## Salvatore Piscuoglio

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8467198/publications.pdf

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191 papers 8,120 citations

50170 46 h-index 84 g-index

211 all docs

211 docs citations

times ranked

211

13121 citing authors

#	Article	IF	CITATIONS
1	Cerebrospinal fluid-derived circulating tumour DNA better represents the genomic alterations of brain tumours than plasma. Nature Communications, 2015, 6, 8839.	5.8	605
2	Genomic characterization of metastatic breast cancers. Nature, 2019, 569, 560-564.	13.7	448
3	Long noncoding RNA HOTTIP/HOXA13 expression is associated with disease progression and predicts outcome in hepatocellular carcinoma patients. Hepatology, 2014, 59, 911-923.	3.6	382
4	Capturing intra-tumor genetic heterogeneity by de novo mutation profiling of circulating cell-free tumor DNA: a proof-of-principle. Annals of Oncology, 2014, 25, 1729-1735.	0.6	308
5	Organoid Models of Human Liver Cancers Derived from Tumor Needle Biopsies. Cell Reports, 2018, 24, 1363-1376.	2.9	288
6	Cancer-associated fibroblasts release exosomal microRNAs that dictate an aggressive phenotype in breast cancer. Oncotarget, 2017, 8, 19592-19608.	0.8	267
7	Breast cancer intra-tumor heterogeneity. Breast Cancer Research, 2014, 16, 210.	2.2	256
8	YAP/TAZ and ATF4 drive resistance to Sorafenib in hepatocellular carcinoma by preventing ferroptosis. EMBO Molecular Medicine, 2021, 13, e14351.	3.3	204
9	Diverse <i>BRCA1</i> and <i>BRCA2</i> Reversion Mutations in Circulating Cell-Free DNA of Therapy-Resistant Breast or Ovarian Cancer. Clinical Cancer Research, 2017, 23, 6708-6720.	3.2	194
10	Hotspot activating PRKD1 somatic mutations in polymorphous low-grade adenocarcinomas of the salivary glands. Nature Genetics, 2014, 46, 1166-1169.	9.4	188
11	Massively Parallel Sequencing-Based Clonality Analysis of Synchronous Endometrioid Endometrial and Ovarian Carcinomas. Journal of the National Cancer Institute, 2015, 108, djv427.	3.0	164
12	The protein histidine phosphatase LHPP is a tumour suppressor. Nature, 2018, 555, 678-682.	13.7	151
13	Genomic landscape of adenoid cystic carcinoma of the breast. Journal of Pathology, 2015, 237, 179-189.	2.1	133
14	The Landscape of Somatic Genetic Alterations in Metaplastic Breast Carcinomas. Clinical Cancer Research, 2017, 23, 3859-3870.	3.2	129
15	The Genomic Landscape of Male Breast Cancers. Clinical Cancer Research, 2016, 22, 4045-4056.	3.2	119
16	Benchmarking mutation effect prediction algorithms using functionally validated cancer-related missense mutations. Genome Biology, 2014, 15, 484.	3.8	117
17	Whole-genome single-cell copy number profiling from formalin-fixed paraffin-embedded samples. Nature Medicine, 2017, 23, 376-385.	15.2	111
18	Intra-tumor genetic heterogeneity and alternative driver genetic alterations in breast cancers with heterogeneous HER2 gene amplification. Genome Biology, 2015, 16, 107.	3.8	109

