Citation Report
List of articles citing

The clonal and mutational evolution spectrum of primary triple-negative breast cancers

DOI: 10.1038/nature10933
Nature, 2012, 486, 395-9.

Source: https://exaly.com/paper-pdf/54383918/citation-report.pdf
Version: 2024-04-23

This report has been generated based on the citations recorded by exaly.com for the above article. 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.

#	Paper	IF	Citations
1633	Stroke in the young: coming of age. **2002**, 59, 6-7		12
1632	Cooperativity of Rb, Brca1, and p53 in malignant breast cancer evolution. **2012**, 8, e1003027		18
1631	Genomic Determinants of PI3K Pathway Inhibitor Response in Cancer. **2012**, 2, 109		60
1630	Triple-negative breast cancer in focus: from biology to novel therapeutics. Editorial. **2012**, 23 Suppl 6, vi5-6		1
1629	nFuse: discovery of complex genomic rearrangements in cancer using high-throughput sequencing. **2012**, 22, 2250-61		58
1628	Next-generation sequencing in breast cancer: first take home messages. **2012**, 24, 597-604		62
1627	Integrative analysis of genome-wide loss of heterozygosity and monoallelic expression at nucleotide resolution reveals disrupted pathways in triple-negative breast cancer. **2012**, 22, 1995-2007		181
1626	Targeting the PyMT Oncogene to Diverse Mammary Cell Populations Enhances Tumor Heterogeneity and Generates Rare Breast Cancer Subtypes. **2012**, 3, 550-63		15
1625	Genome-based diagnostics and predictive tools: a new epoch for breast cancer management. **2012**, 8, 1211-4		
1624	Functional analysis of receptor tyrosine kinase mutations in lung cancer identifies oncogenic extracellular domain mutations of ERBB2. **2012**, 109, 14476-81		208
1623	Advances in Breast Cancer - Looking Back over the Year. **2012**, 72, 1117-1129		16
1622	Functional impact bias reveals cancer drivers. **2012**, 40, e169		238
1621	Annotating cancer variants and anti-cancer therapeutics in reactome. **2012**, 4, 1180-211		232
1620	Keeping an open mind: highlights and controversies of the breast cancer stem cell theory. **2012**, 4, 155-66		15
1619	THE FUTURE OF GENOME-BASED MEDICINE. **2012**,		
1618	Profiling the immune stromal interface in breast cancer and its potential for clinical impact. **2012**, 7, 273-80		6
1617	Mechanisms of acquired resistance to anti-EGF receptor treatment in colorectal cancer. **2012**, 1, 491-502		1

1616	Cancer in light of experimental evolution. **2012**, 22, R762-71		89
1615	The transcriptional landscape and mutational profile of lung adenocarcinoma. **2012**, 22, 2109-19		435
1614	Regulation of mRNA expression in breast cancer - a cis-tematic trans-action. **2012**, 14, 322		1
1613	Who's driving anyway? Herculean efforts to identify the drivers of breast cancer. **2012**, 14, 323		7
1612	Bioinformatics for cancer immunology and immunotherapy. **2012**, 61, 1885-903		32
1611	Zukünftige Entwicklung der gynäkologischen Onkologie. **2012**, 45, 678-683		
1610	Imaging mitochondrial redox potential and its possible link to tumor metastatic potential. **2012**, 44, 645-53		25
1609	Molecular biology in breast cancer: should molecular classifiers be assessed by conventional tools or by gene expression arrays?. **2012**, 84 Suppl 1, e58-69		10
1608	CHAPTER 11:Breast Cancer �Importance of Life Stage with Respect to Environmental Influences. **2012**, 293-330		
1607	Whole-genome sequencing of liver cancers identifies etiological influences on mutation patterns and recurrent mutations in chromatin regulators. **2012**, 44, 760-4		671
1606	Molecular oncology: The positive in the negative. *Nature*, **2012**, 485, S52-3	50.4	4
1605	The rebel angel: mutant p53 as the driving oncogene in breast cancer. **2012**, 33, 2007-17		199
1604	Impact of genetic dynamics and single-cell heterogeneity on development of nonstandard personalized medicine strategies for cancer. **2012**, 109, 14586-91		76
1603	What are we learning from the cancer genome?. **2012**, 9, 621-30		43
1602	Intratumor heterogeneity: evolution through space and time. **2012**, 72, 4875-82		628
1601	Navigating cancer network attractors for tumor-specific therapy. **2012**, 30, 842-8		115
1600	Targeted therapy in rare cancers--adopting the orphans. **2012**, 9, 631-42		25
1599	Evolution of the cancer genome. **2012**, 13, 795-806		424

1598	SnapShot: breast cancer. **2012**, 22, 562-562.e1		54
1597	Expression of epithelial to mesenchymal transition-related markers in lymph node metastases as a surrogate for primary tumor metastatic potential in breast cancer. **2012**, 10, 226		40
1596	Overcoming implementation challenges of personalized cancer therapy. **2012**, 9, 542-8		96
1595	Comprehensive molecular portraits of human breast tumours. *Nature*, **2012**, 490, 61-70	50.4	8025
1594	Breast cancer intratumor genetic heterogeneity: causes and implications. **2012**, 12, 1021-32		57
1593	What history tells us XXVIII. What is really new in the current evolutionary theory of cancer?. **2012**, 37, 609-12		3
1592	Cancer sequencing unravels clonal evolution. **2012**, 30, 408-10		32
1591	DriverNet: uncovering the impact of somatic driver mutations on transcriptional networks in cancer. **2012**, 13, R124		156
1590	PIK3R1 (phosphoinositide-3-kinase, regulatory subunit 1 (alpha)). **2012**,		
1589	Use of mutation profiles to refine the classification of endometrial carcinomas. **2012**, 228, 20-30		227
1588	Genomics: the breast cancer landscape. *Nature*, **2012**, 486, 328-9	50.4	30
1587	Breast cancer: divide and conquer?. **2012**, 12, 375		
1586	High intratumor genetic heterogeneity is related to worse outcome in patients with head and neck squamous cell carcinoma. **2013**, 119, 3034-42		138
1585	Targeting triple negative breast cancer: is p53 the answer?. **2013**, 39, 541-50		89
1584	Cancer Genomics. **2013**,		4
1583	Relapsed triple-negative breast cancer: challenges and treatment strategies. **2013**, 73, 1257-65		34
1582	Next generation sequencing in cancer research and clinical application. **2013**, 15, 4		76
1581	A novel min-cost flow method for estimating transcript expression with RNA-Seq. **2013**, 14 Suppl 5, S15		48

1580	Comparing somatic mutation-callers: beyond Venn diagrams. **2013**, 14, 189	57
1579	Discovery of structural alterations in solid tumor oligodendroglioma by single molecule analysis. **2013**, 14, 505	25
1578	Gene rearrangements in hormone receptor negative breast cancers revealed by mate pair sequencing. **2013**, 14, 165	28
1577	Signaling pathway switch in breast cancer. **2013**, 13, 66	22
1576	Next generation analysis of breast cancer genomes for precision medicine. **2013**, 339, 1-7	19
1575	How integrins control breast biology. **2013**, 25, 633-41	43
1574	A new genome-driven integrated classification of breast cancer and its implications. **2013**, 32, 617-28	212
1573	Personal genomes, quantitative dynamic omics and personalized medicine. **2013**, 1, 71-90	26
1572	The complex genetic landscape of familial breast cancer. **2013**, 132, 845-63	94
1571	Personalized therapy for breast cancer: a dream or a reality?. **2013**, 9, 1105-19	23
1570	Array Comparative Genomic Hybridization. **2013**,	1
1569	The RasGAP gene, RASAL2, is a tumor and metastasis suppressor. **2013**, 24, 365-78	102
1568	Molecular targets on the horizon for kidney and urothelial cancer. **2013**, 10, 557-70	18
1567	Clonal evolution of high-grade serous ovarian carcinoma from primary to recurrent disease. **2013**, 229, 515-24	73
1566	Genomics of lymphoid malignancies reveal major activation pathways in lymphocytes. **2013**, 45, 15-23	2
1565	Recessive cancer genes engage in negative genetic interactions with their functional paralogs. **2013**, 5, 1519-26	14
1564	Cell to extracellular matrix interactions and their reciprocal nature in cancer. **2013**, 319, 1663-70	39
1563	Combined Wnt/□catenin, Met, and CXCL12/CXCR4 signals characterize basal breast cancer and predict disease outcome. **2013**, 5, 1214-27	57

1562	Triple-negative breast cancer and the need for new therapeutic targets. **2013**, 183, 1064-1074		110
1561	MAST2 and NOTCH1 translocations in breast carcinoma and associated pre-invasive lesions. **2013**, 44, 2837-44		10
1560	Beyond BRCA1/2: polygenic, 'polyfunctional' molecular circuitry model to predict breast cancer risk. **2013**, 7, 675-8		2
1559	The mitochondrial and autosomal mutation landscapes of prostate cancer. **2013**, 63, 702-8		80
1558	Mutational analysis of breast cancer: guiding personalized treatments. **2013**, 22 Suppl 2, S19-21		12
1557	DGIdb: mining the druggable genome. **2013**, 10, 1209-10		317
1556	From integrative genomics to therapeutic targets. **2013**, 73, 3483-8		16
1555	Molecular pathways: PI3K pathway targets in triple-negative breast cancers. **2013**, 19, 3738-44		49
1554	MATH, a novel measure of intratumor genetic heterogeneity, is high in poor-outcome classes of head and neck squamous cell carcinoma. **2013**, 49, 211-5		191
1553	Cell and Molecular Biology of Breast Cancer. **2013**,		8
1552	Identification of prognosis-relevant subgroups in patients with chemoresistant triple-negative breast cancer. **2013**, 19, 2723-33		119
1551	A tale of two approaches: complementary mechanisms of cytotoxic and targeted therapy resistance may inform next-generation cancer treatments. **2013**, 34, 725-38		68
1550	Profiles of Basal and stimulated receptor signaling networks predict drug response in breast cancer lines. **2013**, 6, ra84		75
1549	From next-generation sequencing to nanopore sequencing technology: paving the way to personalized genomic medicine. **2013**, 10, 1-6		60
1548	Breast carcinoma: is molecular evaluation a necessary part of current pathological analysis?. **2013**, 30, 321-8		6
1547	The causes and consequences of genetic heterogeneity in cancer evolution. *Nature*, **2013**, 501, 338-45	50.4	1473
1546	Video Q&A: molecular profiling of breast cancer. **2013**, 11, 150		
1545	Semiautomated isolation and molecular characterisation of single or highly purified tumour cells from CellSearch enriched blood samples using dielectrophoretic cell sorting. **2013**, 108, 1358-67		131

1544	Integration of Gene Signatures and Genomic Data into Radiation Oncology Practice. **2013**, 29-46		
1543	Glucocorticoid receptor antagonism as a novel therapy for triple-negative breast cancer. **2013**, 19, 6163-72		119
1542	A simple consensus approach improves somatic mutation prediction accuracy. **2013**, 5, 90		29
1541	Intra-relation reconstruction from inter-relation: miRNA to gene expression. **2013**, 7 Suppl 3, S8		10
1540	THetA: inferring intra-tumor heterogeneity from high-throughput DNA sequencing data. **2013**, 14, R80		160
1539	Critical research gaps and translational priorities for the successful prevention and treatment of breast cancer. **2013**, 15, R92		248
1538	Emerging patterns of somatic mutations in cancer. **2013**, 14, 703-18		366
1537	Genetically engineered mouse models of PI3K signaling in breast cancer. **2013**, 7, 146-64		28
1536	Tumour heterogeneity and cancer cell plasticity. *Nature*, **2013**, 501, 328-37	50.4	1532
1535	Deep sequencing and integrative genome analysis: approaching a new class of biomarkers and therapeutic targets for breast cancer. **2013**, 14, 5-8		3
1534	Economic and environmental impacts of microbial biodiesel. **2013**, 31, 789-93		70
1533	Systematic investigation of cancer-associated somatic point mutations in SNP databases. **2013**, 31, 787-9		15
1532	A genome-wide siRNA screen identifies proteasome addiction as a vulnerability of basal-like triple-negative breast cancer cells. **2013**, 24, 182-96		114
1531	Reliable identification of genomic variants from RNA-seq data. **2013**, 93, 641-51		247
1530	Next-generation sequencing in cancer research & diagnostics. **2013**, 20-40		
1529	Chronic lymphocytic leukemia: molecular heterogeneity revealed by high-throughput genomics. **2013**, 5, 47		35
1528	Intra-tumor heterogeneity: lessons from microbial evolution and clinical implications. **2013**, 5, 101		36
1527	Needles in a haystack: finding recurrent genomic changes in breast cancer. **2013**, 14, 304		2

1526	The genomic map of breast cancer: which roads lead to better targeted therapies?. **2013**, 15, 209	10
1525	Cancer Modeling: A Personal Perspective. **2013**, 60, 304	13
1524	KLF6-SV1 drives breast cancer metastasis and is associated with poor survival. **2013**, 5, 169ra12	58
1523	Activating HER2 mutations in HER2 gene amplification negative breast cancer. **2013**, 3, 224-37	561
1522	Deep sequencing in cancer research. **2013**, 43, 110-5	16
1521	Genome and transcriptome sequencing in prospective metastatic triple-negative breast cancer uncovers therapeutic vulnerabilities. **2013**, 12, 104-16	170
1520	Recurrent SETBP1 mutations in atypical chronic myeloid leukemia. **2013**, 45, 18-24	272
1519	Cancer stem cells, the epithelial to mesenchymal transition (EMT) and radioresistance: potential role of hypoxia. **2013**, 341, 63-72	161
1518	The genomic landscape of breast cancer as a therapeutic roadmap. **2013**, 3, 27-34	161
1517	iReckon: simultaneous isoform discovery and abundance estimation from RNA-seq data. **2013**, 23, 519-29	92
1516	Cancer heterogeneity and "the struggle for existence": diagnostic and analytical challenges. **2013**, 340, 220-6	20
1515	Prognostic evaluation of the B cell/IL-8 metagene in different intrinsic breast cancer subtypes. **2013**, 137, 407-16	22
1514	A phase II study of UCN-01 in combination with irinotecan in patients with metastatic triple negative breast cancer. **2013**, 137, 483-92	82
1513	Evolution and impact of subclonal mutations in chronic lymphocytic leukemia. **2013**, 152, 714-26	1006
1512	Promise of personalized omics to precision medicine. **2013**, 5, 73-82	188
1511	Endocrine-therapy-resistant ESR1 variants revealed by genomic characterization of breast-cancer-derived xenografts. **2013**, 4, 1116-30	447
1510	Summary of the 2013 American Association for Cancer Research (AACR) Annual Meeting. **2013**, 130, 6-8	
1509	Tackling the diversity of triple-negative breast cancer. **2013**, 19, 6380-8	120

1508	Statin induces inhibition of triple negative breast cancer (TNBC) cells via PI3K pathway. **2013**, 439, 275-9	40
1507	Aldehyde dehydrogenase 1/epidermal growth factor receptor coexpression is characteristic of a highly aggressive, poor-prognosis subgroup of high-grade serous ovarian carcinoma. **2013**, 44, 1465-71	29
1506	Functional analysis-make or break for cancer predictability. **2013**, 743-744, 132-141	4
1505	Progression from ductal carcinoma in situ to invasive breast cancer: revisited. **2013**, 7, 859-69	146
1504	Integrative deep-sequencing analysis of cancer samples: discoveries and clinical challenges. **2013**, 13, 205-8	3
1503	Breast cancer: Tamoxifen--when more might be better. **2013**, 10, 125-6	3
1502	Plasma-derived tumor DNA analysis at whole-genome resolution. **2013**, 59, 6-8	5
1501	Distinguishing somatic and germline copy number events in cancer patient DNA hybridized to whole-genome SNP genotyping arrays. **2013**, 973, 355-72	5
1500	Analysis of circulating tumor DNA to monitor metastatic breast cancer. **2013**, 368, 1199-209	1560
1499	Therapeutic targets in triple negative breast cancer. **2013**, 66, 530-42	104
1498	Translating genomics to the clinic: implications of cancer heterogeneity. **2013**, 59, 127-37	20
1497	The implications of clonal genome evolution for cancer medicine. **2013**, 368, 842-51	275
1496	Emerging targeted agents in metastatic breast cancer. **2013**, 10, 191-210	138
1495	Alterations of EGFR, p53 and PTEN that mimic changes found in basal-like breast cancer promote transformation of human mammary epithelial cells. **2013**, 14, 246-53	25
1494	FOXA1 mutations in hormone-dependent cancers. **2013**, 3, 20	42
1493	Next-generation sequencing: a powerful tool for the discovery of molecular markers in breast ductal carcinoma in situ. **2013**, 13, 151-65	36
1492	Cancer genome-sequencing study design. **2013**, 14, 321-32	85
1491	Genomic sequencing in cancer. **2013**, 340, 161-70	20

1490	Non-invasive analysis of acquired resistance to cancer therapy by sequencing of plasma DNA. *Nature*, **2013**, 497, 108-12	50.4	1220
1489	Understanding genomic alterations in cancer genomes using an integrative network approach. **2013**, 340, 261-9		49
1488	The detection and implication of genome instability in cancer. **2013**, 32, 341-52		100
1487	Proteomic and bioinformatic analysis of mammalian SWI/SNF complexes identifies extensive roles in human malignancy. **2013**, 45, 592-601		765
1486	Adapting clinical paradigms to the challenges of cancer clonal evolution. **2013**, 182, 1962-71		36
1485	Circulating tumour cells and cell-free DNA as tools for managing breast cancer. **2013**, 10, 377-89		146
1484	Molecular and clinicopathological markers of prognosis in breast cancer. **2013**, 13, 481-98		4
1483	Parallel evolution of tumour subclones mimics diversity between tumours. **2013**, 230, 356-64		70
1482	Genetic heterogeneity in breast cancer: the road to personalized medicine?. **2013**, 11, 151		42
1481	Cancer networks and beyond: interpreting mutations using the human interactome and protein structure. **2013**, 23, 219-26		19
1480	The evolving landscape of protein kinases in breast cancer: clinical implications. **2013**, 39, 68-76		19
1479	Genomics-driven oncology: framework for an emerging paradigm. **2013**, 31, 1806-14		251
1478	High-throughput gene expression and mutation profiling: current methods and future perspectives. **2013**, 8, 401-6		11
1477	Isogenic human mammary epithelial cell lines: novel tools for target identification and validation. Comprehensive characterization of an isogenic human mammary epithelial cell model provides evidence for epithelial-mesenchymal transition. **2013**, 138, 437-56		2
1476	Genomic profiling in triple-negative breast cancer. **2013**, 8, 408-13		20
1475	Clonal heterogeneity as detected by metaphase karyotyping is an indicator of poor prognosis in acute myeloid leukemia. **2013**, 31, 3898-905		52
1474	Breast-conserving therapy achieves locoregional outcomes comparable to mastectomy in women with T1-2N0 triple-negative breast cancer. **2013**, 20, 3469-76		95
1473	Integrating NGS and third-generation sequencing technologies into clinical genomic medicine. **2013** , 6-18		

1472	Tumour heterogeneity in the clinic. *Nature*, **2013**, 501, 355-64	50.4	770
1471	Hierarchy in somatic mutations arising during genomic evolution and progression of follicular lymphoma. **2013**, 121, 1604-11		218
1470	Progress in breast cancer: overview. **2013**, 19, 6353-9		6
1469	Research resource: global identification of estrogen receptor target genes in triple negative breast cancer cells. **2013**, 27, 1762-75		42
1468	Fine mapping of breast cancer genome-wide association studies loci in women of African ancestry identifies novel susceptibility markers. **2013**, 34, 1520-8		24
1467	[Personalized medicine and breast cancer: anticipatory medicine, prognostic evaluation and therapeutic targeting]. **2013**, 100, 1295-310		3
1466	Integrated clinical genomics: new horizon for diagnostic and biomarker discoveries in cancer. **2013**, 13, 1-4		8
1465	ANTXR1, a stem cell-enriched functional biomarker, connects collagen signaling to cancer stem-like cells and metastasis in breast cancer. **2013**, 73, 5821-33		81
1464	An evolutionary perspective on anti-tumor immunity. **2012**, 2, 202		12
1463	Bringing precision medicine to the clinic: from genomic profiling to the power of clinical observation. **2013**, 24, 1956-7		17
1462	Integrative analysis of cancer-related signaling pathways. **2013**, 4, 124		9
1461	Overview of diagnostic/targeted treatment combinations in personalized medicine for breast cancer patients. **2013**, 7, 1-19		8
1460	Novel Integrative Genomics Approach for Associating GWAS Information with Intrinsic Subtypes of Breast Cancer. **2013**, 12, 125-42		4
1459	Genome-wide signatures of transcription factor activity: connecting transcription factors, disease, and small molecules. **2013**, 9, e1003198		18
1458	Expanding the prion concept to cancer biology: dominant-negative effect of aggregates of mutant p53 tumour suppressor. **2013**, 33,		41
1457	Comprehensive analysis of transcriptome variation uncovers known and novel driver events in T-cell acute lymphoblastic leukemia. **2013**, 9, e1003997		94
1456	Going with the flow: from circulating tumor cells to DNA. **2013**, 5, 207ps14		90
1455	Targeting receptor tyrosine kinases in HER2-negative breast cancer. **2013**, 25, 594-601		9

1454	A deterministic model for the occurrence and dynamics of multiple mutations in hierarchically organized tissues. **2013**, 10, 20130349	35
1453	Revealing targeted therapeutic opportunities in triple-negative breast cancers: a new strategy. **2013**, 12, 2705-6	10
1452	Functional analysis of genes in regions commonly amplified in high-grade serous and endometrioid ovarian cancer. **2013**, 19, 1411-21	41
1451	An empirical Bayesian framework for somatic mutation detection from cancer genome sequencing data. **2013**, 41, e89	129
1450	Polo-like kinase 1: a potential therapeutic option in combination with conventional chemotherapy for the management of patients with triple-negative breast cancer. **2013**, 73, 813-23	125
1449	Next-Generation Sequencing & Molecular Diagnostics. **2013**,	1
1448	Oncogenic miR-181a/b affect the DNA damage response in aggressive breast cancer. **2013**, 12, 1679-87	88
1447	Somatic mutation profiling and associations with prognosis and trastuzumab benefit in early breast cancer. **2013**, 105, 960-7	112
1446	Clinical relevance of miRNAs in cancer. **2013**, 42-62	
1445	[Triple-negative breast cancer: histoclinical and molecular features, therapeutic management and perspectives]. **2013**, 100, 453-64	14
1444	Breast Cancer Genomics: From Portraits to Landscapes. **2013**, 255-294	
1443	The mutational landscape of chromatin regulatory factors across 4,623 tumor samples. **2013**, 14, r106	78
1442	Clinical response to a lapatinib-based therapy for a Li-Fraumeni syndrome patient with a novel HER2V659E mutation. **2013**, 3, 1238-44	38
1441	Circulating tumour cells: insights into tumour heterogeneity. **2013**, 274, 137-43	37
1440	An Integrative Genomics Approach for Associating GWAS Information with Triple-Negative Breast Cancer. **2013**, 12, 1-20	14
1439	Current Challenges for HER2 Testing in Diagnostic Pathology: State of the Art and Controversial Issues. **2013**, 3, 129	51
1438	Somatic mutations in GRM1 in cancer alter metabotropic glutamate receptor 1 intracellular localization and signaling. **2013**, 83, 770-80	20
1437	TrAp: a tree approach for fingerprinting subclonal tumor composition. **2013**, 41, e165	90

1436	Immunotherapeutic approaches in triple-negative breast cancer: latest research and clinical prospects. **2013**, 5, 169-81	121
1435	Triple-negative breast cancers: associations between imaging and pathological findings for triple-negative tumors compared with hormone receptor-positive/human epidermal growth factor receptor-2-negative breast cancers. **2013**, 18, 802-11	47
1434	Trastuzumab emtansine for advanced HER2-positive breast cancer and beyond: genome landscape-based targets. **2013**, 13, 5-8	10
1433	Genome evolution during progression to breast cancer. **2013**, 23, 1097-108	86
1432	Genomic medicine frontier in human solid tumors: prospects and challenges. **2013**, 31, 1874-84	90
1431	HER2's new mutations. **2013**, 6, 26-26	
1430	Triple-negative breast cancer: molecular characterization and targeted therapies. **2013**, 2, 417-430	1
1429	Diagnostic perspectives in the epoch of next-generation sequencing. **2013**, 98-111	
1428	Prognostic microRNA/mRNA signature from the integrated analysis of patients with invasive breast cancer. **2013**, 110, 7413-7	128
1427	Incorporating genomics into breast cancer clinical trials and care. **2013**, 19, 6371-9	14
1426	MET and ERBB2 are coexpressed in ERBB2+ breast cancer and contribute to innate resistance. **2013** , 11, 1112-21	28
1425	Relapsed classic E-cadherin (CDH1)-mutated invasive lobular breast cancer shows a high frequency of HER2 (ERBB2) gene mutations. **2013**, 19, 2668-76	101
1424	Genome function, ChIP-Seq and personalized diagnostics. **2013**, 78-96	
1423	Comprehensive whole genome and transcriptome analysis for novel diagnostics. **2013**, 64-76	
1422	Targeted-capture massively-parallel sequencing enables robust detection of clinically informative mutations from formalin-fixed tumours. **2013**, 3, 3494	38
1421	Emerging treatments for metastatic breast cancer: update from 2012. **2013**, 2, 33-45	
1420	Distinct evolutionary trajectories of primary high-grade serous ovarian cancers revealed through spatial mutational profiling. **2013**, 231, 21-34	292
1419	Endobiogeny: a global approach to systems biology (part 1 of 2). **2013**, 2, 64-78	7

