Gene expression profiling in breast cancer: understanding the molecular basis of histologic grade to improve prognosis

#	Paper	IF	Citations
1704	Identification of human triple-negative breast cancer subtypes and preclinical models for selection of targeted therapies. **2011**, 121, 2750		11
1703	Regularized Multivariate Regression for Identifying Master Predictors with Application to Integrative Genomics Study of Breast Cancer. **2010**, 4, 53-77		82
1702	.		
1701	The impact of the Oncotype DX Recurrence Score on treatment decisions and clinical outcomes in patients with early breast cancer: the Maccabi Healthcare Services experience with a unified testing policy. **2013**, 7, 380		13
1700	International Agency for Research on Cancer workshop on 'Expression array analyses in breast cancer taxonomy'. **2006**, 8, 303		6
1699	Classification and risk stratification of invasive breast carcinomas using a real-time quantitative RT-PCR assay. **2006**, 8, R23		150
1698	A consensus prognostic gene expression classifier for ER positive breast cancer. **2006**, 7, R101		75
1697	High-throughput genomic technology in research and clinical management of breast cancer. Exploiting the potential of gene expression profiling: is it ready for the clinic?. **2006**, 8, 214		25
1696	Gene expression profiling and clinical outcome in breast cancer. **2006**, 10, 429-43		47
1695	Quantitative profiling of drug-associated proteomic alterations by combined 2-nitrobenzenesulfenyl chloride (NBS) isotope labeling and 2DE/MS identification. **2006**, 5, 2194-206		37
1694	Gene Expression Profiling to Predict Chemotherapy Response in Primary Breast Cancer. **2006**, 1, 362-367		2
1693	Personalized medicine for breast cancer: moving forward and going back. **2006**, 3, 363-370		1
1692	WS11Comprehensive investigation of the transcriptome. **2006**, 29, 36-37		
1691	WS12Measuring biological effects in the target species using proteomics: detection of the illegal treatment of cattle with performance enhancing agents. **2006**, 29, 37-39		21
1690	A signature of chromosomal instability inferred from gene expression profiles predicts clinical outcome in multiple human cancers. **2006**, 38, 1043-8		782
1689	The challenges of gene expression microarrays for the study of human cancer. **2006**, 9, 333-9		80
1688	Tumor progression--targets for differential therapy. **2006**, 209, 589-91		3

1687   Prediction of metastasis from low-malignant breast cancer by gene expression profiling. **2007**, 120, 1070-5   23

1686   Breast cancer expression profiling: the impact of microarray testing on clinical decision making. **2006**, 7, 2069-78   7

1685   Proliferation: the most prominent predictor of clinical outcome in breast cancer. **2006**, 5, 2198-202   67

1684   Nachweis zirkulierender Tumorzellen für die Prognose, Diagnostik und Therapie unter besonderer Berücksichtigung des Mammakarzinoms. **2006**, 38, 123-128

1683   Genetic reclassification of histologic grade delineates new clinical subtypes of breast cancer. **2006**, 66, 10292-301   531

1682   Gene expression profiling in breast cancer. **2006**, 17 Suppl 10, x259-62   24

1681   Analysis of oncogenic signaling networks in glioblastoma identifies ASPM as a molecular target. **2006**, 103, 17402-7   503

1680   Molecular profiling of laser-microdissected matched tumor and normal breast tissue identifies karyopherin alpha2 as a potential novel prognostic marker in breast cancer. **2006**, 12, 3950-60   124

1679   Limitations of pharmacogenomic predictor discovery in Phase II clinical trials. **2007**, 8, 1443-8   7

1678   Clinical and therapeutic perspectives of gene expression profiling for breast cancer. **2007**, 18 Suppl 6, vi58-62   3

1677   Breast cancer prognostication and prediction: are we making progress?. **2007**, 18 Suppl 8, viii3-7   42

1676   Elucidating the altered transcriptional programs in breast cancer using independent component analysis. **2007**, 3, e161   92

1675   Cancer du sein. **2007**,   2

1674   Definition of clinically distinct molecular subtypes in estrogen receptor-positive breast carcinomas through genomic grade. **2007**, 25, 1239-46   650

1673   RB in breast cancer: at the crossroads of tumorigenesis and treatment. **2007**, 6, 667-71   87

1672   Expression profiling in breast carcinoma: new insights on old prognostic factors?. **2007**, 25, 4316-7; author reply 4317-8   1

1671   Microtubule-associated protein-tau is a bifunctional predictor of endocrine sensitivity and chemotherapy resistance in estrogen receptor-positive breast cancer. **2007**, 13, 2061-7   102

1670   Different prognostic value of cytokeratin-19 mRNA positive circulating tumor cells according to estrogen receptor and HER2 status in early-stage breast cancer. **2007**, 25, 5194-202   208

| 1669 | Poor outcome in estrogen receptor-positive breast cancers predicted by loss of plexin B1. **2007**, 13, 1115-22 | 59 |

| 1668 | In Reply. **2007**, 25, 4317-4318 | |

| 1667 | Pharmacogenomic predictor discovery in phase II clinical trials for breast cancer. **2007**, 13, 6080-6 | 52 |

| 1666 | Breast Cancer. **2007**, | |

| 1665 | The transcription factor snail mediates epithelial to mesenchymal transitions by repression of estrogen receptor-alpha. **2007**, 21, 2907-18 | 151 |

| 1664 | Nonparametric pathway-based regression models for analysis of genomic data. **2007**, 8, 265-84 | 54 |

| 1663 | RAD51 up-regulation bypasses BRCA1 function and is a common feature of BRCA1-deficient breast tumors. **2007**, 67, 9658-65 | 128 |

| 1662 | The prognostic biomarkers HOXB13, IL17BR, and CHDH are regulated by estrogen in breast cancer. **2007**, 13, 6327-34 | 59 |

| 1661 | Gene expression signatures to predict the development of metastasis in breast cancer. **2006**, 26, 149-56 | 15 |

| 1660 | The phenotypic spectrum of basal-like breast cancers: a critical appraisal. **2007**, 14, 358-73 | 64 |

| 1659 | Diverse correlation structures in gene expression data and their utility in improving statistical inference. **2007**, 1, | 22 |

| 1658 | Gene expression profiling in breast cancer. **2007**, 19, 547-51 | 40 |

| 1657 | Comparison of gene sets for expression profiling: prediction of metastasis from low-malignant breast cancer. **2007**, 13, 5355-60 | 30 |

| 1656 | Changes to the dihydropyrimidine dehydrogenase gene copy number influence the susceptibility of cancers to 5-FU-based drugs: Data mining of the NCI-DTP data sets and validation with human tumour xenografts. **2007**, 43, 791-8 | 9 |

| 1655 | Prognostic factors in invasive breast carcinoma: Do new molecular techniques/profiling add significantly to traditional histological factors?. **2007**, 13, 116-125 | |

| 1654 | Is the benefit of postmastectomy irradiation limited to patients with four or more positive nodes, as recommended in international consensus reports? A subgroup analysis of the DBCG 82 b&c randomized trials. **2007**, 82, 247-53 | 326 |

| 1653 | Determination of oestrogen-receptor status and ERBB2 status of breast carcinoma: a gene-expression profiling study. **2007**, 8, 203-11 | 157 |

| 1652 | To bury TNM classification in breast cancer or to praise it?. **2007**, 5, 23-29 | |