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19	Recurrent hotspot mutations in HRAS Q61 and PI3K-AKT pathway genes as drivers of breast adenomyoepitheliomas. Nature Communications, 2018, 9, 1816.	5.8	105
20	Massively parallel sequencing of phyllodes tumours of the breast reveals actionable mutations, and <i><scp>TERT</scp></i> promoter hotspot mutations and <i>TERT</i> gene amplification as likely drivers of progression. Journal of Pathology, 2016, 238, 508-518.	2.1	102
21	A survey of DICER1 hotspot mutations in ovarian and testicular sex cord-stromal tumors. Modern Pathology, 2015, 28, 1603-1612.	2.9	100
22	<i>IDH2</i> Mutations Define a Unique Subtype of Breast Cancer with Altered Nuclear Polarity. Cancer Research, 2016, 76, 7118-7129.	0.4	99
23	Genetic alterations of triple negative breast cancer by targeted next-generation sequencing and correlation with tumor morphology. Modern Pathology, 2016, 29, 476-488.	2.9	95
24	Uterine adenosarcomas are mesenchymal neoplasms. Journal of Pathology, 2016, 238, 381-388.	2.1	94
25	Cancer Diagnosis Using a Liquid Biopsy: Challenges and Expectations. Diagnostics, 2018, 8, 31.	1.3	94
26	Genetic Heterogeneity in Therapy-Na $\tilde{A}$ -ve Synchronous Primary Breast Cancers and Their Metastases. Clinical Cancer Research, 2017, 23, 4402-4415.	3.2	91
27	TP53 Mutational Spectrum in Endometrioid and Serous Endometrial Cancers. International Journal of Gynecological Pathology, 2016, 35, 289-300.	0.9	89
28	Characterization of the genomic features and expressed fusion genes in micropapillary carcinomas of the breast. Journal of Pathology, 2014, 232, 553-565.	2.1	88
29	HMGA1 and HMGA2 protein expression correlates with advanced tumour grade and lymph node metastasis in pancreatic adenocarcinoma. Histopathology, 2012, 60, 397-404.	1.6	82
30	<i>MED12</i> somatic mutations in fibroadenomas and phyllodes tumours of the breast. Histopathology, 2015, 67, 719-729.	1.6	78
31	Reliability of Whole-Exome Sequencing for Assessing Intratumor Genetic Heterogeneity. Cell Reports, 2018, 25, 1446-1457.	2.9	76
32	Role of specialized composition of SWI/SNF complexes in prostate cancer lineage plasticity. Nature Communications, 2020, 11, 5549.	5.8	76
33	Patient-derived xenografts and organoids model therapy response in prostate cancer. Nature Communications, 2021, 12, 1117.	5.8	76
34	Genetic profiling using plasma-derived cell-free DNA in therapy-na $\tilde{A}$ -ve hepatocellular carcinoma patients: a pilot study. Annals of Oncology, 2018, 29, 1286-1291.	0.6	74
35	The Role of Long Non-Coding RNAs in Hepatocarcinogenesis. International Journal of Molecular Sciences, 2018, 19, 682.	1.8	73
36	The Tumor Profiler Study: integrated, multi-omic, functional tumor profiling for clinical decision support. Cancer Cell, 2021, 39, 288-293.	7.7	71