1418	Clinical application of high-throughput genomic technologies for treatment selection in breast cancer. **2013**, 15, R97	13
1417	Using multigene tests to select treatment for early-stage breast cancer. **2013**, 11, 174-82; quiz 182	37
1416	A network-heuristic approach to improve the impact of genomic data on drug discovery. **2013**, 93, 295-7	0
1415	Wnt signaling in triple negative breast cancer is associated with metastasis. **2013**, 13, 537	173
1414	Glutamate signaling in benign and malignant disorders: current status, future perspectives, and therapeutic implications. **2013**, 9, 728-42	55
1413	Identifying potential cancer driver genes by genomic data integration. **2013**, 3, 3538	45
1412	Glycoprotein non-metastatic b (GPNMB): A metastatic mediator and emerging therapeutic target in cancer. **2013**, 6, 839-52	70
1411	Germline DNA copy number aberrations identified as potential prognostic factors for breast cancer recurrence. **2013**, 8, e53850	17
1410	Genomic interaction profiles in breast cancer reveal altered chromatin architecture. **2013**, 8, e73974	30
1409	Triple negative breast tumors in African-American and Hispanic/Latina women are high in CD44+, low in CD24+, and have loss of PTEN. **2013**, 8, e78259	46
1408	Spectrum of EGFR gene copy number changes and KRAS gene mutation status in Korean triple negative breast cancer patients. **2013**, 8, e79014	19
1407	Neoadjuvant therapy in operable breast cancer: application to triple negative breast cancer. **2013**, 2013, 219869	12
1406	Translating complex genomic discoveries into molecular diagnostic tests. **2013**, 2-5	
1405	PIK3CA mutations are a predictor of docetaxel plus epirubicin neoadjuvant chemotherapy clinical efficacy in breast cancer. **2014**, 61, 461-7	11
1404	Metabotropic glutamate receptor-1 contributes to progression in triple negative breast cancer. **2014**, 9, e81126	33
1403	Candidate luminal B breast cancer genes identified by genome, gene expression and DNA methylation profiling. **2014**, 9, e81843	42
1402	Phenotypic diversity of breast cancer-related mutations in metalloproteinase-disintegrin ADAM12. **2014**, 9, e92536	11
1401	Highly adaptable triple-negative breast cancer cells as a functional model for testing anticancer agents. **2014**, 9, e109487	14

1400	Characterization of X chromosome inactivation using integrated analysis of whole-exome and mRNA sequencing. **2014**, 9, e113036	12
1399	Identification of p53 and its isoforms in human breast carcinoma cells. **2014**, 2014, 618698	14
1398	ReactomeFIViz: the Reactome FI Cytoscape app for pathway and network-based data analysis. **2014** , 3, 146	118
1397	Loss of the multifunctional RNA-binding protein RBM47 as a source of selectable metastatic traits in breast cancer. **2014**, 3,	79
1396	Computational prognostic indicators for breast cancer. **2014**, 6, 301-12	7
1395	A novel use of biomarkers in the modeling of cancer activity based on the theory of endobiogeny. **2014**, 3, 55-60	3
1394	[Stochastic phenomena and the tumoral process]. **2014**, 30, 693-8	0
1393	Subtyping of breast cancer using reverse phase protein arrays. **2014**, 11, 757-70	13
1392	Next-generation sequencing in multiple myeloma: insights into the molecular heterogeneity of the disease. **2014**, 3, 367-376	2
1391	A general framework for analyzing tumor subclonality using SNP array and DNA sequencing data. **2014**, 15, 473	52
1390	Genome-driven integrated classification of breast cancer validated in over 7,500 samples. **2014**, 15, 431	130
1389	The intra-tumor heterogeneity of cell signaling factors in breast cancer: p4E-BP1 and peIF4E are diffusely expressed and are real potential targets. **2014**, 16, 937-41	19
1388	SubcloneSeeker: a computational framework for reconstructing tumor clone structure for cancer variant interpretation and prioritization. **2014**, 15, 443	47
1387	Cancer genomic research at the crossroads: realizing the changing genetic landscape as intratumoral spatial and temporal heterogeneity becomes a confounding factor. **2014**, 14, 115	31
1386	Genome-based approaches for the diagnosis of breast cancer: a review with perspective. **2014**, 3, 173-193	
1385	The AURORA initiative for metastatic breast cancer. **2014**, 111, 1881-7	68
1384	A cancer theory kerfuffle can lead to new lines of research. **2015**, 107,	57
1383	A combinatorial approach for analyzing intra-tumor heterogeneity from high-throughput sequencing data. **2014**, 30, i78-86	78

1382	Spaced seed data structures. **2014**,	1
1381	SciClone: inferring clonal architecture and tracking the spatial and temporal patterns of tumor evolution. **2014**, 10, e1003665	301
1380	Suppression of invasion and metastasis of triple-negative breast cancer lines by pharmacological or genetic inhibition of slug activity. **2014**, 16, 1047-58	61
1379	Longitudinal study of recurrent metastatic melanoma cell lines underscores the individuality of cancer biology. **2014**, 134, 1389-1396	2
1378	Induction of Wnt-inducible signaling protein-1 correlates with invasive breast cancer oncogenesis and reduced type 1 cell-mediated cytotoxic immunity: a retrospective study. **2014**, 10, e1003409	35
1377	Tracking genomic cancer evolution for precision medicine: the lung TRACERx study. **2014**, 12, e1001906	136
1376	Inferring clonal composition from multiple sections of a breast cancer. **2014**, 10, e1003703	84
1375	Clonal architecture of secondary acute myeloid leukemia defined by single-cell sequencing. **2014**, 10, e1004462	94
1374	The relationship between delay period eye movements and visuospatial memory. **2014**, 14,	47
1373	Antagonism of EGFR and HER3 enhances the response to inhibitors of the PI3K-Akt pathway in triple-negative breast cancer. **2014**, 7, ra29	93
1372	Tumor heterogeneity and personalized cancer medicine: are we being outnumbered?. **2014**, 10, 417-28	16
1371	Systems consequences of amplicon formation in human breast cancer. **2014**, 24, 1559-71	21
1370	TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequence data. **2014**, 24, 1881-93	218
1369	What is the potential of using PI3K inhibitors in the management of breast cancer in the clinic?. **2014**, 3, 345-357	
1368	Metronomic Chemotherapy. **2014**,	2
1367	Personalized oncology: genomic screening in phase 1. **2014**, 122, 723-33	16
1366	Molecular profiling of the residual disease of triple-negative breast cancers after neoadjuvant chemotherapy identifies actionable therapeutic targets. **2014**, 4, 232-45	310
1365	Combined deletion of Pten and p53 in mammary epithelium accelerates triple-negative breast cancer with dependency on eEF2K. **2014**, 6, 1542-60	80

1364	Triple negative breast carcinoma EGFR amplification is not associated with EGFR, Kras or ALK mutations. **2014**, 110, 1045-52	26
1363	Lessons learned from the intrinsic subtypes of breast cancer in the quest for precision therapy. **2014**, 101, 925-38	30
1362	GATA3 mutations define a unique subtype of luminal-like breast cancer with improved survival. **2014**, 120, 1329-37	48
1361	DNA barcoding reveals diverse growth kinetics of human breast tumour subclones in serially passaged xenografts. **2014**, 5, 5871	66
1360	Genome network medicine: innovation to overcome huge challenges in cancer therapy. **2014**, 6, 201-8	6
1359	Polarity gene alterations in pure invasive micropapillary carcinomas of the breast. **2014**, 16, R46	30
1358	Successful treatment of a patient with Li-Fraumeni syndrome and metastatic lung adenocarcinoma harboring synchronous EGFR L858R and ERBB2 extracellular domain S310F mutations with the pan-HER inhibitor afatinib. **2014**, 15, 970-4	7
1357	CLImAT: accurate detection of copy number alteration and loss of heterozygosity in impure and aneuploid tumor samples using whole-genome sequencing data. **2014**, 30, 2576-83	32
1356	A fine-scale dissection of the DNA double-strand break repair machinery and its implications for breast cancer therapy. **2014**, 42, 6106-27	53
1355	Towards accurate characterization of clonal heterogeneity based on structural variation. **2014**, 15, 299	7
1354	High expression of GEM and EDNRA is associated with metastasis and poor outcome in patients with advanced bladder cancer. **2014**, 14, 638	20
1353	Molecular characterisation of isogenic taxane resistant cell lines identify novel drivers of drug resistance. **2014**, 14, 762	11
1352	Evaluation of an integrated clinical workflow for targeted next-generation sequencing of low-quality tumor DNA using a 51-gene enrichment panel. **2014**, 7, 62	25
1351	New concepts in breast cancer genomics and genetics. **2014**, 16, 460	23
1350	Triple-negative breast cancer: molecular subtypes and targeted therapy. **2014**, 26, 34-40	26
1349	Autophagy inhibition augments the anticancer effects of epirubicin treatment in anthracycline-sensitive and -resistant triple-negative breast cancer. **2014**, 20, 3159-73	101
1348	NCI Workshop Report: Clinical and Computational Requirements for Correlating Imaging Phenotypes with Genomics Signatures. **2014**, 7, 556-69	60
1347	Favorable prognostic impact in loss of TP53 and PIK3CA mutations after neoadjuvant chemotherapy in breast cancer. **2014**, 74, 3399-407	31

1346	Frequent promoter hypermethylation and expression reduction of the glucocorticoid receptor gene in breast tumors. **2014**, 9, 851-9	30
1345	Theranostic and molecular classification of breast cancer. **2014**, 138, 44-56	35
1344	HER2 mutation status in Japanese HER2-negative breast cancer patients. **2014**, 44, 619-23	9
1343	Association of H3K9me3 and H3K27me3 repressive histone marks with breast cancer subtypes in the Nurses' Health Study. **2014**, 147, 639-51	37
1342	Omics Approaches in Breast Cancer. **2014**,	8
1341	Breast Cancer Genomics. **2014**, 53-103	
1340	EXPANDS: expanding ploidy and allele frequency on nested subpopulations. **2014**, 30, 50-60	93
1339	Clinical Trials Using LV-P140K-MGMT for Gliomas. **2014**, 379-391	1
1338	Whole exome sequencing for cancer – is there evidence of clinical utility?. **2014**, 115	2
1337	Patient-derived xenografts of triple-negative breast cancer reproduce molecular features of patient tumors and respond to mTOR inhibition. **2014**, 16, R36	55
1336	Individualizing breast cancer treatment-The dawn of personalized medicine. **2014**, 320, 1-11	24
1335	Animal models of disease: pre-clinical animal models of cancer and their applications and utility in drug discovery. **2014**, 87, 150-61	224
1334	Clonal evolution in hematological malignancies and therapeutic implications. **2014**, 28, 34-43	120
1333	Mutations in EGFR, BRAF and RAS are rare in triple-negative and basal-like breast cancers from Caucasian women. **2014**, 143, 385-92	43
1332	Characterizing the heterogeneity of triple-negative breast cancers using microdissected normal ductal epithelium and RNA-sequencing. **2014**, 143, 57-68	25
1331	An emerging role of PARK2 in cancer. **2014**, 92, 31-42	73
1330	Genomic architecture and evolution of clear cell renal cell carcinomas defined by multiregion sequencing. **2014**, 46, 225-233	866
1329	Follicle-stimulating hormone receptor (FSHR) alternative skipping of exon 2 or 3 affects ovarian response to FSH. **2014**, 20, 630-43	20

1328	Causal Network Models for Predicting Compound Targets and Driving Pathways in Cancer. **2014**, 19, 791-802	21
1327	Mutational signatures: the patterns of somatic mutations hidden in cancer genomes. **2014**, 24, 52-60	299
1326	Wnt modulates MCL1 to control cell survival in triple negative breast cancer. **2014**, 14, 124	44
1325	Inferring clonal evolution of tumors from single nucleotide somatic mutations. **2014**, 15, 35	163
1324	Decreased expression of key tumour suppressor microRNAs is associated with lymph node metastases in triple negative breast cancer. **2014**, 14, 51	62
1323	Molecular tests as prognostic factors in breast cancer. **2014**, 464, 283-91	30
1322	Serological proteome analysis of dogs with breast cancer unveils common serum biomarkers with human counterparts. **2014**, 35, 901-10	20
1321	The prognostic significance of the aberrant extremes of p53 immunophenotypes in breast cancer. **2014**, 65, 340-52	54
1320	Second-Generation Sequencing for Cancer Genome Analysis. **2014**, 13-30	1
1319	Widespread genetic heterogeneity in multiple myeloma: implications for targeted therapy. **2014**, 25, 91-101	657
1318	Epistatic interactions and drug response. **2014**, 232, 255-63	19
1317	Novel role of Engrailed 1 as a prosurvival transcription factor in basal-like breast cancer and engineering of interference peptides block its oncogenic function. **2014**, 33, 4767-77	51
1316	Principles and methods of integrative genomic analyses in cancer. **2014**, 14, 299-313	245
1315	The challenge of intratumour heterogeneity in precision medicine. **2014**, 276, 41-51	50
1314	Genomic and molecular characterization of esophageal squamous cell carcinoma. **2014**, 46, 467-73	398
1313	Cancer Transcriptome Sequencing and Analysis. **2014**, 31-47	1
1312	Characterization of the genomic features and expressed fusion genes in micropapillary carcinomas of the breast. **2014**, 232, 553-65	75
1311	The emergence of targeted drugs in breast cancer to prevent resistance to endocrine treatment and chemotherapy. **2014**, 15, 681-700	40

1310	Whole-genome sequencing identifies genomic heterogeneity at a nucleotide and chromosomal level in bladder cancer. **2014**, 111, E672-81	59
1309	Enriched variations in TEKT4 and breast cancer resistance to paclitaxel. **2014**, 5, 3802	25
1308	Triple-negative breast cancer: bridging the gap from cancer genomics to predictive biomarkers. **2014**, 6, 88-100	29
1307	Glioblastomas are composed of genetically divergent clones with distinct tumourigenic potential and variable stem cell-associated phenotypes. **2014**, 127, 203-19	69
1306	The need for complex 3D culture models to unravel novel pathways and identify accurate biomarkers in breast cancer. **2014**, 69-70, 42-51	234
1305	Clonal analysis via barcoding reveals diverse growth and differentiation of transplanted mouse and human mammary stem cells. **2014**, 14, 253-63	46
1304	Nesprins in health and disease. **2014**, 29, 169-79	50
1303	Breast Cancer Genomics. **2014**, 213-232	2
1302	The evolution of the unstable cancer genome. **2014**, 24, 61-7	52
1301	Bias from removing read duplication in ultra-deep sequencing experiments. **2014**, 30, 1073-1080	30
1300	Inactivating CUX1 mutations promote tumorigenesis. **2014**, 46, 33-8	89
1299	Comprehensive genomic analysis of rhabdomyosarcoma reveals a landscape of alterations affecting a common genetic axis in fusion-positive and fusion-negative tumors. **2014**, 4, 216-31	417
1298	Identification and use of biomarkers in treatment strategies for triple-negative breast cancer subtypes. **2014**, 232, 142-50	267
1297	PTEN/PIK3CA genes are frequently mutated in spontaneous and medroxyprogesterone acetate-accelerated 7,12-dimethylbenz(a)anthracene-induced mammary tumours of tree shrews. **2014**, 50, 3230-42	19
1296	Eribulin mesilate suppresses experimental metastasis of breast cancer cells by reversing phenotype from epithelial-mesenchymal transition (EMT) to mesenchymal-epithelial transition (MET) states. **2014**, 110, 1497-505	227
1295	Identifying driver mutations in sequenced cancer genomes: computational approaches to enable precision medicine. **2014**, 6, 5	127
1294	Biology of breast cancer in young women. **2014**, 16, 427	201
1293	The promise of circulating tumor cell analysis in cancer management. **2014**, 15, 448	38

1292	Cancer genomics: one cell at a time. **2014**, 15, 452	202
1291	Deciphering intratumor heterogeneity and temporal acquisition of driver events to refine precision medicine. **2014**, 15, 453	139
1290	Nonstandard personalized medicine strategies for cancer may lead to improved patient outcomes. **2014**, 11, 705-719	4
1289	The kinome associated with estrogen receptor-positive status in human breast cancer. **2014**, 21, R357-70	4
1288	Breast cancer intra-tumor heterogeneity. **2014**, 16, 210	188
1287	Reconstructing Mutational History in Multiply Sampled Tumors Using Perfect Phylogeny Mixtures. **2014**, 354-367	10
1286	Genomic Resource Projects. **2014**, 153-171	
1285	Recurrent somatic mutations of PTPN1 in primary mediastinal B cell lymphoma and Hodgkin lymphoma. **2014**, 46, 329-35	141
1284	Leveraging the complementary nature of RNA-Seq and shotgun proteomics data. **2014**, 14, 2676-87	45
1283	The persistent contributions of RNA to eukaryotic gen(om)e architecture and cellular function. **2014**, 6, a016089	9
1282	Patient-derived xenograft models: an emerging platform for translational cancer research. **2014**, 4, 998-1013	1018
1281	Genomics of uterine leiomyomas: insights from high-throughput sequencing. **2014**, 102, 621-9	112
1280	New strategies for triple-negative breast cancer--deciphering the heterogeneity. **2014**, 20, 782-90	210
1279	Phase I clinical trial of nintedanib plus paclitaxel in early HER-2-negative breast cancer (CNIO-BR-01-2010/GEICAM-2010-10 study). **2014**, 111, 1060-4	22
1278	Clonal evolution in breast cancer revealed by single nucleus genome sequencing. *Nature*, **2014**, 512, 155-60 5004	730
1277	Parameterizing cell-to-cell regulatory heterogeneities via stochastic transcriptional profiles. **2014**, 111, E626-35	29
1276	Functional characterization of CFI-400945, a Polo-like kinase 4 inhibitor, as a potential anticancer agent. **2014**, 26, 163-76	121
1275	Personalized medicine for patients with advanced cancer in the phase I program at MD Anderson: validation and landmark analyses. **2014**, 20, 4827-36	150

1274	Next generation sequencing and tumor mutation profiling: are we ready for routine use in the oncology clinic?. **2014**, 12, 140	30
1273	PIK3CA mutations in androgen receptor-positive triple negative breast cancer confer sensitivity to the combination of PI3K and androgen receptor inhibitors. **2014**, 16, 406	199
1272	Biased estimates of clonal evolution and subclonal heterogeneity can arise from PCR duplicates in deep sequencing experiments. **2014**, 15, 420	22
1271	A systematic approach to identify novel cancer drug targets using machine learning, inhibitor design and high-throughput screening. **2014**, 6, 57	67
1270	Cancer: evolution within a lifetime. **2014**, 48, 215-36	146
1269	Expanding the computational toolbox for mining cancer genomes. **2014**, 15, 556-70	146
1268	Systematic analysis of metastasis-associated genes identifies miR-17-5p as a metastatic suppressor of basal-like breast cancer. **2014**, 146, 487-502	38
1267	Capturing intra-tumor genetic heterogeneity by de novo mutation profiling of circulating cell-free tumor DNA: a proof-of-principle. **2014**, 25, 1729-1735	258
1266	Molecular Heterogeneity of Triple Negative Breast Cancer. **2014**, 6, 154-158	43
1265	Expression microarray identifies the unliganded glucocorticoid receptor as a regulator of gene expression in mammary epithelial cells. **2014**, 14, 275	17
1264	PyClone: statistical inference of clonal population structure in cancer. **2014**, 11, 396-8	584
1263	Zebrafish as a model to assess cancer heterogeneity, progression and relapse. **2014**, 7, 755-62	35
1262	Integrins and epithelial cell polarity. **2014**, 127, 3217-25	77
1261	Epithelial-to-mesenchymal transition rewires the molecular path to PI3K-dependent proliferation. **2014**, 4, 186-99	74
1260	Advances in patient-derived tumor xenografts: from target identification to predicting clinical response rates in oncology. **2014**, 91, 135-43	129
1259	Algorithms in Bioinformatics. **2014**,	3
1258	Discovery of biomarkers predictive of GSI response in triple-negative breast cancer and adenoid cystic carcinoma. **2014**, 4, 1154-67	92
1257	The 41st David A. Karnofsky Memorial Award Lecture: Academic research worldwide--quo vadis?. **2014**, 32, 347-54	31

1256	Establishing the origin of metastatic deposits in the setting of multiple primary malignancies: the role of massively parallel sequencing. **2014**, 8, 150-8	34
1255	Collection, integration and analysis of cancer genomic profiles: from data to insight. **2014**, 24, 92-8	17
1254	Personalized medicine: present and future of breast cancer management. **2014**, 91, 223-33	40
1253	KIF14 promotes AKT phosphorylation and contributes to chemoresistance in triple-negative breast cancer. **2014**, 16, 247-56, 256.e2	54
1252	Ordering of mutations in preinvasive disease stages of esophageal carcinogenesis. **2014**, 46, 837-843	240
1251	The omics of triple-negative breast cancers. **2014**, 60, 122-33	44
1250	Triple-negative breast carcinoma: current and emerging concepts. **2014**, 141, 462-77	119
1249	Molecular classification of breast cancer. **2014**, 465, 1-14	106
1248	Basal-like and triple-negative breast cancers: searching for positives among many negatives. **2014**, 23, 567-77	65
1247	Predictive chromosomal clusters of synchronous and metachronous brain metastases in clear cell renal cell carcinoma. **2014**, 207, 206-13	8
1246	Brain metastasis: new opportunities to tackle therapeutic resistance. **2014**, 8, 1120-31	28
1245	Mutational context and diverse clonal development in early and late bladder cancer. **2014**, 7, 1649-1663	94
1244	Active kinase profiling, genetic and pharmacological data define mTOR as an important common target in triple-negative breast cancer. **2014**, 33, 148-56	67
1243	High-Throughput Analysis of Plasma Hybrid Markers for Early Detection of Cancers. **2014**, 2, 1-17	7
1242	Profiling the tyrosine phosphoproteome of different mouse mammary tumour models reveals distinct, model-specific signalling networks and conserved oncogenic pathways. **2014**, 16, 437	10
1241	Sequencing of breast cancer stem cell populations indicates a dynamic conversion between differentiation states in vivo. **2014**, 16, R72	47
1240	The Hallmarks of Prostate Cancer Stem Cells. **2014**, 17-37	
1239	Differential and limited expression of mutant alleles in multiple myeloma. **2014**, 124, 3110-7	42

1238	On the complexity of Minimum Path Cover with Subpath Constraints for multi-assembly. **2014**, 15 Suppl 9, S5	14
1237	The inactive X chromosome is epigenetically unstable and transcriptionally labile in breast cancer. **2015**, 25, 488-503	81
1236	Analysis of different HER-2 mutations in breast cancer progression and drug resistance. **2015**, 19, 2691-701	32
1235	Breast cancer heterogeneity: parallel evolution or conscious uncoupling?. **2015**, 237, 1-3	2
1234	Prognostic role of PIK3CA mutations of cell-free DNA in early-stage triple negative breast cancer. **2015**, 106, 1582-9	46
1233	PKC□Promotes Breast Cancer Invasion by Regulating Expression of E-cadherin and Zonula Occludens-1 (ZO-1) via NFB-p65. **2015**, 5, 12520	23
1232	Genomic and epigenomic heterogeneity in chronic lymphocytic leukemia. **2015**, 126, 445-53	103
1231	Leveraging a Multi-Omics Strategy for Prioritizing Personalized Candidate Mutation-Driver Genes: A Proof-of-Concept Study. **2015**, 5, 17564	12
1230	Prolonged Response to Trastuzumab in a Patient With HER2-Nonamplified Breast Cancer With Elevated HER2 Dimerization Harboring an ERBB2 S310F Mutation. **2015**, 13, 1066-70	25
1229	Implementation of In Vitro Drug Resistance Assays: Maximizing the Potential for Uncovering Clinically Relevant Resistance Mechanisms. **2015**, e52879	1
1228	Targeting Breast Cancer Metastasis. **2015**, 9, 23-34	87
1227	Advanced Applications of RNA Sequencing and Challenges. **2015**, 9, 29-46	126
1226	An integrated bioinformatics analysis to dissect kinase dependency in triple negative breast cancer. **2015**, 16 Suppl 12, S2	6
1225	No association between HPV positive breast cancer and expression of human papilloma viral transcripts. **2015**, 5, 18081	13
1224	High EGFR protein expression and exon 9 PIK3CA mutations are independent prognostic factors in triple negative breast cancers. **2015**, 15, 986	13
1223	A co-culture genome-wide RNAi screen with mammary epithelial cells reveals transmembrane signals required for growth and differentiation. **2015**, 17, 4	20
1222	The repertoire of somatic genetic alterations of acinic cell carcinomas of the breast: an exploratory, hypothesis-generating study. **2015**, 237, 166-78	42
1221	Gene expression and splicing alterations analyzed by high throughput RNA sequencing of chronic lymphocytic leukemia specimens. **2015**, 15, 714	13

