

Charlotte K Y Ng

List of Publications by Citations

Source: <https://exaly.com/author-pdf/5315203/charlotte-k-y-ng-publications-by-citations.pdf>

Version: 2024-04-25

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

138
papers

7,054
citations

47
h-index

81
g-index

183
ext. papers

8,851
ext. citations

9.2
avg, IF

5.46
L-index

#	Paper	IF	Citations
138	Mutation tracking in circulating tumor DNA predicts relapse in early breast cancer. <i>Science Translational Medicine</i> , 2015 , 7, 302ra133	17.5	679
137	Cerebrospinal fluid-derived circulating tumour DNA better represents the genomic alterations of brain tumours than plasma. <i>Nature Communications</i> , 2015 , 6, 8839	17.4	416
136	Capturing intra-tumor genetic heterogeneity by de novo mutation profiling of circulating cell-free tumor DNA: a proof-of-principle. <i>Annals of Oncology</i> , 2014 , 25, 1729-1735	10.3	258
135	Genomic characterization of metastatic breast cancers. <i>Nature</i> , 2019 , 569, 560-564	50.4	256
134	Spatial and temporal heterogeneity in high-grade serous ovarian cancer: a phylogenetic analysis. <i>PLoS Medicine</i> , 2015 , 12, e1001789	11.6	230
133	Chromosomal instability determines taxane response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 8671-6	11.5	192
132	Breast cancer intra-tumor heterogeneity. <i>Breast Cancer Research</i> , 2014 , 16, 210	8.3	188
131	A framework to rank genomic alterations as targets for cancer precision medicine: the ESMO Scale for Clinical Actionability of molecular Targets (ESCAT). <i>Annals of Oncology</i> , 2018 , 29, 1895-1902	10.3	181
130	Organoid Models of Human Liver Cancers Derived from Tumor Needle Biopsies. <i>Cell Reports</i> , 2018 , 24, 1363-1376	10.6	166
129	Hotspot activating PRKD1 somatic mutations in polymorphous low-grade adenocarcinomas of the salivary glands. <i>Nature Genetics</i> , 2014 , 46, 1166-9	36.3	150
128	Progression from ductal carcinoma in situ to invasive breast cancer: revisited. <i>Molecular Oncology</i> , 2013 , 7, 859-69	7.9	146
127	Diverse and Reversion Mutations in Circulating Cell-Free DNA of Therapy-Resistant Breast or Ovarian Cancer. <i>Clinical Cancer Research</i> , 2017 , 23, 6708-6720	12.9	132
126	SF3B1 mutations constitute a novel therapeutic target in breast cancer. <i>Journal of Pathology</i> , 2015 , 235, 571-80	9.4	124
125	Genomic analysis of genetic heterogeneity and evolution in high-grade serous ovarian carcinoma. <i>Oncogene</i> , 2010 , 29, 4905-13	9.2	122
124	Massively Parallel Sequencing-Based Clonality Analysis of Synchronous Endometrioid Endometrial and Ovarian Carcinomas. <i>Journal of the National Cancer Institute</i> , 2016 , 108, djv427	9.7	111
123	A recurrent neomorphic mutation in MYOD1 defines a clinically aggressive subset of embryonal rhabdomyosarcoma associated with PI3K-AKT pathway mutations. <i>Nature Genetics</i> , 2014 , 46, 595-600	36.3	107
122	Genomic landscape of adenoid cystic carcinoma of the breast. <i>Journal of Pathology</i> , 2015 , 237, 179-89	9.4	101

