

Charlotte K Y Ng

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5315203/publications.pdf>

Version: 2024-02-01

168
papers

10,290
citations

31902

53
h-index

37111

96
g-index

183
all docs

183
docs citations

183
times ranked

16599
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutation tracking in circulating tumor DNA predicts relapse in early breast cancer. <i>Science Translational Medicine</i> , 2015, 7, 302ra133.	5.8	889
2	Cerebrospinal fluid-derived circulating tumour DNA better represents the genomic alterations of brain tumours than plasma. <i>Nature Communications</i> , 2015, 6, 8839.	5.8	605
3	Genomic characterization of metastatic breast cancers. <i>Nature</i> , 2019, 569, 560-564.	13.7	448
4	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.	0.6	424
5	Spatial and Temporal Heterogeneity in High-Grade Serous Ovarian Cancer: A Phylogenetic Analysis. <i>PLoS Medicine</i> , 2015, 12, e1001789.	3.9	314
6	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.	0.6	308
7	Organoid Models of Human Liver Cancers Derived from Tumor Needle Biopsies. <i>Cell Reports</i> , 2018, 24, 1363-1376.	2.9	288
8	Breast cancer intra-tumor heterogeneity. <i>Breast Cancer Research</i> , 2014, 16, 210.	2.2	256
9	Chromosomal instability determines taxane response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8671-8676.	3.3	244
10	Progression from ductal carcinoma <i>in situ</i> to invasive breast cancer: Revisited. <i>Molecular Oncology</i> , 2013, 7, 859-869.	2.1	195
11	Diverse <i>BRCA1</i> and <i>BRCA2</i> Reversion Mutations in Circulating Cell-Free DNA of Therapy-Resistant Breast or Ovarian Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 6708-6720.	3.2	194
12	Hotspot activating <i>PRKD1</i> somatic mutations in polymorphous low-grade adenocarcinomas of the salivary glands. <i>Nature Genetics</i> , 2014, 46, 1166-1169.	9.4	188
13	<i>SF3B1</i> mutations constitute a novel therapeutic target in breast cancer. <i>Journal of Pathology</i> , 2015, 235, 571-580.	2.1	167
14	Massively Parallel Sequencing-Based Clonality Analysis of Synchronous Endometrioid Endometrial and Ovarian Carcinomas. <i>Journal of the National Cancer Institute</i> , 2015, 108, djv427.	3.0	164
15	Genomic analysis of genetic heterogeneity and evolution in high-grade serous ovarian carcinoma. <i>Oncogene</i> , 2010, 29, 4905-4913.	2.6	153
16	A recurrent neomorphic mutation in <i>MYOD1</i> defines a clinically aggressive subset of embryonal rhabdomyosarcoma associated with <i>PI3K-AKT</i> pathway mutations. <i>Nature Genetics</i> , 2014, 46, 595-600.	9.4	152
17	The protein histidine phosphatase <i>LHPP</i> is a tumour suppressor. <i>Nature</i> , 2018, 555, 678-682.	13.7	151
18	Genomic landscape of adenoid cystic carcinoma of the breast. <i>Journal of Pathology</i> , 2015, 237, 179-189.	2.1	133