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37	Genetic events in the progression of adenoid cystic carcinoma of the breast to high-grade triple-negative breast cancer. Modern Pathology, 2016, 29, 1292-1305.	2.9	68
38	The Genomic Landscape of Mucinous Breast Cancer. Journal of the National Cancer Institute, 2019, 111, 737-741.	3.0	68
39	Genomic and transcriptomic heterogeneity in metaplastic carcinomas of the breast. Npj Breast Cancer, 2017, 3, 48.	2.3	63
40	Mutation Profiling of Key Cancer Genes in Primary Breast Cancers and Their Distant Metastases. Cancer Research, 2018, 78, 3112-3121.	0.4	57
41	The repertoire of somatic genetic alterations of acinic cell carcinomas of the breast: an exploratory, hypothesisâ€generating study. Journal of Pathology, 2015, 237, 166-178.	2.1	53
42	TIA-1 Cytotoxic Granule-Associated RNA Binding Protein Improves the Prognostic Performance of CD8 in Mismatch Repair-Proficient Colorectal Cancer. PLoS ONE, 2010, 5, e14282.	1.1	52
43	Microglandular adenosis associated with tripleâ€negative breast cancer is a neoplastic lesion of tripleâ€negative phenotype harbouring <i><scp>TP53</scp></i> somatic mutations. Journal of Pathology, 2016, 238, 677-688.	2.1	52
44	The genetic landscape of breast carcinomas with neuroendocrine differentiation. Journal of Pathology, 2017, 241, 405-419.	2.1	52
45	Phyllodes tumors with and without fibroadenoma-like areas display distinct genomic features and may evolve through distinct pathways. Npj Breast Cancer, 2017, 3, 40.	2.3	52
46	High Expression of FAP in Colorectal Cancer Is Associated With Angiogenesis and Immunoregulation Processes. Frontiers in Oncology, 2020, 10, 979.	1.3	50
47	Integrative genomic and transcriptomic characterization of papillary carcinomas of the breast. Molecular Oncology, 2014, 8, 1588-1602.	2.1	49
48	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. Modern Pathology, 2017, 30, 69-84.	2.9	48
49	MAGEâ€A10 is a nuclear protein frequently expressed in high percentages of tumor cells in lung, skin and urothelial malignancies. International Journal of Cancer, 2011, 129, 1137-1148.	2.3	46
50	Integrative proteogenomic characterization of hepatocellular carcinoma across etiologies and stages. Nature Communications, 2022, 13, 2436.	5.8	45
51	Lobular Carcinomas <i>In Situ</i> Display Intralesion Genetic Heterogeneity and Clonal Evolution in the Progression to Invasive Lobular Carcinoma. Clinical Cancer Research, 2019, 25, 674-686.	3.2	44
52	Biâ€allelic alterations in DNA repair genes underpin homologous recombination DNA repair defects in breast cancer. Journal of Pathology, 2017, 242, 165-177.	2.1	43
53	ZNRF3 and RNF43 cooperate to safeguard metabolic liver zonation and hepatocyte proliferation. Cell Stem Cell, 2021, 28, 1822-1837.e10.	5.2	42
54	HMGA1 Expression in Human Hepatocellular Carcinoma Correlates with Poor Prognosis and Promotes Tumor Growth and Migration in in vitro Models. Neoplasia, 2016, 18, 724-731.	2.3	41

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55	Targeted capture massively parallel sequencing analysis of LCIS and invasive lobular cancer: Repertoire of somatic genetic alterations and clonal relationships. Molecular Oncology, 2016, 10, 360-370.	2.1	41
56	High expression of HOXA13 correlates with poorly differentiated hepatocellular carcinomas and modulates sorafenib response in in vitro models. Laboratory Investigation, 2018, 98, 95-105.	1.7	41
57	Homologous recombination DNA repair defects in PALB2-associated breast cancers. Npj Breast Cancer, 2019, 5, 23.	2.3	39
58	Circulating Cell-Free DNA in Hepatocellular Carcinoma: Current Insights and Outlook. Frontiers in Medicine, 2018, 5, 78.	1.2	38
59	Skeletal Muscle Disorders: A Noncardiac Source of Cardiac Troponin T. Circulation, 2022, 145, 1764-1779.	1.6	38
60	Are acinic cell carcinomas of the breast and salivary glands distinct diseases?. Histopathology, 2015, 67, 529-537.	1.6	37
61	Contralateral breast cancers: Independent cancers or metastases?. International Journal of Cancer, 2018, 142, 347-356.	2.3	37
62	SCIM: universal single-cell matching with unpaired feature sets. Bioinformatics, 2020, 36, i919-i927.	1.8	37
63	Genetic heterogeneity and actionable mutations in HER2-positive primary breast cancers and their brain metastases. Oncotarget, 2018, 9, 20617-20630.	0.8	36
64	LATS1 but not LATS2 represses autophagy by a kinase-independent scaffold function. Nature Communications, 2019, 10, 5755.	5.8	36
65	Survivin Expression in Renal Cell Carcinoma. Cancer Investigation, 2008, 26, 929-935.	0.6	35
66	Prostate cancer patientâ€derived organoids: detailed outcome from a prospective cohort of 81 clinical specimens. Journal of Pathology, 2021, 254, 543-555.	2.1	35
67	Infiltration by myeloperoxidase-positive neutrophils is an independent prognostic factor in breast cancer. Breast Cancer Research and Treatment, 2019, 177, 581-589.	1.1	34
68	USP29-mediated HIF1 $\hat{l}_{\pm}$ stabilization is associated with Sorafenib resistance of hepatocellular carcinoma cells by upregulating glycolysis. Oncogenesis, 2021, 10, 52.	2.1	33
69	Genomic Analysis Revealed New Oncogenic Signatures in TP53-Mutant Hepatocellular Carcinoma. Frontiers in Genetics, 2018, 9, 2.	1.1	32
70	Infiltrating epitheliosis of the breast: characterization of histological features, immunophenotype and genomic profile. Histopathology, 2016, 68, 1030-1039.	1.6	31
71	Effect of EpCAM, CD44, CD133 and CD166 expression on patient survival in tumours of the ampulla of Vater. Journal of Clinical Pathology, 2012, 65, 140-145.	1.0	30
72	HIPK2 deficiency causes chromosomal instability by cytokinesis failure and increases tumorigenicity. Oncotarget, 2015, 6, 10320-10334.	0.8	30