121	The protein histidine phosphatase LHPP is a tumour suppressor. <i>Nature</i> , 2018 , 555, 678-682	50.4	96
120	Benchmarking mutation effect prediction algorithms using functionally validated cancer-related missense mutations. <i>Genome Biology</i> , 2014 , 15, 484	18.3	95
119	The Landscape of Somatic Genetic Alterations in Metaplastic Breast Carcinomas. <i>Clinical Cancer Research</i> , 2017 , 23, 3859-3870	12.9	92
118	The Genomic Landscape of Male Breast Cancers. <i>Clinical Cancer Research</i> , 2016 , 22, 4045-56	12.9	85
117	Intra-tumor genetic heterogeneity and alternative driver genetic alterations in breast cancers with heterogeneous HER2 gene amplification. <i>Genome Biology</i> , 2015 , 16, 107	18.3	83
116	Whole-genome single-cell copy number profiling from formalin-fixed paraffin-embedded samples. <i>Nature Medicine</i> , 2017 , 23, 376-385	50.5	82
115	Recurrent hotspot mutations in HRAS Q61 and PI3K-AKT pathway genes as drivers of breast adenomyoepitheliomas. <i>Nature Communications</i> , 2018 , 9, 1816	17.4	82
114	Massively parallel sequencing of phyllodes tumours of the breast reveals actionable mutations, and TERT promoter hotspot mutations and TERT gene amplification as likely drivers of progression. <i>Journal of Pathology</i> , 2016 , 238, 508-18	9.4	80
113	Characterization of the genomic features and expressed fusion genes in micropapillary carcinomas of the breast. <i>Journal of Pathology</i> , 2014 , 232, 553-65	9.4	75
112	Breast cancer genomics from microarrays to massively parallel sequencing: paradigms and new insights. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	72
111	Tandem duplication of chromosomal segments is common in ovarian and breast cancer genomes. <i>Journal of Pathology</i> , 2012 , 227, 446-55	9.4	72
110	Uterine adenocarcinomas are mesenchymal neoplasms. <i>Journal of Pathology</i> , 2016 , 238, 381-8	9.4	70
109	IDH2 Mutations Define a Unique Subtype of Breast Cancer with Altered Nuclear Polarity. <i>Cancer Research</i> , 2016 , 76, 7118-7129	10.1	70
108	Genetic Heterogeneity in Therapy-Naïve Synchronous Primary Breast Cancers and Their Metastases. <i>Clinical Cancer Research</i> , 2017 , 23, 4402-4415	12.9	69
107	Cancer Diagnosis Using a Liquid Biopsy: Challenges and Expectations. <i>Diagnostics</i> , 2018 , 8,	3.8	69
106	Genetic alterations of triple negative breast cancer by targeted next-generation sequencing and correlation with tumor morphology. <i>Modern Pathology</i> , 2016 , 29, 476-88	9.8	67
105	HER2 Reactivation through Acquisition of the HER2 L755S Mutation as a Mechanism of Acquired Resistance to HER2-targeted Therapy in HER2 Breast Cancer. <i>Clinical Cancer Research</i> , 2017 , 23, 5123-5134	12.9	64
104	Mechanism of action of a WWTR1(TAZ)-CAMTA1 fusion oncoprotein. <i>Oncogene</i> , 2016 , 35, 929-38	9.2	63

103	Intra-tumour genetic heterogeneity and poor chemoradiotherapy response in cervical cancer. <i>British Journal of Cancer</i> , 2011 , 104, 361-8	8.7	58
102	Breast cancer intratumor genetic heterogeneity: causes and implications. <i>Expert Review of Anticancer Therapy</i> , 2012 , 12, 1021-32	3.5	57
101	Metaplastic breast carcinomas display genomic and transcriptomic heterogeneity [corrected].. <i>Modern Pathology</i> , 2015 , 28, 340-51	9.8	56
100	Loss of osteoclasts contributes to development of osteosarcoma pulmonary metastases. <i>Cancer Research</i> , 2010 , 70, 7063-72	10.1	56
99	Genomic profiling of histological special types of breast cancer. <i>Breast Cancer Research and Treatment</i> , 2013 , 142, 257-69	4.4	55
98	Reliability of Whole-Exome Sequencing for Assessing Intratumor Genetic Heterogeneity. <i>Cell Reports</i> , 2018 , 25, 1446-1457	10.6	55
97	Genetic events in the progression of adenoid cystic carcinoma of the breast to high-grade triple-negative breast cancer. <i>Modern Pathology</i> , 2016 , 29, 1292-1305	9.8	52
96	TP53 Mutational Spectrum in Endometrioid and Serous Endometrial Cancers. <i>International Journal of Gynecological Pathology</i> , 2016 , 35, 289-300	3.2	51
95	Genetic profiling using plasma-derived cell-free DNA in therapy-naïve hepatocellular carcinoma patients: a pilot study. <i>Annals of Oncology</i> , 2018 , 29, 1286-1291	10.3	49
94	The Role of Long Non-Coding RNAs in Hepatocarcinogenesis. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	49
93	Metaplastic breast carcinoma: more than a special type. <i>Nature Reviews Cancer</i> , 2014 , 14, 147-8	31.3	49
92	The role of tandem duplicator phenotype in tumour evolution in high-grade serous ovarian cancer. <i>Journal of Pathology</i> , 2012 , 226, 703-12	9.4	48
91	MYBL1 rearrangements and MYB amplification in breast adenoid cystic carcinomas lacking the MYB-NFIB fusion gene. <i>Journal of Pathology</i> , 2018 , 244, 143-150	9.4	46
90	The repertoire of somatic genetic alterations of acinic cell carcinomas of the breast: an exploratory, hypothesis-generating study. <i>Journal of Pathology</i> , 2015 , 237, 166-78	9.4	42
89	Microglandular adenosis associated with triple-negative breast cancer is a neoplastic lesion of triple-negative phenotype harbouring TP53 somatic mutations. <i>Journal of Pathology</i> , 2016 , 238, 677-88	9.4	42
88	The Genomic Landscape of Mucinous Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2019 , 111, 737-741	9.7	41
87	Integrative genomic and transcriptomic characterization of papillary carcinomas of the breast. <i>Molecular Oncology</i> , 2014 , 8, 1588-602	7.9	38
86	Genomic and transcriptomic heterogeneity in metaplastic carcinomas of the breast. <i>Npj Breast Cancer</i> , 2017 , 3, 48	7.8	38