#	ARTICLE	IF	CITATIONS
19	The Landscape of Somatic Genetic Alterations in Metaplastic Breast Carcinomas. <i>Clinical Cancer Research</i> , 2017, 23, 3859-3870.	3.2	129
20	The Genomic Landscape of Male Breast Cancers. <i>Clinical Cancer Research</i> , 2016, 22, 4045-4056.	3.2	119
21	Benchmarking mutation effect prediction algorithms using functionally validated cancer-related missense mutations. <i>Genome Biology</i> , 2014, 15, 484.	3.8	117
22	Whole-genome single-cell copy number profiling from formalin-fixed paraffin-embedded samples. <i>Nature Medicine</i> , 2017, 23, 376-385.	15.2	111
23	Intra-tumor genetic heterogeneity and alternative driver genetic alterations in breast cancers with heterogeneous HER2 gene amplification. <i>Genome Biology</i> , 2015, 16, 107.	3.8	109
24	Recurrent hotspot mutations in HRAS Q61 and PI3K-AKT pathway genes as drivers of breast adenomyoepitheliomas. <i>Nature Communications</i> , 2018, 9, 1816.	5.8	105
25	Massively parallel sequencing of phyllodes tumours of the breast reveals actionable mutations, and <i>TERT</i> promoter hotspot mutations and <i>TERT</i> gene amplification as likely drivers of progression. <i>Journal of Pathology</i> , 2016, 238, 508-518.	2.1	102
26	<i>IDH2</i> Mutations Define a Unique Subtype of Breast Cancer with Altered Nuclear Polarity. <i>Cancer Research</i> , 2016, 76, 7118-7129.	0.4	99
27	Genetic alterations of triple negative breast cancer by targeted next-generation sequencing and correlation with tumor morphology. <i>Modern Pathology</i> , 2016, 29, 476-488.	2.9	95
28	Uterine adenosarcomas are mesenchymal neoplasms. <i>Journal of Pathology</i> , 2016, 238, 381-388.	2.1	94
29	Cancer Diagnosis Using a Liquid Biopsy: Challenges and Expectations. <i>Diagnostics</i> , 2018, 8, 31.	1.3	94
30	Genetic Heterogeneity in Therapy-Naïve Synchronous Primary Breast Cancers and Their Metastases. <i>Clinical Cancer Research</i> , 2017, 23, 4402-4415.	3.2	91
31	Mechanism of action of a WWTR1(TAZ)-CAMTA1 fusion oncoprotein. <i>Oncogene</i> , 2016, 35, 929-938.	2.6	90
32	TP53 Mutational Spectrum in Endometrioid and Serous Endometrial Cancers. <i>International Journal of Gynecological Pathology</i> , 2016, 35, 289-300.	0.9	89
33	Characterization of the genomic features and expressed fusion genes in micropapillary carcinomas of the breast. <i>Journal of Pathology</i> , 2014, 232, 553-565.	2.1	88
34	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.	0.6	87
35	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.	3.2	85
36	Tandem duplication of chromosomal segments is common in ovarian and breast cancer genomes. <i>Journal of Pathology</i> , 2012, 227, 446-455.	2.1	81

#	ARTICLE	IF	CITATIONS
37	Breast Cancer Genomics From Microarrays to Massively Parallel Sequencing: Paradigms and New Insights. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	80
38	Metastatic breast carcinomas display genomic and transcriptomic heterogeneity. <i>Modern Pathology</i> , 2015, 28, 340-351.	2.9	80
39	Reliability of Whole-Exome Sequencing for Assessing Intratumor Genetic Heterogeneity. <i>Cell Reports</i> , 2018, 25, 1446-1457.	2.9	76
40	Patient-derived xenografts and organoids model therapy response in prostate cancer. <i>Nature Communications</i> , 2021, 12, 1117.	5.8	76
41	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.	0.6	74
42	<i>MYBL1</i> rearrangements and <i>MYB</i> amplification in breast adenoid cystic carcinomas lacking the <i>MYB</i> – <i>NFIB</i> fusion gene. <i>Journal of Pathology</i> , 2018, 244, 143-150.	2.1	74
43	The Role of Long Non-Coding RNAs in Hepatocarcinogenesis. <i>International Journal of Molecular Sciences</i> , 2018, 19, 682.	1.8	73
44	Loss of Osteoclasts Contributes to Development of Osteosarcoma Pulmonary Metastases. <i>Cancer Research</i> , 2010, 70, 7063-7072.	0.4	72
45	The Tumor Profiler Study: integrated, multi-omic, functional tumor profiling for clinical decision support. <i>Cancer Cell</i> , 2021, 39, 288-293.	7.7	71
46	Intra-tumour genetic heterogeneity and poor chemoradiotherapy response in cervical cancer. <i>British Journal of Cancer</i> , 2011, 104, 361-368.	2.9	69
47	Metaplastic breast carcinoma: more than a special type. <i>Nature Reviews Cancer</i> , 2014, 14, 147-148.	12.8	69
48	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.	2.9	68
49	The Genomic Landscape of Mucinous Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2019, 111, 737-741.	3.0	68
50	Breast cancer intratumor genetic heterogeneity: causes and implications. <i>Expert Review of Anticancer Therapy</i> , 2012, 12, 1021-1032.	1.1	65
51	Genomic profiling of histological special types of breast cancer. <i>Breast Cancer Research and Treatment</i> , 2013, 142, 257-269.	1.1	64
52	Genomic and transcriptomic heterogeneity in metaplastic carcinomas of the breast. <i>Npj Breast Cancer</i> , 2017, 3, 48.	2.3	63
53	Comprehensive clinical and molecular analyses of neuroendocrine carcinomas of the breast. <i>Modern Pathology</i> , 2018, 31, 68-82.	2.9	58
54	Mutation Profiling of Key Cancer Genes in Primary Breast Cancers and Their Distant Metastases. <i>Cancer Research</i> , 2018, 78, 3112-3121.	0.4	57