1220	Fast and scalable inference of multi-sample cancer lineages. **2015**, 16, 91	127
1219	Cell-lineage heterogeneity and driver mutation recurrence in pre-invasive breast neoplasia. **2015**, 7, 28	15
1218	Are acinic cell carcinomas of the breast and salivary glands distinct diseases?. **2015**, 67, 529-37	25
1217	Triple-negative breast cancer: advancements in characterization and treatment approach. **2016**, 28, 59-69	63
1216	Functional screening identifies MCT4 as a key regulator of breast cancer cell metabolism and survival. **2015**, 237, 152-65	55
1215	Triple-negative Breast Carcinoma: Morphologic and Molecular Subtypes. **2015**, 22, 306-13	11
1214	Clinical Trials of Precision Medicine through Molecular Profiling: Focus on Breast Cancer. **2015**, e183-90	15
1213	Comprehensive Two- and Three-Dimensional RNAi Screening Identifies PI3K Inhibition as a Complement to MEK Inhibitor AS703026 for Combination Treatment of Triple-Negative Breast Cancer. **2015**, 6, 1306-19	14
1212	Genomic dynamics associated with malignant transformation in IDH1 mutated gliomas. **2015**, 6, 43653-66	11
1211	Application of metabolomics in drug resistant breast cancer research. **2015**, 5, 100-18	38
1210	Mutant p53: Multiple Mechanisms Define Biologic Activity in Cancer. **2015**, 5, 249	64
1209	Cancer stem cell-driven efficacy of trastuzumab (Herceptin): towards a reclassification of clinically HER2-positive breast carcinomas. **2015**, 6, 32317-38	26
1208	Revealing the Molecular Portrait of Triple Negative Breast Tumors in an Understudied Population through Omics Analysis of Formalin-Fixed and Paraffin-Embedded Tissues. **2015**, 10, e0126762	14
1207	Single-Cell Genetic Analysis Using Automated Microfluidics to Resolve Somatic Mosaicism. **2015**, 10, e0135007	37
1206	Analysis of PIK3CA Mutations and Activation Pathways in Triple Negative Breast Cancer. **2015**, 10, e0141763	63
1205	Mutation Screening of 1,237 Cancer Genes across Six Model Cell Lines of Basal-Like Breast Cancer. **2015**, 10, e0144528	5
1204	Somatic mutations in breast and serous ovarian cancer young patients: a systematic review and meta-analysis. **2015**, 61, 474-83	15
1203	Deciphering the Correlation between Breast Tumor Samples and Cell Lines by Integrating Copy Number Changes and Gene Expression Profiles. **2015**, 2015, 901303	6

1202	Spaced Seed Data Structures for De Novo Assembly. **2015**, 2015, 196591	4
1201	Triple-negative breast cancer: immune modulation as the new treatment paradigm. **2015**, e25-30	58
1200	Triple-negative breast cancer: molecular subtypes and new targets for therapy. **2015**, e31-9	83
1199	A novel framework for analyzing somatic copy number aberrations and tumor subclones for paired heterogeneous tumor samples. **2015**, 26 Suppl 1, S1845-53	2
1198	Triple negative breast cancer: looking for the missing link between biology and treatments. **2015**, 6, 26560-74	109
1197	Genomic profiling of breast cancers. **2015**, 27, 34-9	16
1196	Pushing the boundaries of somatic copy-number variation detection: advances and challenges. **2015**, 26, 11-12	
1195	BRCA1-like signature in triple negative breast cancer: Molecular and clinical characterization reveals subgroups with therapeutic potential. **2015**, 9, 1528-38	45
1194	Triple-negative breast cancer: new perspectives for targeted therapies. **2015**, 8, 177-93	94
1193	Advances and applications of single-cell sequencing technologies. **2015**, 58, 598-609	341
1192	Single-cell transcriptogenomics reveals transcriptional exclusion of ENU-mutated alleles. **2015**, 772, 55-62	16
1191	Next-Generation Sequencing for Cancer Biomarker Discovery. **2015**, 103-125	1
1190	Predicting censored survival data based on the interactions between meta-dimensional omics data in breast cancer. **2015**, 56, 220-8	27
1189	Clinical applications of next generation sequencing in cancer: from panels, to exomes, to genomes. **2015**, 6, 215	60
1188	Cell Fusion Connects Oncogenesis with Tumor Evolution. **2015**, 185, 2049-60	44
1187	Genome-wide analysis of alternative transcripts in human breast cancer. **2015**, 151, 295-307	16
1186	Next generation sequencing of triple negative breast cancer to find predictors for chemotherapy response. **2015**, 17, 134	47
1185	Developmental Insights into Breast Cancer Intratumoral Heterogeneity. **2015**, 1, 242-251	16

1184	Teamwork: The tumor cell edition. **2015**, 350, 1174-5	4
1183	Heterozygous bone marrow in a homozygous mature ovarian teratoma: a challenge to the germ cell theory or incidental somatic heterotopia?. **2015**, 68, 666-9	2
1182	Lessons learned from the application of whole-genome analysis to the treatment of patients with advanced cancers. **2015**, 1, a000570	75
1181	Molecular segmentation of luminal breast: Reality in 2015?. **2015**, 24 Suppl 2, S41-3	
1180	Intratumoral heterogeneity: Clonal cooperation in epithelial-to-mesenchymal transition and metastasis. **2015**, 9, 265-76	42
1179	A seven-gene signature can predict distant recurrence in patients with triple-negative breast cancers who receive adjuvant chemotherapy following surgery. **2015**, 136, 1976-84	14
1178	Single cell-derived clonal analysis of human glioblastoma links functional and genomic heterogeneity. **2015**, 112, 851-6	251
1177	Cancer Metastasis: Tracking and Attacking a Moving Target. **2015**, 1-13	
1176	Intratumoral heterogeneity and consequences for targeted therapies. **2015**, 102, 17-23	13
1175	Patient-derived xenograft models of breast cancer and their predictive power. **2015**, 17, 17	195
1174	The evolving cancer stem cell paradigm: implications in veterinary oncology. **2015**, 205, 154-60	11
1173	Clinical actionability enhanced through deep targeted sequencing of solid tumors. **2015**, 61, 544-53	76
1172	CLK2 Is an Oncogenic Kinase and Splicing Regulator in Breast Cancer. **2015**, 75, 1516-26	51
1171	Inter- and intra-tumor profiling of multi-regional colon cancer and metastasis. **2015**, 458, 52-6	26
1170	Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. **2015**, 6, 6120	139
1169	BCL2 is an independent predictor of outcome in basal-like triple-negative breast cancers treated with adjuvant anthracycline-based chemotherapy. **2015**, 36, 4243-52	27
1168	Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. **2015**, 25, 316-27	240
1167	BCL11A is a triple-negative breast cancer gene with critical functions in stem and progenitor cells. **2015**, 6, 5987	94

1166	The future of breast cancer systemic therapy: the next 10 years. **2015**, 93, 119-25	17
1165	Somatic Diseases (Cancer): Amplification-Based Next-Generation Sequencing. **2015**, 297-319	0
1164	Subtyping of triple-negative breast cancer: implications for therapy. **2015**, 121, 8-16	212
1163	Pharmacological profiling of kinase dependency in cell lines across triple-negative breast cancer subtypes. **2015**, 14, 298-306	11
1162	The Molecular Biology of Breast Cancer. **2015**, 523-530.e3	
1161	Understanding and Using Information about Cancer Genomes. **2015**, 357-368.e3	
1160	Early phase clinical trials to identify optimal dosing and safety. **2015**, 9, 997-1007	59
1159	Gene expression analysis identifies global gene dosage sensitivity in cancer. **2015**, 47, 115-25	219
1158	Biological and therapeutic impact of intratumor heterogeneity in cancer evolution. **2015**, 27, 15-26	672
1157	Heterogeneity of triple-negative breast cancer: mammographic, US, and MR imaging features according to androgen receptor expression. **2015**, 25, 419-27	21
1156	Breast cancer genomics from microarrays to massively parallel sequencing: paradigms and new insights. **2015**, 107,	72
1155	Assessing the clinical value of targeted massively parallel sequencing in a longitudinal, prospective population-based study of cancer patients. **2015**, 112, 1411-20	44
1154	p53 status identifies triple-negative breast cancer patients who do not respond to adjuvant chemotherapy. **2015**, 24, 294-7	18
1153	The reverse evolution from multicellularity to unicellularity during carcinogenesis. **2015**, 6, 6367	79
1152	The Sweden Cancerome Analysis Network - Breast (SCAN-B) Initiative: a large-scale multicenter infrastructure towards implementation of breast cancer genomic analyses in the clinical routine. **2015**, 7, 20	70
1151	Hotspot mutation panel testing reveals clonal evolution in a study of 265 paired primary and metastatic tumors. **2015**, 21, 2644-51	63
1150	The origin of breast tumor heterogeneity. **2015**, 34, 5309-16	90
1149	Precision medicine in breast cancer: genes, genomes, and the future of genomically driven treatments. **2015**, 17, 15	22

1148	Translational implications of tumor heterogeneity. **2015**, 21, 1258-66	292
1147	Concepts in solid tumor evolution. **2015**, 31, 208-14	38
1146	Ploidy-Seq: inferring mutational chronology by sequencing polyploid tumor subpopulations. **2015**, 7, 6	6
1145	Intra-tumor genetic heterogeneity and mortality in head and neck cancer: analysis of data from the Cancer Genome Atlas. **2015**, 12, e1001786	171
1144	Gene-Expression-Based Predictors for Breast Cancer. **2015**, 22, 3418-32	19
1143	Fibroblast growth factor receptor signaling in hereditary and neoplastic disease: biologic and clinical implications. **2015**, 34, 479-96	74
1142	Surgery in the era of the ’omics revolution. **2015**, 102, e29-40	9
1141	Spatial and temporal heterogeneity in high-grade serous ovarian cancer: a phylogenetic analysis. **2015**, 12, e1001789	230
1140	Genetic Intratumor Heterogeneity. **2015**, 571-593	1
1139	TIPIN depletion leads to apoptosis in breast cancer cells. **2015**, 9, 1580-98	14
1138	ER▯ inversely correlates with PTEN/PI3K/AKT pathway and predicts a favorable prognosis in triple-negative breast cancer. **2015**, 152, 255-69	59
1137	Clonality and evolutionary history of rhabdomyosarcoma. **2015**, 11, e1005075	40
1136	Somatic Cell Fusions Reveal Extensive Heterogeneity in Basal-like Breast Cancer. **2015**, 11, 1549-63	48
1135	Estrogen receptor mutations and functional consequences for breast cancer. **2015**, 26, 467-76	55
1134	TTF-1 positive breast cancer: a cautionary tale. **2015**, 68, 665-6	2
1133	Cancer in the parasitic protozoans Trypanosoma brucei and Toxoplasma gondii. **2015**, 112, 8835-42	22
1132	Precision medicine for metastatic breast cancer--limitations and solutions. **2015**, 12, 693-704	201
1131	Maintaining Tumor Heterogeneity in Patient-Derived Tumor Xenografts. **2015**, 75, 2963-8	218

1130	Cancer modelling in the NGS era - Part I: Emerging technology and initial modelling. **2015**, 96, 274-307	7
1129	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. **2015**, 21, 751-9	521
1128	Determination of HER2 and p53 Mutations by Sequence Analysis Method and EGFR/Chromosome 7 Gene Status by Fluorescence in Situ Hybridization for the Predilection of Targeted Therapy Modalities in Immunohistochemically Triple Negative Breast Carcinomas in Turkish Population. **2015**, 21, 1223-7	2
1127	Reconstruction of clonal trees and tumor composition from multi-sample sequencing data. **2015**, 31, i62-70	144
1126	Safety and diagnostic accuracy of tumor biopsies in children with cancer. **2015**, 121, 1098-107	9
1125	Protein domain-level landscape of cancer-type-specific somatic mutations. **2015**, 11, e1004147	46
1124	Systemic treatment approaches in her2-negative advanced breast cancer-guidance on the guidelines. **2015**, 22, S29-42	14
1123	Examining the utility of patient-derived xenograft mouse models. **2015**, 15, 311-6	246
1122	Glucocorticoid receptor regulates accurate chromosome segregation and is associated with malignancy. **2015**, 112, 5479-84	34
1121	Nuclear TAZ expression associates with the triple-negative phenotype in breast cancer. **2015**, 22, 443-54	47
1120	Design, Synthesis, and Structure-Activity Relationship Studies of 3-(Phenylethynyl)-1H-pyrazolo[3,4-d]pyrimidin-4-amine Derivatives as a New Class of Src Inhibitors with Potent Activities in Models of Triple Negative Breast Cancer. **2015**, 58, 3957-74	32
1119	Therapies for triple negative breast cancer. **2015**, 16, 983-98	60
1118	Clinical management of breast cancer heterogeneity. **2015**, 12, 381-94	285
1117	Novel role of PELP1 in regulating chemotherapy response in mutant p53-expressing triple negative breast cancer cells. **2015**, 150, 487-99	18
1116	Clonal status of actionable driver events and the timing of mutational processes in cancer evolution. **2015**, 7, 283ra54	417
1115	PhyloWGS: reconstructing subclonal composition and evolution from whole-genome sequencing of tumors. **2015**, 16, 35	242
1114	TET proteins and the control of cytosine demethylation in cancer. **2015**, 7, 9	130
1113	Predictive Biomarker Profiling of > 6000 Breast Cancer Patients Shows Heterogeneity in TNBC, With Treatment Implications. **2015**, 15, 473-481.e3	66

1112	Defining breast cancer intrinsic subtypes by quantitative receptor expression. **2015**, 20, 474-82	102
1111	Resistance to Aromatase Inhibitors in Breast Cancer. **2015**,	1
1110	Whole-exome DNA sequence analysis of Brca2- and Trp53-deficient mouse mammary gland tumours. **2015**, 236, 186-200	11
1109	Next-Generation Genotyping by Digital PCR to Detect and Quantify the BRAF V600E Mutation in Melanoma Biopsies. **2015**, 17, 366-73	31
1108	Next Generation Sequencing in Cancer Research, Volume 2. **2015**,	4
1107	Vimentin-ERK Signaling Uncouples Slug Gene Regulatory Function. **2015**, 75, 2349-62	84
1106	Is androgen receptor targeting an emerging treatment strategy for triple negative breast cancer?. **2015**, 41, 547-53	31
1105	TBCRC009: A Multicenter Phase II Clinical Trial of Platinum Monotherapy With Biomarker Assessment in Metastatic Triple-Negative Breast Cancer. **2015**, 33, 1902-9	281
1104	Mutant allele tumor heterogeneity (MATH) and head and neck squamous cell carcinoma. **2015**, 9, 1-5	31
1103	Mutational landscape and clonal architecture in grade II and III gliomas. **2015**, 47, 458-68	543
1102	Biomarkers in Patients with Metastatic Breast Cancer and the PRAEGNANT Study Network. **2015**, 75, 41-50	54
1101	The first five years of single-cell cancer genomics and beyond. **2015**, 25, 1499-507	238
1100	Adiposity is associated with p53 gene mutations in breast cancer. **2015**, 153, 635-45	4
1099	CDK7-dependent transcriptional addiction in triple-negative breast cancer. **2015**, 163, 174-86	268
1098	Targeted Therapies for Triple-Negative Breast Cancer: Combating a Stubborn Disease. **2015**, 36, 822-846	191
1097	HER2 missense mutations have distinct effects on oncogenic signaling and migration. **2015**, 112, E6205-14	51
1096	Multifocal clonal evolution characterized using circulating tumour DNA in a case of metastatic breast cancer. **2015**, 6, 8760	334
1095	Potentiation of Carboplatin-Mediated DNA Damage by the Mdm2 Modulator Nutlin-3a in a Humanized Orthotopic Breast-to-Lung Metastatic Model. **2015**, 14, 2850-63	28

1094	The path to routine use of genomic biomarkers in the cancer clinic. **2015**, 25, 1508-13		26
1093	Advances in small-molecule drug discovery for triple-negative breast cancer. **2015**, 7, 2019-39		11
1092	Tumor Heterogeneity: Focus on the Leaves, the Trees, or the Forest?. **2015**, 28, 149-50		16
1091	Reactivation of multipotency by oncogenic PIK3CA induces breast tumour heterogeneity. *Nature*, **2015**, 525, 119-23	50.4	213
1090	Sequenza: allele-specific copy number and mutation profiles from tumor sequencing data. **2015**, 26, 64-70		331
1089	Clinical implications of molecular heterogeneity in triple negative breast cancer. **2015**, 24 Suppl 2, S36-40		76
1088	Development of triple-negative breast cancer radiosensitive gene signature and validation based on transcriptome analysis. **2015**, 154, 57-62		7
1087	Classical pathology and mutational load of breast cancer - integration of two worlds. **2015**, 1, 225-38		57
1086	Mutations in the Kinase Domain of the HER2/ERBB2 Gene Identified in a Wide Variety of Human Cancers. **2015**, 17, 487-95		39
1085	Mammakarzinom Update 2014 Die Patientin und derTumor im Mittelpunkt. **2015**, 12, 31-43		
1084	Breast Cancer Update 2014 - Focus on the Patient and the Tumour. **2015**, 75, 170-182		8
1083	Limited evidence that cancer susceptibility regions are preferential targets for somatic mutation. **2015**, 16, 193		17
1082	Mammakarzinom Update 2014 Die Patientin und derTumor im Mittelpunkt. **2015**, 36, 213-225		
1081	Genomic landscape of adenoid cystic carcinoma of the breast. **2015**, 237, 179-89		101
1080	Biomarker f Patientinnen mit metastasiertem Mammakarzinom und das PRAEGNANT-Studiennetzwerk. **2015**, 12, 85-94		
1079	Genetic Testing and Tissue Banking for Personalized Oncology: Analytical and Institutional Factors. **2015**, 42, 713-23		10
1078	The mammary stem cell hierarchy: a looking glass into heterogeneous breast cancer landscapes. **2015**, 22, T161-76		35
1077	Tailoring adjuvant chemotherapy regimens for patients with triple negative breast cancer. **2015**, 24 Suppl 2, S132-5		20

1076	Intra-tumor genetic heterogeneity and alternative driver genetic alterations in breast cancers with heterogeneous HER2 gene amplification. **2015**, 16, 107		83
1075	Mutation tracking in circulating tumor DNA predicts relapse in early breast cancer. **2015**, 7, 302ra133		679
1074	Evolution and social epidemiology. **2015**, 145, 132-7		7
1073	Implications of Tumor Clonal Heterogeneity in the Era of Next-Generation Sequencing. **2015**, 1, 231-241		22
1072	Reversion to an embryonic alternative splicing program enhances leukemia stem cell self-renewal. **2015**, 112, 15444-9		24
1071	Dissecting cancer evolution at the macro-heterogeneity and micro-heterogeneity scale. **2015**, 30, 1-6		52
1070	Enriched transcription factor signatures in triple negative breast cancer indicates possible targeted therapies with existing drugs. **2015**, 4, 129-41		14
1069	Breast Tumor Heterogeneity: Source of Fitness, Hurdle for Therapy. **2015**, 60, 537-46		163
1068	Prognostic value of circulating tumor cells and disseminated tumor cells in patients with ovarian cancer: a systematic review and meta-analysis. **2015**, 8, 38		23
1067	Splicing mutation analysis reveals previously unrecognized pathways in lymph node-invasive breast cancer. **2014**, 4, 7063		31
1066	Comparison of breast cancer recurrence and outcome patterns between patients treated from 1986 to 1992 and from 2004 to 2008. **2015**, 33, 65-73		103
1065	SF3B1 mutations constitute a novel therapeutic target in breast cancer. **2015**, 235, 571-80		124
1064	Molecular markers for breast cancer diagnosis, prognosis and targeted therapy. **2015**, 111, 81-90		23
1063	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. *Nature*, **2015**, 518, 422-6	50.4	451
1062	Driver and passenger mutations in cancer. **2015**, 10, 25-50		179
1061	Gene regulatory networks by transcription factors and microRNAs in breast cancer. **2015**, 31, 76-83		23
1060	Cancer evolution: mathematical models and computational inference. **2015**, 64, e1-25		181
1059	Breast cancer classification: linking molecular mechanisms to disease prognosis. **2015**, 16, 461-74		40

1058	Circulating tumor DNA and circulating tumor cells in metastatic triple negative breast cancer patients. **2015**, 136, 2158-65	115
1057	Triple-negative breast cancer: investigating potential molecular therapeutic target. **2015**, 19, 55-75	39
1056	Mechanism-based cancer therapy: resistance to therapy, therapy for resistance. **2015**, 34, 3617-26	165
1055	Genomic Applications in Pathology. **2015**,	
1054	TP53 mutations and protein immunopositivity may predict for poor outcome but also for trastuzumab benefit in patients with early breast cancer treated in the adjuvant setting. **2016**, 7, 32731-53	25
1053	Anti-EGFR monoclonal antibodies and EGFR tyrosine kinase inhibitors as combination therapy for triple-negative breast cancer. **2016**, 7, 73618-73637	43
1052	Current advances in biomarkers for targeted therapy in triple-negative breast cancer. **2016**, 8, 183-197	25
1051	Genomic Instability: The Pivotal Role of Mutant P53 in Human Cancers. **2016**, 05,	
1050	New generation of breast cancer clinical trials implementing molecular profiling. **2016**, 13, 226-35	3
1049	Evaluation and consequences of heterogeneity in the circulating tumor cell compartment. **2016**, 7, 48625-48643	42
1048	Histone Posttranslational Modifications in Breast Cancer and Their Use in Clinical Diagnosis and Prognosis. **2016**, 467-477	
1047	Association between Mutation and Expression of as a Potential Prognostic Marker of Triple-Negative Breast Cancer. **2016**, 48, 1338-1350	45
1046	Mutations of Chromatin Structure Regulating Genes in Human Malignancies. **2016**, 17, 411-37	14
1045	Pan-cancer analysis of intratumor heterogeneity as a prognostic determinant of survival. **2016**, 7, 10051-63	169
1044	Human plasma metabolomics for identifying differential metabolites and predicting molecular subtypes of breast cancer. **2016**, 7, 9925-38	60
1043	Exosomes: The Link between GPCR Activation and Metastatic Potential?. **2016**, 7, 56	16
1042	Tumor Evolution in Two Patients with Basal-like Breast Cancer: A Retrospective Genomics Study of Multiple Metastases. **2016**, 13, e1002174	62
1041	Tumor Infiltrating Lymphocytes Affect the Outcome of Patients with Operable Triple-Negative Breast Cancer in Combination with Mutated Amino Acid Classes. **2016**, 11, e0163138	8

1040	Refinement of Triple-Negative Breast Cancer Molecular Subtypes: Implications for Neoadjuvant Chemotherapy Selection. **2016**, 11, e0157368	590
1039	A Network-Based Data Integration Approach to Support Drug Repurposing and Multi-Target Therapies in Triple Negative Breast Cancer. **2016**, 11, e0162407	38
1038	RNA-Seq analysis for the potential targets and molecular mechanisms of 17 estradiol in squamous cell lung carcinoma. **2016**, 63, 394-401	1
1037	Triple-negative breast cancer: treatment challenges and solutions. **2016**, 8, 93-107	146
1036	A dried blood spot mass spectrometry metabolomic approach for rapid breast cancer detection. **2016**, 9, 1389-98	38
1035	Somatic gene mutation analysis of triple negative breast cancers. **2016**, 29, 202-7	15
1034	The routes for transformation of follicular lymphoma. **2016**, 23, 385-91	13
1033	Single-cell approaches for molecular classification of endocrine tumors. **2016**, 28, 43-9	2
1032	Microglandular adenosis associated with triple-negative breast cancer is a neoplastic lesion of triple-negative phenotype harbouring TP53 somatic mutations. **2016**, 238, 677-88	42
1031	Discovering potential cancer driver genes by an integrated network-based approach. **2016**, 12, 2921-31	22
1030	A Distributed Network for Intensive Longitudinal Monitoring in Metastatic Triple-Negative Breast Cancer. **2016**, 14, 8-17	17
1029	PD-1 and PD-L1 Immune Checkpoint Blockade to Treat Breast Cancer. **2016**, 11, 385-390	27
1028	Recent developments and translational aspects in targeted therapy for metastatic breast cancer. **2016**, 1, e000036	1
1027	Tracing the origin of disseminated tumor cells in breast cancer using single-cell sequencing. **2016**, 17, 250	48
1026	Patient-derived xenograft (PDX) models in basic and translational breast cancer research. **2016**, 35, 547-573	133
1025	Mutation patterns in small cell and non-small cell lung cancer patients suggest a different level of heterogeneity between primary and metastatic tumors. **2017**, 38, 144-151	21
1024	SNooPer: a machine learning-based method for somatic variant identification from low-pass next-generation sequencing. **2016**, 17, 912	33
1023	miR-564 acts as a dual inhibitor of PI3K and MAPK signaling networks and inhibits proliferation and invasion in breast cancer. **2016**, 6, 32541	40

1022	Diverse, Biologically Relevant, and Targetable Gene Rearrangements in Triple-Negative Breast Cancer and Other Malignancies. **2016**, 76, 4850-60	28
1021	Incidence of BRCA1 somatic mutations and response to neoadjuvant chemotherapy in Chinese women with triple-negative breast cancer. **2016**, 584, 26-30	8
1020	Triple-negative breast cancer: challenges and opportunities of a heterogeneous disease. **2016**, 13, 674-690	1246
1019	Exploring phenotype patterns of breast cancer within somatic mutations: a modicum in the intrinsic code. **2017**, 18, 619-633	2
1018	Sensitizing Triple-Negative Breast Cancer to PI3K Inhibition by Cotargeting IGF1R. **2016**, 15, 1545-56	19
1017	Understanding mutagenesis through delineation of mutational signatures in human cancer. **2016**, 37, 531-40	66
1016	Genetic alterations of triple negative breast cancer by targeted next-generation sequencing and correlation with tumor morphology. **2016**, 29, 476-88	67
1015	Analysis of functional germline variants in APOBEC3 and driver genes on breast cancer risk in Moroccan study population. **2016**, 16, 165	16
1014	Intratumoral Heterogeneity of the Epigenome. **2016**, 29, 440-451	132
1013	Targeting a Cancer-Specific Epitope of the Epidermal Growth Factor Receptor in Triple-Negative Breast Cancer. **2016**, 108,	17
1012	Tree inference for single-cell data. **2016**, 17, 86	155
1011	The role of ctDNA detection and the potential of the liquid biopsy for breast cancer monitoring. **2016**, 16, 751-5	15
1010	Re-Evaluating Clonal Dominance in Cancer Evolution. **2016**, 2, 263-276	33
1009	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. *Nature*, **2016**, 534, 47-54 40.4	1193
1008	Acquired Resistance to Clinical Cancer Therapy: A Twist in Physiological Signaling. **2016**, 96, 805-29	43
1007	Emerging Biomarkers of the Future: Changing Clinical Practice for 2020. **2016**, 8, 60-72	1
1006	MxA expression is associated with tumor-infiltrating lymphocytes and is a prognostic factor in triple-negative breast cancer. **2016**, 156, 597-606	16
1005	Identification of selective cytotoxic and synthetic lethal drug responses in triple negative breast cancer cells. **2016**, 15, 34	44