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73	Massively parallel sequencing analysis of synchronous fibroepithelial lesions supports the concept of progression from fibroadenoma to phyllodes tumor. Npj Breast Cancer, 2016, 2, 16035.	2.3	28
74	NGS-pipe: a flexible, easily extendable and highly configurable framework for NGS analysis. Bioinformatics, 2018, 34, 107-108.	1.8	25
75	Hepatocellular Carcinoma Xenografts Established From Needle Biopsies Preserve the Characteristics of the Originating Tumors. Hepatology Communications, 2019, 3, 971-986.	2.0	24
76	Lack of <i><scp>PRKD</scp>2</i> and <i><scp>PRKD</scp>3</i> kinase domain somatic mutations in <i><scp>PRKD</scp>1</i> wildâ€type classic polymorphous lowâ€grade adenocarcinomas of the salivary gland. Histopathology, 2016, 68, 1055-1062.	1.6	23
77	Resolving quandaries: basaloid adenoid cystic carcinoma or breast cylindroma? The role of massively parallel sequencing. Histopathology, 2016, 68, 262-271.	1.6	22
78	Phosphoprotein enriched in diabetes (PED/PEA15) promotes migration in hepatocellular carcinoma and confers resistance to sorafenib. Cell Death and Disease, 2017, 8, e3138-e3138.	2.7	22
79	Nectin-4 Expression Is an Independent Prognostic Biomarker and Associated With Better Survival in Triple-Negative Breast Cancer. Frontiers in Medicine, 2019, 6, 200.	1.2	22
80	Prevention of dsRNAâ€induced interferon signaling by AGO1x is linked to breast cancer cell proliferation. EMBO Journal, 2020, 39, e103922.	3.5	22
81	The genetic landscape of metaplastic breast cancers and uterine carcinosarcomas. Molecular Oncology, 2021, 15, 1024-1039.	2.1	21
82	Prognostic significance of CD8+ T-cells density in stage III colorectal cancer depends on SDF-1 expression. Scientific Reports, 2021, 11, 775.	1.6	21
83	Preoperative plasma fatty acid metabolites inform risk of prostate cancer progression and may be used for personalized patient stratification. BMC Cancer, 2019, 19, 1216.	1.1	20
84	Mapping of m6A and Its Regulatory Targets in Prostate Cancer Reveals a METTL3-Low Induction of Therapy Resistance. Molecular Cancer Research, 2021, 19, 1398-1411.	1.5	20
85	Adenylosuccinate lyase is oncogenic in colorectal cancer by causing mitochondrial dysfunction and independent activation of NRF2 and mTOR-MYC-axis. Theranostics, 2021, 11, 4011-4029.	4.6	19
86	Response to dual HER2 blockade in a patient with HER3-mutant metastatic breast cancer. Annals of Oncology, 2015, 26, 1704-1709.	0.6	18
87	High mobility group A1 enhances tumorigenicity of human cholangiocarcinoma and confers resistance to therapy. Molecular Carcinogenesis, 2017, 56, 2146-2157.	1.3	17
88	Therapeutic Targeting of CD146/MCAM Reduces Bone Metastasis in Prostate Cancer. Molecular Cancer Research, 2019, 17, 1049-1062.	1.5	17
89	3′-UTR Poly(T/U) Tract Deletions and Altered Expression of <i>EWSR1</i> Are a Hallmark of Mismatch Repair–Deficient Cancers. Cancer Research, 2014, 74, 224-234.	0.4	16
90	HMGA1 overexpression is associated with a particular subset of human breast carcinomas. Journal of Clinical Pathology, 2016, 69, 117-121.	1.0	16