#	ARTICLE	IF	CITATIONS
55	The role of tandem duplicator phenotype in tumour evolution in high-grade serous ovarian cancer. <i>Journal of Pathology</i> , 2012, 226, 703-712.	2.1	56
56	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, 166-178.	2.1	53
57	High-throughput sequencing of nodal marginal zone lymphomas identifies recurrent BRAF mutations. <i>Leukemia</i> , 2018, 32, 2412-2426.	3.3	53
58	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, 677-688.	2.1	52
59	The genetic landscape of breast carcinomas with neuroendocrine differentiation. <i>Journal of Pathology</i> , 2017, 241, 405-419.	2.1	52
60	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.	2.3	52
61	Leiomyoma with bizarre nuclei: a morphological, immunohistochemical and molecular analysis of 31 cases. <i>Modern Pathology</i> , 2017, 30, 1476-1488.	2.9	51
62	High Expression of FAP in Colorectal Cancer Is Associated With Angiogenesis and Immunoregulation Processes. <i>Frontiers in Oncology</i> , 2020, 10, 979.	1.3	50
63	Integrative genomic and transcriptomic characterization of papillary carcinomas of the breast. <i>Molecular Oncology</i> , 2014, 8, 1588-1602.	2.1	49
64	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.	2.9	48
65	Integrative proteogenomic characterization of hepatocellular carcinoma across etiologies and stages. <i>Nature Communications</i> , 2022, 13, 2436.	5.8	45
66	Lobular Carcinomas <i>In Situ</i> Display Intralesion Genetic Heterogeneity and Clonal Evolution in the Progression to Invasive Lobular Carcinoma. <i>Clinical Cancer Research</i> , 2019, 25, 674-686.	3.2	44
67	Biallelic alterations in DNA repair genes underpin homologous recombination DNA repair defects in breast cancer. <i>Journal of Pathology</i> , 2017, 242, 165-177.	2.1	43
68	PI3K Pathway Activation in High-Grade Ductal Carcinoma <i>In Situ</i> —Implications for Progression to Invasive Breast Carcinoma. <i>Clinical Cancer Research</i> , 2014, 20, 2326-2337.	3.2	41
69	HMGA1 Expression in Human Hepatocellular Carcinoma Correlates with Poor Prognosis and Promotes Tumor Growth and Migration in <i>in vitro</i> Models. <i>Neoplasia</i> , 2016, 18, 724-731.	2.3	41
70	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, 360-370.	2.1	41
71	High expression of HOXA13 correlates with poorly differentiated hepatocellular carcinomas and modulates sorafenib response in <i>in vitro</i> models. <i>Laboratory Investigation</i> , 2018, 98, 95-105.	1.7	41
72	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. <i>Molecular Oncology</i> , 2015, 9, 115-127.	2.1	38