85	Mutation Profiling of Key Cancer Genes in Primary Breast Cancers and Their Distant Metastases. <i>Cancer Research</i> , 2018 , 78, 3112-3121	10.1	37
84	PI3K pathway activation in high-grade ductal carcinoma in situ—implications for progression to invasive breast carcinoma. <i>Clinical Cancer Research</i> , 2014 , 20, 2326-37	12.9	37
83	Targeted capture massively parallel sequencing analysis of LCIS and invasive lobular cancer: Repertoire of somatic genetic alterations and clonal relationships. <i>Molecular Oncology</i> , 2016 , 10, 360-70	7.9	36
82	Bi-allelic alterations in DNA repair genes underpin homologous recombination DNA repair defects in breast cancer. <i>Journal of Pathology</i> , 2017 , 242, 165-177	9.4	35
81	The genetic landscape of breast carcinomas with neuroendocrine differentiation. <i>Journal of Pathology</i> , 2017 , 241, 405-419	9.4	35
80	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. <i>Molecular Oncology</i> , 2015 , 9, 115-27	7.9	35
79	Establishing the origin of metastatic deposits in the setting of multiple primary malignancies: the role of massively parallel sequencing. <i>Molecular Oncology</i> , 2014 , 8, 150-8	7.9	34
78	Genetic analysis of microglandular adenosis and acinic cell carcinomas of the breast provides evidence for the existence of a low-grade triple-negative breast neoplasia family. <i>Modern Pathology</i> , 2017 , 30, 69-84	9.8	34
77	Phyllodes tumors with and without fibroadenoma-like areas display distinct genomic features and may evolve through distinct pathways. <i>Npj Breast Cancer</i> , 2017 , 3, 40	7.8	33
76	Comprehensive clinical and molecular analyses of neuroendocrine carcinomas of the breast. <i>Modern Pathology</i> , 2018 , 31, 68-82	9.8	32
75	Proteasome Addiction Defined in Ewing Sarcoma Is Effectively Targeted by a Novel Class of 19S Proteasome Inhibitors. <i>Cancer Research</i> , 2016 , 76, 4525-34	10.1	31
74	Circulating Cell-Free DNA in Hepatocellular Carcinoma: Current Insights and Outlook. <i>Frontiers in Medicine</i> , 2018 , 5, 78	4.9	31
73	Leiomyoma with bizarre nuclei: a morphological, immunohistochemical and molecular analysis of 31 cases. <i>Modern Pathology</i> , 2017 , 30, 1476-1488	9.8	31
72	Lobular Carcinomas Display Intralesion Genetic Heterogeneity and Clonal Evolution in the Progression to Invasive Lobular Carcinoma. <i>Clinical Cancer Research</i> , 2019 , 25, 674-686	12.9	31
71	High expression of HOXA13 correlates with poorly differentiated hepatocellular carcinomas and modulates sorafenib response in in vitro models. <i>Laboratory Investigation</i> , 2018 , 98, 95-105	5.9	30
70	Neoantigen prediction and computational perspectives towards clinical benefit: recommendations from the ESMO Precision Medicine Working Group. <i>Annals of Oncology</i> , 2020 , 31, 978-990	10.3	29
69	High-throughput sequencing of nodal marginal zone lymphomas identifies recurrent BRAF mutations. <i>Leukemia</i> , 2018 , 32, 2412-2426	10.7	29
68	Gene expression profiling of lobular carcinoma in situ reveals candidate precursor genes for invasion. <i>Molecular Oncology</i> , 2015 , 9, 772-82	7.9	29