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91	Expression of RET is associated with Oestrogen receptor expression but lacks prognostic significance in breast cancer. BMC Cancer, 2019, 19, 41.	1.1	16
92	PIKing the type and pattern of PI3K pathway mutations in endometrioid endometrial carcinomas. Gynecologic Oncology, 2015, 137, 321-328.	0.6	15
93	Vascular endothelial growth factor A amplification in colorectal cancer is associated with reduced M1 and M2 macrophages and diminished PD-1-expressing lymphocytes. PLoS ONE, 2017, 12, e0175563.	1.1	15
94	Diagnostic Targeted Sequencing Panel for Hepatocellular Carcinoma Genomic Screening. Journal of Molecular Diagnostics, 2018, 20, 836-848.	1.2	15
95	Deciphering the clonal relationship between glandular and squamous components in adenosquamous carcinoma of the lung using whole exome sequencing. Lung Cancer, 2020, 150, 132-138.	0.9	15
96	Infiltration by IL22-Producing T Cells Promotes Neutrophil Recruitment and Predicts Favorable Clinical Outcome in Human Colorectal Cancer. Cancer Immunology Research, 2020, 8, 1452-1462.	1.6	15
97	Reliability of liquid biopsy analysis: an inter-laboratory comparison of circulating tumor DNA extraction and sequencing with different platforms. Laboratory Investigation, 2020, 100, 1475-1484.	1.7	15
98	Establishing standardized immune phenotyping of metastatic melanoma by digital pathology. Laboratory Investigation, 2021, 101, 1561-1570.	1.7	15
99	Genomic characterization of small cell carcinomas of the uterine cervix. Molecular Oncology, 2022, 16, 833-845.	2.1	14
100	mTOR signaling mediates ILC3-driven immunopathology. Mucosal Immunology, 2021, 14, 1323-1334.	2.7	14
101	Transcriptional Enhancer Factor Domain Family member 4 Exerts an Oncogenic Role in Hepatocellular Carcinoma by Hippoâ€Independent Regulation of Heat Shock Protein 70 Family Members. Hepatology Communications, 2021, 5, 661-674.	2.0	13
102	Alterations in homologous recombination repair genes in prostate cancer brain metastases. Nature Communications, 2022, 13, 2400.	5.8	13
103	Multi-omics data integration reveals novel drug targets in hepatocellular carcinoma. BMC Genomics, 2021, 22, 592.	1.2	12
104	Preclinical evaluation of the PARP inhibitor BMN-673 for the treatment of ovarian clear cell cancer. Oncotarget, 2017, 8, 6057-6066.	0.8	12
105	Genetic analysis of uterine adenosarcomas and phyllodes tumors of the breast. Molecular Oncology, 2017, 11, 913-926.	2.1	11
106	Molecular classification of hepatocellular carcinoma: The view from metabolic zonation. Hepatology, 2017, 66, 1377-1380.	3.6	11
107	Pregnancy at early age is associated with a reduction of progesterone-responsive cells and epithelial Wnt signaling in human breast tissue. Oncotarget, 2017, 8, 22353-22360.	0.8	11
108	PipelT. Journal of Molecular Diagnostics, 2019, 21, 884-894.	1.2	11