1004	Clinical Actionability of Comprehensive Genomic Profiling for Management of Rare or Refractory Cancers. **2016**, 21, 1315-1325	49
1003	A saltationist theory of cancer evolution. **2016**, 48, 1102-3	15
1002	CloneCNA: detecting subclonal somatic copy number alterations in heterogeneous tumor samples from whole-exome sequencing data. **2016**, 17, 310	22
1001	The genomic landscape of breast cancer and its interaction with host immunity. **2016**, 29, 241-50	130
1000	Patient-derived tumour xenografts for breast cancer drug discovery. **2016**, 23, T259-T270	10
999	Identifying candidate drivers of drug response in heterogeneous cancer by mining high throughput genomics data. **2016**, 17, 638	6
998	Simul-seq: combined DNA and RNA sequencing for whole-genome and transcriptome profiling. **2016**, 13, 953-958	20
997	Anti-androgen therapy in triple-negative breast cancer. **2016**, 8, 305-8	17
996	Paired Exome Analysis Reveals Clonal Evolution and Potential Therapeutic Targets in Urothelial Carcinoma. **2016**, 76, 5894-5906	65
995	Genetic events in the progression of adenoid cystic carcinoma of the breast to high-grade triple-negative breast cancer. **2016**, 29, 1292-1305	52
994	Deciphering and Targeting Oncogenic Mutations and Pathways in Breast Cancer. **2016**, 21, 1063-78	35
993	Protein Tyrosine Phosphatases in Cancer. **2016**,	3
992	Role of PTPN11 (SHP2) in Cancer. **2016**, 115-143	7
991	Validated biomarkers: The key to precision treatment in patients with breast cancer. **2016**, 29, 192-201	34
990	An investigation of the association of genetic susceptibility risk with somatic mutation burden in breast cancer. **2016**, 115, 752-60	10
989	Comprehensive comparison of molecular portraits between cell lines and tumors in breast cancer. **2016**, 17 Suppl 7, 525	97
988	The hedgehog pathway in triple-negative breast cancer. **2016**, 5, 2989-3006	71
987	Three-dimensional modelling identifies novel genetic dependencies associated with breast cancer progression in the isogenic MCF10 model. **2016**, 240, 315-328	24

986	Punctuated copy number evolution and clonal stasis in triple-negative breast cancer. **2016**, 48, 1119-30	290
985	An Evolutionary Genetic Perspective on Cancer Biology. **2016**, 47, 25-49	6
984	The molecular landscape of high-risk early breast cancer: comprehensive biomarker analysis of a phase III adjuvant population. **2016**, 2, 16022	18
983	Triple-negative breast cancer: the importance of molecular and histologic subtyping, and recognition of low-grade variants. **2016**, 2, 16036	89
982	The Mechanisms of Therapy Resistance in Cancer Stem Cells. **2016**, 395-410	1
981	A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. **2016**, 167, 260-274.e22	274
980	Breast cancer classification and prognostication through diverse systems along with recent emerging findings in this respect; the dawn of new perspectives in the clinical applications. **2016**, 37, 14479-14499	5
979	Novel targets for paclitaxel nano formulations: Hopes and hypes in triple negative breast cancer. **2016**, 111, 577-591	26
978	CRISPR-Barcoding for Intratumor Genetic Heterogeneity Modeling and Functional Analysis of Oncogenic Driver Mutations. **2016**, 63, 526-38	40
977	Biology and Management of Patients With Triple-Negative Breast Cancer. **2016**, 21, 1050-62	131
976	Spatial intratumoral heterogeneity and temporal clonal evolution in esophageal squamous cell carcinoma. **2016**, 48, 1500-1507	139
975	EGFR and SYNE2 are associated with p21 expression and SYNE2 variants predict post-operative clinical outcomes in HBV-related hepatocellular carcinoma. **2016**, 6, 31237	12
974	Transposon mutagenesis identifies genes that cooperate with mutant Pten in breast cancer progression. **2016**, 113, E7749-E7758	43
973	A microscopic landscape of the invasive breast cancer genome. **2016**, 6, 27545	19
972	Progress in the clinical detection of heterogeneity in breast cancer. **2016**, 5, 3475-3488	39
971	Alternative Polyadenylation in Triple-Negative Breast Tumors Allows NRAS and c-JUN to Bypass PUMILIO Posttranscriptional Regulation. **2016**, 76, 7231-7241	32
970	Big Data Analytics in Genomics. **2016**,	4
969	SSA-ME Detection of cancer driver genes using mutual exclusivity by small subnetwork analysis. **2016**, 6, 36257	9

968	The somatic mutation profiles of 2,433 breast cancers refines their genomic and transcriptomic landscapes. **2016**, 7, 11479	779
967	A Bioinformatics Approach for Understanding GenotypePhenotype Correlation in Breast Cancer. **2016**, 397-428	0
966	The Role of Mediator Complex Subunit 12 in Leiomyoma Biology. **2016**, 4, 196-206	
965	Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers. **2016**, 7, 12498	47
964	Constitutively activated PI3K accelerates tumor initiation and modifies histopathology of breast cancer. **2016**, 5, e267	23
963	The DNA cytosine deaminase APOBEC3B promotes tamoxifen resistance in ER-positive breast cancer. **2016**, 2, e1601737	118
962	Primary breast cancer cell culture yields intra-tumor heterogeneous subpopulations expressing exclusive patterns of receptor tyrosine kinases. **2016**, 16, 740	9
961	Long range personalized cancer treatment strategies incorporating evolutionary dynamics. **2016**, 11, 56	10
960	Integrative exploration of genomic profiles for triple negative breast cancer identifies potential drug targets. **2016**, 95, e4321	17
959	Clinicopathogenomic analysis of mismatch repair proficient colorectal adenocarcinoma uncovers novel prognostic subgroups with differing patterns of genetic evolution. **2016**, 139, 1546-56	15
958	The Tyrosine Kinome Dictates Breast Cancer Heterogeneity and Therapeutic Responsiveness. **2016**, 117, 1971-90	10
957	Current and Evolving Methods to Visualize Biological Data in Cancer Research. **2016**, 108,	13
956	Proteasome machinery is instrumental in a common gain-of-function program of the p53 missense mutants in cancer. **2016**, 18, 897-909	142
955	Women at high risk of breast cancer: Molecular characteristics, clinical presentation and management. **2016**, 28, 136-44	67
954	The Role of Proliferation in Determining Response to Neoadjuvant Chemotherapy in Breast Cancer: A Gene Expression-Based Meta-Analysis. **2016**, 22, 6039-6050	32
953	p53 deficiency linked to B cell translocation gene 2 (BTG2) loss enhances metastatic potential by promoting tumor growth in primary and metastatic sites in patient-derived xenograft (PDX) models of triple-negative breast cancer. **2016**, 18, 13	31
952	PI3K-mTOR in Cancer and Cancer Therapy. **2016**,	3
951	PI3K-AKT-mTOR Pathway Cooperates with the DNA Damage Repair Pathway: Carcinogenesis in Triple-Negative Breast Cancers and Beyond. **2016**, 65-108	

950	Subtelomeric p53 binding prevents accumulation of DNA damage at human telomeres. **2016**, 35, 193-207	37
949	Genomic tumor evolution of breast cancer. **2016**, 23, 4-11	19
948	Imaging tumour cell heterogeneity following cell transplantation into optically clear immune-deficient zebrafish. **2016**, 7, 10358	62
947	Cell-free circulating tumour DNA as a liquid biopsy in breast cancer. **2016**, 10, 464-74	82
946	Functional Genomic Landscape of Human Breast Cancer Drivers, Vulnerabilities, and Resistance. **2016**, 164, 293-309	259
945	Circulating tumor DNA for triple-negative breast cancer diagnosis and treatment decisions. **2016**, 16, 39-50	9
944	HER2 mutation status in Japanese HER2-positive breast cancer patients. **2016**, 23, 902-907	7
943	Metabolomics in Breast Cancer: Current Status and Perspectives. **2016**, 882, 217-34	21
942	Intratumor Heterogeneity in Breast Cancer. **2016**, 882, 169-89	81
941	Randomized phase II trial of cyclophosphamide and the oral poly (ADP-ribose) polymerase inhibitor veliparib in patients with recurrent, advanced triple-negative breast cancer. **2016**, 34, 355-63	46
940	Novel Biomarkers in the Continuum of Breast Cancer. **2016**,	9
939	Prognostic Implications of CTC in Breast Cancer. **2016**, 233-254	
938	Somatic mutation detection using ensemble of flexible neural tree model. **2016**, 179, 161-168	6
937	Molecular Testing and the Pathologist's Role in Clinical Trials of Breast Cancer. **2016**, 16, 166-79	14
936	Circulating Tumor Cells. **2016**,	4
935	ALK(R1275Q) perturbs extracellular matrix, enhances cell invasion and leads to the development of neuroblastoma in cooperation with MYCN. **2016**, 35, 4447-58	18
934	Breast cancer survival among young women: a review of the role of modifiable lifestyle factors. **2016**, 27, 459-72	46
933	Single-cell proteomics: potential implications for cancer diagnostics. **2016**, 16, 579-89	21

932	Hsp90 Inhibition Results in Glucocorticoid Receptor Degradation in Association with Increased Sensitivity to Paclitaxel in Triple-Negative Breast Cancer. **2016**, 7, 114-26	15
931	Histone deacetylase inhibitors suppress mutant p53 transcription via HDAC8/YY1 signals in triple negative breast cancer cells. **2016**, 28, 506-515	54
930	Crossroad between linear and nonlinear transcription concepts in the discovery of next-generation sequencing systems-based anticancer therapies. **2016**, 21, 663-73	12
929	Whole exome sequencing of rare aggressive breast cancer histologies. **2016**, 156, 21-32	26
928	Long-term outcomes after adjuvant treatment of sequential versus combination docetaxel with doxorubicin and cyclophosphamide in node-positive breast cancer: BCIRG-005 randomized trial. **2016**, 27, 1041-1047	32
927	High-throughput «Omics» technologies: New tools for the study of triple-negative breast cancer. **2016**, 382, 77-85	24
926	Endoplasmic Reticulum-resident Heat Shock Protein 90 (HSP90) Isoform Glucose-regulated Protein 94 (GRP94) Regulates Cell Polarity and Cancer Cell Migration by Affecting Intracellular Transport. **2016**, 291, 8309-23	22
925	Disentangling the aneuploidy and senescence paradoxes: a study of triploid breast cancers non-responsive to neoadjuvant therapy. **2016**, 145, 497-508	23
924	Catalog of genetic progression of human cancers: breast cancer. **2016**, 35, 49-62	14
923	Liquid Biopsy and its Potential for Management of Hepatocellular Carcinoma. **2016**, 47, 157-67	22
922	Filamin A (FLNA) modulates chemosensitivity to docetaxel in triple-negative breast cancer through the MAPK/ERK pathway. **2016**, 37, 5107-15	17
921	Clonal evolution and tumor-initiating cells: New dimensions in cancer patient treatment. **2016**, 53, 40-51	14
920	Breast Disease. **2016**,	3
919	Quantum dot-based in situ simultaneous molecular imaging and quantitative analysis of EGFR and collagen IV and identification of their prognostic value in triple-negative breast cancer. **2016**, 37, 2509-18	7
918	An overview of triple-negative breast cancer. **2016**, 293, 247-69	268
917	Comprehensive profiling of biological processes reveals two major prognostic subtypes in breast cancer. **2016**, 37, 3365-70	
916	Evaluation of targeted therapies in advanced breast cancer: the need for large-scale molecular screening and transformative clinical trial designs. **2016**, 35, 1743-9	11
915	MDM4 is a rational target for treating breast cancers with mutant p53. **2017**, 241, 661-670	24

914	Targeting the PI3K/AKT pathway via GLI1 inhibition enhanced the drug sensitivity of acute myeloid leukemia cells. **2017**, 7, 40361	32
913	Tumor evolution: Linear, branching, neutral or punctuated?. **2017**, 1867, 151-161	135
912	Interrogating open issues in cancer precision medicine with patient-derived xenografts. **2017**, 17, 254-268	369
911	Genomic insights in gynecologic cancer. **2017**, 41, 8-36	7
910	Splicing imbalances in basal-like breast cancer underpin perturbation of cell surface and oncogenic pathways and are associated with patients' survival. **2017**, 7, 40177	8
909	Catch my drift? Making sense of genomic intra-tumour heterogeneity. **2017**, 1867, 95-100	15
908	Male breast cancer precursor lesions: analysis of the EORTC 10085/TBCRC/BIG/NABCG International Male Breast Cancer Program. **2017**, 30, 509-518	22
907	A review of estrogen receptor/androgen receptor genomics in male breast cancer. **2017**, 24, R27-R34	18
906	Stress-induced EGF receptor signaling through STAT3 and tumor progression in triple-negative breast cancer. **2017**, 451, 24-30	13
905	Exploring the pharmacological mechanism of Yanghe Decoction on HER2-positive breast cancer by a network pharmacology approach. **2017**, 199, 68-85	68
904	Breast Cancer Heterogeneity: Roles in Tumorigenesis and Therapeutic Implications. **2017**, 9, 34-44	9
903	Inhibition of ROS production, autophagy or apoptosis signaling reversed the anticancer properties of Antrodia salmonea in triple-negative breast cancer (MDA-MB-231) cells. **2017**, 103, 1-17	30
902	In situ localization of tumor cells associated with the epithelial-mesenchymal transition marker Snail and the prognostic impact of lymphocytes in the tumor microenvironment in invasive ductal breast cancer. **2017**, 102, 268-275	7
901	Cancer cells exhibit clonal diversity in phenotypic plasticity. **2017**, 7,	21
900	Inhibition of Ubc13-mediated Ubiquitination by GPS2 Regulates Multiple Stages of B Cell Development. **2017**, 292, 2754-2772	14
899	A Randomized Phase II Neoadjuvant Study of Cisplatin, Paclitaxel With or Without Everolimus in Patients with Stage II/III Triple-Negative Breast Cancer (TNBC): Responses and Long-term Outcome Correlated with Increased Frequency of DNA Damage Response Gene Mutations, TNBC Subtype, AR Status, and Ki67. **2017**, 23, 4035-4045	79
898	Functional characterization of CFI-402257, a potent and selective Mps1/TTK kinase inhibitor, for the treatment of cancer. **2017**, 114, 3127-3132	53
897	Functional germline variants in driver genes of breast cancer. **2017**, 28, 259-271	7

896	Identification of frequent somatic mutations in inflammatory breast cancer. **2017**, 163, 263-272	20
895	A Transposon-based Analysis Reveals Is Involved in Triple-Negative Breast Cancer. **2017**, 77, 1357-1368	25
894	Silencing the roadblocks to effective triple-negative breast cancer treatments by siRNA nanoparticles. **2017**, 24, R81-R97	16
893	PARP inhibitor increases chemosensitivity by upregulating miR-664b-5p in BRCA1-mutated triple-negative breast cancer. **2017**, 7, 42319	13
892	Transposon insertional mutagenesis in mice identifies human breast cancer susceptibility genes and signatures for stratification. **2017**, 114, E2215-E2224	24
891	A population genetics perspective on the determinants of intra-tumor heterogeneity. **2017**, 1867, 109-126	29
890	Advances in understanding tumour evolution through single-cell sequencing. **2017**, 1867, 127-138	58
889	Improved systemic treatment for early breast cancer improves cure rates, modifies metastatic pattern and shortens post-metastatic survival: 35-year results from the Munich Cancer Registry. **2017**, 143, 1701-1712	23
888	Natural and Chemotherapy-Induced Clonal Evolution of Tumors. **2017**, 82, 413-425	18
887	HER2 somatic mutations are associated with poor survival in HER2-negative breast cancers. **2017**, 108, 671-677	32
886	CLImAT-HET: detecting subclonal copy number alterations and loss of heterozygosity in heterogeneous tumor samples from whole-genome sequencing data. **2017**, 10, 15	12
885	Emerging therapies for breast cancer. **2017**, 10, 98	37
884	p53 Maintains Baseline Expression of Multiple Tumor Suppressor Genes. **2017**, 15, 1051-1062	39
883	4-1BB-Enhanced Expansion of CD8 TIL from Triple-Negative Breast Cancer Unveils Mutation-Specific CD8 T Cells. **2017**, 5, 439-445	32
882	Hedgehog signalling pathway orchestrates angiogenesis in triple-negative breast cancers. **2017**, 116, 1425-1435	50
881	How to study and overcome tumor heterogeneity with circulating biomarkers: The breast cancer case. **2017**, 44, 106-116	32
880	Resistance to Taxanes in Triple-Negative Breast Cancer Associates with the Dynamics of a CD49f+ Tumor-Initiating Population. **2017**, 8, 1392-1407	53
879	Mitophagy and age-related pathologies: Development of new therapeutics by targeting mitochondrial turnover. **2017**, 178, 157-174	75

878	Breast Cancer Neoantigens Can Induce CD8 T-Cell Responses and Antitumor Immunity. **2017**, 5, 516-523	40
877	Neoadjuvant Therapy for Breast Cancer: Established Concepts and Emerging Strategies. **2017**, 77, 1313-1336	25
876	Targeting the Molecular Subtypes of Triple Negative Breast Cancer: Understanding the Diversity to Progress the Field. **2017**, 22, 1086-1093	53
875	Targeting the duality of cancer. **2017**, 1,	23
874	Intratumor Heterogeneity: Novel Approaches for Resolving Genomic Architecture and Clonal Evolution. **2017**, 15, 1127-1137	31
873	The Transcriptional Landscape of p53 Signalling Pathway. **2017**, 20, 109-119	30
872	Genomic profiling of breast secretory carcinomas reveals distinct genetics from other breast cancers and similarity to mammary analog secretory carcinomas. **2017**, 30, 1086-1099	41
871	Gender-related prognostic value and genomic pattern of intra-tumor heterogeneity in colorectal cancer. **2017**, 38, 837-846	14
870	assessment of drug response on breast cancer primary tissue with preserved microenvironments. **2017**, 6, e1331798	24
869	Isolation and Molecular Characterization of Circulating Tumor Cells. **2017**,	2
868	Molecular Profiling and Significance of Circulating Tumor Cell Based Genetic Signatures. **2017**, 994, 143-167	2
867	Targeting long non-coding RNA ASBEL with oligonucleotide antagonist for breast cancer therapy. **2017**, 489, 386-392	15
866	Translational Genomics: Practical Applications of the Genomic Revolution in Breast Cancer. **2017**, 23, 2630-2639	15
865	Mutational Signatures in Breast Cancer: The Problem at the DNA Level. **2017**, 23, 2617-2629	73
864	Genetic Alterations in the Molecular Subtypes of Bladder Cancer: Illustration in the Cancer Genome Atlas Dataset. **2017**, 72, 354-365	126
863	Wnt signaling in triple-negative breast cancer. **2017**, 6, e310	159
862	Initiative for Molecular Profiling and Advanced Cancer Therapy and challenges in the implementation of precision medicine. **2017**, 41, 176-181	15
861	Robotic Mammosphere Assay for High-Throughput Screening in Triple-Negative Breast Cancer. **2017**, 22, 827-836	1

860	New Developments in Breast Cancer and Their Impact on Daily Practice in Pathology. **2017**, 141, 490-498	37
859	Biological Subtypes of Triple-Negative Breast Cancer. **2017**, 12, 8-14	48
858	Germline Mutations in Triple-Negative Breast Cancer. **2017**, 12, 15-19	32
857	Molecular alterations in triple-negative breast cancer-the road to new treatment strategies. **2017**, 389, 2430-2442	394
856	The genetic landscape of breast carcinomas with neuroendocrine differentiation. **2017**, 241, 405-419	35
855	Survival with metastatic breast cancer based on initial presentation, de novo versus relapsed. **2017**, 161, 549-556	92
854	Metabotypes of breast cancer cell lines revealed by non-targeted metabolomics. **2017**, 43, 173-186	19
853	Lesion-Directed Therapies and Monitoring Tumor Evolution Using Liquid Biopsies. **2017**, 7,	6
852	DNA damage repair in breast cancer and its therapeutic implications. **2017**, 49, 156-165	36
851	Tissue disruption increases stochastic gene expression thus producing tumors: Cancer initiation without driver mutation. **2017**, 140, 2408-2413	16
850	Antrodia salmonea induces G cell-cycle arrest in human triple-negative breast cancer (MDA-MB-231) cells and suppresses tumor growth in athymic nude mice. **2017**, 196, 9-19	13
849	Dynamics of clonal evolution in myelodysplastic syndromes. **2017**, 49, 204-212	228
848	The recurrent architecture of tumour initiation, progression and drug sensitivity. **2017**, 17, 116-130	97
847	Delayed Sequential Co-Delivery of Gefitinib and Doxorubicin for Targeted Combination Chemotherapy. **2017**, 14, 4551-4559	20
846	Unusually high levels of serum p53 antibody in recurrent gastric cancer. **2017**, 10, 503-507	1
845	A Targetable EGFR-Dependent Tumor-Initiating Program in Breast Cancer. **2017**, 21, 1140-1149	45
844	Mapping genomic and transcriptomic alterations spatially in epithelial cells adjacent to human breast carcinoma. **2017**, 8, 1245	10
843	Sample Size Calculation for Differential Expression Analysis of RNA-Seq Data. **2017**, 359-379	

842	Frontiers of Biostatistical Methods and Applications in Clinical Oncology. **2017**,	
841	Sweepstake evolution revealed by population-genetic analysis of copy-number alterations in single genomes of breast cancer. **2017**, 4, 171060	11
840	Unravelling biology and shifting paradigms in cancer with single-cell sequencing. **2017**, 17, 557-569	157
839	Panel sequencing of 264 candidate susceptibility genes and segregation analysis in a cohort of non-BRCA1, non-BRCA2 breast cancer families. **2017**, 166, 937-949	4
838	Complete regression of cutaneous metastases with systemic immune response in a patient with triple negative breast cancer receiving p53MVA vaccine with pembrolizumab. **2017**, 6, e1363138	11
837	Neutral tumor evolution in myeloma is associated with poor prognosis. **2017**, 130, 1639-1643	14
836	Decoding nervous system by single-cell RNA sequencing. **2017**, 5, 210-214	1
835	Tumor Sequencing and Patient-Derived Xenografts in the Neoadjuvant Treatment of Breast Cancer. **2017**, 109,	40
834	Piecing together the puzzle: nanopore technology in detection and quantification of cancer biomarkers. **2017**, 7, 42653-42666	11
833	Basal-A Triple-Negative Breast Cancer Cells Selectively Rely on RNA Splicing for Survival. **2017**, 16, 2849-2861	24
832	Fidelity and Stability of PDX Models. **2017**, 29-42	1
831	Studies of Cancer Heterogeneity Using PDX Models. **2017**, 59-69	
830	Identification of New Tumor Suppressor Genes in Triple-Negative Breast Cancer. **2017**, 77, 4089-4101	21
829	Intratumor heterogeneity predicts metastasis of triple-negative breast cancer. **2017**, 38, 900-909	43
828	The Evolving Role of Companion Diagnostics for Breast Cancer in an Era of Next-Generation Omics. **2017**, 187, 2185-2198	9
827	Breast Cancer Molecular Stratification: From Intrinsic Subtypes to Integrative Clusters. **2017**, 187, 2152-2162	114
826	The Spectrum of Triple-Negative Breast Disease: High- and Low-Grade Lesions. **2017**, 187, 2139-2151	78
825	Triple-Negative Breast Cancer: Next-Generation Sequencing for Target Identification. **2017**, 187, 2133-2138	42

824	Tumor-infiltrating lymphocytes in breast cancer according to tumor subtype: Current state of the art. **2017**, 35, 142-150	66
823	A functional BRCA1 coding sequence genetic variant contributes to prognosis of triple-negative breast cancer, especially after radiotherapy. **2017**, 166, 109-116	10
822	Genomic Evolution of Breast Cancer Metastasis and Relapse. **2017**, 32, 169-184.e7	346
821	Resistance to Targeted Therapies in Breast Cancer. **2017**,	
820	Comprehensive statistical inference of the clonal structure of cancer from multiple biopsies. **2017**, 7, 16943	1
819	Role of epithelial to mesenchymal transition associated genes in mammary gland regeneration and breast tumorigenesis. **2017**, 8, 1669	36
818	Relevance of Stem Cells. **2017**, 883-888	
817	Network Analysis of miRNA and Protein Expression Profiles in Breast Cancer Patients. **2017**,	
816	Breast Cancer Genomics. **2017**, 149-156	
815	Fundamental Pathways in Breast Cancer 2: Maintenance of Genomic Stability. **2017**, 13-17	
814	Mouse Models of Breast Cancer: Deceptions that Reveal the Truth. **2017**, 49-60	
813	Lowly methylated region analysis identifies EBF1 as a potential epigenetic modifier in breast cancer. **2017**, 12, 964-972	11
812	The Expression of Connexins and SOX2 Reflects the Plasticity of Glioma Stem-Like Cells. **2017**, 10, 555-569	13
811	Body mass index mediates the prognostic significance of circulating tumor cells in inflammatory breast cancer. **2017**, 214, 666-671	6
810	Intratumoral heterogeneity and subclonal diversification of early breast cancer. **2017**, 34 Suppl 1, S36-S42	12
809	Patient-Derived Xenograft Models of Human Cancer. **2017**,	5
808	Identification of Interacting Stromal Axes in Triple-Negative Breast Cancer. **2017**, 77, 4673-4683	21
807	Precision medicine in breast cancer: reality or utopia?. **2017**, 15, 139	38