67	Structural analysis of the genome of breast cancer cell line ZR-75-30 identifies twelve expressed fusion genes. <i>BMC Genomics</i> , 2012 , 13, 719	4.5	28
66	Genetic heterogeneity and actionable mutations in HER2-positive primary breast cancers and their brain metastases. <i>Oncotarget</i> , 2018 , 9, 20617-20630	3.3	26
65	HMGA1 Expression in Human Hepatocellular Carcinoma Correlates with Poor Prognosis and Promotes Tumor Growth and Migration in in vitro Models. <i>Neoplasia</i> , 2016 , 18, 724-731	6.4	25
64	Are acinic cell carcinomas of the breast and salivary glands distinct diseases?. <i>Histopathology</i> , 2015 , 67, 529-37	7.3	25
63	Contralateral breast cancers: Independent cancers or metastases?. <i>International Journal of Cancer</i> , 2018 , 142, 347-356	7.5	23
62	Massively parallel sequencing analysis of synchronous fibroepithelial lesions supports the concept of progression from fibroadenoma to phyllodes tumor. <i>Npj Breast Cancer</i> , 2016 , 2, 16035	7.8	23
61	Infiltration by myeloperoxidase-positive neutrophils is an independent prognostic factor in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2019 , 177, 581-589	4.4	22
60	LATS1 but not LATS2 represses autophagy by a kinase-independent scaffold function. <i>Nature Communications</i> , 2019 , 10, 5755	17.4	22
59	The repertoire of genetic alterations in salivary duct carcinoma including a novel HNRNP3-ALK rearrangement. <i>Human Pathology</i> , 2019 , 88, 66-77	3.7	21
58	Genomic Analysis Revealed New Oncogenic Signatures in -Mutant Hepatocellular Carcinoma. <i>Frontiers in Genetics</i> , 2018 , 9, 2	4.5	21
57	The Tumor Profiler Study: integrated, multi-omic, functional tumor profiling for clinical decision support. <i>Cancer Cell</i> , 2021 , 39, 288-293	24.3	21
56	Lack of PRKD2 and PRKD3 kinase domain somatic mutations in PRKD1 wild-type classic polymorphous low-grade adenocarcinomas of the salivary gland. <i>Histopathology</i> , 2016 , 68, 1055-62	7.3	21
55	Infiltrating epitheliosis of the breast: characterization of histological features, immunophenotype and genomic profile. <i>Histopathology</i> , 2016 , 68, 1030-9	7.3	21
54	Patient-derived xenografts and organoids model therapy response in prostate cancer. <i>Nature Communications</i> , 2021 , 12, 1117	17.4	18
53	High Expression of FAP in Colorectal Cancer Is Associated With Angiogenesis and Immunoregulation Processes. <i>Frontiers in Oncology</i> , 2020 , 10, 979	5.3	17
52	Phosphoprotein enriched in diabetes (PED/PEA15) promotes migration in hepatocellular carcinoma and confers resistance to sorafenib. <i>Cell Death and Disease</i> , 2017 , 8, e3138	9.8	17
51	DNA Copy Number Aberrations, and Human Papillomavirus Status in Penile Carcinoma. Clinico-Pathological Correlations and Potential Driver Genes. <i>PLoS ONE</i> , 2016 , 11, e0146740	3.7	17
50	Response to dual HER2 blockade in a patient with HER3-mutant metastatic breast cancer. <i>Annals of Oncology</i> , 2015 , 26, 1704-9	10.3	16