#	ARTICLE	IF	CITATIONS
73	Circulating Cell-Free DNA in Hepatocellular Carcinoma: Current Insights and Outlook. <i>Frontiers in Medicine</i> , 2018, 5, 78.	1.2	38
74	The repertoire of genetic alterations in salivary duct carcinoma including a novel HNRNPH3-ALK rearrangement. <i>Human Pathology</i> , 2019, 88, 66-77.	1.1	38
75	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, 150-158.	2.1	37
76	Are acinic cell carcinomas of the breast and salivary glands distinct diseases?. <i>Histopathology</i> , 2015, 67, 529-537.	1.6	37
77	Contralateral breast cancers: Independent cancers or metastases?. <i>International Journal of Cancer</i> , 2018, 142, 347-356.	2.3	37
78	SCIM: universal single-cell matching with unpaired feature sets. <i>Bioinformatics</i> , 2020, 36, i919-i927.	1.8	37
79	Genetic heterogeneity and actionable mutations in HER2-positive primary breast cancers and their brain metastases. <i>Oncotarget</i> , 2018, 9, 20617-20630.	0.8	36
80	LATS1 but not LATS2 represses autophagy by a kinase-independent scaffold function. <i>Nature Communications</i> , 2019, 10, 5755.	5.8	36
81	Infiltration by myeloperoxidase-positive neutrophils is an independent prognostic factor in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2019, 177, 581-589.	1.1	34
82	Proteasome Addiction Defined in Ewing Sarcoma Is Effectively Targeted by a Novel Class of 19S Proteasome Inhibitors. <i>Cancer Research</i> , 2016, 76, 4525-4534.	0.4	33
83	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.	1.2	32
84	Gene expression profiling of lobular carcinoma in situ reveals candidate precursor genes for invasion. <i>Molecular Oncology</i> , 2015, 9, 772-782.	2.1	32
85	Genomic Analysis Revealed New Oncogenic Signatures in TP53-Mutant Hepatocellular Carcinoma. <i>Frontiers in Genetics</i> , 2018, 9, 2.	1.1	32
86	Infiltrating epitheliosis of the breast: characterization of histological features, immunophenotype and genomic profile. <i>Histopathology</i> , 2016, 68, 1030-1039.	1.6	31
87	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.	2.3	28
88	NGS-pipe: a flexible, easily extendable and highly configurable framework for NGS analysis. <i>Bioinformatics</i> , 2018, 34, 107-108.	1.8	25
89	Hepatocellular Carcinoma Xenografts Established From Needle Biopsies Preserve the Characteristics of the Originating Tumors. <i>Hepatology Communications</i> , 2019, 3, 971-986.	2.0	24
90	Lack of <i>PRKD2</i> and <i>PRKD3</i> kinase domain somatic mutations in wild-type classic polymorphous low-grade adenocarcinomas of the salivary gland. <i>Histopathology</i> , 2016, 68, 1055-1062.	1.6	23

#	ARTICLE	IF	CITATIONS
91	Resolving quandaries: basaloid adenoid cystic carcinoma or breast cylindroma? The role of massively parallel sequencing. <i>Histopathology</i> , 2016, 68, 262-271.	1.6	22
92	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-e3138.	2.7	22
93	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.	1.2	22
94	Predictive Performance of Microarray Gene Signatures: Impact of Tumor Heterogeneity and Multiple Mechanisms of Drug Resistance. <i>Cancer Research</i> , 2014, 74, 2946-2961.	0.4	20
95	The Dilemma of HER2 Double-equivocal Breast Carcinomas. <i>American Journal of Surgical Pathology</i> , 2018, 42, 1190-1200.	2.1	20
96	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.	1.1	20
97	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.	4.6	19
98	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.	1.1	19
99	Response to dual HER2 blockade in a patient with HER3-mutant metastatic breast cancer. <i>Annals of Oncology</i> , 2015, 26, 1704-1709.	0.6	18
100	Therapeutic Targeting of CD146/MCAM Reduces Bone Metastasis in Prostate Cancer. <i>Molecular Cancer Research</i> , 2019, 17, 1049-1062.	1.5	17
101	Expression of RET is associated with Oestrogen receptor expression but lacks prognostic significance in breast cancer. <i>BMC Cancer</i> , 2019, 19, 41.	1.1	16
102	PIKING the type and pattern of PI3K pathway mutations in endometrioid endometrial carcinomas. <i>Gynecologic Oncology</i> , 2015, 137, 321-328.	0.6	15
103	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.	1.1	15
104	Diagnostic Targeted Sequencing Panel for Hepatocellular Carcinoma Genomic Screening. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 836-848.	1.2	15
105	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.	1.6	15
106	Establishing standardized immune phenotyping of metastatic melanoma by digital pathology. <i>Laboratory Investigation</i> , 2021, 101, 1561-1570.	1.7	15
107	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.	2.0	13
108	Interferon lambda 4 impairs hepatitis C viral antigen presentation and attenuates T cell responses. <i>Nature Communications</i> , 2021, 12, 4882.	5.8	13