806	Posttranslationally modified progesterone receptors direct ligand-specific expression of breast cancer stem cell-associated gene programs. **2017**, 10, 89	43
805	miR-629-3p may serve as a novel biomarker and potential therapeutic target for lung metastases of triple-negative breast cancer. **2017**, 19, 72	30
804	Mechanisms of resistance of chemotherapy in early-stage triple negative breast cancer (TNBC). **2017**, 34 Suppl 1, S27-S30	64
803	Deciphering Genetic Intratumor Heterogeneity and Its Impact on Cancer Evolution. **2017**, 1, 223-240	16
802	Genome evolution in ductal carcinoma in situ: invasion of the clones. **2017**, 241, 208-218	51
801	Transcriptional Regulation by Wild-Type and Cancer-Related Mutant Forms of p53. **2017**, 7,	56
800	TP53 Mutations in Breast and Ovarian Cancer. **2017**, 7,	65
799	Towards Precision Medicine in the Clinic: From Biomarker Discovery to Novel Therapeutics. **2017**, 38, 25-40	62
798	Cardamonin, a chalcone, inhibits human triple negative breast cancer cell invasiveness by downregulation of Wnt/▯catenin signaling cascades and reversal of epithelial-mesenchymal transition. **2017**, 43, 152-169	50
797	Pathology and Molecular Pathology of Breast Cancer. **2017**, 173-231	0
796	Parkin and mitophagy in cancer. **2017**, 36, 1315-1327	124
795	The role of cancer stem cells in tumor heterogeneity and resistance to therapy. **2017**, 95, 1-15	32
794	Irreversible electroporation inhibits pro-cancer inflammatory signaling in triple negative breast cancer cells. **2017**, 113, 42-50	16
793	Mutant p53: a novel target for the treatment of patients with triple-negative breast cancer?. **2017**, 140, 234-246	56
792	Predicting and Overcoming Chemotherapeutic Resistance in Breast Cancer. **2017**, 1026, 59-104	32
791	The Dawning of Translational Breast Cancer: From Bench to Bedside. **2017**, 1026, 1-25	
790	New agents for the management of resistant metastatic breast cancer. **2017**, 18, 1815-1831	5
789	Participant Attitudes Toward an Intensive Trial of Multiple Biopsies, Multidimensional Molecular Analysis, and Reporting of Results in Metastatic Triple-Negative Breast Cancer. **2017**, 1,	2

788	Mutation Clusters from Cancer Exome. **2017**, 8,	0
787	Morphological Evaluation of Tumor-Infiltrating Lymphocytes (TILs) to Investigate Invasive Breast Cancer Immunogenicity, Reveal Lymphocytic Networks and Help Relapse Prediction: A Retrospective Study. **2017**, 18,	10
786	Viral-Cellular DNA Junctions as Molecular Markers for Assessing Intra-Tumor Heterogeneity in Cervical Cancer and for the Detection of Circulating Tumor DNA. **2017**, 18,	13
785	Transcription Factors in Breast Cancer-Lessons From Recent Genomic Analyses and Therapeutic Implications. **2017**, 107, 223-273	10
784	Metabolomics Applications in Precision Medicine: An Oncological Perspective. **2017**, 17, 2740-2751	55
783	The Consequences of Chromosome Segregation Errors in Mitosis and Meiosis. **2017**, 6,	64
782	Alternative Splicing in Breast Cancer and the Potential Development of Therapeutic Tools. **2017**, 8,	16
781	Tumor Heterogeneity in Breast Cancer. **2017**, 4, 227	211
780	Genetic Mutations and Epigenetic Modifications: Driving Cancer and Informing Precision Medicine. **2017**, 2017, 9620870	32
779	The past and future of breast cancer treatment-from the papyrus to individualised treatment approaches. **2017**, 11, 746	26
778	Integrative analysis of genomic alterations in triple-negative breast cancer in association with homologous recombination deficiency. **2017**, 13, e1006853	32
777	Intra-tumor heterogeneity in breast cancer has limited impact on transcriptomic-based molecular profiling. **2017**, 17, 802	5
776	The emerging roles of CDK12 in tumorigenesis. **2017**, 12, 7	39
775	ReMixT: clone-specific genomic structure estimation in cancer. **2017**, 18, 140	18
774	Characterization of potential driver mutations involved in human breast cancer by computational approaches. **2017**, 8, 50252-50272	28
773	[Triple-negative breast cancer therapy via nectin-4 targeting]. **2017**, 33, 936-939	0
772	Mutation Clusters from Cancer Exome. **2017**,	
771	Response of a Metastatic Breast Carcinoma With a Previously Uncharacterized ERBB2 G776V Mutation to Human Epidermal Growth Factor Receptor 2-Targeted Therapy.. **2017**, 1, 1-9	

770	Homologous Recombination Deficiency in Breast Cancer: A Clinical Review.. **2017**, 1, 1-13		11
769	Practical Approach to Triple-Negative Breast Cancer. **2017**, 13, 293-300		45
768	Tumor Heterogeneity. **2017**, 37-55		4
767	Targeted exome sequencing of Korean triple-negative breast cancer reveals homozygous deletions associated with poor prognosis of adjuvant chemotherapy-treated patients. **2017**, 8, 61538-61550		11
766	Adenoid cystic carcinomas of the salivary gland, lacrimal gland, and breast are morphologically and genetically similar but have distinct microRNA expression profiles. **2018**, 31, 1211-1225		20
765	Tumor-infiltrating lymphocytes and ductal carcinoma in situ of the breast: friends or foes?. **2018**, 31, 1012-1025		19
764	Mass Spectrometry-Based Proteomics Reveals Potential Roles of NEK9 and MAP2K4 in Resistance to PI3K Inhibition in Triple-Negative Breast Cancers. **2018**, 78, 2732-2746		34
763	Untargeted and stable isotope-assisted metabolomic analysis of MDA-MB-231 cells under hypoxia. **2018**, 14, 40		9
762	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. *Nature*, **2018**, 555, 371-376	50.4	380
761	Towards predictive biomarkers for immunotherapy response in breast cancer patients. **2018**, 7, BMT05		4
760	Update on the Treatment of Early-Stage Triple-Negative Breast Cancer. **2018**, 19, 22		41
759	MicroSPECT imaging of triple negative breast cancer cell tumor xenografted in athymic mice with radioiodinated anti-ICAM-1 monoclonal antibody. **2018**, 139, 20-25		10
758	c-Src inhibitor selectively inhibits triple-negative breast cancer overexpressed Vimentin in vitro and in vivo. **2018**, 109, 1648-1659		13
757	Chemoresistance Evolution in Triple-Negative Breast Cancer Delineated by Single-Cell Sequencing. **2018**, 173, 879-893.e13		427
756	Multiscale blind source separation. **2018**, 46,		7
755	Clinically actionable mutation profiles in patients with cancer identified by whole-genome sequencing. **2018**, 4,		11
754	The Use of Transcriptomics in Clinical Applications. **2018**, 49-66		
753	Development of a personalized therapeutic strategy for ERBB-gene-mutated cancers. **2018**, 10, 1758834017746040		10

752	Accurity: accurate tumor purity and ploidy inference from tumor-normal WGS data by jointly modelling somatic copy number alterations and heterozygous germline single-nucleotide-variants. **2018**, 34, 2004-2011	14
751	Pathologic Evaluation of Triple-Negative Breast Cancer. **2018**, 1-22	2
750	An update on first line therapies for metastatic breast cancer. **2018**, 19, 243-252	5
749	Identification of a rhodium(iii) complex as a Wee1 inhibitor against TP53-mutated triple-negative breast cancer cells. **2018**, 54, 2463-2466	32
748	Integrative network-based approach identifies central genetic and transcriptomic elements in triple-negative breast cancer. **2018**, 18, 113-124	6
747	Protein biomarkers for subtyping breast cancer and implications for future research. **2018**, 15, 131-152	35
746	Molecular Oncology of Breast Cancer. **2018**, 282-307.e5	5
745	Expression of GHRH-R, a Potentially Targetable Biomarker, in Triple-negative Breast Cancer. **2018**, 26, 1-5	1
744	Theranostics of Triple-Negative Breast Cancer Based on Conjugated Polymer Nanoparticles. **2018**, 10, 10634-10646	48
743	Triple-Negative Breast Cancer. **2018**,	
742	Management of Metastatic Triple-Negative Breast Cancer. **2018**, 95-116	
741	Orai1 is critical for Notch-driven aggressiveness under hypoxic conditions in triple-negative breast cancers. **2018**, 1864, 975-986	22
740	Multiclonal Invasion in Breast Tumors Identified by Topographic Single Cell Sequencing. **2018**, 172, 205-217.e12	200
739	Breast cancer intratumour heterogeneity: current status and clinical implications. **2018**, 73, 717-731	21
738	OCT4 but not SOX2 expression correlates with worse prognosis in surgical patients with triple-negative breast cancer. **2018**, 25, 447-455	23
737	Mutational analysis of triple-negative breast cancers within the International Breast Cancer Study Group (IBCSG) Trial 22-00. **2018**, 170, 351-360	5
736	An integrative bioinformatics approach reveals coding and non-coding gene variants associated with gene expression profiles and outcome in breast cancer molecular subtypes. **2018**, 118, 1107-1114	17
735	Mutant p53 in breast cancer: potential as a therapeutic target and biomarker. **2018**, 170, 213-219	73

734	Integrated genomics and functional validation identifies malignant cell specific dependencies in triple negative breast cancer. **2018**, 9, 1044	29
733	Identification of differentially expressed genes regulated by molecular signature in breast cancer-associated fibroblasts by bioinformatics analysis. **2018**, 297, 161-183	7
732	Mutant p53 as a therapeutic target for the treatment of triple-negative breast cancer: Preclinical investigation with the anti-p53 drug, PK11007. **2018**, 414, 99-106	38
731	Analysis of Genomes and Transcriptomes of Hepatocellular Carcinomas Identifies Mutations and Gene Expression Changes in the Transforming Growth Factor-Pathway. **2018**, 154, 195-210	68
730	Therapeutic targeting of p53: all mutants are equal, but some mutants are more equal than others. **2018**, 15, 13-30	196
729	Computational approaches for inferring tumor evolution from single-cell genomic data. **2018**, 7, 16-25	12
728	Breast Cancers Activate Stromal Fibroblast-Induced Suppression of Progenitors in Adjacent Normal Tissue. **2018**, 10, 196-211	8
727	Genetic alterations in sporadic triple negative breast cancer. **2018**, 38, 30-38	15
726	Identifying and Targeting Sporadic Oncogenic Genetic Aberrations in Mouse Models of Triple-Negative Breast Cancer. **2018**, 8, 354-369	40
725	Mitochondrial quality control: The role of mitophagy in aging. **2018**, 28, 246-260	46
724	Metastatic triple negative breast cancer: Optimizing treatment options, new and emerging targeted therapies. **2018**, 14, 32-39	63
723	Are There Any Clinically Relevant Subgroups of Triple-Negative Breast Cancer in 2018?. **2018**, 14, 281-289	8
722	Association of Cell-Free DNA Tumor Fraction and Somatic Copy Number Alterations With Survival in Metastatic Triple-Negative Breast Cancer. **2018**, 36, 543-553	113
721	Circulating Tumor DNA Guides Prognosis in Metastatic Triple-Negative Breast Cancer. **2018**, 36, 523-524	2
720	Actionable gene alterations in an Asian population with triple-negative breast cancer. **2018**, 2,	1
719	Bayesian Modeling Approaches for Temporal Dynamics in RNA-seq Data. **2018**,	2
718	Integrated Modeling of GC-Content, Mappability, Tumor Impurity and Aneuploidy for Accurate Detection of Genomic Aberrations. **2018**, 6, 64096-64106	
717	Overexpression of MUC1 predicts poor prognosis in patients with breast cancer. **2019**, 41, 801-810	48

716	Potential Management of Circulating Tumor DNA as a Biomarker in Triple-Negative Breast Cancer. **2018**, 9, 4627-4634	16
715	Frequent downregulation of LRRC26 by epigenetic alterations is involved in the malignant progression of triple-negative breast cancer. **2018**, 52, 1539-1558	4
714	High-resolution clonal mapping of multi-organ metastasis in triple negative breast cancer. **2018**, 9, 5079	52
713	Fractal-Radiomics as Complexity Analysis of CT and MRI Cancer Images. **2018**,	2
712	Genetic heterogeneity and actionable mutations in HER2-positive primary breast cancers and their brain metastases. **2018**, 9, 20617-20630	26
711	MicroRNAs and DNA-Damaging Drugs in Breast Cancer: Strength in Numbers. **2018**, 8, 352	12
710	Updates on Molecular Classification of Triple Negative Breast Cancer. **2018**, 10, 289-295	1
709	Restoring guardianship of the genome: Anticancer drug strategies to reverse oncogenic mutant p53 misfolding. **2018**, 71, 19-31	4
708	DNA Methylation Predicts the Response of Triple-Negative Breast Cancers to All-Trans Retinoic Acid. **2018**, 10,	15
707	Precision medicine based on tumorigenic signaling pathways for triple-negative breast cancer. **2018** , 16, 4984-4996	18
706	Somatic mutations, clinicopathologic characteristics, and survival in patients with untreated breast cancer with bone-only and non-bone sites of first metastasis. **2018**, 9, 3640-3646	13
705	Characterization of Nigerian breast cancer reveals prevalent homologous recombination deficiency and aggressive molecular features. **2018**, 9, 4181	45
704	Precision medicine and bladder cancer heterogeneity. **2018**, 105, 925-931	15
703	miR-3178 inhibits cell proliferation and metastasis by targeting Notch1 in triple-negative breast cancer. **2018**, 9, 1059	26
702	Detection of copy number variants and loss of heterozygosity from impure tumor samples using whole exome sequencing data. **2018**, 16, 4713-4720	2
701	The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. **2018**, 34, 427-438.e6	339
700	The Mutant p53-Targeting Compound APR-246 Induces ROS-Modulating Genes in Breast Cancer Cells. **2018**, 11, 1343-1349	14
699	Tumor-stroma interactions differentially alter drug sensitivity based on the origin of stromal cells. **2018**, 14, e8322	14

698	The prognostic effects of somatic mutations in ER-positive breast cancer. **2018**, 9, 3476	51
697	Unravelling subclonal heterogeneity and aggressive disease states in TNBC through single-cell RNA-seq. **2018**, 9, 3588	187
696	Cyclin E Overexpression Sensitizes Triple-Negative Breast Cancer to Wee1 Kinase Inhibition. **2018**, 24, 6594-6610	36
695	In vivo phosphoproteomics reveals kinase activity profiles that predict treatment outcome in triple-negative breast cancer. **2018**, 9, 3501	26
694	Somatic EP300-G211S mutations are associated with overall somatic mutational patterns and breast cancer specific survival in triple-negative breast cancer. **2018**, 172, 339-351	6
693	Quantification of subclonal selection in cancer from bulk sequencing data. **2018**, 50, 895-903	138
692	How shall we treat early triple-negative breast cancer (TNBC): from the current standard to upcoming immuno-molecular strategies. **2018**, 3, e000357	78
691	Molecular Biology of Breast Cancer. **2018**, 569-588	3
690	Self-digitization chip for single-cell genotyping of cancer-related mutations. **2018**, 13, e0196801	1
689	The cJUN NH-terminal kinase (JNK) signaling pathway promotes genome stability and prevents tumor initiation. **2018**, 7,	18
688	Epigenetics of Breast Cancer. **2018**, 141-168	
687	Structural Prediction of Protein-Protein Interactions by Docking: Application to Biomedical Problems. **2018**, 110, 203-249	9
686	Cytokeratin 5/6 and cytokeratin 8/18 expression in triple negative breast cancers: clinicopathologic significance in South-Asian population. **2018**, 11, 372	15
685	Mutational landscape and clonal diversity of pulmonary adenoid cystic carcinoma. **2018**, 19, 898-903	8
684	Genetic Markers in Triple-Negative Breast Cancer. **2018**, 18, e841-e850	61
683	Phase I/II clinical trial of everolimus combined with gemcitabine/cisplatin for metastatic triple-negative breast cancer. **2018**, 9, 1145-1151	12
682	Engineering cell heterogeneity into organs-on-a-chip. **2018**, 18, 2378-2395	12
681	PIK3CA mutation profiling in patients with breast cancer, using a highly sensitive detection system. **2018**, 109, 2558-2566	23

680	Neoadjuvant Treatment of Stage IIB/III Triple Negative Breast Cancer with Cyclophosphamide, Doxorubicin, and Cisplatin (CAP Regimen): A Single Arm, Single Center Phase II Study (GBECAM 2008/02). **2017**, 7, 329	8
679	The association of genomic lesions and PD-1/PD-L1 expression in resected triple-negative breast cancers. **2018**, 20, 71	36
678	The Landscape of Small Non-Coding RNAs in Triple-Negative Breast Cancer. **2018**, 9,	14
677	Effects of PTEN Loss and Activated KRAS Overexpression on Mechanical Properties of Breast Epithelial Cells. **2018**, 19,	6
676	Long non-coding RNAs: implications in targeted diagnoses, prognosis, and improved therapeutic strategies in human non- and triple-negative breast cancer. **2018**, 10, 88	36
675	Therapeutic landscape in mutational triple negative breast cancer. **2018**, 17, 99	40
674	An Introduction to the Computational Challenges in Next Generation Sequencing. **2018**, 37-45	
673	The Making of a PreCancer Atlas: Promises, Challenges, and Opportunities. **2018**, 4, 523-536	23
672	Microenvironment-Induced Non-sporadic Expression of the AXL and cKIT Receptors Are Related to Epithelial Plasticity and Drug Resistance. **2018**, 6, 41	18
671	Predictors of breast cancer cell types and their prognostic power in breast cancer patients. **2018**, 19, 137	8
670	The histone deacetylase inhibitor OBP-801 and eribulin synergistically inhibit the growth of triple-negative breast cancer cells with the suppression of survivin, Bcl-xL, and the MAPK pathway. **2018**, 171, 43-52	12
669	Applications of RNA Indexes for Precision Oncology in Breast Cancer. **2018**, 16, 108-119	11
668	Phase II study of ruxolitinib, a selective JAK1/2 inhibitor, in patients with metastatic triple-negative breast cancer. **2018**, 4, 10	58
667	New therapeutic strategies to treat human cancers expressing mutant p53 proteins. **2018**, 37, 30	112
666	New insights from the widening homogeneity perspective to target intratumor heterogeneity. **2018**, 38, 17	6
665	Tumor mutational burden is a determinant of immune-mediated survival in breast cancer. **2018**, 7, e1490854	129
664	Patient advocate involvement in the design and conduct of breast cancer clinical trials requiring the collection of multiple biopsies. **2018**, 4, 22	1
663	Synthetic Lethality: From Research to Precision Cancer Nanomedicine. **2018**, 18, 337-346	14

662	Mutational Intratumor Heterogeneity is a Complex and Early Event in the Development of Adult T-cell Leukemia/Lymphoma. **2018**, 20, 883-893	7
661	Integrative analysis of the inter-tumoral heterogeneity of triple-negative breast cancer. **2018**, 8, 11807	23
660	Cancer-Associated MORC2-Mutant M276I Regulates an hnRNPM-Mediated CD44 Splicing Switch to Promote Invasion and Metastasis in Triple-Negative Breast Cancer. **2018**, 78, 5780-5792	40
659	Linking transcriptional and genetic tumor heterogeneity through allele analysis of single-cell RNA-seq data. **2018**, 28, 1217-1227	90
658	The Spatiotemporal Evolution of Lymph Node Spread in Early Breast Cancer. **2018**, 24, 4763-4770	21
657	Light-Activatable Assembled Nanoparticles to Improve Tumor Penetration and Eradicate Metastasis in Triple Negative Breast Cancer. **2018**, 28, 1801738	23
656	Characterization of cancer genomic heterogeneity by next-generation sequencing advances precision medicine in cancer treatment. **2018**, 1, 29-48	49
655	Profiling molecular regulators of recurrence in chemorefractory triple-negative breast cancers. **2019**, 21, 87	10
654	Influence of BRCA1 Germline Mutations in the Somatic Mutational Burden of Triple-Negative Breast Cancer. **2019**, 12, 1453-1460	2
653	Single-Cell Omics: Deciphering Tumor Clonal Architecture. **2019**, 61-97	3
652	Landscape of transcriptomic interactions between breast cancer and its microenvironment. **2019**, 10, 3116	12
651	MicroRNA-based potential diagnostic, prognostic and therapeutic applications in triple-negative breast cancer. **2019**, 47, 2800-2809	24
650	Emerging Role of Genomics and Cell-Free DNA in Breast Cancer. **2019**, 20, 68	6
649	A general overview of systems theory, integrative physiology, and the theory of Endobiogeny. **2019**, 17-29	
648	Prognostic impact of PIK3CA protein expression in triple negative breast cancer and its subtypes. **2019**, 145, 2051-2059	9
647	PhISCS: a combinatorial approach for subperfect tumor phylogeny reconstruction via integrative use of single-cell and bulk sequencing data. **2019**, 29, 1860-1877	28
646	DNA methylation exploration for ARDS: a multi-omics and multi-microarray interrelated analysis. **2019**, 17, 345	12
645	Dissociation of solid tumor tissues with cold active protease for single-cell RNA-seq minimizes conserved collagenase-associated stress responses. **2019**, 20, 210	77

644	SiCloneFit: Bayesian inference of population structure, genotype, and phylogeny of tumor clones from single-cell genome sequencing data. **2019**, 29, 1847-1859	40
643	Targeted exosome-encapsulated erastin induced ferroptosis in triple negative breast cancer cells. **2019**, 110, 3173-3182	101
642	Tumor clonal status predicts clinical outcomes of lung adenocarcinoma with EGFR-TKI sensitizing mutation. **2019**, 10, 5549-5556	3
641	Biomarker predictors for immunotherapy benefit in breast: beyond PD-L1. **2019**, 11, 217-227	3
640	Deconvolution of the Genomic and Epigenomic Interaction Landscape of Triple-Negative Breast Cancer. **2019**, 11,	3
639	Evolution and Impact of Subclonal Mutations in Papillary Thyroid Cancer. **2019**, 105, 959-973	11
638	Identification of Single Nucleotide Polymorphism in Red Clover () Using Targeted Genomic Amplicon Sequencing and RNA-seq. **2019**, 10, 1257	4
637	Novel therapeutic avenues in triple-negative breast cancer: PI3K/AKT inhibition, androgen receptor blockade, and beyond. **2019**, 11, 1758835919880429	22
636	The HER2 S310F Mutant Can Form an Active Heterodimer with the EGFR, Which Can Be Inhibited by Cetuximab but Not by Trastuzumab as well as Pertuzumab. **2019**, 9,	5
635	Patterns of Mutation Enrichment in Metastatic Triple-Negative Breast Cancer. **2019**, 13, 1179554919868482	5
634	Breast Cancer Heterogeneity in Primary and Metastatic Disease. **2019**, 1152, 75-104	13
633	What sustains the multidrug resistance phenotype beyond ABC efflux transporters? Looking beyond the tip of the iceberg. **2019**, 46, 100643	38
632	Dynamic clonal remodelling in breast cancer metastases is associated with subtype conversion. **2019**, 120, 54-64	13
631	The Dual Roles of the Atypical Protein Kinase Cs in Cancer. **2019**, 36, 218-235	25
630	Triple-Negative Breast Cancer: Current Understanding and Future Therapeutic Breakthrough Targeting Cancer Stemness. **2019**, 11,	85
629	FRET biosensor-based kinase inhibitor screen for ERK and AKT activity reveals differential kinase dependencies for proliferation in TNBC cells. **2019**, 169, 113640	5
628	Novel and Alternative Targets Against Breast Cancer Stemness to Combat Chemoresistance. **2019**, 9, 1003	27
627	Designing Highly Crystalline Multifunctional Multicolor Luminescence Nanosystem for Tracking Breast Cancer Heterogeneity. **2019**, 1, 1021-1034	3

626	EGFR/Notch Antagonists Enhance the Response to Inhibitors of the PI3K-Akt Pathway by Decreasing Tumor-Initiating Cell Frequency. **2019**, 25, 2835-2847	18
625	Unstable Genome and Transcriptome Dynamics during Tumor Metastasis Contribute to Therapeutic Heterogeneity in Colorectal Cancers. **2019**, 25, 2821-2834	8
624	Insights into Molecular Classifications of Triple-Negative Breast Cancer: Improving Patient Selection for Treatment. **2019**, 9, 176-198	364
623	A subgroup of microRNAs defines PTEN-deficient, triple-negative breast cancer patients with poorest prognosis and alterations in RB1, MYC, and Wnt signaling. **2019**, 21, 18	20
622	Personalized medicine in breast cancer: pharmacogenomics approaches. **2019**, 12, 59-73	24
621	Using State Space Exploration to Determine How Gene Regulatory Networks Constrain Mutation Order in Cancer Evolution. **2019**, 133-153	3
620	Tumor mutational profile of triple negative breast cancer patients in Thailand revealed distinctive genetic alteration in chromatin remodeling gene. **2019**, 7, e6501	9
619	Shear Wave Elastography of Breast Lesions: Quantitative Analysis of Elastic Heterogeneity Improves Diagnostic Performance. **2019**, 45, 1909-1917	6
618	The Genomic and Immune Landscapes of Lethal Metastatic Breast Cancer. **2019**, 27, 2690-2708.e10	58
617	Array comparative genomic hybridization analysis discloses chromosome copy number alterations as indicators of patient outcome in lymph node-negative breast cancer. **2019**, 19, 521	6
616	Oncogenic lncRNA downregulates cancer cell antigen presentation and intrinsic tumor suppression. **2019**, 20, 835-851	147
615	State of art of advanced triple negative breast cancer. **2019**, 25, 967-970	13
614	Cytoplasmic HAX1 Is an Independent Risk Factor for Breast Cancer Metastasis. **2019**, 2019, 6375025	4
613	Tensor clustering with algebraic constraints gives interpretable groups of crosstalk mechanisms in breast cancer. **2019**, 16, 20180661	3
612	Biomarkers to diagnose metastatic breast carcinoma to the pancreas: A case report and update. **2019**, 47, 912-917	1
611	Novel key genes in triple-negative breast cancer identified by weighted gene co-expression network analysis. **2019**, 120, 16900-16912	12
610	Resistance to neoadjuvant chemotherapy in triple-negative breast cancer mediated by a reversible drug-tolerant state. **2019**, 11,	93
609	Targeting the PI3-kinase pathway in triple-negative breast cancer. **2019**, 30, 1051-1060	86