49	Resolving quandaries: basaloid adenoid cystic carcinoma or breast cylindroma? The role of massively parallel sequencing. <i>Histopathology</i> , 2016 , 68, 262-71	7.3	16
48	Hepatocellular Carcinoma Xenografts Established From Needle Biopsies Preserve the Characteristics of the Originating Tumors. <i>Hepatology Communications</i> , 2019 , 3, 971-986	6	15
47	PIKING the type and pattern of PI3K pathway mutations in endometrioid endometrial carcinomas. <i>Gynecologic Oncology</i> , 2015 , 137, 321-8	4.9	14
46	Predictive performance of microarray gene signatures: impact of tumor heterogeneity and multiple mechanisms of drug resistance. <i>Cancer Research</i> , 2014 , 74, 2946-2961	10.1	14
45	Vascular endothelial growth factor A amplification in colorectal cancer is associated with reduced M1 and M2 macrophages and diminished PD-1-expressing lymphocytes. <i>PLoS ONE</i> , 2017 , 12, e0175563	3.7	12
44	Therapeutic Targeting of CD146/MCAM Reduces Bone Metastasis in Prostate Cancer. <i>Molecular Cancer Research</i> , 2019 , 17, 1049-1062	6.6	12
43	NGS-pipe: a flexible, easily extendable and highly configurable framework for NGS analysis. <i>Bioinformatics</i> , 2018 , 34, 107-108	7.2	11
42	The Dilemma of HER2 Double-equivocal Breast Carcinomas: Genomic Profiling and Implications for Treatment. <i>American Journal of Surgical Pathology</i> , 2018 , 42, 1190-1200	6.7	10
41	Diagnostic Targeted Sequencing Panel for Hepatocellular Carcinoma Genomic Screening. <i>Journal of Molecular Diagnostics</i> , 2018 , 20, 836-848	5.1	9
40	Expression of RET is associated with Oestrogen receptor expression but lacks prognostic significance in breast cancer. <i>BMC Cancer</i> , 2019 , 19, 41	4.8	8
39	SCIM: universal single-cell matching with unpaired feature sets. <i>Bioinformatics</i> , 2020 , 36, i919-i927	7.2	8
38	Preoperative plasma fatty acid metabolites inform risk of prostate cancer progression and may be used for personalized patient stratification. <i>BMC Cancer</i> , 2019 , 19, 1216	4.8	8
37	Nectin-4 Expression Is an Independent Prognostic Biomarker and Associated With Better Survival in Triple-Negative Breast Cancer. <i>Frontiers in Medicine</i> , 2019 , 6, 200	4.9	7
36	Radiogenomics Analysis of Intratumor Heterogeneity in a Patient With High-Grade Serous Ovarian Cancer. <i>JCO Precision Oncology</i> , 2019 , 3,	3.6	7
35	Adenylosuccinate lyase is oncogenic in colorectal cancer by causing mitochondrial dysfunction and independent activation of NRF2 and mTOR-MYC-axis. <i>Theranostics</i> , 2021 , 11, 4011-4029	12.1	7
34	Genetic analysis of uterine adenocarcinomas and phyllodes tumors of the breast. <i>Molecular Oncology</i> , 2017 , 11, 913-926	7.9	6
33	Pregnancy at early age is associated with a reduction of progesterone-responsive cells and epithelial Wnt signaling in human breast tissue. <i>Oncotarget</i> , 2017 , 8, 22353-22360	3.3	6
32	High-resolution genomic profiling of thyroid lesions uncovers preferential copy number gains affecting mitochondrial biogenesis loci in the oncogenic variants. <i>American Journal of Cancer Research</i> , 2015 , 5, 1954-71	4.4	6