4

| 1633 | The use of gene-expression profiling to better understand the clinical heterogeneity of estrogen receptor positive breast cancers and tamoxifen response. **2007**, 61, 187-94 | 37 |

| 1632 | RNA quality in frozen breast cancer samples and the influence on gene expression analysis--a comparison of three evaluation methods using microcapillary electrophoresis traces. **2007**, 8, 38 | 83 |

| 1631 | Oxidative stress pathways highlighted in tumor cell immortalization: association with breast cancer outcome. **2007**, 26, 6269-79 | 32 |

| 1630 | Expression profiling technology: its contribution to our understanding of breast cancer. **2008**, 52, 67-81 | 34 |

| 1629 | A gene expression bar code for microarray data. **2007**, 4, 911-3 | 109 |

| 1628 | Taking gene-expression profiling to the clinic: when will molecular signatures become relevant to patient care?. **2007**, 7, 545-53 | 382 |

| 1627 | Phosphohistone H3 expression has much stronger prognostic value than classical prognosticators in invasive lymph node-negative breast cancer patients less than 55 years of age. **2007**, 20, 1307-15 | 90 |

| 1626 | Molecular and morphologic distinctions between infiltrating ductal and lobular carcinoma of the breast. **2007**, 13, 172-9 | 59 |

| 1625 | Impact of an increase in grading categories and double reporting on the reliability of breast cancer grade. **2007**, 115, 360-6 | 5 |

| 1624 | Pathway analysis of gene signatures predicting metastasis of node-negative primary breast cancer. **2007**, 7, 182 | 94 |

| 1623 | The erbB2+ cluster of the intrinsic gene set predicts tumor response of breast cancer patients receiving neoadjuvant chemotherapy with docetaxel, doxorubicin and cyclophosphamide within the GEPARTRIO trial. **2007**, 16, 235-40 | 53 |

| 1622 | Pathological definitions of invasion, metastatic potential and responsiveness to targeted therapies. **2007**, 16 Suppl 2, S55-8 | 12 |

| 1621 | The evolution of treatment strategies: aiming at the target. **2007**, 16 Suppl 2, S10-6 | 25 |

| 1620 | Molecular definition of breast tumor heterogeneity. **2007**, 11, 259-73 | 1135 |

| 1619 | Thymosin beta-NB is the human isoform of rat thymosin beta15. **2007**, 1112, 286-96 | 15 |

| 1618 | Correlation of levels and patterns of genomic instability with histological grading of DCIS. **2007**, 14, 3070-7 | 20 |

| 1617 | Molecular profiling of breast cancer: transcriptomic studies and beyond. **2007**, 64, 3185-200 | 11 |

| 1616 | Molecular basis of invasion in breast cancer. **2007**, 64, 3201-18 | 70 |

1597	Implications of applied research for prognosis and therapy of breast cancer. **2008**, 65, 223-34	6
1596	A significant proportion of elderly patients develop hormone-dependant "luminal-B" tumours associated with aggressive characteristics. **2008**, 67, 80-92	46
1595	Molecular diagnosis in breast cancer. **2008**, 14, 202-213	8
1594	Clinical application of the 70-gene profile: the MINDACT trial. **2008**, 26, 729-35	396
1593	Elevated thymosin beta15 expression is associated with progression and metastasis of non-small cell lung cancer. **2008**, 116, 484-90	7
1592	Robust prognostic value of a knowledge-based proliferation signature across large patient microarray studies spanning different cancer types. **2008**, 99, 1884-90	43
1591	An embryonic stem cell-like gene expression signature in poorly differentiated aggressive human tumors. **2008**, 40, 499-507	1885
1590	Stromal gene expression predicts clinical outcome in breast cancer. **2008**, 14, 518-27	1297
1589	Tailoring to RB: tumour suppressor status and therapeutic response. **2008**, 8, 714-24	263
1588	An update on prognosis in breast cancer patients with extensive axillary disease. **2008**, 14, 76-80	5
1587	The changing focus of microarray analysis. **2008**, 62, 364-373	
1586	Merging microarray data from separate breast cancer studies provides a robust prognostic test. **2008**, 9, 125	69
1585	Integrative bioinformatics analysis of transcriptional regulatory programs in breast cancer cells. **2008**, 9, 404	27
1584	A gene sets approach for identifying prognostic gene signatures for outcome prediction. **2008**, 9, 177	13
1583	Predicting prognosis using molecular profiling in estrogen receptor-positive breast cancer treated with tamoxifen. **2008**, 9, 239	272
1582	Comparison of prognostic gene expression signatures for breast cancer. **2008**, 9, 394	110
1581	Gene expression meta-analysis identifies metastatic pathways and transcription factors in breast cancer. **2008**, 8, 394	54
1580	The use of genomic tools for the molecular understanding of breast cancer and to guide personalized medicine. **2008**, 13, 481-7	13

1579   Down-regulation of osteopontin attenuates breast tumour progression in vivo. **2008**, 12, 2305-18   39

1578   Using microarray analysis as a prognostic and predictive tool in oncology: focus on breast cancer and normal tissue toxicity. **2008**, 18, 105-14   39

1577   High throughput molecular diagnostics in bladder cancer - on the brink of clinical utility. **2008**, 1, 384-94   13

1576   Arylamine N-acetyltransferases: from structure to function. **2008**, 40, 479-510   106

1575   [Prognostic classification of breast cancer and gene expression profiling]. **2008**, 24, 599-606   4

1574   Advances in Breast Cancer Management, Second Edition. **2008**,   1

1573   A comprehensive analysis of prognostic signatures reveals the high predictive capacity of the proliferation, immune response and RNA splicing modules in breast cancer. **2008**, 10, R93   104

1572   A functional Notch-survivin gene signature in basal breast cancer. **2008**, 10, R97   91

1571   A candidate molecular signature associated with tamoxifen failure in primary breast cancer. **2008**, 10, R88   48

1570   Meta-analysis of gene expression profiles in breast cancer: toward a unified understanding of breast cancer subtyping and prognosis signatures. **2008**, 10, R65   658

1569   A robust classifier of high predictive value to identify good prognosis patients in ER-negative breast cancer. **2008**, 10, R73   78

1568   Effects of common germline genetic variation in cell cycle control genes on breast cancer survival: results from a population-based cohort. **2008**, 10, R47   29

1567   Evaluation of biological pathways involved in chemotherapy response in breast cancer. **2008**, 10, R37   50

1566   Re-evaluating early breast neoplasia. **2008**, 10, 302   19

1565   Correction of technical bias in clinical microarray data improves concordance with known biological information. **2008**, 9, R26   50

1564   Innovative Endocrinology of Cancer. **2008**,   5

1563   Prognostic differences of World Health Organization-assessed mitotic activity index and mitotic impression by quick scanning in invasive ductal breast cancer patients younger than 55 years. **2008**, 39, 584-90   18

1562   [The use of breast cancer subtype classification to predict local and distant recurrence. A review]. **2008**, 12, 577-83   8

| 1561 | Forkhead-box A1 (FOXA1) expression in breast cancer and its prognostic significance. **2008**, 44, 1541-51 | 74 |

| 1560 | Combining biological gene expression signatures in predicting outcome in breast cancer: An alternative to supervised classification. **2008**, 44, 2319-29 | 18 |

| 1559 | Gene expression predictors in breast cancer: current status, limitations and perspectives. **2008**, 44, 2714-20 | 45 |

| 1558 | Molecular analysis of hormone receptor positive (luminal) breast cancers: what have we learnt?. **2008**, 44, 2813-8 | 17 |

| 1557 | Functional genomics of cancer. **2008**, 18, 251-6 | 17 |

| 1556 | Are gene signatures better than traditional clinical factors?. **2008**, 9, 197-8; author reply 198-9 | 2 |

| 1555 | A transcriptional fingerprint of estrogen in human breast cancer predicts patient survival. **2008**, 10, 79-88 | 30 |

| 1554 | Biological processes associated with breast cancer clinical outcome depend on the molecular subtypes. **2008**, 14, 5158-65 | 641 |

| 1553 | Basal-like breast cancer: a critical review. **2008**, 26, 2568-81 | 657 |

| 1552 | Multigene predictors in early-stage breast cancer: moving in or moving out?. **2008**, 8, 129-35 | 11 |

| 1551 | Application of gene set enrichment method to ChIP-chip data analysis. **2008**, | |

| 1550 | A five-gene molecular grade index and HOXB13:IL17BR are complementary prognostic factors in early stage breast cancer. **2008**, 14, 2601-8 | 240 |

| 1549 | Gene expression profiling of breast cancer. **2008**, 3, 67-97 | 56 |

| 1548 | A comparative study of survival models for breast cancer prognostication based on microarray data: does a single gene beat them all?. **2008**, 24, 2200-8 | 157 |

| 1547 | Learning on Weighted Hypergraphs to Integrate Protein Interactions and Gene Expressions for Cancer Outcome Prediction. **2008**, | 27 |

| 1546 | Treatment tailoring based on molecular characterizations. **2008**, 19 Suppl 7, vii46-50 | 3 |

| 1545 | Algebraic stability indicators for ranked lists in molecular profiling. **2008**, 24, 258-64 | 65 |

| 1544 | Commercialized multigene predictors of clinical outcome for breast cancer. **2008**, 13, 477-93 | 210 |