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109	A Pygopus 2-Histone Interaction Is Critical for Cancer Cell Dedifferentiation and Progression in Malignant Breast Cancer. Cancer Research, 2020, 80, 3631-3648.	0.4	11
110	ESR1 and endocrine therapy resistance: more than just mutations. Annals of Oncology, 2018, 29, 787-789.	0.6	10
111	Genetic Alterations in Benign Breast Biopsies of Subsequent Breast Cancer Patients. Frontiers in Medicine, 2019, 6, 166.	1.2	10
112	SH2D4A is frequently downregulated in hepatocellular carcinoma and cirrhotic nodules. European Journal of Cancer, 2014, 50, 731-738.	1.3	9
113	Circulating Cell-Free DNA Captures the Intratumor Heterogeneity in Multinodular Hepatocellular Carcinoma. JCO Precision Oncology, 2022, 6, e2100335.	1.5	9
114	RNASeq analysis reveals biological processes governing the clinical behaviour of endometrioid and serous endometrial cancers. European Journal of Cancer, 2016, 64, 149-158.	1.3	8
115	miRâ€579â€3p Controls Hepatocellular Carcinoma Formation by Regulating the Phosphoinositide 3â€Kinase–Protein Kinase B Pathway in Chronically Inflamed Liver. Hepatology Communications, 2022, 6, 1467-1481.	2.0	8
116	GATA3 and MDM2 are synthetic lethal in estrogen receptor-positive breast cancers. Communications Biology, 2022, 5, 373.	2.0	7
117	Nestin and CD34 expression in colorectal cancer predicts improved overall survival. Acta $Oncol\tilde{A}^3$ gica, 2021, 60, 727-734.	0.8	5
118	Genomic analysis of focal nodular hyperplasia with associated hepatocellular carcinoma unveils its malignant potential: a case report. Communications Medicine, 2022, 2, .	1.9	5
119	Patient-derived tumor organoids for personalized medicine in a patient with rare hepatocellular carcinoma with neuroendocrine differentiation: a case report. Communications Medicine, 2022, 2, .	1.9	5
120	90 HOXA13 AND HOTTIP EXPRESSION LEVELS PREDICT PATIENTS' SURVIVAL AND METASTASIS FORMATION IN HEPATOCELLULAR CARCINOMA. Journal of Hepatology, 2013, 58, S39-S40.	1.8	4
121	Hormone receptor and HER2 assessment in breast carcinoma metastatic to bone: A comparison between FNA cell blocks and decalcified core needle biopsies. Cancer Cytopathology, 2020, 128, 133-145.	1.4	4
122	Systematic identification of novel cancer genes through analysis of deep shRNA perturbation screens. Nucleic Acids Research, 2021, 49, 8488-8504.	6.5	4
123	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
124	The Genomic Landscape of Serrated Lesion of the Colorectum: Similarities and Differences With Tubular and Tubulovillous Adenomas. Frontiers in Oncology, 2021, 11, 668466.	1.3	4
125	Standardizing Patient-Derived Organoid Generation Workflow to Avoid Microbial Contamination From Colorectal Cancer Tissues. Frontiers in Oncology, 2021, 11, 781833.	1.3	4
126	Hepatocellular Carcinoma: Pathology and Genetics. , 2018, , 198-198.		3