31	Genetic Alterations in Benign Breast Biopsies of Subsequent Breast Cancer Patients. <i>Frontiers in Medicine</i> , 2019 , 6, 166	4.9	5
30	PipeIT: A Singularity Container for Molecular Diagnostic Somatic Variant Calling on the Ion Torrent Next-Generation Sequencing Platform. <i>Journal of Molecular Diagnostics</i> , 2019 , 21, 884-894	5.1	5
29	RNASeq analysis reveals biological processes governing the clinical behaviour of endometrioid and serous endometrial cancers. <i>European Journal of Cancer</i> , 2016 , 64, 149-58	7.5	4
28	Prognostic signatures in breast cancer: correlation does not imply causation. <i>Breast Cancer Research</i> , 2012 , 14, 313	8.3	4
27	Stroma Transcriptomic and Proteomic Profile of Prostate Cancer Metastasis Xenograft Models Reveals Prognostic Value of Stroma Signatures. <i>Cancers</i> , 2020 , 12,	6.6	4
26	Abstract S4-03: A functional assay for homologous recombination (HR) DNA repair and whole exome sequencing reveal that HR-defective sporadic breast cancers are enriched for genetic alterations in DNA repair genes 2016 ,		3
25	Infiltration by IL22-Producing T Cells Promotes Neutrophil Recruitment and Predicts Favorable Clinical Outcome in Human Colorectal Cancer. <i>Cancer Immunology Research</i> , 2020 , 8, 1452-1462	12.5	3
24	Transcriptional Enhancer Factor Domain Family member 4 Exerts an Oncogenic Role in Hepatocellular Carcinoma by Hippo-Independent Regulation of Heat Shock Protein 70 Family Members. <i>Hepatology Communications</i> , 2021 , 5, 661-674	6	3
23	Alterations in homologous recombination repair genes in prostate cancer brain metastases.. <i>Nature Communications</i> , 2022 , 13, 2400	17.4	3
22	Abstract 927: Targeted capture next generation sequencing of fresh frozen lobular carcinoma in situ and invasive lobular cancer identifies a common repertoire of mutations 2014 ,		2
21	Reliability of Whole-Exome Sequencing for Assessing Intratumor Genetic Heterogeneity. <i>SSRN Electronic Journal</i> ,	1	2
20	The Genomic Landscape of Prostate Cancer Brain Metastases		2
19	Discovery of synthetic lethal interactions from large-scale pan-cancer perturbation screens		2
18	Nestin and CD34 expression in colorectal cancer predicts improved overall survival. <i>Acta Oncologica</i> , 2021 , 60, 727-734	3.2	2
17	Interferon lambda 4 impairs hepatitis C viral antigen presentation and attenuates T cell responses. <i>Nature Communications</i> , 2021 , 12, 4882	17.4	2
16	Identification of Somatic Mutations in Thirty-year-old Serum Cell-free DNA From Patients With Breast Cancer: A Feasibility Study. <i>Clinical Breast Cancer</i> , 2020 , 20, 413-421.e1	3	1
15	Combining two antibodies to define E-cadherin loss of expression in non-lobular breast carcinomas: when less is more. <i>Histopathology</i> , 2013 , 63, 439-40	7.3	1
14	Patient-derived xenografts and organoids model therapy response in prostate cancer		1

13	Fibroepithelial Breast Lesion: When Sequencing Can Help to Make a Clinical Decision. A Case Report. <i>Clinical Breast Cancer</i> , 2019 , 19, e1-e6	3	1
12	Multi-omics data integration reveals novel drug targets in hepatocellular carcinoma. <i>BMC Genomics</i> , 2021 , 22, 592	4.5	1
11	Circulating Cell-Free DNA Captures the Intratumor Heterogeneity in Multinodular Hepatocellular Carcinoma.. <i>JCO Precision Oncology</i> , 2022 , 6, e2100335	3.6	1
10	Integrative proteogenomic characterization of hepatocellular carcinoma across etiologies and stages.. <i>Nature Communications</i> , 2022 , 13, 2436	17.4	1
9	Hepatocellular Carcinoma: Pathology and Genetics 2018 , 198-198		0
8	The Genomic Landscape of Serrated Lesion of the Colorectum: Similarities and Differences With Tubular and Tubulovillous Adenomas. <i>Frontiers in Oncology</i> , 2021 , 11, 668466	5.3	0
7	Cell-free DNA in hepatocellular carcinoma 2020 , 199-209		0
6	Genomic evolutionary trajectory of metastatic squamous cell carcinoma of the lung. <i>Translational Lung Cancer Research</i> , 2021 , 10, 1792-1803	4.4	0
5	Systematic identification of novel cancer genes through analysis of deep shRNA perturbation screens. <i>Nucleic Acids Research</i> , 2021 , 49, 8488-8504	20.1	0
4	Establishing standardized immune phenotyping of metastatic melanoma by digital pathology. <i>Laboratory Investigation</i> , 2021 , 101, 1561-1570	5.9	0
3	GATA3 and MDM2 are synthetic lethal in estrogen receptor-positive breast cancers.. <i>Communications Biology</i> , 2022 , 5, 373	6.7	0
2	Discovery of heterozygous KRT10 alterations in MAUIE cases underlines the importance of regular skin cancer screening in ichthyosis with confetti. <i>British Journal of Dermatology</i> , 2020 , 183, 954-955	4	
1	PipeIT2: Somatic Variant Calling Workflow for Ion Torrent Sequencing Data. <i>Methods in Molecular Biology</i> , 2022 , 195-204	1.4	