608	Role of Hedgehog Signaling in Breast Cancer: Pathogenesis and Therapeutics. **2019**, 8,	44
607	Imaging tools to enhance animal tumor models for cancer research and drug discovery. **2019**, 75-106	
606	Personalized chemotherapy in triple-negative breast cancer: are we ready for prime time?. **2019**, 6, 4	1
605	Engineering Multidimensional Evolutionary Forces to Combat Cancer. **2019**, 9, 587-604	10
604	TP53 Status as a Determinant of Pro- vs Anti-Tumorigenic Effects of Estrogen Receptor-Beta in Breast Cancer. **2019**, 111, 1202-1215	26
603	PDLIM2 Is a Marker of Adhesion and Catenin Activity in Triple-Negative Breast Cancer. **2019**, 79, 2619-2633	9
602	A breast one-patient panel of heterogeneous genomes reveals genetic alterations driving DCIS into invasive lesions. **2019**, 15, 1565-1576	1
601	Cancer Treatment in the Genomic Era. **2019**, 88, 247-280	14
600	Branched clonal evolution: nodal follicular lymphoma and primary diffuse large B-cell lymphoma of the central nervous system. **2019**, 104, e326-e329	1
599	Genomic and Transcriptomic Landscape of Triple-Negative Breast Cancers: Subtypes and Treatment Strategies. **2019**, 35, 428-440.e5	239
598	Integrating Germline and Somatic Mutation Information for the Discovery of Biomarkers in Triple-Negative Breast Cancer. **2019**, 16,	8
597	Triple Negative Breast Cancer Profile, from Gene to microRNA, in Relation to Ethnicity. **2019**, 11,	21
596	Genetic alterations of triple negative breast cancer (TNBC) in women from Northeastern Mexico. **2019**, 17, 3581-3588	6
595	Breast Disease. **2019**,	
594	Intratumor heterogeneity index of breast carcinomas based on DNA methylation profiles. **2019**, 19, 328	4
593	Integrated Somatic and Germline Whole-Exome Sequencing Analysis in Women with Lung Cancer after a Previous Breast Cancer. **2019**, 11,	1
592	Patterns of Genomic Instability in Breast Cancer. **2019**, 40, 198-211	38
591	Prognostic value of CD8 + PD-1+ immune infiltrates and PDCD1 gene expression in triple negative breast cancer. **2019**, 7, 34	44

590	Precise targeting of POLR2A as a therapeutic strategy for human triple negative breast cancer. **2019**, 14, 388-397	69
589	Tumour targeted contrast enhanced ultrasound imaging dual-modal microbubbles for diagnosis and treatment of triple negative breast cancer.. **2019**, 9, 5682-5691	10
588	Barcoding reveals complex clonal behavior in patient-derived xenografts of metastatic triple negative breast cancer. **2019**, 10, 766	52
587	Targeted-Gene Sequencing to Catch Triple Negative Breast Cancer Heterogeneity before and after Neoadjuvant Chemotherapy. **2019**, 11,	7
586	Flip the coin: IL-7 and IL-7R in health and disease. **2019**, 20, 1584-1593	83
585	Invariant patterns of clonal succession determine specific clinical features of myelodysplastic syndromes. **2019**, 10, 5386	29
584	JNK-Dependent cJun Phosphorylation Mitigates TGF▯and EGF-Induced Pre-Malignant Breast Cancer Cell Invasion by Suppressing AP-1-Mediated Transcriptional Responses. **2019**, 8,	4
583	Targeting of the Eukaryotic Translation Initiation Factor 4A Against Breast Cancer Stemness. **2019**, 9, 1311	21
582	Association of p53 expression with poor prognosis in patients with triple-negative breast invasive ductal carcinoma. **2019**, 98, e15449	20
581	Concordance of Genomic Variants in Matched Primary Breast Cancer, Metastatic Tumor, and Circulating Tumor DNA: The MIRROR Study.. **2019**, 3, 1-16	3
580	TPX2/Aurora kinase A signaling as a potential therapeutic target in genomically unstable cancer cells. **2019**, 38, 852-867	21
579	Genomic Applications in Breast Carcinoma. **2019**, 347-361	
578	Molecular Regulation Mechanisms and Interactions Between Reactive Oxygen Species and Mitophagy. **2019**, 38, 10-22	43
577	Genomic Applications in Ovarian Cancer. **2019**, 471-482	
576	Immunological therapy: A novel thriving area for triple-negative breast cancer treatment. **2019**, 442, 409-428	26
575	Intratumor Heterogeneity. **2019**, 17-30	1
574	Explore Genomic Profiles for Triple-Negative Breast Cancer to Discover Drug Targets. **2019**, 423-440	
573	Basal biomarkers nestin and INPP4B predict gemcitabine benefit in metastatic breast cancer: Samples from the phase III SBG0102 clinical trial. **2019**, 144, 2578-2586	7

572	Estrogen Receptor and Breast Cancer. **2019**,	3
571	Germline TP53 and MSH6 mutations implicated in sporadic triple-negative breast cancer (TNBC): a preliminary study. **2019**, 13, 4	6
570	Raloxifene nano-micelles effect on triple-negative breast cancer is mediated through estrogen receptor-□and epidermal growth factor receptor. **2019**, 27, 903-916	9
569	Molecular features of premenopausal breast cancers in Latin American women: Pilot results from the PRECAMA study. **2019**, 14, e0210372	5
568	Optical Imaging of Triple-Negative Breast Cancer Cells in Xenograft Athymic Mice Using an ICAM-1-Targeting Small-Molecule Probe. **2019**, 21, 835-841	2
567	Breast tumour organoids: promising models for the genomic and functional characterisation of breast cancer. **2019**, 47, 109-117	15
566	NFIB promotes cell survival by directly suppressing p21 transcription in TP53-mutated triple-negative breast cancer. **2019**, 247, 186-198	27
565	Molecular Mechanisms of Endocrine Resistance. **2019**, 265-307	4
564	Comprehensive analysis of coexpressed long noncoding RNAs and genes in breast cancer. **2019**, 45, 428-437	6
563	Ductal Carcinoma in Situ Biomarkers in a Precision Medicine Era: Current and Future Molecular-Based Testing. **2019**, 189, 956-965	10
562	Thirty years of neuroendocrinology: Technological advances pave the way for molecular discovery. **2019**, 31, e12653	1
561	Targeting homologous repair deficiency in breast and ovarian cancers: Biological pathways, preclinical and clinical data. **2019**, 133, 58-73	20
560	CRTC1-MAML2 fusion in mucoepidermoid carcinoma of the breast. **2019**, 74, 463-473	19
559	A Four-gene Decision Tree Signature Classification of Triple-negative Breast Cancer: Implications for Targeted Therapeutics. **2019**, 18, 204-212	14
558	Molecular characterization of metaplastic breast carcinoma via next-generation sequencing. **2019**, 86, 85-92	17
557	Evolving and Expanding the Roles of Mitophagy as a Homeostatic and Pathogenic Process. **2019**, 99, 853-892	77
556	Outcome for triple negative breast cancer in a retrospective cohort with an emphasis on response to platinum-based neoadjuvant therapy. **2019**, 174, 1-13	12
555	Genomic analysis of racial differences in triple negative breast cancer. **2019**, 111, 1529-1542	12

554	Cancer Target Gene Screening: a web application for breast cancer target gene screening using multi-omics data analysis. **2020**, 21, 663-675	10
553	Mitochondria as playmakers of apoptosis, autophagy and senescence. **2020**, 98, 139-153	121
552	COTI-2 reactivates mutant p53 and inhibits growth of triple-negative breast cancer cells. **2020**, 179, 47-56	18
551	Effects of normothermic microwave irradiation on CD44/CD24 in breast cancer MDA-MB-231 and MCF-7 cell lines. **2020**, 84, 103-110	3
550	Tumor Liquid Biopsies. **2020**,	5
549	Know your enemy: Genetics, aging, exposomic and inflammation in the war against triple negative breast cancer. **2020**, 60, 285-293	9
548	The potential of ctDNA analysis in breast cancer. **2020**, 57, 54-72	7
547	NOTCH and DNA repair pathways are more frequently targeted by genomic alterations in inflammatory than in non-inflammatory breast cancers. **2020**, 14, 504-519	13
546	Phytochemicals inhibit migration of triple negative breast cancer cells by targeting kinase signaling. **2020**, 20, 4	11
545	Capivasertib Plus Paclitaxel Versus Placebo Plus Paclitaxel As First-Line Therapy for Metastatic Triple-Negative Breast Cancer: The PAKT Trial. **2020**, 38, 423-433	123
544	TBCRC 032 IB/II Multicenter Study: Molecular Insights to AR Antagonist and PI3K Inhibitor Efficacy in Patients with AR Metastatic Triple-Negative Breast Cancer. **2020**, 26, 2111-2123	41
543	Brain metastasis. **2020**, 20, 4-11	77
542	Phosphorylation of RAB7 by TBK1/IKK□Regulates Innate Immune Signaling in Triple-Negative Breast Cancer. **2020**, 80, 44-56	16
541	F-FDG PET imaging for monitoring the early anti-tumor effect of albendazole on triple-negative breast cancer. **2020**, 27, 372-380	6
540	The JAK2 V617F mutation in breast cancer?. **2020**, 26, 592	
539	Recent treatment progress of triple negative breast cancer. **2020**, 151, 40-53	39
538	Tumor mutation burden, immune checkpoint crosstalk and radiosensitivity in single-cell RNA sequencing data of breast cancer. **2020**, 142, 202-209	26
537	Personalized treatment in metastatic triple-negative breast cancer: The outlook in 2020. **2020**, 26, 69-80	14

536	GeTallele: A Method for Analysis of DNA and RNA Allele Frequency Distributions. **2020**, 8, 1021	1
535	Applications of Machine Learning in Drug Discovery II: Biomarker Discovery, Patient Stratification and Pharmacoeconomics. **2020**,	
534	Claudin 1 inhibits cell migration and increases intercellular adhesion in triple-negative breast cancer cell line. **2020**, 47, 7643-7653	1
533	The effects of p53 gene inactivation on mutant proteome expression in a human melanoma cell model. **2020**, 1864, 129722	2
532	Exosomes as Biomarkers of Human and Feline Mammary Tumours; A Comparative Medicine Approach to Unravelling the Aggressiveness of TNBC. **2020**, 1874, 188431	5
531	St. John's Wort Suppresses Growth in Triple-Negative Breast Cancer Cell Line MDA-MB-231 by Inducing Prodeath Autophagy and Apoptosis. **2020**, 12,	4
530	Practical classification of triple-negative breast cancer: intratumoral heterogeneity, mechanisms of drug resistance, and novel therapies. **2020**, 6, 54	58
529	Genetic and clinical landscape of breast cancers with germline BRCA1/2 variants. **2020**, 3, 578	7
528	Anti gC1qR/p32/HABP1 Antibody Therapy Decreases Tumor Growth in an Orthotopic Murine Xenotransplant Model of Triple Negative Breast Cancer. **2020**, 9,	2
527	Delineation of the Germline and Somatic Mutation Interaction Landscape in Triple-Negative and Non-Triple-Negative Breast Cancer. **2020**, 2020, 2641370	0
526	RNF181 modulates Hippo signaling and triple negative breast cancer progression. **2020**, 20, 291	3
525	Oncogenic Mutations in Tumorigenesis and Targeted Therapy in Breast Cancer. **2020**, 6, 116-125	9
524	Increased number of subclones in lung squamous cell carcinoma elicits overexpression of immune related genes. **2020**, 9, 659-669	2
523	Comprehensive Genomic Profile of Heterogeneous Long Follow-Up Triple-Negative Breast Cancer and Its Clinical Characteristics Shows DNA Repair Deficiency Has Better Prognostic. **2020**, 11,	3
522	Novel miRNA Targets and Therapies in the Triple-Negative Breast Cancer Microenvironment: An Emerging Hope for a Challenging Disease. **2020**, 21,	10
521	Triple-Negative Breast Cancer Comparison With Canine Mammary Tumors From Light Microscopy to Molecular Pathology. **2020**, 10, 563779	2
520	Multi-Omics Characterization of the 4T1 Murine Mammary Gland Tumor Model. **2020**, 10, 1195	24
519	Genome-wide chromosomal instability by cell-free DNA sequencing predicts survival in patients with metastatic breast cancer. **2020**, 53, 111-118	1

518	Effects of Cancer Stem Cells in Triple-Negative Breast Cancer and Brain Metastasis: Challenges and Solutions. **2020**, 12,	10
517	Genomic Profiling Comparison of Germline and Non- Carriers Reveals Amplification as a Risk Factor for Non- Carriers in Patients With Triple-Negative Breast Cancer. **2020**, 10, 583314	1
516	Honeybee venom and melittin suppress growth factor receptor activation in HER2-enriched and triple-negative breast cancer. **2020**, 4, 24	33
515	Subclonal reconstruction of tumors by using machine learning and population genetics. **2020**, 52, 898-907	24
514	FOXA1 Mutations Reveal Distinct Chromatin Profiles and Influence Therapeutic Response in Breast Cancer. **2020**, 38, 534-550.e9	19
513	Co-targeting of lysosome and mitophagy in cancer stem cells with chloroquine analogues and antibiotics. **2020**, 24, 11667-11679	7
512	Targeting homologous recombination (HR) repair mechanism for cancer treatment: discovery of new potential UCHL-3 inhibitors virtual screening, molecular dynamics and binding mode analysis. **2020**, 1-14	2
511	Discrete Adaptive Responses to MEK Inhibitor in Subpopulations of Triple-Negative Breast Cancer. **2020**, 18, 1685-1698	1
510	Chebulinic acid inhibits MDA-MB-231 breast cancer metastasis and promotes cell death through down regulation of SOD1 and induction of autophagy. **2020**, 44, 2553-2569	7
509	Non-epigenetic induction of HEXIM1 by DNMT1 inhibitors and functional relevance. **2020**, 10, 21015	1
508	Proteomic Resistance Biomarkers for PI3K Inhibitor in Triple Negative Breast Cancer Patient-Derived Xenograft Models. **2020**, 12,	4
507	Methodological Advancements for Investigating Intra-tumoral Heterogeneity in Breast Cancer at the Bench and Bedside. **2020**, 25, 289-304	1
506	PyClone-VI: scalable inference of clonal population structures using whole genome data. **2020**, 21, 571	13
505	Extended transcriptome analysis reveals genome-wide lncRNA-mediated epigenetic dysregulation in colorectal cancer. **2020**, 18, 3507-3517	1
504	Frequency and spectrum of PIK3CA somatic mutations in breast cancer. **2020**, 22, 45	55
503	Therapeutic Potential of Combining PARP Inhibitor and Immunotherapy in Solid Tumors. **2020**, 10, 570	56
502	Tumor membrane-based vaccine immunotherapy in combination with anti-CTLA-4 antibody confers protection against immune checkpoint resistant murine triple-negative breast cancer. **2020**, 16, 3184-3193	5
501	Computer-Aided Ligand Discovery for Estrogen Receptor Alpha. **2020**, 21,	14

500	Neoadjuvant Treatment for Triple Negative Breast Cancer: Recent Progresses and Challenges. **2020** , 12,	36
499	N083E (Alliance): long-term outcomes of patients treated in a pilot phase II study of docetaxel, carboplatin, trastuzumab, and lapatinib as adjuvant therapy for early-stage HER2-positive breast cancer. **2020**, 182, 613-622	
498	Invasive apocrine carcinoma of the breast: clinicopathologic features and comprehensive genomic profiling of 18 pure triple-negative apocrine carcinomas. **2020**, 33, 2473-2482	12
497	Clinical Development of PD-1/PD-L1 Inhibitors in Breast Cancer: Still a Long Way to Go. **2020**, 21, 59	6
496	NEK10 tyrosine phosphorylates p53 and controls its transcriptional activity. **2020**, 39, 5252-5266	7
495	Chemogenomic profiling of breast cancer patient-derived xenografts reveals targetable vulnerabilities for difficult-to-treat tumors. **2020**, 3, 310	11
494	Unraveling the Genomic-Epigenomic Interaction Landscape in Triple Negative and Non-Triple Negative Breast Cancer. **2020**, 12,	4
493	Combined p53- and PTEN-deficiency activates expression of mesenchyme homeobox 1 (MEOX1) required for growth of triple-negative breast cancer. **2020**, 295, 12188-12202	6
492	The novel camptothecin derivative, CPT211, induces cell cycle arrest and apoptosis in models of human breast cancer. **2020**, 128, 110309	6
491	Biology of the Triple-Negative Breast Cancer: Immunohistochemical, RNA, and DNA Features. **2020**, 15, 208-216	2
490	The INPP4B Tumor Suppressor Modulates EGFR Trafficking and Promotes Triple-Negative Breast Cancer. **2020**, 10, 1226-1239	12
489	Insights into the Role of Estrogen Receptor □in Triple-Negative Breast Cancer. **2020**, 12,	15
488	Plasma DNA as a "liquid biopsy" incompletely complements tumor biopsy for identification of mutations in a case series of four patients with oligometastatic breast cancer. **2020**, 182, 665-677	1
487	Targeting MYCN-expressing triple-negative breast cancer with BET and MEK inhibitors. **2020**, 12,	22
486	Regulation of Hippo signaling and triple negative breast cancer progression by an ubiquitin ligase RNF187. **2020**, 9, 36	11
485	Positive progress: current and evolving role of immune checkpoint inhibitors in metastatic triple-negative breast cancer. **2020**, 12, 1758835920909091	7
484	Therapeutic Delivery of Polymeric Tadpole Nanostructures with High Selectivity to Triple Negative Breast Cancer Cells. **2020**, 21, 4457-4468	5
483	Breast Cancer: A Molecularly Heterogenous Disease Needing Subtype-Specific Treatments. **2020**, 8,	28

482	Tumor Microenvironment. **2020**,	6
481	Integrative analysis of genomic amplification-dependent expression and loss-of-function screen identifies ASAP1 as a driver gene in triple-negative breast cancer progression. **2020**, 39, 4118-4131	7
480	Molecular Classification and Future Therapeutic Challenges of Triple-negative Breast Cancer. **2020**, 34, 1715-1727	8
479	Sterile, abscess-like cerebral lesion during trastuzumab therapy after HER2 status switch in a triple negative breast cancer patient: a case report and literature review. **2020**, 20, 615	1
478	Long non-coding RNA LINC-PINT attenuates paclitaxel resistance in triple-negative breast cancer cells via targeting the RNA-binding protein NONO. **2020**, 52, 801-809	8
477	Age-related mutational signature negatively associated with immune activity and survival outcome in triple-negative breast cancer. **2020**, 9, 1788252	11
476	Immune checkpoint inhibitors: Key trials and an emerging role in breast cancer. **2020**,	39
475	Growth pattern can be used as a new characteristic to predict malignancy in breast cancer. **2020**, 27, 445-455	0
474	Integrative Transcriptomic Analysis Reveals a Multiphasic Epithelial-Mesenchymal Spectrum in Cancer and Non-tumorigenic Cells. **2019**, 9, 1479	14
473	Therapeutic opportunities for PLK1 inhibitors: Spotlight on BRCA1-deficiency and triple negative breast cancers. **2020**, 821, 111693	7
472	Response of metastatic mouse invasive lobular carcinoma to mTOR inhibition is partly mediated by the adaptive immune system. **2020**, 9, 1724049	6
471	Genetic heterogeneity and clonal evolution during metastasis in breast cancer patient-derived tumor xenograft models. **2020**, 18, 323-331	9
470	Ret Receptor Has Distinct Alterations and Functions in Breast Cancer. **2020**, 25, 13-26	5
469	Integrated analysis of gene expression, alteration and clinical significance of carcinoembryonic antigen-related cell adhesion molecule 1 in cancer. **2020**, 10, 132	2
468	ARID1A determines luminal identity and therapeutic response in estrogen-receptor-positive breast cancer. **2020**, 52, 198-207	62
467	Germline Variants in Driver Genes of Breast Cancer and Their Association with Familial and Early-Onset Breast Cancer Risk in a Chilean Population. **2020**, 12,	0
466	Ras-Mediated Activation of NF-B and DNA Damage Response in Carcinogenesis. **2020**, 38, 185-208	8
465	TGF and EGF signaling orchestrates the AP-1- and p63 transcriptional regulation of breast cancer invasiveness. **2020**, 39, 4436-4449	18

464	The Landscape of Targeted Therapies in TNBC. **2020**, 12,	92
463	Anti-cancer Activity of Extract in Triple Negative Breast Cancer via Inhibition of AKT, NF-B, and STAT3 Signaling Pathways. **2020**, 10, 491	11
462	Systematic Review and Meta-analysis of the Malignant Ultrasound Features of Triple-Negative Breast Cancer. **2020**, 39, 2013-2025	4
461	Co-targeting EGFR and mTOR with gefitinib and everolimus in triple-negative breast cancer cells. **2020**, 10, 6367	21
460	Sporadic activation of an oxidative stress-dependent NRF2-p53 signaling network in breast epithelial spheroids and premalignancies. **2020**, 13,	12
459	Response of Breast Cancer Cells to PARP Inhibitors Is Independent of BRCA Status. **2020**, 9,	34
458	Expression pattern, regulation, and clinical significance of TOX in breast cancer. **2021**, 70, 349-363	4
457	Integrated analysis of single-cell RNA-seq and bulk RNA-seq unravels tumour heterogeneity plus M2-like tumour-associated macrophage infiltration and aggressiveness in TNBC. **2021**, 70, 189-202	29
456	Multi-color clonal tracking reveals intra-stage proliferative heterogeneity during mammary tumor progression. **2021**, 40, 12-27	6
455	Molecular Heterogeneity and Evolution in Breast Cancer. **2021**, 5, 79-94	5
454	Mutation profile differences in younger and older patients with advanced breast cancer using circulating tumor DNA (ctDNA). **2021**, 185, 639-646	1
453	Insulin-Induced Gene 2 Expression Is Associated with Breast Cancer Metastasis. **2021**, 191, 385-395	1
452	Anti-pyroptotic function of TGF-is suppressed by a synthetic dsRNA analogue in triple negative breast cancer cells. **2021**, 15, 1289-1307	3
451	Targeted metabolomics reveals dynamic portrayal of amino acids and derivatives in triple-negative breast cancer cells and culture media. **2021**, 17, 142-152	2
450	Research advances and new challenges in overcoming triple-negative breast cancer. **2021**, 4, 517-542	3
449	Tumor Profiling at the Service of Cancer Therapy. **2020**, 10, 595613	2
448	Defining Breast Cancer. **2021**, 1-31	
447	Long Non-coding RNA BTG3-7:1 and JUND Co-regulate to Promote Triple-Negative Breast Cancer Progress. **2020**, 7, 605623	

446	3D Functional Genomics Screens Identify CREBBP as a Targetable Driver in Aggressive Triple-Negative Breast Cancer. **2021**, 81, 847-859	2
445	Antecedents and consequences of panic buying: The case of COVID-19.	33
444	Adjuvant and Neoadjuvant Treatment of Triple-Negative Breast Cancer With Chemotherapy. **2021**, 27, 41-49	5
443	Graphene nanoribbon-based supramolecular ensembles with dual-receptor targeting function for targeted photothermal tumor therapy. **2021**, 12, 11089-11097	4
442	p66ShcA potentiates the cytotoxic response of triple-negative breast cancers to PARP inhibitors. **2021**, 6,	
441	Bone marrow mesenchymal stem cell-mediated ultrasmall gold nanoclusters and hNIS gene synergize radiotherapy for breast cancer. **2021**, 9, 2866-2876	5
440	MicroRNA-205-5p targets the HOXD9-Snail1 axis to inhibit triple negative breast cancer cell proliferation and chemoresistance. **2021**, 13, 3945-3956	4
439	Liquid Biopsy in Breast Cancer: Circulating Tumor Cells and Circulating Tumor DNA. **2021**, 1187, 337-361	1
438	Small molecules targeting misfolded mutants of p53 as a rescue strategy to improve glioblastoma chemotherapy. **2021**, 749-771	
437	The advance of adjuvant treatment for triple-negative breast cancer. **2021**,	1
436	Rational design of aqueous conjugated polymer nanoparticles as potential theranostic agents of breast cancer.	4
435	A High-Dimensional Window into the Micro-Environment of Triple Negative Breast Cancer. **2021**, 13,	8
434	Therapeutic Advances in Oncology. **2021**, 22,	5
433	Role of PRPS2 as a prognostic and therapeutic target in osteosarcoma. **2021**, 74, 321-326	0
432	Advanced Approaches to Breast Cancer Classification and Diagnosis. **2020**, 11, 632079	15
431	CIBERSORT analysis of TCGA and METABRIC identifies subgroups with better outcomes in triple negative breast cancer. **2021**, 11, 4691	13
430	Extracts of var. (Odash.) Kudo Leaves Have Antitumor Effects on Breast Cancer Cells by Suppressing YAP Activity. **2021**, 2021, 5619761	1
429	Molecular mechanics and dynamic simulations of well-known Kabuki syndrome-associated KDM6A variants reveal putative mechanisms of dysfunction. **2021**, 16, 66	3