1525	hsa-miR-210 Is induced by hypoxia and is an independent prognostic factor in breast cancer. **2008**, 14, 1340-8	555
1524	The humoral immune system has a key prognostic impact in node-negative breast cancer. **2008**, 68, 5405-13	585
1523	An ideal prognostic test for estrogen receptor-positive breast cancer?. **2008**, 26, 4058-9	7
1522	Functional genomics in translational cancer research: focus on breast cancer. **2008**, 7, 1-7	3
1521	Prediction of nodal involvement in breast cancer based on multiparametric protein analyses from preoperative core needle biopsies of the primary lesion. **2008**, 14, 3345-53	18
1520	Prognostic Value of Gene Signatures and Tumorbiological Characteristics in Breast Cancer Patients Treated with Anthracycline-containing Chemotherapy. **2008**, 68, 1171-1177	2
1519	Bedeutung von Biomarkern in der Klassifizierung und Therapie des Mammakarzinoms. **2008**, 5, 257-263	1
1518	Revealing Significant Biological Knowledge via Gene Ontologies and Pathways. **2008**,	
1517	Serine 2481-autophosphorylation of mammalian target of rapamycin (mTOR) couples with chromosome condensation and segregation during mitosis: Confocal microscopy characterization and immunohistochemical validation of PP-mTORSer2481 as a novel high-contrast mitosis marker in breast cancer core biopsies. **2009**, 36,	
1516	Molecular Biology of Breast Cancer. **2009**, 501-517	1
1515	Genomic heterogeneity of breast tumor pathogenesis. **2009**, 3, 77-85	1
1514	[Innovation in adjuvant radiotherapy for breast cancer: new biologic parameters, a perspective for treatment tailoring]. **2009**, 96, 111-21	1
1513	Adjuvant Therapy of Breast Cancer: Can We Do Better?. **2009**, 4, 292-293	
1512	Cross-study projections of genomic biomarkers: an evaluation in cancer genomics. **2009**, 4, e4523	12
1511	Evaluation of microarray preprocessing algorithms based on concordance with RT-PCR in clinical samples. **2009**, 4, e5645	67
1510	A Systems Biology Approach to Identify Affected Regulatory and Signaling Circuits in Protein Interaction Networks. **2009**,	
1509	The Impact of Tumor Biology on Cancer Treatment and Multidisciplinary Strategies. **2009**,	10
1508	Using Frequent Co-expression Network to Identify Gene Clusters for Breast Cancer Prognosis. **2009**, 428-434	12

1507	Sam-pointed domain containing Ets transcription factor in luminal breast cancer pathogenesis. **2009**, 18, 1899-903	21
1506	Acid ceramidase 1 expression correlates with a better prognosis in ER-positive breast cancer. **2009**, 12, 502-13	33
1505	A Proposal for Gene Signature Integration. **2009**,	1
1504	Cyclin A is a proliferative marker with good prognostic value in node-negative breast cancer. **2009**, 18, 2501-6	22
1503	Prediction of local recurrence, distant metastases, and death after breast-conserving therapy in early-stage invasive breast cancer using a five-biomarker panel. **2009**, 27, 4701-8	253
1502	DNA methylation as a biomarker in breast cancer. **2009**, 5, 1245-56	48
1501	Case records of the Massachusetts General Hospital. Case 25-2009. A 36-year-old woman with hormone-receptor-positive breast cancer. **2009**, 361, 699-707	2
1500	Estrogen regulation of cyclin E2 requires cyclin D1 but not c-Myc. **2009**, 29, 4623-39	53
1499	A radiation-derived gene expression signature predicts clinical outcome for breast cancer patients. **2009**, 171, 141-54	8
1498	HtrA serine proteases as potential therapeutic targets in cancer. **2009**, 9, 451-68	96
1497	The HOXB13:IL17BR gene-expression ratio: a biomarker providing information above and beyond tumor grade. **2009**, 3, 99-102	5
1496	A high-sensitivity, medium-density, and target amplification-free planar waveguide microarray system for gene expression analysis of formalin-fixed and paraffin-embedded tissue. **2009**, 55, 1995-2003	6
1495	Integrated Analysis of Gene Expression Profiling Studies âExamples in Breast Cancer. **2009**, 85-114	1
1494	Zur Rolle von Her-2/neu in der Karzinogenese des Mammakarzinoms âwann und wo?. **2009**, 69, 711-716	
1493	CT-X antigen expression in human breast cancer. **2009**, 106, 13493-8	78
1492	Hierarchically penalized Cox regression with grouped variables. **2009**, 96, 307-322	50
1491	Prognostic applications of gene expression signatures in breast cancer. **2009**, 77 Suppl 1, 2-8	18
1490	LRpath: a logistic regression approach for identifying enriched biological groups in gene expression data. **2009**, 25, 211-7	138

1489	Breast cancer subtypes and response to docetaxel in node-positive breast cancer: use of an immunohistochemical definition in the BCIRG 001 trial. **2009**, 27, 1168-76	411
1488	Improved survival for women with stage I breast cancer in south-east Sweden: a comparison between two time periods before and after increased use of adjuvant systemic therapy. **2009**, 48, 504-13	3
1487	Genomic grade index is associated with response to chemotherapy in patients with breast cancer. **2009**, 27, 3185-91	153
1486	Hormone Receptors in Breast Cancer. **2009**,	
1485	Microarray-based gene expression profiling as a clinical tool for breast cancer management: are we there yet?. **2009**, 17, 285-302	56
1484	Immutable functional attributes of histologic grade revealed by context-independent gene expression in primary breast cancer cells. **2009**, 69, 7826-34	17
1483	Coactivator function defines the active estrogen receptor alpha cistrome. **2009**, 29, 3413-23	65
1482	Overexpression and mislocalization of the chromosomal segregation protein separase in multiple human cancers. **2009**, 15, 2703-10	60
1481	Integrative analysis of cyclin protein levels identifies cyclin b1 as a classifier and predictor of outcomes in breast cancer. **2009**, 15, 3654-62	109
1480	Bioinformatics and breast cancer: what can high-throughput genomic approaches actually tell us?. **2009**, 62, 879-85	29
1479	Gene expression profiling: decoding breast cancer. **2009**, 18, 366-78	25
1478	The ordering of expression among a few genes can provide simple cancer biomarkers and signal BRCA1 mutations. **2009**, 10, 256	29
1477	Selecting control genes for RT-QPCR using public microarray data. **2009**, 10, 42	49
1476	Classification across gene expression microarray studies. **2009**, 10, 453	13
1475	Systematic identification of transcription factors associated with patient survival in cancers. **2009**, 10, 225	10
1474	Relationship between estrogen receptor alpha location and gene induction reveals the importance of downstream sites and cofactors. **2009**, 10, 381	6
1473	Improvement of the clinical applicability of the Genomic Grade Index through a qRT-PCR test performed on frozen and formalin-fixed paraffin-embedded tissues. **2009**, 10, 424	67
1472	Intrinsic bias in breast cancer gene expression data sets. **2009**, 9, 214	2

1453 Gene expression of topoisomerase II alpha (TOP2A) by microarray analysis is highly prognostic in estrogen receptor (ER) positive breast cancer. **2009**, 113, 457-66 — 48

1452 Validating the prognostic value of proliferation measured by Phosphohistone H3 (PPH3) in invasive lymph node-negative breast cancer patients less than 71 years of age. **2009**, 114, 39-45 — 40

1451 The role and regulation of the nuclear receptor co-activator AIB1 in breast cancer. **2009**, 116, 225-37 — 72

1450 The epidemiology of triple-negative breast cancer, including race. **2009**, 20, 1071-82 — 234

1449 A mouse mammary gland involution mRNA signature identifies biological pathways potentially associated with breast cancer metastasis. **2009**, 14, 99-116 — 43

1448 Prognostic and predictive factors and genetic analysis of early breast cancer. **2009**, 11, 634-42 — 6

1447 Molecular changes in primary breast tumors and the Nottingham Histologic Score. **2009**, 15, 541-7 — 8

1446 Mammakarzinom. **2009**, 42, 841-846

1445 [Genome-wide expression profiling as a clinical tool: are we there yet?]. **2009**, 30, 141-6 — 3

1444 Overexpression of TFAP2C in invasive breast cancer correlates with a poorer response to anti-hormone therapy and reduced patient survival. **2009**, 217, 32-41 — 48

1443 Mammosphere-derived gene set predicts outcome in patients with ER-positive breast cancer. **2009**, 218, 316-26 — 35

1442 PrognoScan: a new database for meta-analysis of the prognostic value of genes. **2009**, 2, 18 — 507

1441 Gene expression profiling identifies activated growth factor signaling in poor prognosis (Luminal-B) estrogen receptor positive breast cancer. **2009**, 2, 37 — 39

1440 The Gene expression Grade Index: a potential predictor of relapse for endocrine-treated breast cancer patients in the BIG 1-98 trial. **2009**, 2, 40 — 58

1439 Gene expression meta-analysis supports existence of molecular apocrine breast cancer with a role for androgen receptor and implies interactions with ErbB family. **2009**, 2, 59 — 40