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127	Genomic evolutionary trajectory of metastatic squamous cell carcinoma of the lung. Translational Lung Cancer Research, 2021, 10, 1792-1803.	1.3	3
128	Non-viral gene delivery of the oncotoxic protein NS1 for treatment of hepatocellular carcinoma. Journal of Controlled Release, 2021, 334, 138-152.	4.8	3
129	High Density of CD16+ Tumor-Infiltrating Immune Cells in Recurrent Ovarian Cancer Is Associated with Enhanced Responsiveness to Chemotherapy and Prolonged Overall Survival. Cancers, 2021, 13, 5783.	1.7	3
130	Epigenetic priming in chronic liver disease impacts the transcriptional and genetic landscapes of hepatocellular carcinoma. Molecular Oncology, 2022, 16, 665-682.	2.1	3
131	Genetic analysis of a morphologically heterogeneous ovarian endometrioid carcinoma. Histopathology, 2017, 71, 480-487.	1.6	2
132	Convergent Evolution of Copy Number Alterations in Multi-Centric Hepatocellular Carcinoma. Scientific Reports, 2019, 9, 4611.	1.6	2
133	Fibroepithelial Breast Lesion: When Sequencing Can Help to Make a Clinical Decision. A Case Report. Clinical Breast Cancer, 2019, 19, e1-e6.	1.1	2
134	Discovery of heterozygous <i>KRT10</i> alterations in MAUIE cases underlines the importance of regular skin cancer screening in ichthyosis with confetti. British Journal of Dermatology, 2020, 183, 954-955.	1.4	2
135	Identification of Somatic Mutations in Thirty-year-old Serum Cell-free DNA From Patients With Breast Cancer: A Feasibility Study. Clinical Breast Cancer, 2020, 20, 413-421.e1.	1.1	2
136	Utility of Serial cfDNA NGS for Prospective Genomic Analysis of Patients on a Phase I Basket Study. JCO Precision Oncology, 2021, 5, 6-16.	1.5	2
137	Reliability of Whole-Exome Sequencing for Assessing Intratumor Genetic Heterogeneity. SSRN Electronic Journal, 0, , .	0.4	2
138	Abstract 930: Analysis of cell-free tumor DNA in cerebrospinal fluid to characterize and monitor the genetic alterations of brain tumors. Cancer Research, 2015, 75, 930-930.	0.4	2
139	Abstract GS1-08: Genomic characterisation of metastatic breast cancer., 2019,,.		2
140	The Role of Chronic Liver Diseases in the Emergence and Recurrence of Hepatocellular Carcinoma: An Omics Perspective. Frontiers in Medicine, 0, 9, .	1.2	2
141	The Potential Tumor-Suppressor DHRS7 Inversely Correlates with EGFR Expression in Prostate Cancer Cells and Tumor Samples. Cancers, 2022, 14, 3074.	1.7	2
142	High-Resolution Breakpoint Analysis Provides Evidence for the Sequence-Directed Nature of Genome Rearrangements in Hereditary Disorders. Human Mutation, 2015, 36, 250-259.	1.1	1
143	Genetic profiling using plasma-derived cell-free DNA in therapy-naÃ <sup>-</sup> ve hepatocellular carcinoma patients: A pilot study. Digestive and Liver Disease, 2018, 50, 27.	0.4	1
144	Cell-free DNA in hepatocellular carcinoma. , 2020, , 199-209.		1

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145	Abstract 100: The landscape of somatic genetic alterations in BRCA1 and BRCA2 breast cancers. , 2016, , .		1
146	Abstract S6-06: The genomic landscape of male breast cancers. , 2015, , .		1
147	Pilot trial of an implantable microdevice for In Vivo drug sensitivity testing in patients with early stage, triple negative breast cancer receiving neoadjuvant therapy Journal of Clinical Oncology, 2016, 34, TPS1101-TPS1101.	0.8	1
148	Abstract 138: Solid papillary carcinoma with reverse polarization are driven by IDH2 and PI3K pathway mutations. , 2016, , .		1
149	Abstract 3379: Massively parallel sequencing analysis of breast adenomyoepitheliomas reveals the heterogeneity of the disease and identifies a subset driven by HRAShotspot mutations., 2017,,.		1
150	Cost-effective target sequencing panel for hepatocellular carcinoma mutational screening. Journal of Hepatology, 2018, 68, S680.	1.8	0
151	Nectin-4 expression is a prognostic biomarker and associated with worse survival in triple-negative breast cancer. Breast, 2019, 44, S99.	0.9	O
152	Infiltration by Myeloperoxidase positive neutrophils is an independent prognostic factor in breast cancer. Breast, 2019, 44, S98-S99.	0.9	0
153	292 Patients with MAUIE syndrome are carriers of heterozygous IWC-associated KRT10 variants. Journal of Investigative Dermatology, 2019, 139, S264.	0.3	0
154	Uterine carcinosarcomas and metaplastic breast carcinomas: Genetically related cancers?. Gynecologic Oncology, 2020, 159, 323.	0.6	0
155	Abstract 2853: Transposon-activatedPOU5F1Bpromotes colorectal cancer growth and metastasis., 2021,,.		O
156	Abstract 3081: Loss of Shoca-2 expression in colorectal cancer correlates with metastasis as Shoca-2 represses EGF-regulated STAT3 activation via recruitment of PP1beta., 2010,,.		0
157	Abstract 3195: HMGA1 and HMGA2 over-expression in human lung carcinoma. , 2011, , .		O
158	Abstract 3802: EWSR1: Identification and functional characterization of a novel target gene locus in Lynch syndrome. , 2011, , .		0
159	Abstract 4496: UBCH10 overexpression in human colorectal cancers. , 2012, , .		O
160	Abstract 4685: SH2D4A is frequently downregulated in hepatocellular carcinoma , 2013, , .		0
161	Abstract S6-06: High-depth massively parallel sequencing reveals heterogeneity between primary tumor and metastatic deposits in de novo metastatic breast cancer patients prior to exposure to systemic therapy. , 2013, , .		0
162	Abstract P4-04-08: Genomic and transcriptomic characterization of papillary carcinomas of the breast. , 2013, , .		0