428	Epigenetic Alterations in Triple-Negative Breast Cancer-The Critical Role of Extracellular Matrix. **2021**, 13,	11
427	Targeting LDHC dysregulates the cell cycle and improves sensitivity to cisplatin and olaparib.	
426	Response to Vemurafenib in Metastatic Triple-Negative Breast Cancer Harbouring a BRAF V600E Mutation: A Case Report and Electronically Captured Patient-Reported Outcome. **2021**, 14, 616-621	1
425	Genetic and Non-Genetic Mechanisms Underlying Cancer Evolution. **2021**, 13,	7
424	Faciogenital Dysplasia 5 supports cancer stem cell traits in basal-like breast cancer by enhancing EGFR stability. **2021**, 13,	2
423	Precision Oncology, Signaling and Anticancer Agents in Cancer Therapeutics. **2021**,	1
422	Tumor mutational burden as a predictor of immunotherapy response in breast cancer. **2021**, 12, 394-400	13
421	Identification of Hub Genes and Pathways of Triple Negative Breast Cancer by Expression Profiles Analysis. **2021**, 13, 2095-2104	2
420	Cancer Cell Intrinsic and Immunologic Phenotypes Determine Clinical Outcomes in Basal-like Breast Cancer. **2021**, 27, 3079-3093	5
419	Single-Cell Transcriptome Analysis Uncovers Intratumoral Heterogeneity and Underlying Mechanisms for Drug Resistance in Hepatobiliary Tumor Organoids. **2021**, 8, e2003897	5
418	New Insight into Triple-Negative Breast Cancer Therapy: The Potential Roles of Endoplasmic Reticulum Stress and Autophagy Mechanisms. **2021**, 21, 679-691	3
417	Clinical and genomic assessment of PD-L1 SP142 expression in triple-negative breast cancer. **2021**, 188, 165-178	6
416	6-lncRNA Assessment Model for Monitoring and Prognosis of HER2-Positive Breast Cancer: Based on Transcriptome Data. **2021**, 27, 609083	2
415	DNA damage response inhibitors: An avenue for TNBC treatment. **2021**, 1875, 188521	5
414	Exosomal microRNAs: Pleiotropic Impacts on Breast Cancer Metastasis and Their Clinical Perspectives. **2021**, 10,	1
413	Breast cancer as an example of tumour heterogeneity and tumour cell plasticity during malignant progression. **2021**, 125, 164-175	25
412	In silico screening using bulk and single-cell RNA-seq data identifies RIMS2 as a prognostic marker in basal-like breast cancer: A retrospective study. **2021**, 100, e25414	2
411	Understanding Molecular Process and Chemotherapeutics for the Management of Breast Cancer. **2021**, 15, 69-84	1

410	Unique evolutionary trajectories of breast cancers with distinct genomic and spatial heterogeneity. **2021**, 11, 10571		
409	Adamantyl Isothiocyanates as Mutant p53 Rescuing Agents and Their Structure-Activity Relationships. **2021**, 64, 6621-6633		4
408	Triple-negative breast cancer: A run-through of features, classification and current therapies. **2021**, 22, 512		10
407	Therapeutic Strategies for Metastatic Triple-Negative Breast Cancers: From Negative to Positive. **2021**, 14,		4
406	Phenotypic Heterogeneity of Triple-Negative Breast Cancer Mediated by Epithelial-Mesenchymal Plasticity. **2021**, 13,		8
405	In vivo genome-wide CRISPR screen reveals breast cancer vulnerabilities and synergistic mTOR/Hippo targeted combination therapy. **2021**, 12, 3055		9
404	Metastasis is altered through multiple processes regulated by the E2F1 transcription factor. **2021**, 11, 9502		2
403	Genomic features of rapid versus late relapse in triple negative breast cancer. **2021**, 21, 568		2
402	HDAC6 inhibitors sensitize non-mesenchymal triple-negative breast cancer cells to cysteine deprivation. **2021**, 11, 10956		2
401	RASAL2 Confers Collateral MEK/EGFR Dependency in Chemoresistant Triple-Negative Breast Cancer. **2021**, 27, 4883-4897		5
400	The impact of mutational processes on structural genomic plasticity in cancer cells.		2
399	Targeting of lactate dehydrogenase C dysregulates the cell cycle and sensitizes breast cancer cells to DNA damage response targeted therapy. **2021**,		2
398	Clinical utility of whole-genome sequencing in precision oncology. **2021**,		7
397	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. *Nature*, **2021**, 595, 585-590	50.4	10
396	The Natural Products and Extracts: Anti-Triple-Negative Breast Cancer in Vitro. **2021**, 18, e2001047		5
395	Potentiating Therapeutic Effects of Epidermal Growth Factor Receptor Inhibition in Triple-Negative Breast Cancer. **2021**, 14,		7
394	Inter-Metastatic Heterogeneity of Tumor Marker Expression and Microenvironment Architecture in a Preclinical Cancer Model. **2021**, 22,		3
393	Specific cell differentiation in breast cancer: a basis for histological classification. **2021**,		1

392	miRNome and Functional Network Analysis of PGRMC1 Regulated miRNA Target Genes Identify Pathways and Biological Functions Associated With Triple Negative Breast Cancer. **2021**, 11, 710337	1
391	Uncovering the Subtype-Specific Molecular Characteristics of Breast Cancer by Multiomics Analysis of Prognosis-Associated Genes, Driver Genes, Signaling Pathways, and Immune Activity. **2021**, 9, 689028	1
390	Akt Isoforms: A Family Affair in Breast Cancer. **2021**, 13,	8
389	Precision Medicine and Triple-Negative Breast Cancer: Current Landscape and Future Directions. **2021**, 13,	7
388	Multi-Gene Testing Overview with a Clinical Perspective in Metastatic Triple-Negative Breast Cancer. **2021**, 22,	2
387	Sociodemographic Factors Associated With Rapid Relapse in Triple-Negative Breast Cancer: A Multi-Institution Study. **2021**, 19, 797-804	3
386	Acquired Resistance to Third-Generation EGFR Tyrosine Kinase Inhibitors in Patients With De Novo EGFR-Mutant NSCLC. **2021**, 16, 1859-1871	2
385	Comprehensive characterization of distinct genetic alterations in metastatic breast cancer across various metastatic sites. **2021**, 7, 93	3
384	Performance Comparisons of AlexNet and GoogLeNet in Cell Growth Inhibition IC50 Prediction. **2021**, 22,	4
383	Nanotechnology-based siRNA delivery strategies for treatment of triple negative breast cancer. **2021**, 605, 120835	19
382	Intra-Tumor Heterogeneity Revealed by Mass Spectrometry Imaging Is Associated with the Prognosis of Breast Cancer. **2021**, 13,	4
381	Survival-Based Biomarker Module Identification Associated with Oral Squamous Cell Carcinoma (OSCC). **2021**, 10,	1
380	Patient-derived triple negative breast cancer organoids provide robust model systems that recapitulate tumor intrinsic characteristics.	1
379	Recurrence biomarkers of triple negative breast cancer treated with neoadjuvant chemotherapy and anti-EGFR antibodies. **2021**, 7, 124	1
378	Triple negative breast cancer and non-small cell lung cancer: Clinical challenges and nano-formulation approaches. **2021**, 337, 27-58	11
377	Targeting cytokinesis bridge proteins to kill high-CIN type tumors. **2021**, 1, 752-752	1
376	Metabolic Flexibility Is a Determinant of Breast Cancer Heterogeneity and Progression. **2021**, 13,	4
375	Single-Cell RNA-Seq Reveals Heterogeneous lncRNA Expression in Xenografted Triple-Negative Breast Cancer Cells. **2021**, 10,	1

374	Molecular Classification of Triple Negative Breast Cancer and the Emergence of Targeted Therapies. **2021**, 21, 509-520	1
373	Griffin: Framework for clinical cancer subtyping from nucleosome profiling of cell-free DNA.	0
372	Progress and challenges of immunotherapy in triple-negative breast cancer. **2021**, 1876, 188593	14
371	Circular RNA: A potential diagnostic, prognostic, and therapeutic biomarker for human triple-negative breast cancer. **2021**, 26, 63-80	7
370	Vitamin C sensitizes triple negative breast cancer to PI3K inhibition therapy. **2021**, 11, 3552-3564	2
369	Prune-1 drives polarization of tumor-associated macrophages (TAMs) within the lung metastatic niche in triple-negative breast cancer. **2021**, 24, 101938	4
368	Clinical genomic profiling to identify actionable alterations for very early relapsed triple-negative breast cancer patients in the Chinese population. **2021**, 53, 1358-1369	4
367	Genetic Susceptibility to Triple-Negative Breast Cancers.	1
366	An Integrated Human Mammary Epithelial Cell Culture System for Studying Carcinogenesis and Aging. **2013**, 323-361	16
365	Future Paradigm of Breast Cancer Resistance and Treatment. **2017**, 155-178	2
364	Metronomic Chemotherapy in Breast Cancers. **2014**, 93-110	1
363	Molecular Profiling of Breast Cancer in Clinical Trials: A Perspective. **2020**, 313-332	4
362	Somatic mutations of triple-negative breast cancer: a comparison between Black and White women. **2020**, 182, 503-509	5
361	Targeted therapy and drug resistance in triple-negative breast cancer: the EGFR axis. **2020**, 48, 657-665	26
360	Computational modelling in single-cell cancer genomics: methods and future directions. **2020**, 17, 061001	1
359	A survey of genes modulated by host cell infection. **2020**, 6,	8
358	Single cell fitness landscapes induced by genetic and pharmacologic perturbations in cancer.	3
357	Age Influences on the Molecular Presentation of Tumours.	2

356	Model-based tumor subclonal reconstruction.	4
355	Machine learning predicts rapid relapse of triple negative breast cancer.	1
354	Dissociation of solid tumour tissues with cold active protease for single-cell RNA-seq minimizes conserved collagenase-associated stress responses.	2
353	Death-associated protein kinase 1 promotes growth of p53-mutant cancers. **2015**, 125, 2707-20	34
352	MEL-18 loss mediates estrogen receptor-□downregulation and hormone independence. **2015**, 125, 1801-14	21
351	Integrated RNA and DNA sequencing reveals early drivers of metastatic breast cancer. **2018**, 128, 1371-1383	83
350	Spatially distinct tumor immune microenvironments stratify triple-negative breast cancers. **2019**, 129, 1785-1800	125
349	Eya3 promotes breast tumor-associated immune suppression via threonine phosphatase-mediated PD-L1 upregulation. **2018**, 128, 2535-2550	16
348	Cancer quasispecies and stem-like adaptive aneuploidy. **2013**, 2, 268	2
347	ReactomeFIViz: the Reactome FI Cytoscape app for pathway and network-based data analysis. **2014**, 3, 146	118
346	High-resolution mutational profiling suggests the genetic validity of glioblastoma patient-derived pre-clinical models. **2013**, 8, e56185	21
345	The relative timing of mutations in a breast cancer genome. **2013**, 8, e64991	17
344	Genome aberrations in canine mammary carcinomas and their detection in cell-free plasma DNA. **2013**, 8, e75485	39
343	RB1 status in triple negative breast cancer cells dictates response to radiation treatment and selective therapeutic drugs. **2013**, 8, e78641	52
342	Evolution of pre-existing versus acquired resistance to platinum drugs and PARP inhibitors in BRCA-associated cancers. **2014**, 9, e105724	10
341	Unsupervised deconvolution of dynamic imaging reveals intratumor vascular heterogeneity and repopulation dynamics. **2014**, 9, e112143	9
340	Folate receptor-□(FOLR1) expression and function in triple negative tumors. **2015**, 10, e0122209	71
339	Transcriptome analysis of Wnt3a-treated triple-negative breast cancer cells. **2015**, 10, e0122333	43

338	Evaluation of two highly-multiplexed custom panels for massively parallel semiconductor sequencing on paraffin DNA. **2015**, 10, e0128818	13
337	Analysis of Paired Primary-Metastatic Hormone-Receptor Positive Breast Tumors (HRPBC) Uncovers Potential Novel Drivers of Hormonal Resistance. **2016**, 11, e0155840	16
336	Important Role of FTO in the Survival of Rare Panresistant Triple-Negative Inflammatory Breast Cancer Cells Facing a Severe Metabolic Challenge. **2016**, 11, e0159072	54
335	Mutant PIK3CA Induces EMT in a Cell Type Specific Manner. **2016**, 11, e0167064	3
334	Identification of Post-Transcriptional Modulators of Breast Cancer Transcription Factor Activity Using MINDy. **2016**, 11, e0168770	3
333	Prediction of adjuvant chemotherapy response in triple negative breast cancer with discovery and targeted proteomics. **2017**, 12, e0178296	16
332	Novel putative drivers revealed by targeted exome sequencing of advanced solid tumors. **2018**, 13, e0194790	2
331	The mutational landscape of the SCAN-B real-world primary breast cancer transcriptome. **2020**, 12, e12118	11
330	Review of Triple Negative Breast Cancer and the Impact of Inducible Nitric Oxide Synthase on Tumor Biology and Patient Outcomes. **2016**, 21, 333-351	27
329	Robust genomic copy number predictor of pan cancer metastasis. **2018**, 9, 66-77	5
328	Tyrosine phosphorylation regulates ER□ubiquitination, protein turnover, and inhibition of breast cancer. **2016**, 7, 42585-42597	12
327	Targeting mTOR pathway inhibits tumor growth in different molecular subtypes of triple-negative breast cancers. **2016**, 7, 48206-48219	25
326	Triple negative breast cancer: shedding light onto the role of pi3k/akt/mtor pathway. **2016**, 7, 60712-60722	79
325	Inhibition of cyclin dependent kinase 9 by dinaciclib suppresses cyclin B1 expression and tumor growth in triple negative breast cancer. **2016**, 7, 56864-56875	38
324	Differentially expressed miRNAs in triple negative breast cancer between African-American and non-Hispanic white women. **2016**, 7, 79274-79291	28
323	Systematic screening of isogenic cancer cells identifies DUSP6 as context-specific synthetic lethal target in melanoma. **2017**, 8, 23760-23774	14
322	High Myc expression and transcription activity underlies intra-tumoral heterogeneity in triple-negative breast cancer. **2017**, 8, 28101-28115	13
321	Increased risk of brain metastases in women with breast cancer and p16 expression in metastatic lymph-nodes. **2017**, 8, 37332-37341	4

320	Concurrent somatic mutations in driver genes were significantly correlated with lymph node metastasis and pathological types in solid tumors. **2017**, 8, 68746-68757	6
319	The prognostic significance of combined androgen receptor, E-Cadherin, Ki67 and CK5/6 expression in patients with triple negative breast cancer. **2017**, 8, 76974-76986	24
318	Combined targeting of Raf and Mek synergistically inhibits tumorigenesis in triple negative breast cancer model systems. **2017**, 8, 80804-80819	17
317	Targeted therapy for metastatic triple negative breast cancer: The next frontier in precision oncology. **2017**, 8, 106167-106168	19
316	Mitochondrial dysfunction activates lysosomal-dependent mitophagy selectively in cancer cells. **2018**, 9, 995-1011	23
315	Therapeutic potential of ERK5 targeting in triple negative breast cancer. **2014**, 5, 11308-18	35
314	Molecular and clinical features of the signature gene expression profile in early-stage breast cancer. **2018**, 9, 14193-14206	7
313	Mutational profiles in triple-negative breast cancer defined by ultradeep multigene sequencing show high rates of PI3K pathway alterations and clinically relevant entity subgroup specific differences. **2014**, 5, 9952-65	52
312	Prevalence of MDM2 amplification and coalterations in 523 advanced cancer patients in the MD Anderson phase 1 clinic. **2018**, 9, 33232-33243	15
311	PI3K inhibition enhances the anti-tumor effect of eribulin in triple negative breast cancer. **2019**, 10, 3667-3680	4
310	Differential gene expression analysis of HNSCC tumors deciphered tobacco dependent and independent molecular signatures. **2019**, 10, 6168-6183	11
309	BCATc modulates crosstalk between the PI3K/Akt and the Ras/ERK pathway regulating proliferation in triple negative breast cancer. **2020**, 11, 1971-1987	2
308	Identification of a new class of natural product MDM2 inhibitor: In vitro and in vivo anti-breast cancer activities and target validation. **2015**, 6, 2623-40	48
307	Genomic differences between pure ductal carcinoma in situ and synchronous ductal carcinoma in situ with invasive breast cancer. **2015**, 6, 7597-607	53
306	Antitumor activity of the novel multi-kinase inhibitor EC-70124 in triple negative breast cancer. **2015**, 6, 27923-37	19
305	Global phosphotyrosine survey in triple-negative breast cancer reveals activation of multiple tyrosine kinase signaling pathways. **2015**, 6, 29143-60	34
304	Auranofin is a potent suppressor of osteosarcoma metastasis. **2016**, 7, 831-44	28
303	The combinatorial activation of the PI3K and Ras/MAPK pathways is sufficient for aggressive tumor formation, while individual pathway activation supports cell persistence. **2015**, 6, 35231-46	16

302	Two classes of intrahepatic cholangiocarcinoma defined by relative abundance of mutations and copy number alterations. **2016**, 7, 23825-36	8
301	CD74 and intratumoral immune response in breast cancer. **2017**, 8, 12664-12674	25
300	Neoadjuvant tamoxifen synchronizes ER□binding and gene expression profiles related to outcome and proliferation. **2016**, 7, 33901-18	11
299	Cellular plasticity and metastasis in breast cancer: a pre- and post-malignant problem. **2019**, 5,	5
298	Lectin-like transcript 1 as a natural killer cell-mediated immunotherapeutic target for triple negative breast cancer and prostate cancer. **2019**, 2019,	1
297	Next-generation sequencing and its clinical application. **2019**, 16, 4-10	23
296	Therapeutic targeting of cancers with loss of PTEN function. **2014**, 15, 65-79	154
295	BRCA Mutational Status is a Promising Predictive Biomarker for Platinum- based Chemotherapy in Triple-Negative Breast Cancer. **2020**, 21, 962-973	6
294	Targeting Different Pathways Using Novel Combination Therapy in Triple Negative Breast Cancer. **2020**, 20, 586-602	39
293	Prognostic Evaluation of Epidermal Growth Factor Receptor (EGFR) Genotype and Phenotype Parameters in Triple-negative Breast Cancers. **2017**, 14, 181-195	19
292	Histone Deacetylases as New Therapeutic Targets in Triple-negative Breast Cancer: Progress and Promises. **2017**, 14, 299-313	26
291	BRAF, KRAS and PIK3CA Mutation and Sensitivity to Trastuzumab in Breast Cancer Cell Line Model. **2017**, 18, 2209-2213	11
290	Mediator kinase module and human tumorigenesis. **2015**, 50, 393-426	73
289	Comparison of Circulating Tumour DNA and Extracellular Vesicle DNA by Low-Pass Whole-Genome Sequencing Reveals Molecular Drivers of Disease in a Breast Cancer Patient. **2020**, 9,	5
288	Revealing the Complexity of Breast Cancer by Next Generation Sequencing. **2015**, 7, 2183-200	23
287	Three-microRNA expression signature predicts survival in triple-negative breast cancer. **2020**, 19, 301-308	12
286	Bioinformatics analysis of the expression of HOXC13 and its role in the prognosis of breast cancer. **2020**, 19, 899-907	9
285	Expression and clinical significance of MAPK and EGFR in triple-negative breast cancer. **2020**, 19, 1842-1848	15

284	ZW10 interacting kinetochore protein may serve as a prognostic biomarker for human breast cancer: An integrated bioinformatics analysis. **2020**, 19, 2163-2174	9
283	Gene expression profiling identified TP53PIK3CA as a potential biomarker for patients with triple-negative breast cancer treated with immune checkpoint inhibitors. **2020**, 19, 2817-2824	6
282	Knockdown of SERPINE1 reverses resistance of triple-negative breast cancer to paclitaxel via suppression of VEGFA. **2020**, 44, 1875-1884	10
281	Current Issues and Clinical Evidence in Tumor-Infiltrating Lymphocytes in Breast Cancer. **2015**, 49, 355-63	29
280	The Role of Genomic Profiling in Advanced Breast Cancer: The Two Faces of Janus. **2016**, 8, 1-7	2
279	Using Systems Biology to Understand Cancer as an Evolutionary Process. **2014**, 2, 1-8	2
278	Preventive and Risk Reduction Strategies for Women at High Risk of Developing Breast Cancer: a Review. **2016**, 17, 895-904	5
277	Data Mining for Identification of Molecular Targets in Ovarian Cancer. **2016**, 17, 1691-9	4
276	Novel insights into breast cancer copy number genetic heterogeneity revealed by single-cell genome sequencing. **2020**, 9,	20
275	Molecular Targets and Promising Therapeutics of Triple-Negative Breast Cancer. **2021**, 14,	5
274	Centrosome Aberrations as Drivers of Chromosomal Instability in Breast Cancer. **2021**, 162,	0
273	Clonal populations of a human TNBC model display significant functional heterogeneity and divergent growth dynamics in distinct contexts. **2021**,	2
272	MYTH: An algorithm to score intratumour heterogeneity based on alterations of DNA methylation profiles. **2021**, 11, e611	0
271	Comprehensive Analysis of the Implication of PGRMC1 in Triple-Negative Breast Cancer. **2021**, 9, 714030	1
270	Identifying High-Risk Triple-Negative Breast Cancer Patients by Molecular Subtyping.. **2021**, 16, 637-647	2
269	Neoadjuvant in situ immunomodulation enhances systemic antitumor immunity against highly metastatic tumors. **2021**,	2
268	CallSim: Evaluation of Base Calls Using Sequencing Simulation. **2012**, 2012, 371718	
267	Index. **2013**, 112-113	

266	Translating genomic research into clinical practice: promise and pitfalls. **2013**, 15-23	4
265	Are mutations in K-RAS, BRAF and PIK3CA genes critical for response to adjuvant trastuzumab treatment in patients with HER-2 positive breast cancer?. **2014**, 3, 3	2
264	The global cancer genomics consortium's third annual symposium: from oncogenomics to cancer care. **2014**, 5, 64-70	1
263	Next Generation Sequencing in Cancer Research and Clinical Application. **2014**, 71-94	1
262	Genomic Applications in Epithelial Ovarian Malignancies. **2015**, 489-502	
261	Genomic Applications in Breast Carcinoma. **2015**, 359-382	
260	Chromatin and Epigenetic Determinants of Resistance to Aromatase Inhibitors. **2015**, 145-168	
259	Next-Generation Sequencing Applications in Head and Neck Oncology. **2015**, 401-422	
258	Tumors of the breast. 426-446	
257	Gene Expression Analysis: Current Methods. **2016**, 107-136	0
256	Genomic Markers in ER-Negative Breast Cancer. **2016**, 283-298	
255	Next-Generation Sequencing Based Testing for Breast Cancer. **2016**, 299-328	
254	Biology and Genetics of Breast Cancer. **2016**, 145-160	1
253	Gene Expression Analysis: Applications. **2016**, 137-149	
252	Tree inference for single-cell data.	
251	A Key Cytoskeletal Regulator of Ubiquitination Amplifies TGFβ Signaling During Mouse Developmental Vascular Patterning.	
250	Genomic Analysis and In Vivo Functional Validation of Brain Somatic Mutations Leading to Focal Cortical Malformations. **2017**, 299-327	
249	Molecular Classification of Breast Cancer. **2017**, 1-22	

248	ConsensusDriver improves upon individual algorithms for predicting driver alterations in different cancer types and individual patients □a toolbox for precision oncology.	0
247	Comprehensive statistical inference of the clonal structure of cancer from multiple biopsies.	
246	Fibroblasts from metastatic sites induce broad-spectrum drug desensitization via modulation of mitochondrial priming.	
245	The prognostic effects of somatic mutations in ER-positive breast cancer.	
244	Diagnosis and Preparing Patients for Their Oncology Consultations. **2018**, 125-147	
243	COMPARISON OF CLINICO-PATHOLOGICAL FEATURES AND PROGNOSIS OF TRIPLE-NEGATIVE AND NON-TRIPLE-NEGATIVE FEMALE BREAST CANCER PATIENTS. **2018**, 7, 3412-3418	
242	Molecular features of premenopausal breast cancers in Latin American women: pilot results from the PRECAMA study.	
241	Novel Approaches to Immunotherapy in Triple Negative Breast Cancer. **2018**, In Press,	1
240	GeTallele: a method for integrative analysis and visualization of DNA and RNA allele frequencies.	1
239	NEK10 tyrosine phosphorylates p53 and controls its transcriptional activity.	
238	Biology and Genetics of Breast Cancer. **2019**, 125-142	
237	Tumor Evolution Decoder (TED): Unveiling Tumor Evolution Based on Mutation Profiles of Subclones or Single Cells.	1
236	Sporadic activation of an oxidative stress-dependent NRF2□p53 signaling network in breast epithelial spheroids and premalignancies.	2
235	Metastasis is altered through multiple processes regulated by the E2F1 transcription factor.	
234	A Comprehensive Survey of Genomic Mutations in Breast Cancer Reveals Recurrent Neoantigens as Potential Therapeutic Targets.	
233	A tyrosine kinase protein interaction map reveals targetable EGFR network oncogenesis in lung cancer.	
232	Ancestry Influences on the Molecular Presentation of Tumours.	
231	Current and Emerging Molecular Therapies for Head and Neck Squamous Cell Carcinoma. **2021**, 13,	4