1438 A taxonomy of epithelial human cancer and their metastases. **2009**, 2, 69 — 15

1437 Distant metastasis: not out of reach any more. **2009**, 8, 28 — 10

1436 Coordinated expression of ER, PR and HER2 define different prognostic subtypes among poorly differentiated breast carcinomas. **2009**, 55, 346-52 — 22

1435	Histological grading of invasive breast carcinoma--a simplification of existing methods in a large conservation series with long-term follow-up. **2009**, 55, 724-31	24
1434	Clinicopathological relevance of UbcH10 in breast cancer. **2009**, 100, 238-48	22
1433	AP-2gamma promotes proliferation in breast tumour cells by direct repression of the CDKN1A gene. **2009**, 28, 3591-601	30
1432	A stroma-related gene signature predicts resistance to neoadjuvant chemotherapy in breast cancer. **2009**, 15, 68-74	477
1431	Biological determinants of endocrine resistance in breast cancer. **2009**, 9, 631-43	950
1430	Histological and molecular types of breast cancer: is there a unifying taxonomy?. **2009**, 6, 718-30	296
1429	The GAB2 signaling scaffold promotes anchorage independence and drives a transcriptional response associated with metastatic progression of breast cancer. **2009**, 28, 4444-55	17
1428	Cell-cycle-phase progression analysis identifies unique phenotypes of major prognostic and predictive significance in breast cancer. **2009**, 100, 959-70	67
1427	Review of gene-expression profiling and its clinical use in breast cancer. **2009**, 69, 1-11	30
1426	Microarray methods to identify factors determining breast cancer progression: potentials, limitations, and challenges. **2009**, 70, 1-11	16
1425	Gene-expression signatures in breast cancer. **2009**, 360, 790-800	1095
1424	Extracellular matrix 1 (ECM1) expression is a novel prognostic marker for poor long-term survival in breast cancer: a Hospital-based Cohort Study in Iowa. **2009**, 16, 2280-7	37
1423	The role of molecular analysis in breast cancer. **2009**, 41, 77-88	41
1422	Supervised risk predictor of breast cancer based on intrinsic subtypes. **2009**, 27, 1160-7	2866
1421	TGF-beta3 and cancer: a review. **2009**, 20, 305-17	64
1420	Loss of Plexin B1 is highly prognostic in low proliferating ER positive breast cancers--results of a large scale microarray analysis. **2009**, 45, 405-13	30
1419	Daily clinical practice of fresh tumour tissue freezing and gene expression profiling; logistics pilot study preceding the MINDACT trial. **2009**, 45, 1201-1208	28
1418	A Mutant-p53/Smad complex opposes p63 to empower TGFbeta-induced metastasis. **2009**, 137, 87-98	629

| 1381 | Evidence for a transcriptional signature of breast cancer. **2010**, 122, 65-75 | 11 |

| 1380 | Clinical relevance of the putative stem cell marker p63 in breast cancer. **2010**, 122, 765-75 | 21 |

| 1379 | An online survival analysis tool to rapidly assess the effect of 22,277 genes on breast cancer prognosis using microarray data of 1,809 patients. **2010**, 123, 725-31 | 1940 |

| 1378 | The predictive value of the 70-gene signature for adjuvant chemotherapy in early breast cancer. **2010**, 120, 655-61 | 203 |

| 1377 | Gene expression profiling of response to mTOR inhibitor everolimus in pre-operatively treated post-menopausal women with oestrogen receptor-positive breast cancer. **2010**, 122, 419-28 | 38 |

| 1376 | ROCK: a breast cancer functional genomics resource. **2010**, 124, 567-72 | 26 |

| 1375 | Metastasis-related miRNAs, active players in breast cancer invasion, and metastasis. **2010**, 29, 785-99 | 80 |

| 1374 | Linking the septin expression with carcinogenesis. **2010**, 37, 3601-8 | 33 |

| 1373 | Detection of gene pathways with predictive power for breast cancer prognosis. **2010**, 11, 1 | 273 |

| 1372 | A semi-parametric Bayesian model for unsupervised differential co-expression analysis. **2010**, 11, 234 | 28 |

| 1371 | Detecting disease associated modules and prioritizing active genes based on high throughput data. **2010**, 11, 26 | 62 |

| 1370 | An eScience-Bayes strategy for analyzing omics data. **2010**, 11, 282 | 4 |

| 1369 | Enumerating the gene sets in breast cancer, a "direct" alternative to hierarchical clustering. **2010**, 11, 482 | 3 |

| 1368 | Molecular risk assessment of BIG 1-98 participants by expression profiling using RNA from archival tissue. **2010**, 10, 37 | 8 |

| 1367 | Cellular processes of v-Src transformation revealed by gene profiling of primary cells--implications for human cancer. **2010**, 10, 41 | 12 |

| 1366 | Improved prognostic classification of breast cancer defined by antagonistic activation patterns of immune response pathway modules. **2010**, 10, 604 | 104 |

| 1365 | Increased entropy of signal transduction in the cancer metastasis phenotype. **2010**, 4, 104 | 70 |

| 1364 | Genomic distance entrained clustering and regression modelling highlights interacting genomic regions contributing to proliferation in breast cancer. **2010**, 4, 127 | 9 |

1345	Array-based DNA methylation profiling for breast cancer subtype discrimination. **2010**, 5, e12616	68
1344	Protein-protein interaction reveals synergistic discrimination of cancer phenotype. **2010**, 9, 61-6	6
1343	Context-specific gene regulatory networks subdivide intrinsic subtypes of breast cancer. **2010**,	
1342	SRp20 is a proto-oncogene critical for cell proliferation and tumor induction and maintenance. **2010**, 6, 806-26	140
1341	Tamoxifen in early-stage estrogen receptor-positive breast cancer: overview of clinical use and molecular biomarkers for patient selection. **2010**, 4, 1-11	22
1340	CARMA3: A novel scaffold protein in regulation of NF-B activation and diseases. **2010**, 1, 353-61	23
1339	Molecular profiling: moving away from tumor philately. **2010**, 2, 47ps43	61
1338	Clinical implications of gene dosage and gene expression patterns in diploid breast carcinoma. **2010**, 16, 3860-74	73
1337	Session 2: Marqueurs moléculaires pronostiques et prédictifs de réponse au traitement des cancers du sein. **2010**, 97, S12-S13	
1336	Predictive and prognostic molecular markers for cancer medicine. **2010**, 2, 125-48	138
1335	New developments in hormone receptor-positive disease. **2010**, 15 Suppl 5, 18-28	7
1334	The embryonic transcription cofactor LBH is a direct target of the Wnt signaling pathway in epithelial development and in aggressive basal subtype breast cancers. **2010**, 30, 4267-79	66
1333	14-3-3Tau regulates ubiquitin-independent proteasomal degradation of p21, a novel mechanism of p21 downregulation in breast cancer. **2010**, 30, 1508-27	49
1332	FKBPL regulates estrogen receptor signaling and determines response to endocrine therapy. **2010**, 70, 1090-100	30
1331	Predictive biomarkers of sensitivity to the phosphatidylinositol 3' kinase inhibitor GDC-0941 in breast cancer preclinical models. **2010**, 16, 3670-83	226
1330	LYN is a mediator of epithelial-mesenchymal transition and a target of dasatinib in breast cancer. **2010**, 70, 2296-306	110
1329	[Molecular prognostic and predictive markers of breast cancer treatment]. **2010**, 97, 1297-304	0
1328	DNA microarrays are predictive of cancer prognosis: a re-evaluation. **2010**, 16, 629-36	47

1309	Biomarker research in breast cancer. **2010**, 14, 771-83	3
1308	The impact of inter-observer variation in pathological assessment of node-negative breast cancer on clinical risk assessment and patient selection for adjuvant systemic treatment. **2010**, 21, 40-7	48
1307	A genome-wide RNAi screen identifies multiple RSK-dependent regulators of cell migration. **2010**, 24, 2654-65	69
1306	Cell cycle proteins in epithelial cell differentiation: implications for breast cancer. **2010**, 9, 1918-28	59
1305	Dual association by TFAP2A during activation of the p21cip/CDKN1A promoter. **2010**, 9, 4525-32	17
1304	Do predictive signatures really predict response to cancer chemotherapy?. **2010**, 9, 4836-40	46
1303	The CINSARC signature: prognostic and predictive of response to chemotherapy?. **2010**, 9, 4025-7	9
1302	RB-pathway disruption in breast cancer: differential association with disease subtypes, disease-specific prognosis and therapeutic response. **2010**, 9, 4153-63	131
1301	[Identification of basal-like carcinomas in clinical practice: "triple zero/BRCA1-like" carcinomas]. **2010**, 97, 357-63	6
1300	The prognostic value of Ki67 is dependent on estrogen receptor status and histological grade in premenopausal patients with node-negative breast cancer. **2010**, 23, 251-9	60
1299	Prognostic and predictive biomarkers in resected colon cancer: current status and future perspectives for integrating genomics into biomarker discovery. **2010**, 15, 390-404	135
1298	Clinical application of gene expression profiling in breast cancer. **2010**, 19, 581-606	17
1297	Trefoil factor 3 is oncogenic and mediates anti-estrogen resistance in human mammary carcinoma. **2010**, 12, 1041-53	45
1296	Ron receptor tyrosine kinase activation confers resistance to tamoxifen in breast cancer cell lines. **2010**, 12, 650-8	52
1295	DNA amplifications in breast cancer: genotypic-phenotypic correlations. **2010**, 6, 967-84	18
1294	A Bayesian hierarchical model for high-dimensional meta-analysis. **2010**, 620, 538-46	1
1293	Neoadyuvancia en cãcer de mama: Papel del patllogo. **2010**, 43, 90-93	1
1292	Histological types of breast cancer: how special are they?. **2010**, 4, 192-208	255

