal novel mutations. Lung Cancer, 2018, 119, 64-70.	0.9	23
105	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
106	Evaluation of the role of Finnish ataxia-telangiectasia mutations in hereditary predisposition to breast cancer. Carcinogenesis, 2006, 28, 1040-1045.	1.3	21
107	Non-coding RNAs underlie genetic predisposition to breast cancer. Genome Biology, 2020, 21, 7.	3.8	21
108	CRISPR/Cas9â€mediated genome editing of Schistosoma mansoni acetylcholinesterase. FASEB Journal, 2021, 35, e21205.	0.2	21

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109	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
110	Mutation load in melanoma is affected by <scp>MC</scp>1R genotype. Pigment Cell and Melanoma Research, 2017, 30, 255-258.	1.5	19
111	BRAF Mutations in Low-Grade Serous Ovarian Cancer and Response to BRAF Inhibition. JCO Precision Oncology, 2018, 2, 1-14.	1.5	19
112	Complex structural rearrangements are present in high-grade dysplastic Barrettâ€™s oesophagus samples. BMC Medical Genomics, 2019, 12, 31.	0.7	19
113	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. Npj Breast Cancer, 2020, 6, 33.	2.3	19
114	Radiomics Biomarkers Correlate with CD8 Expression and Predict Immune Signatures in Melanoma Patients. Molecular Cancer Research, 2021, 19, 950-956.	1.5	19
115	Characterization of the breast cancer associatedATM7271T>G (V2424G) mutation by gene expression profiling. Genes Chromosomes and Cancer, 2006, 45, 1169-1181.	1.5	17
116	RON is not a prognostic marker for resectable pancreatic cancer. BMC Cancer, 2012, 12, 395.	1.1	17
117	Early Changes in CD4+ T-Cell Activation During Blood-Stage Plasmodium falciparum Infection. Journal of Infectious Diseases, 2018, 218, 1119-1129.	1.9	17
118	Sequencing transcriptomes in toto. Integrative Biology (United Kingdom), 2011, 3, 522.	0.6	16
119	Patient-derived xenograft models capture genomic heterogeneity in endometrial cancer. Genome Medicine, 2022, 14, 3.	3.6	16
120	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
121	The Prognostic Significance of Low-Frequency Somatic Mutations in Metastatic Cutaneous Melanoma. Frontiers in Oncology, 2018, 8, 584.	1.3	14
122	Pathogenic germline variants are associated with poor survival in stage III/IV melanoma patients. Scientific Reports, 2020, 10, 17687.	1.6	14
123	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
124	Copy number profiles of paired primary and metastatic colorectal cancers. Oncotarget, 2018, 9, 3394-3405.	0.8	14
125	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
126	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

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127	The Genomic Landscape of Lobular Breast Cancer. Cancers, 2021, 13, 1950.	1.7	13
128	Queensland Genomics: an adaptive approach for integrating genomics into a public healthcare system. Npj Genomic Medicine, 2021, 6, 71.	1.7	13
129	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
130	Comparative microRNA profiling of sporadic and BRCA1 associated basal-like breast cancers. BMC Cancer, 2015, 15, 506.	1.1	12
131	Developing a gene panel for pharmacoresistant epilepsy: a review of epilepsy pharmacogenetics. Pharmacogenomics, 2021, 22, 225-234.	0.6	12
132	Microarrayâ€based DNA profiling to study genomic aberrations. IUBMB Life, 2008, 60, 437-440.	1.5	11
133	Targeting novel LSD1-dependent ACE2 demethylation domains inhibits SARS-CoV-2 replication. Cell Discovery, 2021, 7, 37.	3.1	11
134	Histone Modifying Enzymes in Gynaecological Cancers. Cancers, 2021, 13, 816.	1.7	10
135	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
136	Evaluation of Crizotinib Treatment in a Patient With Unresectable GOPC-ROS1 Fusion Agminated Spitz Nevi. JAMA Dermatology, 2021, 157, 836-841.	2.0	9
137	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
138	Ask the people: developing guidelines for genomic research with Aboriginal and Torres Strait Islander peoples. BMJ Global Health, 2021, 6, e007259.	2.0	8
139	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
140	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
141	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
142	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
143	Tumor Signature Analysis Implicates Hereditary Cancer Genes in Endometrial Cancer Development. Cancers, 2021, 13, 1762.	1.7	5
144	qmotif: determination of telomere content from whole-genome sequence data. Bioinformatics Advances, 2022, 2, .	0.9	5

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145	The application of nonsense-mediated mRNA decay inhibition to the identification of breast cancer susceptibility genes. BMC Cancer, 2012, 12, 246.	1.1	4
146	Queensland Consumersâ€™ Awareness and Understanding of Clinical Genetics Services. Frontiers in Genetics, 2020, 11, 537743.	1.1	4
147	ROR1 and ROR2 expression in pancreatic cancer. BMC Cancer, 2021, 21, 1199.	1.1	4
148	DNA methylome of familial breast cancer identifies distinct profiles defined by mutation status. Breast Cancer Research, 2010, 12, .	2.2	3
149	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
150	Precision diagnostics: Integration of tissue pathology and genomics in cancer. Pathology, 2021, 53, 809-817.	0.3	2
151	Evaluation of a Genetics Education Program for Health Interpreters: A Pilot Study. Frontiers in Genetics, 2021, 12, 771892.	1.1	2
152	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
153	Abstract A27: Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. , 2016, , .		1
154	Morphological and molecular analysis of a breast cancer cluster at the ABC Studio in Toowong. Pathology, 2012, 44, 469-472.	0.3	0
155	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. BioTechniques, 2014, 57, 31-38.	0.8	0
156	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
157	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
158	Abstract 479:BRAFandKRAS mutation define distinct subtypes of the CpG island methylator phenotype in colorectal cancers. , 2019, , .		0