#	ARTICLE	IF	CITATIONS
109	Alterations in homologous recombination repair genes in prostate cancer brain metastases. <i>Nature Communications</i> , 2022, 13, 2400.	5.8	13
110	Multi-omics data integration reveals novel drug targets in hepatocellular carcinoma. <i>BMC Genomics</i> , 2021, 22, 592.	1.2	12
111	Genetic analysis of uterine adenosarcomas and phyllodes tumors of the breast. <i>Molecular Oncology</i> , 2017, 11, 913-926.	2.1	11
112	Molecular classification of hepatocellular carcinoma: The view from metabolic zonation. <i>Hepatology</i> , 2017, 66, 1377-1380.	3.6	11
113	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.	0.8	11
114	PipeIT. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 884-894.	1.2	11
115	ESR1 and endocrine therapy resistance: more than just mutations. <i>Annals of Oncology</i> , 2018, 29, 787-789.	0.6	10
116	Genetic Alterations in Benign Breast Biopsies of Subsequent Breast Cancer Patients. <i>Frontiers in Medicine</i> , 2019, 6, 166.	1.2	10
117	Radiogenomics Analysis of Intratumor Heterogeneity in a Patient With High-Grade Serous Ovarian Cancer. <i>JCO Precision Oncology</i> , 2019, 3, 1-9.	1.5	10
118	Circulating Cell-Free DNA Captures the Intratumor Heterogeneity in Multinodular Hepatocellular Carcinoma. <i>JCO Precision Oncology</i> , 2022, 6, e2100335.	1.5	9
119	RNASeq analysis reveals biological processes governing the clinical behaviour of endometrioid and serous endometrial cancers. <i>European Journal of Cancer</i> , 2016, 64, 149-158.	1.3	8
120	Stroma Transcriptomic and Proteomic Profile of Prostate Cancer Metastasis Xenograft Models Reveals Prognostic Value of Stroma Signatures. <i>Cancers</i> , 2020, 12, 3786.	1.7	8
121	GATA3 and MDM2 are synthetic lethal in estrogen receptor-positive breast cancers. <i>Communications Biology</i> , 2022, 5, 373.	2.0	7
122	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.	1.4	6
123	Nestin and CD34 expression in colorectal cancer predicts improved overall survival. <i>Acta Oncologica</i> , 2021, 60, 727-734.	0.8	5
124	Genomic analysis of focal nodular hyperplasia with associated hepatocellular carcinoma unveils its malignant potential: a case report. <i>Communications Medicine</i> , 2022, 2, .	1.9	5
125	Prognostic signatures in breast cancer: correlation does not imply causation. <i>Breast Cancer Research</i> , 2012, 14, 313.	2.2	4
126	Systematic identification of novel cancer genes through analysis of deep shRNA perturbation screens. <i>Nucleic Acids Research</i> , 2021, 49, 8488-8504.	6.5	4

#	ARTICLE	IF	CITATIONS
127	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, , .		4
128	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.	1.3	4
129	Hepatocellular Carcinoma: Pathology and Genetics. , 2018, , 198-198.		3
130	Genomic evolutionary trajectory of metastatic squamous cell carcinoma of the lung. <i>Translational Lung Cancer Research</i> , 2021, 10, 1792-1803.	1.3	3
131	Epigenetic priming in chronic liver disease impacts the transcriptional and genetic landscapes of hepatocellular carcinoma. <i>Molecular Oncology</i> , 2022, 16, 665-682.	2.1	3
132	Fibroepithelial Breast Lesion: When Sequencing Can Help to Make a Clinical Decision. A Case Report. <i>Clinical Breast Cancer</i> , 2019, 19, e1-e6.	1.1	2
133	Discovery of heterozygous <i>KRT10</i> alterations in MALIE cases underlines the importance of regular skin cancer screening in ichthyosis with confetti. <i>British Journal of Dermatology</i> , 2020, 183, 954-955.	1.4	2
134	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.	1.1	2
135	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
136	Reliability of Whole-Exome Sequencing for Assessing Intratumor Genetic Heterogeneity. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2
137	Abstract 930: Analysis of cell-free tumor DNA in cerebrospinal fluid to characterize and monitor the genetic alterations of brain tumors. <i>Cancer Research</i> , 2015, 75, 930-930.	0.4	2
138	The Role of Chronic Liver Diseases in the Emergence and Recurrence of Hepatocellular Carcinoma: An Omics Perspective. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	2
139	Combining two antibodies to define E-cadherin loss of expression in non-lobular breast carcinomas: when less is more. <i>Histopathology</i> , 2013, 63, 439-440.	1.6	1
140	Genetic profiling using plasma-derived cell-free DNA in therapy-naïve hepatocellular carcinoma patients: A pilot study. <i>Digestive and Liver Disease</i> , 2018, 50, 27.	0.4	1
141	Cell-free DNA in hepatocellular carcinoma. , 2020, , 199-209.		1
142	Abstract PD05-08: Genomic characterisation of invasive breast cancers with heterogeneous HER2 gene amplification. , 2012, , .		1
143	Abstract 100: The landscape of somatic genetic alterations in BRCA1 and BRCA2 breast cancers. , 2016, , .		1
144	Abstract S6-06: The genomic landscape of male breast cancers. , 2015, , .		1