1291   Molecular basis for therapy resistance. **2010**, 4, 284-300   36

1290   Preinvasive breast cancer. **2010**, 5, 193-221   67

1289   High expression levels of putative hepatic stem/progenitor cell biomarkers related to tumour angiogenesis and poor prognosis of hepatocellular carcinoma. **2010**, 59, 953-62   206

1288   A multigene predictor of metastatic outcome in early stage hormone receptor-negative and triple-negative breast cancer. **2010**, 12, R85   140

1287   Prognostic gene network modules in breast cancer hold promise. **2010**, 12, 317

1286   Development of a diagnostic microarray assay to assess the risk of recurrence of prostate cancer based on PITX2 DNA methylation. **2010**, 12, 345-53   24

1285   Expression of Long-chain Fatty Acyl-CoA Synthetase 4 in Breast and Prostate Cancers Is Associated with Sex Steroid Hormone Receptor Negativity. **2010**, 3, 91-8   58

1284   Classification and prognosis of invasive breast cancer: from morphology to molecular taxonomy. **2010**, 23 Suppl 2, S60-4   241

1283   Classification moléculaire des cancers du sein : utilité en clinique. **2010**, 34, 32-43   1

1282   Personalized treatment of early-stage breast cancer: present concepts and future directions. **2010**, 36, 584-94   40

1281   Prognostic impact of thymidine phosphorylase expression in breast cancer--comparison of microarray and immunohistochemical data. **2010**, 46, 549-57   16

1280   Is there a niche for DNA microarrays in molecular diagnostics?. **2010**, 10, 875-82   19

1279   The future of diagnostic gene-expression microarrays: bridging the gap between bench and bedside. **2010**, 2, 249-62   7

1278   Genomic index of sensitivity to endocrine therapy for breast cancer. **2010**, 28, 4111-9   203

1277   Molecular profiling currently offers no more than tumour morphology and basic immunohistochemistry. **2010**, 12 Suppl 4, S5   70

1276   Mammostrat as a tool to stratify breast cancer patients at risk of recurrence during endocrine therapy. **2010**, 12, R47   92

1275   A fuzzy gene expression-based computational approach improves breast cancer prognostication. **2010**, 11, R18   36

1274   Bioinformatics Methods in Clinical Research. **2010**,   9

1273   Breast cancer prognostic classification in the molecular era: the role of histological grade. **2010**, 12, 207   459

1272   Gene-expression-based prognostic assays for breast cancer. **2010**, 7, 340-7   132

1271   Identifying Transcription Factors and microRNAs as Key Regulators of Pathways Using Bayesian Inference on Known Pathway Structures. **2011**,

1270   G-DOC: a systems medicine platform for personalized oncology. **2011**, 13, 771-83   42

1269   Deconstructing the molecular portraits of breast cancer. **2011**, 5, 5-23   841

1268   Personalized medicine: the road ahead. **2011**, 11, 20-6   40

1267   Lack of sufficiently strong informative features limits the potential of gene expression analysis as predictive tool for many clinical classification problems. **2011**, 12, 463   10

1266   Ki67, chemotherapy response, and prognosis in breast cancer patients receiving neoadjuvant treatment. **2011**, 11, 486   211

1265   Expression analysis of mitotic spindle checkpoint genes in breast carcinoma: role of NDC80/HEC1 in early breast tumorigenicity, and a two-gene signature for aneuploidy. **2011**, 10, 23   43

1264   Chronic obstructive pulmonary disease-specific gene expression signatures of alveolar macrophages as well as peripheral blood monocytes overlap and correlate with lung function. **2011**, 81, 499-510   37

1263   Immunohistology of the Breast. **2011**, 763-819   0

1262   Breast Cancer and its Precursor Lesions. **2011**,   0

1261   Cancer Systems Biology, Bioinformatics and Medicine. **2011**,   3

1260   Guidelines for Molecular Analysis in Archive Tissues. **2011**,   14

1259   The Hippo transducer TAZ confers cancer stem cell-related traits on breast cancer cells. **2011**, 147, 759-72   886

1258   Gene profiling in breast cancer: time to move forward. **2011**, 37, 416-21   8

1257   Application of molecular findings to the diagnosis and management of breast disease: recent advances and challenges. **2011**, 42, 153-65   5

1256   The Use of Molecular Profiles in the Management of Breast Cancer. **2011**, 319-326

1255   Prognostic value of an RNA expression signature derived from cell cycle proliferation genes in patients with prostate cancer: a retrospective study. **2011**, 12, 245-55   523

1254   Microarrays in the 2010s: the contribution of microarray-based gene expression profiling to breast cancer classification, prognostication and prediction. **2011**, 13, 212   92

1253   'Omic approaches to preventing or managing metastatic breast cancer. **2011**, 13, 230   19

1252   Breast tumors from CHEK2 1100delC-mutation carriers: genomic landscape and clinical implications. **2011**, 13, R90   40

1251   A new gene expression signature, the ClinicoMolecular Triad Classification, may improve prediction and prognostication of breast cancer at the time of diagnosis. **2011**, 13, R92   20

1250   A clinically relevant gene signature in triple negative and basal-like breast cancer. **2011**, 13, R97   238

1249   Gene expression profiling in breast cancer: classification, prognostication, and prediction. **2011**, 378, 1812-23   519

1248   Imaging-related anatomy and pathology. 22-47

1247   A signature inferred from Drosophila mitotic genes predicts survival of breast cancer patients. **2011**, 6, e14737   9

1246   Biologic characteristics of premalignant breast disease. **2010**, 9, 177-92   13

1245   Detecting cancer gene networks characterized by recurrent genomic alterations in a population. **2011**, 6, e14437   18

1244   Combining gene signatures improves prediction of breast cancer survival. **2011**, 6, e17845   33

1243   GOBO: gene expression-based outcome for breast cancer online. **2011**, 6, e17911   295

1242   Distinctive responsiveness to stromal signaling accompanies histologic grade programming of cancer cells. **2011**, 6, e20016   9

1241   A tri-marker proliferation index predicts biochemical recurrence after surgery for prostate cancer. **2011**, 6, e20293   31

1240   Induction of stable drug resistance in human breast cancer cells using a combinatorial zinc finger transcription factor library. **2011**, 6, e21112   10

1239   Sprouty 2 is an independent prognostic factor in breast cancer and may be useful in stratifying patients for trastuzumab therapy. **2011**, 6, e23772   37