230	Molecular-Genetic Portrait of Breast Cancer with Triple Negative Phenotype. **2021**, 13,	0
229	Retrospective analysis of The Two Sister Study using haplotype-based association testing to identify loci associated with early-onset breast cancer.	
228	A Mechanistic Investigation on the Anticancer Properties of SYA013, a Homopiperazine Analogue of Haloperidol with Activity against Triple Negative Breast Cancer Cells. **2020**, 5, 32907-32918	1
227	Dissecting the heterogeneity and tumorigenesis of BRCA1 deficient mammary tumors via single cell RNA sequencing. **2021**, 11, 9967-9987	1
226	A personalized medicine approach to drug repurposing for the treatment of breast cancer molecular subtypes. **2020**, 191-211	
225	The Mutational Landscape of the SCAN-B Real-World Primary Breast Cancer Transcriptome.	0
224	The Immune Landscape in Women Cancers. **2020**, 180, 215-249	1
223	Histo- and clinico-pathological analysis of a large series of triple-negative breast cancer in a single center in China: Evidences on necessity of histological subtyping and grading. **2020**, 32, 580-595	2
222	Local, multimodal intralesional therapy renders distant brain metastases susceptible to PD-L1 blockade in a preclinical model of triple-negative breast cancer. **2021**, 11, 21992	0
221	Multi-omics analysis identifies therapeutic vulnerabilities in triple-negative breast cancer subtypes. **2021**, 12, 6276	10
220	Multiplexed immunofluorescence identifies high stromal CD68PD-L1 macrophages as a predictor of improved survival in triple negative breast cancer. **2021**, 11, 21608	3
219	PyClone-VI: Scalable inference of clonal population structures using whole genome data.	
218	Whole-genome analysis of Nigerian patients with breast cancer reveals ethnic-driven somatic evolution and distinct genomic subtypes.	
217	Mutations in TP53 and other heterogeneous genes help to distinguish metastases from new primary malignancies.	
216	Mutant p53 protein expression and antioxidant status deficiency in breast cancer. **2014**, 13, 691-708	4
215	Autophagy is decreased in triple-negative breast carcinoma involving likely the MUC1-EGFR-NEU1 signalling pathway. **2015**, 8, 4344-55	7
214	A perspective on anti-EGFR therapies targeting triple-negative breast cancer. **2016**, 6, 1609-23	115
213	Disease evolution and heterogeneity in bilateral breast cancer. **2016**, 6, 2611-2630	4

212	The fate of BRCA1-related germline mutations in triple-negative breast tumors. **2017**, 7, 98-114	4
211	The future of genome-based medicine. **2013**, 456-8	
210	Leukotriene Receptor Antagonists Inhibit Mitogenic Activity in Triple Negative Breast Cancer Cells. **2018**, 19, 833-837	0
209	PI3K inhibition enhances the anti-tumor effect of eribulin in triple negative breast cancer. **2019**, 10, 3667-3680	4
208	Principles of digital PCR and its applications in current obstetrical and gynecological diseases. **2019**, 11, 7209-7222	6
207	Birinapant (TL32711) Improves Responses to GEM/AZD7762 Combination Therapy in Triple-negative Breast Cancer Cell Lines. **2016**, 36, 2649-57	4
206	PIK3CA mutations and downstream effector p-mTOR expression: implication for prognostic factors and therapeutic targets in triple negative breast cancer. **2017**, 10, 7682-7691	3
205	Safety in multi-assembly via paths appearing in all path covers of a DAG. **2021**, PP,	1
204	Whole-genome analysis of Nigerian patients with breast cancer reveals ethnic-driven somatic evolution and distinct genomic subtypes. **2021**, 12, 6946	1
203	RDAClone: Deciphering Tumor Heterozygosity through Single-Cell Genomics Data Analysis with Robust Deep Autoencoder.. **2021**, 12,	0
202	Reconstructing mutational lineages in breast cancer by multi-patient-targeted single cell DNA sequencing.	1
201	Association of 17q22 Amplicon Via Cell-Free DNA With Platinum Chemotherapy Response in Metastatic Triple-Negative Breast Cancer. **2021**, 5,	0
200	An adaptive method of defining negative mutation status for multi-sample comparison using next-generation sequencing. **2021**, 14, 32	
199	Research Progress of Mutant p53 as a Potential Therapeutic Target for Breast Cancer. **2021**, 11, 5455-5460	
198	MAPK4 promotes triple negative breast cancer growth and reduces tumor sensitivity to PI3K blockade.. **2022**, 13, 245	2
197	Biomarkers in Breast Carcinomas. **2022**, 309-333	
196	Age influences on the molecular presentation of tumours.. **2022**, 13, 208	1
195	The role of mediator subunit 12 in tumorigenesis and cancer therapeutics.. **2022**, 23, 74	0

194	The impact of young age at diagnosis (age . **2021**, 61, 77-83	5
193	Tumour genotypes account for survival differences in right- and left-sided colon cancers.. **2022**,	3
192	Copy number alterations analysis of primary tumor tissue and circulating tumor cells from patients with early-stage triple negative breast cancer.. **2022**, 12, 1470	0
191	In vivo genome-editing screen identifies tumor suppressor genes that cooperate with Trp53 loss during mammary tumorigenesis.. **2022**,	1
190	Retinoblastoma protein regulates carcinogen susceptibility at heterochromatic cancer driver loci.. **2022**, 5,	0
189	Pathogenesis of Triple-Negative Breast Cancer.. **2022**, 17, 181-204	10
188	A Prognostic Model for Breast Cancer Based on Cancer Incidence-Related DNA Methylation Pattern.. **2021**, 12, 814480	
187	Immunogenomic Landscape in Breast Cancer Reveals Immunotherapeutically Relevant Gene Signatures.. **2022**, 13, 805184	0
186	HSP90 inhibitors induce GPNMB cell-surface expression by modulating lysosomal positioning and sensitize breast cancer cells to glembatumumab vedotin.. **2022**,	1
185	Metformin Bicarbonate-Mediated Efficient RNAi for Precise Targeting of Deficiency in Colon and Rectal Cancers.. **2022**, 43, 101406-101406	2
184	Dynein axonemal heavy chain 9 M4374I variation may have an effect on imatinib mesylate resistance in CML. **2022**, 2,	
183	Integration of multiple lineage measurements from the same cell reconstructs parallel tumor evolution. **2022**, 2, 100096	2
182	Recent advances of transcriptomics and proteomics in triple-negative breast cancer prognosis assessment.. **2022**,	2
181	Comparison of mutational profiles between triple-negative and hormone receptor-positive/human epidermal growth factor receptor 2-negative breast cancers in T2N0-1M0 stage: Implications of TP53 and PIK3CA mutations in Korean early-stage breast cancers.. **2022**, 46, 100843	0
180	Deciphering the Increased Prevalence of TP53 Mutations in Metastatic Prostate Cancer.. **2022**, 21, 11769351221087046	0
179	Proteomic analysis of archival breast cancer clinical specimens identifies biological subtypes with distinct survival outcomes.. **2022**, 13, 896	4
178	Co-Expression and Combined Prognostic Value of CSPG4 and PDL1 in -Aberrant Triple-Negative Breast Cancer.. **2022**, 12, 804466	0
177	Patient-Derived Triple-Negative Breast Cancer Organoids Provide Robust Model Systems That Recapitulate Tumor Intrinsic Characteristics.. **2022**, 82, 1174-1192	3

176	SIEVE: joint inference of single-nucleotide variants and cell phylogeny from single-cell DNA sequencing data.	0
175	Integrative Analysis of Gene Expression and DNA Methylation Depicting the Impact of Obesity on Breast Cancer.. **2022**, 10, 818082	0
174	Selective Photo-Assisted Eradication of Triple-Negative Breast Cancer Cells through Aptamer Decoration of Doped Conjugated Polymer Nanoparticles.. **2022**, 14,	3
173	A Comprehensive Survey of Genomic Mutations in Breast Cancer Reveals Recurrent Neoantigens as Potential Therapeutic Targets.. **2022**, 12, 786438	0
172	Therapeutic progress and challenges for triple negative breast cancer: targeted therapy and immunotherapy.. **2022**, 3, 8	5
171	Exploring the Neoantigen burden in Breast Carcinoma Patients.	0
170	The role of microRNA-4723-5p regulated by c-myc in triple-negative breast cancer.. **2022**, 13, 9097-9105	1
169	Subclonal heterogeneity and evolution in breast cancer.. **2021**, 7, 155	3
168	Differential survival and therapy benefit of breast cancer patients are characterized by distinct epithelial and immune cell microenvironments.. **2021**,	0
167	Discordance of PIK3CA and TP53 mutations between breast cancer brain metastases and matched primary tumors. **2021**, 11, 23548	1
166	Somatic Mutational Profile of High-Grade Serous Ovarian Carcinoma and Triple-Negative Breast Carcinoma in Young and Elderly Patients: Similarities and Divergences.. **2021**, 10,	0
165	Challenges and Gaps in Clinical Trial Genomic Data Management.. **2022**, 6, e2100193	
164	Panel Informativity Optimizer (PIO): an R package to improve cancer NGS panel informativity.. **2022** ,	
163	The top 100 most cited articles on triple-negative breast cancer: a bibliometric analysis.. **2022**, 1	0
162	Notes. 179-189	
161	DataSheet1.zip. **2018**,	
160	Image_1.pdf. **2020**,	
159	Table_1.pdf. **2020**,	

158 Data_Sheet_1.docx. **2018**,

157 Image_1.jpg. **2020**,

156 Image_2.jpg. **2020**,

155 Image_3.tif. **2020**,

154 Image_4.jpg. **2020**,

153 Image_5.jpg. **2020**,

152 Table_1.DOCX. **2020**,

151 Table_2.DOCX. **2020**,

150 Table_3.DOCX. **2020**,

149 Table_4.DOCX. **2020**,

148 Table_5.DOCX. **2020**,

147 Table_6.DOCX. **2020**,

146 Image_1.PNG. **2020**,

145 Image_2.TIF. **2020**,

144 Image_3.TIFF. **2020**,

143 Image_4.TIF. **2020**,

142 Image_5.TIFF. **2020**,

141 Image_6.PNG. **2020**,

140 Image_7.PNG. **2020**,

139 Image_8.TIFF. **2020**,

138 Table_1.XLSX. **2020**,

137 Table_10.XLSX. **2020**,

136 Table_11.XLSX. **2020**,

135 Table_2.XLSX. **2020**,

134 Table_3.XLSX. **2020**,

133 Table_4.XLSX. **2020**,

132 Table_5.XLSX. **2020**,

131 Table_6.XLSX. **2020**,

130 Table_7.XLSX. **2020**,

129 Table_8.XLSX. **2020**,

128 Table_9.XLSX. **2020**,

127 Image_1.TIF. **2019**,

126 Image_2.TIF. **2019**,

125 Image_3.TIF. **2019**,

124 Image_4.TIF. **2019**,

123 Data_Sheet_1.xlsx. **2020**,

122	Presentation_1.zip. **2020**,	
121	DataSheet_1.fasta. **2019**,	
120	DataSheet_2.xlsx. **2019**,	
119	DataSheet_3.pdf. **2019**,	
118	Table_1.xls. **2019**,	
117	Table_2.xls. **2019**,	
116	Table_3.xlsx. **2019**,	
115	Triple-negative breast cancer - an aggressive subtype of breast cancer. **2022**, 1-28	
114	Novel biomarkers in triple-negative breast cancer - role and perspective. **2022**, 29-60	
113	Fast, Flexible, and�Exact Minimum Flow Decompositions via�ILP. **2022**, 230-245	1
112	DNA Copy Number Aberrations and Expression of ABC Transporter Genes in Breast Tumour: Correlation with the Effect of Neoadjuvant Chemotherapy and Prognosis of the Disease. **2022**, 14, 948	2
111	PI3K Inhibitors in Advanced Breast Cancer: The Past, The Present, New Challenges and Future Perspectives.. **2022**, 14,	1
110	Potential epigenetic modifications implicated in triple- to quadruple-negative breast cancer transition: a review.. **2022**,	1
109	Personalisierte Medizin�innovative Therapiem�glichkeiten f� das metastasierte Mammakarzinom. **2022**, 55, 335-343	
108	Statistical Methods for Minimax Estimation in Linear Models with Unknown Design Over Finite Alphabets. **2022**, 4, 490-513	0
107	Paradoxical Behavior of Oncogenes Undermines the Somatic Mutation Theory. **2022**, 12, 662	1
106	Identification of a five genes prognosis signature for triple-negative breast cancer using multi-omics methods and bioinformatics analysis.. **2022**,	1
105	NPC1 confers metabolic flexibility in Triple Negative Breast Cancer.	

104	The translational challenges of precision oncology.. **2022**,	3
103	Comparative characterization of 3D chromatin organization in triple-negative breast cancers.. **2022**,	0
102	Targeted Treatment for High-Risk Early-Stage Triple-Negative Breast Cancer: Spotlight on Pembrolizumab.. **2022**, 14, 113-123	2
101	Triple-Negative Breast Cancer: the Current Aspects of Pathogenesis and Therapies. 1	0
100	siRNA-based nanocarriers for targeted drug delivery to control breast cancer. **2022**, 100047	1
99	Heritable genomic diversity in breast cancer driver genes and associations with risk in a Chilean population. **2022**, 55,	
98	Development and Verification of a Prognostic Ferroptosis-Related Gene Model in Triple-Negative Breast Cancer. 12,	0
97	Focal Adhesion Kinase (FAK)-Hippo/YAP transduction signaling mediates the stimulatory effects exerted by S100A8/A9-RAGE system in triple-negative breast cancer (TNBC). **2022**, 41,	2
96	Beyond Genetics: Metastasis as an Adaptive Response in Breast Cancer. **2022**, 23, 6271	0
95	A Multiomics Signature Highlights Alterations Underlying Homologous Recombination Deficiency in Triple-Negative Breast Cancer.	0
94	Long noncoding RNA (lncRNA) metallothionein 1 J, pseudogene (MT1JP) is downregulated in triple-negative breast cancer and upregulates microRNA-138 (miR-138) to downregulate hypoxia-inducible factor-1□(HIF-1□). **2022**, 13, 13718-13727	0
93	Serial Tumor Molecular Profiling of Newly Diagnosed HER2-Negative Breast Cancers During Chemotherapy in Combination with Angiogenesis Inhibitors. **2022**, 17, 355-368	
92	Mapping Phenotypic Plasticity upon the Cancer Cell State Landscape Using Manifold Learning. OF1-OF13	3
91	Classification of triple negative breast cancer by epithelial mesenchymal transition and the tumor immune microenvironment. **2022**, 12,	0
90	Breast carcinomas with osteoclast-like giant cells: a comprehensive clinico-pathological and molecular portrait and evidence of RANK-L expression.	0
89	Antiprogestins reduce epigenetic field cancerization in breast tissue of young healthy women. **2022**, 14,	1
88	Heterogeneity of triple-negative breast cancer: understanding the Daedalian labyrinth and how it could reveal new drug targets. 1-17	1
87	MUC1 expressing tumor growth was retarded after human mucin 1 (MUC1) plasmid DNA immunization. **2022**, 36, 039463202211123	

86	The Maximum Entropy Principle For Compositional Data.	
85	Functional screening reveals HORMAD1-driven gene dependencies associated with translesion synthesis and replication stress tolerance.	1
84	Research progress on immunotherapy in triple-negative breast cancer (Review). **2022**, 61,	0
83	Triple-Negative Breast Cancer Analysis Based on Metabolic Gene Classification and Immunotherapy. 10,	0
82	Recent advances in multifunctional dendrimer-based nanoprobes for breast cancer theranostics. 1-44	1
81	The Roles of ATP13A2 Gene Mutations Leading to Abnormal Aggregation of �Synuclein in Parkinson� Disease. 16,	0
80	Biological Random Walks: multi-omics integration for disease gene prioritization.	0
79	Anticancer Activity of Bee Venom Components against Breast Cancer. **2022**, 14, 460	1
78	NPC1 Confers Metabolic Flexibility in Triple Negative Breast Cancer. **2022**, 14, 3543	
77	Comprehensive characterization of clonality of driver genes revealing their clinical relevance in colorectal cancer. **2022**, 20,	0
76	Ordered and deterministic cancer genome evolution after p53 loss. **2022**, 608, 795-802	1
75	Identification of necroptosis-related subtypes and prognosis model in triple negative breast cancer. 13,	0
74	Accurate determination of CRISPR-mediated gene fitness in transplantable tumours. **2022**, 13,	
73	Covalent JNK inhibitor, JNK-IN-8, suppresses tumor growth in triple-negative breast cancer by activating TFEB and TFE3 mediated lysosome biogenesis and autophagy.	0
72	Precision Breast Cancer Medicine: Early Stage Triple Negative Breast Cancer�A Review of Molecular Characterisation, Therapeutic Targets and Future Trends. 12,	3
71	non-coding RNAs, another side of immune regulation during Triple-Negative Breast Cancer. **2022**, 154132	0
70	Recent advances in therapeutic strategies for triple-negative breast cancer. **2022**, 15,	7
69	ABL kinases regulate translation in HER2+ cells through Y-box-binding protein 1 to facilitate colonization of the brain. **2022**, 40, 111268	0

68	Heterogeneity of triple negative breast cancer: Current advances in subtyping and treatment implications. **2022**, 41,	4
67	Identification of cuproptosis-related patterns and construction of a scoring system for predicting prognosis, tumor microenvironment-infiltration characteristics, and immunotherapy efficacy in breast cancer. 12,	0
66	Uncovering novel mutational signatures by de novo extraction with SigProfilerExtractor. **2022**, 100179	4
65	Impact of TP53 mutations in Triple Negative Breast Cancer. **2022**, 6,	0
64	Targeting the Heterogeneous Genomic Landscape in Triple-Negative Breast Cancer through Inhibitors of the Transcriptional Machinery. **2022**, 14, 4353	0
63	The Predictive Effect of Tumor Mutation Burden on prognosis in Breast cancer: A Systematic Review and Meta-Analysis.	0
62	The Gardener and the Walled Garden. **2022**, 149-172	0
61	Spatial transcriptomic analysis of a diverse patient cohort reveals a conserved architecture in triple-negative breast cancer.	0
60	RBCK1 is an endogenous inhibitor for triple negative breast cancer via hippo/YAP axis. **2022**, 20,	0
59	Novel BH4-BCL-2 Domain Antagonists Induce BCL-2-Mediated Apoptosis in Triple-Negative Breast Cancer. **2022**, 14, 5241	0
58	Prognosis and stratification of breast cancer immune infiltration status based on a mitochondria-related gene signature..	0
57	Elevated NRAS expression during DCIS is a potential driver for progression to basal-like properties and local invasiveness. **2022**, 24,	0
56	Efficient Minimum Flow Decomposition via Integer Linear Programming.	0
55	The maximum entropy principle for compositional data. **2022**, 23,	0
54	Single-cell genomic variation induced by mutational processes in cancer.	3
53	The Predictive and Prognostic Role of RAS/RAF/MEK/ERK Pathway Alterations in Breast Cancer: Revision of the Literature and Comparison with the Analysis of Cancer Genomic Datasets. **2022**, 14, 5306	0
52	Core promoter in TNBC is highly mutated with rich ethnic signature.	0
51	Determining prognostic factors and optimal surgical intervention for early-onset triple-negative breast cancer. 12,	0

50	Integrating Genomic Information with Tumor-Immune Microenvironment in Triple-Negative Breast Cancer. **2022**, 19, 13901	0
49	Neoplasms of the Breast. 1-62	0
48	A Case Series Exploration of Multi-Regional Expression Heterogeneity in Triple-Negative Breast Cancer Patients. **2022**, 23, 13322	0
47	Identification of HLA class I-restricted immunogenic neoantigens in triple negative breast cancer. 13,	0
46	Voltage imaging reveals the dynamic electrical signatures of human breast cancer cells. **2022**, 5,	0
45	Reconstructing mutational lineages in breast cancer by multi-patient-targeted single-cell DNA sequencing. **2022**, 100215	0
44	Tumor suppressor DEAR1 regulates mammary epithelial cell fate and predicts early onset and metastasis in triple negative breast cancer. **2022**, 12,	0
43	Androgen receptor function and targeted therapeutics across breast cancer subtypes. **2022**, 24,	2
42	Tanshinone IIA promotes apoptosis by downregulating BCL2 and upregulating TP53 in triple-negative breast cancer.	0
41	The prognostic role of tumor mutation burden on survival of breast cancer: a systematic review and meta-analysis. **2022**, 22,	1
40	The role of MEOX1 in non-neoplastic and neoplastic diseases. **2023**, 158, 114068	0
39	Research Progress of Tumor-Associated Macrophages in the Regulation of Breast Cancer Microenvironment. **2022**, 12, 10722-10727	0
38	Gallic acid suppresses the progression of triple-negative breast cancer HCC1806 cells via modulating PI3K/AKT/EGFR and MAPK signaling pathways. 13,	0
37	Comprehensive evaluation of breast cancer immunotherapy and tumor microenvironment characterization based on interleukin genes-related risk model. **2022**, 12,	0
36	Genetic Heterogeneity, Tumor Microenvironment and Immunotherapy in Triple-Negative Breast Cancer. **2022**, 23, 14937	0
35	SIEVE: joint inference of single-nucleotide variants and cell phylogeny from single-cell DNA sequencing data. **2022**, 23,	0
34	SETD7 Expression Is Associated with Breast Cancer Survival Outcomes for Specific Molecular Subtypes: A Systematic Analysis of Publicly Available Datasets. **2022**, 14, 6029	0
33	Phosphoproteomic analysis of neoadjuvant breast cancer suggests that increased sensitivity to paclitaxel is driven by CDK4 and filamin A. **2022**, 13,	1

32	HER3 Alterations in Cancer and Potential Clinical Implications. **2022**, 14, 6174	0
31	Advances in Single-Cell Sequencing Technology and Its Applications in Triple-Negative Breast Cancer. Volume 14, 465-474	1
30	A framework for clinical cancer subtyping from nucleosome profiling of cell-free DNA. **2022**, 13,	1
29	A Clinical Cognizance of Molecular and Pathological Diagnostic Approach of TNBC. **2023**, 26-46	0
28	Cancer Vaccines for Triple-Negative Breast Cancer: A Systematic Review. **2023**, 11, 146	1
27	Molecular Sub-Typing and Exploration of Key Signalling Pathways Involved in Complicating the Disease. **2023**, 47-72	0
26	Ethnic disparities in the immune microenvironment of triple negative breast cancer and its role in therapeutic outcomes.	0
25	PDJ amplicon in triple negative breast cancer. **2023**, 13,	0
24	Pre-Clinical and Clinical Evidence of Recent Therapeutic Trends and Spotting Possibility of Cure in Near Future. **2023**, 73-98	0
23	Inhibition of WNT signaling by conjugated microRNA nano-carriers: A new therapeutic approach for treating triple-negative breast cancer a perspective review. **2023**, 182, 103901	0
22	A randomized phase 2 study of neoadjuvant carboplatin and paclitaxel with or without atezolizumab in triple negative breast cancer (TNBC) - NCI 10013. **2022**, 8,	0
21	MiR-526b targets lncRNA SLC16A1-AS1 to suppress cell proliferation in triple-negative breast cancer.	0
20	Predictive Biomarkers for Response to Immunotherapy in Triple Negative Breast Cancer: Promises and Challenges. **2023**, 12, 953	0
19	EGFR/Notch antagonists enhance the response to inhibitors of the PI3K-Akt pathway by decreasing tumor-initiating cell frequency. **2023**, 155-160	0
18	Single cell lineage tracing reveals subclonal dynamics of anti-EGFR therapy resistance in triple negative breast cancer.	0
17	Deciphering breast cancer: from biology to the clinic. **2023**, 186, 1708-1728	0
16	Syndecan-1 as an immunogene in Triple-negative breast cancer: regulation tumor-infiltrating lymphocyte in the tumor microenviroment and EMT by TGFb1/Smad pathway. **2023**, 23,	0
15	Searching for DNA methylation in patients triple-negative breast cancer: a liquid biopsy approach. **2023**, 23, 41-51	0

14	2,2-Diphenethyl Isothiocyanate Enhances Topoisomerase Inhibitor-Induced Cell Death and Suppresses Multi-Drug Resistance 1 in Breast Cancer Cells. **2023**, 15, 928	0
13	A bibliometric analysis of 16,826 triple-negative breast cancer publications using multiple machine learning algorithms: Progress in the past 17 years. 10,	0
12	Chemoresistome Mapping in Individual Breast Cancer Patients Unravels Diversity in Dynamic Transcriptional Adaptation.	0
11	Discovering New Targets in Triple-Negative Breast Cancer (TNBC): The Androgen Receptor and the Estrogen Receptor **2023**,	0
10	Drugging the PI3K/AKT/mTOR Pathway in ER+ Breast Cancer. **2023**, 24, 4522	0
9	Biochemical Studies of Systemic Lupus Erythematosus-Associated Mutations in Nonreceptor Tyrosine Kinases Ack1 and Brk. **2023**, 62, 1124-1137	0
8	Identification of Kinase Targets for Enhancing the Antitumor Activity of Eribulin in Triple-Negative Breast Cell Lines. **2023**, 11, 735	0
7	Copy number alteration is an independent prognostic biomarker in triple-negative breast cancer patients.	0
6	Chamomile Essential Oil: Chemical Constituents and Antitumor Activity in MDA-MB-231 Cells through PI3K/Akt/mTOR Signaling Pathway.	0
5	Upregulation of the ferroptosis-related STEAP3 gene is a specific predictor of poor triple-negative breast cancer patient outcomes. 13,	0
4	Proteolysis Targeting Chimera (PROTAC) as a promising novel therapeutic modality for the treatment of triple-negative breast cancer (TNBC).	0
3	Targeting chemotherapy resistance in mesenchymal triple-negative breast cancer: a phase II trial of neoadjuvant angiogenic and mTOR inhibition with chemotherapy.	0
2	Molecular portraits of lung cancer evolution. **2023**, 616, 435-436	0
1	Mutation detection of urinary cell-free DNA via catch-and-release isolation on nanowires for liquid biopsy. **2023**, 115318	0