#	ARTICLE	IF	CITATIONS
145	Abstract PD3-4: Reliability of whole exome sequencing for assessing intratumor heterogeneity from breast tumor biopsies. , 2015, , .		1
146	Abstract 2989: Intra-tumor heterogeneity and clonal changes in the progression of DCIS to invasiveness: Combined tumor bulk and single cell analysis. , 2015, , .		1
147	Abstract 138: Solid papillary carcinoma with reverse polarization are driven by IDH2 and PI3K pathway mutations. , 2016, , .		1
148	575 SF3B1 mutations are associated with alternative splicing in ER-positive breast cancer. European Journal of Cancer, 2014, 50, 186.	1.3	0
149	SU30ANALYSIS OF WGS DATA FROM 108 INDIVIDUALS OF 8 SPANISH FAMILIES AFFECTED WITH BIPOLAR DISORDER. European Neuropsychopharmacology, 2019, 29, S1283-S1284.	0.3	0
150	Abstract 4029: The impact of multiple drug resistance mechanisms on microarray predictive gene signature performance.. , 2013, , .		0
151	Abstract P4-04-05: Molecular subtyping reveals the heterogeneity of metaplastic breast cancers. , 2013, , .		0
152	Abstract P4-04-08: Genomic and transcriptomic characterization of papillary carcinomas of the breast. , 2013, , .		0
153	Abstract 1544: The clinical behavior of endometrioid and serous endometrial carcinomas is governed by distinct biological processes. , 2014, , .		0
154	Abstract 4258: Benchmarking algorithms for mutation impact prediction using functionally validated missense mutations. , 2014, , .		0
155	Abstract P2-03-09: Benchmarking mutation function prediction algorithms using validated cancer driver and passenger mutations. , 2015, , .		0
156	Abstract P2-03-08: Mutational landscape of metaplastic breast carcinomas. , 2015, , .		0
157	Abstract 3889: Genetic heterogeneity and distinct driver mutations in synchronous primary and metastatic breast cancers from therapy-naïve patients. , 2015, , .		0
158	Abstract 2971: Whole exome sequencing reveals heterogeneity within lobular carcinoma in situ (LCIS) and clonal selection in the progression to malignant lesions. , 2015, , .		0
159	Abstract 4817: Microsatellite instability status in endometrioid endometrial carcinomas is associated with distinct types and patterns of PI3K pathway mutations. , 2015, , .		0
160	Abstract S4-04: Lobular carcinoma in situ displays intra-lesion genetic heterogeneity and its progression to invasive disease involves clonal selection and variations in mutational processes. , 2016, , .		0
161	Abstract P6-07-04: Distinct repertoires of somatic mutations affecting driver genes in mucinous and neuroendocrine carcinomas of the breast. , 2016, , .		0
162	Abstract P2-01-02: Capturing intra-tumor genetic heterogeneity in cell-free plasma DNA from patients with oligometastatic breast cancer. , 2016, , .		0

#	ARTICLE	IF	CITATIONS
163	Abstract P6-06-02: Germline CDH1 mutations in lobular carcinoma in situ. , 2016, , .		0
164	Abstract P6-03-10: Genomic and transcriptomic heterogeneity in metaplastic breast carcinomas. , 2016, , .		0
165	Abstract 91: The mutational landscape of mucinous carcinomas of the breast. , 2016, , .		0
166	Abstract 134: Mutational landscape of breast cancers from PALB2 germline mutation carriers. , 2016, , .		0
167	Abstract 4612: HOXA13 drives hepatocytes proliferation and liver tumorigenesis in mice. , 2019, , .		0
168	Abstract 2821: Gut commensal bacteria modulate functions of tumor-associated neutrophils in human colorectal cancer. , 2019, , .		0