1238   Network based consensus gene signatures for biomarker discovery in breast cancer. **2011**, 6, e25364   20

| 1237 | Homogeneous datasets of triple negative breast cancers enable the identification of novel prognostic and predictive signatures. **2011**, 6, e28403 | 63 |

| 1236 | Development of commercial gene-expression-based signatures: review of the scientific strategies. **2011**, 8, 253-269 | |

| 1235 | Molecular predictors of response to therapy for breast cancer. **2011**, 17, 96-103 | 19 |

| 1234 | Characteristics of breast cancers detected by ultrasound screening in women with negative mammograms. **2011**, 102, 1862-7 | 37 |

| 1233 | Identification of a claudin-4 and E-cadherin score to predict prognosis in breast cancer. **2011**, 102, 2248-54 | 42 |

| 1232 | Fine tuning of the Van Nuys prognostic index (VNPI) 2003 by integrating the genomic grade index (GGI): new tools for ductal carcinoma in situ (DCIS). **2011**, 17, 343-51 | 20 |

| 1231 | High-dimensional variable selection in meta-analysis for censored data. **2011**, 67, 504-12 | 7 |

| 1230 | Les signatures molšulaires des cancers du sein : le point de vue du pathologiste. **2011**, 2011, 43-47 | 2 |

| 1229 | Control of EVI-1 oncogene expression in metastatic breast cancer cells through microRNA miR-22. **2011**, 30, 1290-301 | 95 |

| 1228 | Breast tumor progression induced by loss of BTG2 expression is inhibited by targeted therapy with the ErbB/HER inhibitor lapatinib. **2011**, 30, 3084-95 | 48 |

| 1227 | Asf1b, the necessary Asf1 isoform for proliferation, is predictive of outcome in breast cancer. **2011**, 30, 480-93 | 112 |

| 1226 | S04 Molecular classification of breast cancer and its emerging clinical relevance. **2011**, 20, S2-S3 | 1 |

| 1225 | S05 Molecular mechanisms which predict response to chemotherapy. **2011**, 20, S3 | 4 |

| 1224 | Adjuvant chemotherapy in luminal breast cancers. **2011**, 20 Suppl 3, S128-31 | 13 |

| 1223 | Complementary gene signature integration in multiplatform microarray experiments. **2011**, 15, 155-63 | 3 |

| 1222 | Multiple-input multiple-output causal strategies for gene selection. **2011**, 12, 458 | 2 |

| 1221 | AnyExpress: integrated toolkit for analysis of cross-platform gene expression data using a fast interval matching algorithm. **2011**, 12, 75 | 10 |

| 1220 | E2F1 and KIAA0191 expression predicts breast cancer patient survival. **2011**, 4, 95 | 12 |

1219 Integration of gene signatures using biological knowledge. **2011**, 53, 57-71   4

1218 SATB1 gene expression and breast cancer prognosis. **2011**, 20, 309-13   36

1217 Twist1-induced invadopodia formation promotes tumor metastasis. **2011**, 19, 372-86   350

1216 Proinvasion metastasis drivers in early-stage melanoma are oncogenes. **2011**, 20, 92-103   116

1215 A Pin1/mutant p53 axis promotes aggressiveness in breast cancer. **2011**, 20, 79-91   209

1214 Management and outcome of HER2-positive early breast cancer treated with or without trastuzumab in the adjuvant trastuzumab era. **2011**, 11, 93-102   13

1213 Gene profiling assay and application: the predictive role in primary therapy. **2011**, 2011, 124-7   8

1212 Ep-CAM RNA expression predicts metastasis-free survival in three cohorts of untreated node-negative breast cancer. **2011**, 125, 637-46   22

1211 A gene expression signature identifies two prognostic subgroups of basal breast cancer. **2011**, 126, 407-20   192

1210 Gene expression profile predicts outcome after anthracycline-based adjuvant chemotherapy in early breast cancer. **2011**, 127, 363-73   7

1209 Patterns and incidence of chromosomal instability and their prognostic relevance in breast cancer subtypes. **2011**, 128, 23-30   67

1208 MIB1/Ki-67 labelling index can classify grade 2 breast cancer into two clinically distinct subgroups. **2011**, 127, 591-9   82

1207 Development of 95-gene classifier as a powerful predictor of recurrences in node-negative and ER-positive breast cancer patients. **2011**, 128, 633-41   36

1206 High-resolution analyses of gene copy number reveal new insights into the prognosis and progression of breast cancers. **2011**, 128, 41-3

1205 Time to move forward from "first-generation" prognostic gene signatures in early breast cancer. **2011**, 128, 643-5   1

1204 Gene expression profiling of luminal B breast cancers reveals NHERF1 as a new marker of endocrine resistance. **2011**, 130, 409-20   27

1203 Breast cancer as heterogeneous disease: contributing factors and carcinogenesis mechanisms. **2011**, 128, 483-93   32

1202 Biologic markers determine both the risk and the timing of recurrence in breast cancer. **2011**, 129, 607-16   75

1201	First generation prognostic gene signatures for breast cancer predict both survival and chemotherapy sensitivity and identify overlapping patient populations. **2011**, 130, 155-64	31
1200	Multidimensional scaling with discrimination coefficients for supervised visualization of high-dimensional data. **2011**, 20, 1211-1218	1
1199	Molecular characterization of early adenocarcinoma of the uterine cervix by oligonucleotide microarray. **2011**, 283, 861-9	1
1198	Prise en charge du cancer du sein infiltrant de la femme âge de 40 ans ou moins. **2011**, 13, 703-726	1
1197	CEACAM1 cytoplastic expression is closely related to tumor angiogenesis and poorer relapse-free survival after curative resection of hepatocellular carcinoma. **2011**, 35, 2259-65	11
1196	Empirical study for the agreement between statistical methods in quality assessment and control of microarray data. **2011**, 26, 259-277	1
1195	Molecular genetic tests in the prediction of the prognosis of breast cancer. **2011**, 4, 158	
1194	Protein expression based multimarker analysis of breast cancer samples. **2011**, 11, 230	30
1193	A simple method for assigning genomic grade to individual breast tumours. **2011**, 11, 306	3
1192	PAX2 is activated by estradiol in breast cancer cells of the luminal subgroup selectively, to confer a low invasive phenotype. **2011**, 10, 148	19
1191	Kinome expression profiling and prognosis of basal breast cancers. **2011**, 10, 86	40
1190	Postmastectomy irradiation in breast in breast cancer patients with T1-2 and 1-3 positive axillary lymph nodes: is there a role for radiation therapy?. **2011**, 6, 28	28
1189	Inferring causal genomic alterations in breast cancer using gene expression data. **2011**, 5, 121	46
1188	Quantifying differential gene connectivity between disease states for objective identification of disease-relevant genes. **2011**, 5, 89	15
1187	Building prognostic models for breast cancer patients using clinical variables and hundreds of gene expression signatures. **2011**, 4, 3	104
1186	A Normalized Tree Index for identification of correlated clinical parameters in microarray experiments. **2011**, 4, 2	2
1185	Consistent metagenes from cancer expression profiles yield agent specific predictors of chemotherapy response. **2011**, 12, 310	2
1184	Context-specific gene regulatory networks subdivide intrinsic subtypes of breast cancer. **2011**, 12 Suppl 2, S3	3

1165	Handbook of Metastatic Breast Cancer. **2011**,		
1164	Differential gene expression in primary breast tumors associated with lymph node metastasis. **2011**, 2011, 142763		13
1163	Paradoxical relationship between chromosomal instability and survival outcome in cancer. **2011**, 71, 3447-52		234
1162	Low residual proliferation after short-term letrozole therapy is an early predictive marker of response in high proliferative ER-positive breast cancer. **2011**, 18, 721-30		6
1161	New developments in hormone receptor-positive disease. **2011**, 16 Suppl 1, 40-50		13
1160	PRO_10--a new tissue-based prognostic multigene marker in patients with early estrogen receptor-positive breast cancer. **2011**, 78, 140-8		3
1159	Molecular classification of breast cancer: is it time to pack up our microscopes?. **2011**, 43, 1-8		20
1158	Traitements mďicaux des cancers du sein RH+ Her2â**2011**, 98, 655-670		4
1157	Activation of the glucocorticoid receptor is associated with poor prognosis in estrogen receptor-negative breast cancer. **2011**, 71, 6360-70		172
1156	Can some patients avoid adjuvant chemotherapy for early-stage breast cancer?. **2011**, 8, 272-9		25
1155	Basal phenotype breast cancer: implications for treatment and prognosis. **2011**, 7, 181-202		19
1154	A CD133-related gene expression signature identifies an aggressive glioblastoma subtype with excessive mutations. **2011**, 108, 1591-6		94
1153	Independent surrogate variable analysis to deconvolve confounding factors in large-scale microarray profiling studies. **2011**, 27, 1496-505		194
1152	Effects of tissue handling on RNA integrity and microarray measurements from resected breast cancers. *Journal of the National Cancer Institute*, **2011**, 103, 1871-83	9.7	84
1151	Manipulating protein acetylation in breast cancer: a promising approach in combination with hormonal therapies?. **2011**, 2011, 856985		25
1150	Molecular characterization of the tumor-suppressive function of nischarin in breast cancer. *Journal of the National Cancer Institute*, **2011**, 103, 1513-28	9.7	46
1149	Gene signatures of genomic instability as prognostic tools for breast cancer. **2011**, 7, 591-4		7
1148	Relationship of extreme chromosomal instability with long-term survival in a retrospective analysis of primary breast cancer. **2011**, 20, 2183-94		114

1147   Most random gene expression signatures are significantly associated with breast cancer outcome. **2011**, 7, e1002240   384