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163	Abstract 1386: Enhanced expression of HMGA1 and THY1 in human hepatocellular carcinoma correlates with poor prognosis. , 2014, , .		0
164	Abstract 1544: The clinical behavior of endometrioid and serous endometrial carcinomas is governed by distinct biological processes. , 2014, , .		0
165	Abstract 4258: Benchmarking algorithms for mutation impact prediction using functionally validated missense mutations. , 2014, , .		0
166	Abstract P6-03-05: Dual HER2 blockade of an activating driverHER3mutation: A proof of principle study in a metastatic breast cancer patient., 2015,,.		0
167	Abstract P2-03-08: Mutational landscape of metaplastic breast carcinomas. , 2015, , .		0
168	Abstract 3889: Genetic heterogeneity and distinct driver mutations in synchronous primary and metastatic breast cancers from therapy-na $\tilde{A}$ ve patients., 2015,,.		0
169	Abstract 2971: Whole exome sequencing reveals heterogeneity within lobular carcinomain situ(LCIS) and clonal selection in the progression to malignant lesions. , $2015$ , , .		0
170	Abstract 3885: Mutational landscape and copy number alterations of mucinous breast carcinoma. , 2015, , .		0
171	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. , $2016, \ldots$		0
172	Abstract P6-07-04: Distinct repertoires of somatic mutations affecting driver genes in mucinous and neuroendocrine carcinomas of the breast. , $2016$ , , .		0
173	Abstract P2-01-02: Capturing intra-tumor genetic heterogeneity in cell-free plasma DNA from patients with oligometastatic breast cancer. , $2016$ , , .		0
174	Abstract P6-03-10: Genomic and transcriptomic heterogeneity in metaplastic breast carcinomas. , 2016, , .		0
175	Serial next generation sequencing (NGS) of cell free DNA (cfDNA) and clonal evolution of <i>AKT1</i> E17K mutant tumors: Analyses from patients (pts) enrolled on a phase I basket study of an AKT inhibitor (AZD5363) Journal of Clinical Oncology, 2016, 34, 11500-11500.	0.8	0
176	Abstract 91: The mutational landscape of mucinous carcinomas of the breast. , 2016, , .		0
177	Abstract 134: Mutational landscape of breast cancers from PALB2 germline mutation carriers. , 2016, , .		0
178	Abstract P2-03-01: Mutational landscape of breast cancers from PALB2 germline mutation carriers. , 2017, , .		0
179	Abstract P1-05-03: The genomic landscape of breast metaplastic carcinoma., 2017,,.		0
180	Abstract S2-02: The landscape of somatic genetic alterations in BRCA1 and BRCA2 breast cancers. , 2017, , .		0

#	Article	lF	CITATIONS
181	Abstract 350: Pregnancy at early age is associated with a reduction of progesterone-responsive cells and epithelial Wnt signaling in human breast tissue. , 2017, , .		0
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