1146   Oestrogen receptor-co-factor-chromatin specificity in the transcriptional regulation of breast cancer. **2011**, 30, 4764-76   95

1145   An "elite hacker": breast tumors exploit the normal microenvironment program to instruct their progression and biological diversity. **2012**, 6, 236-48   29

1144   Prediction of breast cancer metastasis by gene expression profiles: a comparison of metagenes and single genes. **2012**, 11, 193-217   5

1143   Genomic analyses to select patients for adjuvant chemotherapy: trials and tribulations. **2012**, 23 Suppl 10, x211-8   17

1142   Applying the 2011 St Gallen panel of prognostic markers on a large single hospital cohort of consecutively treated primary operable breast cancers. **2012**, 23, 2578-2584   40

1141   Application of microarray in breast cancer: An overview. **2012**, 4, 21-6   39

1140   Interactome-transcriptome integration for predicting distant metastasis in breast cancer. **2012**, 28, 672-8   21

1139   Lost in translation? Estrogen receptor status and endocrine responsiveness in breast cancer. **2012**, 30, 686-9   24

1138   Opposing effects of Runx2 and estradiol on breast cancer cell proliferation: in vitro identification of reciprocally regulated gene signature related to clinical letrozole responsiveness. **2012**, 18, 901-11   39

1137   Caveats and pitfalls of ROC analysis in clinical microarray research (and how to avoid them). **2012**, 13, 83-97   68

1136   Molecular classification of estrogen receptor-positive/luminal breast cancers. **2012**, 19, 39-53   53

1135   Induction of the RNA regulator LIN28A is required for the growth and pathogenesis of RESTless breast tumors. **2012**, 72, 3207-16   11

1134   A 50-gene intrinsic subtype classifier for prognosis and prediction of benefit from adjuvant tamoxifen. **2012**, 18, 4465-72   215

1133   Cancers du sein triples nǵatifs: Jusquâ€doit-on aller dans le bilan histologique?. **2012**, 565-570

1132   Microarrays in Diagnostics and Biomarker Development. **2012**,   3

1131   Assessing the clinical relevance of oncogenic pathways in neoadjuvant breast cancer. **2012**, 30, 1912-5   6

1130   Elucidating prognosis and biology of breast cancer arising in young women using gene expression profiling. **2012**, 18, 1341-51   239

1129   Prognose beim Mammakarzinom. **2012**, 44, 17-25   1

1128   Integrating breast cancer genetics into clinical practice. **2012**, 8, 99-112   4

1127   Decision-making tools to assist prognosis and treatment choices in early breast cancer: a review. **2012**, 12, 1033-43   3

1126   Immunoglobulin kappa chain as an immunologic biomarker of prognosis and chemotherapy response in solid tumors. **2012**, 1, 1156-1158   15

1125   Targeting of the adaptor protein Tab2 as a novel approach to revert tamoxifen resistance in breast cancer cells. **2012**, 31, 4353-61   21

1124   Genomic Grade Index predicts postoperative clinical outcome of GIST. **2012**, 107, 1433-41   13

1123   Independent and functional validation of a multi-tumour-type proliferation signature. **2012**, 107, 508-15   9

1122   A three-gene model to robustly identify breast cancer molecular subtypes. *Journal of the National Cancer Institute*, **2012**, 104, 311-25   9.7   218

1121   Characterization and clinical evaluation of CD10+ stroma cells in the breast cancer microenvironment. **2012**, 18, 1004-14   39

1120   Cyclin E2 overexpression is associated with endocrine resistance but not insensitivity to CDK2 inhibition in human breast cancer cells. **2012**, 11, 1488-99   101

1119   Cancer du sein. **2012**,

1118   Search for a gene expression signature of breast cancer local recurrence in young women. **2012**, 18, 1704-15   56

1117   Expression profiling during mammary epithelial cell three-dimensional morphogenesis identifies PTPRO as a novel regulator of morphogenesis and ErbB2-mediated transformation. **2012**, 32, 3913-24   29

1116   Immunohistochemical analysis of the ubiquitin-conjugating enzyme UbcH10 in lung cancer: a useful tool for diagnosis and therapy. **2012**, 60, 359-65   24

1115   Gene modules and response to neoadjuvant chemotherapy in breast cancer subtypes: a pooled analysis. **2012**, 30, 1996-2004   167

1114   YB-1, the E2F pathway, and regulation of tumor cell growth. *Journal of the National Cancer Institute*, **2012**, 104, 133-46   9.7   79

1113   Protein arginine methyltransferase 6-dependent gene expression and splicing: association with breast cancer outcomes. **2012**, 19, 509-26   25

1112   Systems vaccinology: its promise and challenge for HIV vaccine development. **2012**, 7, 24-31   43

1111   Profiling the immune stromal interface in breast cancer and its potential for clinical impact. **2012**, 7, 273-80   6

1110   Systems analysis of eleven rodent disease models reveals an inflammatome signature and key drivers. **2012**, 8, 594   95

1109   A gene signature for predicting outcome in patients with basal-like breast cancer. **2012**, 2, 227   48

1108   Basal breast cancer: a complex and deadly molecular subtype. **2012**, 12, 96-110   139

1107   Molecular profiling for stage II colon cancer. **2012**, 1, 479-490

1106   Hierarchical modularity in ERÂ transcriptional network is associated with distinct functions and implicates clinical outcomes. **2012**, 2, 875   24

1105   Global gene expression profiling in mouse plasma cell tumor precursor and bystander cells reveals potential intervention targets for plasma cell neoplasia. **2012**, 119, 1018-28   5

1104   Molecular biology in breast cancer: intrinsic subtypes and signaling pathways. **2012**, 38, 698-707   342

1103   Molecular pathology of breast cancer: what a pathologist needs to know. **2012**, 138, 770-80   66

1102   Explaining Subgroups through Ontologies. **2012**, 625-636   1

1101   Predictive biomarkers in breast cancer: their value in neoadjuvant chemotherapy. **2012**, 30, 663-78   15

1100   microRNAs in cancer management. **2012**, 13, e249-58   596

1099   Centromere protein-A, an essential centromere protein, is a prognostic marker for relapse in estrogen receptor-positive breast cancer. **2012**, 14, R72   80

1098   The gene expression landscape of breast cancer is shaped by tumor protein p53 status and epithelial-mesenchymal transition. **2012**, 14, R113   36

1097   Proliffation et signatures ADN de complexit° gÎomique pour la dÎfinition du pronostic des carcinomes mammaires. **2012**, 14, 502-505

1096   Les signatures molČulaires sur paraffine dans le cancer du sein : le point de vue du pathologiste. **2012**, 14, 506-511

1095   PAM50 assay and the three-gene model for identifying the major and clinically relevant molecular subtypes of breast cancer. **2012**, 135, 301-6   117

1094   A prognostic model of early breast cancer relapse after standard adjuvant therapy and comparison with metastatic disease on initial presentation. **2012**, 136, 565-72   12

1093	Nuclear karyopherin a2: a novel biomarker for infiltrative astrocytomas. **2012**, 109, 545-53	42
1092	The prognostic value of temporal in vitro and in vivo derived hypoxia gene-expression signatures in breast cancer. **2012**, 102, 436-43	37
1091	Association of autotaxin and lysophosphatidic acid receptor 3 with aggressiveness of human breast carcinoma. **2012**, 33, 2237-43	38
1090	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
1089	Global enhancement of nuclear localization-dependent nuclear transport in transformed cells. **2012**, 26, 1181-93	43
1088	Prediction of histologic grade in breast cancer using an artificial neural network. **2012**,	1
1087	Integrated proteomic, transcriptomic, and biological network analysis of breast carcinoma reveals molecular features of tumorigenesis and clinical relapse. **2012**, 11, M111.014910	38
1086	A mitotically active, cellular tumor stroma and/or inflammatory cells associated with tumor cells may contribute to intermediate or high Oncotype DX Recurrence Scores in low-grade invasive breast carcinomas. **2012**, 25, 556-66	50
1085	Binding of FoxM1 to G2/M gene promoters is dependent upon B-Myb. **2012**, 1819, 855-62	64
1084	Estrogen receptor positive breast cancer identified by 95-gene classifier as at high risk for relapse shows better response to neoadjuvant chemotherapy. **2012**, 324, 42-7	10
1083	[Radiobiology and breast cancer molecular classification: present or future?]. **2012**, 16, 29-33	3
1082	Core module biomarker identification with network exploration for breast cancer metastasis. **2012**, 13, 12	31
1081	Prognostic gene signatures for patient stratification in breast cancer: accuracy, stability and interpretability of gene selection approaches using prior knowledge on protein-protein interactions. **2012**, 13, 69	34
1080	Improving biomarker list stability by integration of biological knowledge in the learning process. **2012**, 13 Suppl 4, S22	12
1079	Molecular characterisation of cell line models for triple-negative breast cancers. **2012**, 13, 619	60
1078	Peritumoral vascular invasion and NHERF1 expression define an immunophenotype of grade 2 invasive breast cancer associated with poor prognosis. **2012**, 12, 106	22
1077	Expression of aurora kinase A is associated with metastasis-free survival in node-negative breast cancer patients. **2012**, 12, 562	42
1076	A target based approach identifies genomic predictors of breast cancer patient response to chemotherapy. **2012**, 5, 16	13

1057	Amplified loci on chromosomes 8 and 17 predict early relapse in ER-positive breast cancers. **2012**, 7, e38575	24
1056	Identification of common prognostic gene expression signatures with biological meanings from microarray gene expression datasets. **2012**, 7, e45894	15
1055	[Genomics and clinical research for breast cancer]. **2012**, 28 Spec No 1, 14-8	2
1054	Using Variable Precision Rough Set for Selection and Classification of Biological Knowledge Integrated in DNA Gene Expression. **2012**, 9, 1-17	10
1053	[Are expression signatures worthless?]. **2012**, 28, 547-50	0
1052	Functional heterogeneity within the CD44 high human breast cancer stem cell-like compartment reveals a gene signature predictive of distant metastasis. **2012**, 18, 1109-21	67
1051	Robust microarray meta-analysis identifies differentially expressed genes for clinical prediction. **2012**, 2012, 989637	11
1050	Gene expression profiles for predicting metastasis in breast cancer: a cross-study comparison of classification methods. **2012**, 2012, 380495	7
1049	Identification of breast cancer prognosis markers using integrative sparse boosting. **2012**, 51, 152-61	5
1048	Estrogen receptor alpha deletion enhances the metastatic phenotype of Ron overexpressing mammary tumors in mice. **2012**, 11, 2	6
1047	A Ki67/BCL2 index based on immunohistochemistry is highly prognostic in ER-positive breast cancer. **2012**, 226, 97-107	61
1046	CERT depletion predicts chemotherapy benefit and mediates cytotoxic and polyploid-specific cancer cell death through autophagy induction. **2012**, 226, 482-94	42
1045	Biomarker discovery using a comparative omics approach in a mouse model developing heterogeneous mammary cancer subtypes. **2012**, 12, 2149-57	5
1044	Strategies for the discovery and development of therapies for metastatic breast cancer. **2012**, 11, 479-97	249
1043	Integrated cross-species transcriptional network analysis of metastatic susceptibility. **2012**, 109, 3184-9	42
1042	Are expression profiles meaningless for cancer studies?. **2012**, 34, 730-3	3
1041	The present and future of gene profiling in breast cancer. **2012**, 31, 41-6	12
1040	Expression of the novel human gene, UBE2Q1, in breast tumors. **2012**, 39, 5135-41	13

1039	A prognostic model for lymph node-negative breast cancer patients based on the integration of proliferation and immunity. **2012**, 132, 499-509	15
1038	RecurrenceOnline: an online analysis tool to determine breast cancer recurrence and hormone receptor status using microarray data. **2012**, 132, 1025-34	76
1037	Characterisation of amplification patterns and target genes at chromosome 11q13 in CCND1-amplified sporadic and familial breast tumours. **2012**, 133, 583-94	37
1036	SLC22A5/OCTN2 expression in breast cancer is induced by estrogen via a novel intronic estrogen-response element (ERE). **2012**, 134, 101-15	32
1035	Nucleobindin 2 in human breast carcinoma as a potent prognostic factor. **2012**, 103, 136-43	43
1034	A review of the biological and clinical characteristics of luminal-like oestrogen receptor-positive breast cancer. **2012**, 60, 854-63	18
1033	Improved modeling of clinical data with kernel methods. **2012**, 54, 103-14	11
1032	Genomic analysis: toward a new approach in breast cancer management. **2012**, 81, 207-23	20
1031	Identification of Breast Cancer Prognosis Markers via Integrative Analysis. **2012**, 56, 2718-2728	3
1030	Immunohistochemical Ki67 labeling index has similar proliferation predictive power to various gene signatures in breast cancer. **2012**, 103, 1508-12	39
1029	Tailored chemotherapy based on tumour gene expression analysis: breast cancer patients' misinterpretations and positive attitudes. **2012**, 21, 242-50	22
1028	Identifying transcription factors and microRNAs as key regulators of pathways using Bayesian inference on known pathway structures. **2012**, 10 Suppl 1, S15	6
1027	Prognostic value of proliferation assay in the luminal, HER2-positive, and triple-negative biologic classes of breast cancer. **2012**, 14, R3	94
1026	Combination of the proliferation marker cyclin A, histological grade, and estrogen receptor status in a new variable with high prognostic impact in breast cancer. **2012**, 131, 33-40	12
1025	The application of gene co-expression network reconstruction based on CNVs and gene expression microarray data in breast cancer. **2012**, 39, 1627-37	15
1024	Principal Composite Kernel Feature Analysis: Data-Dependent Kernel Approach. **2013**, 25, 1863-1875	20
1023	Interactions between immunity, proliferation and molecular subtype in breast cancer prognosis. **2013**, 14, R34	131
1022	Molecular profiling of prostatic acinar morphogenesis identifies PDCD4 and KLF6 as tissue architecture-specific prognostic markers in prostate cancer. **2013**, 182, 363-74	9

| 1021 | Cancer Genomics. **2013**, | 4 |

| 1020 | A meta-analysis of gene expression-based biomarkers predicting outcome after tamoxifen treatment in breast cancer. **2013**, 140, 219-32 | 140 |

| 1019 | The emerging role of the molecular diagnostics laboratory in breast cancer personalized medicine. **2013**, 183, 1075-1083 | 28 |

| 1018 | Gene expression profiling of breast cancer survivability by pooled cDNA microarray analysis using logistic regression, artificial neural networks and decision trees. **2013**, 14, 100 | 24 |

| 1017 | Biclustering reveals breast cancer tumour subgroups with common clinical features and improves prediction of disease recurrence. **2013**, 14, 102 | 19 |

| 1016 | Luminal breast cancer: from biology to treatment. **2013**, 10, 494-506 | 123 |

| 1015 | Caractéristiques des carcinomes mammaires triple-négatifs dans lâOuest-algérien. **2013**, 5, 155-161 | 2 |

| 1014 | Multigene assays and molecular markers in breast cancer: systematic review of health economic analyses. **2013**, 139, 621-37 | 66 |

| 1013 | ROCK: a resource for integrative breast cancer data analysis. **2013**, 139, 907-21 | 27 |

| 1012 | Molecular subtypes, histopathological grade and survival in a historic cohort of breast cancer patients. **2013**, 140, 463-73 | 143 |

| 1011 | Breast Cancer Metastasis and Drug Resistance. **2013**, | 5 |

| 1010 | Breast Cancer Heterogeneity in Primary and Metastatic Disease. **2013**, 65-95 | 1 |

| 1009 | FOXM1 (Forkhead box M1) in tumorigenesis: overexpression in human cancer, implication in tumorigenesis, oncogenic functions, tumor-suppressive properties, and target of anticancer therapy. **2013**, 119, 191-419 | 115 |

| 1008 | Genomic classifications and radiotherapy for breast cancer. **2013**, 717, 67-70 | 8 |

| 1007 | Influence of genomics on adjuvant treatments for pre-invasive and invasive breast cancer. **2013**, 22 Suppl 2, S83-7 | 5 |

| 1006 | Pitfalls in outcome prediction of breast cancer. **2013**, 66, 458-64 | 26 |

| 1005 | Breast Cancer Biomarkers: Utility in Clinical Practice. **2013**, 5, 284 | 15 |

| 1004 | Prognostische und prädiktive Faktoren. **2013**, 183-201 | |

985	Comparison of Oncotype DX and Mammostrat risk estimations and correlations with histologic tumor features in low-grade, estrogen receptor-positive invasive breast carcinomas. **2013**, 26, 1451-60	25
984	Gene expression profiling in breast cancer: a clinical perspective. **2013**, 22, 109-120	56
983	Change in the microenvironment of breast cancer studied by FTIR imaging. **2013**, 138, 4058-65	65
982	Molecular and clinicopathological markers of prognosis in breast cancer. **2013**, 13, 481-98	4
981	The combination of Ki67, histological grade and estrogen receptor status identifies a low-risk group among 1,854 chemo-naïve women with N0/N1 primary breast cancer. **2013**, 2, 111	11
980	A categorical network approach for discovering differentially expressed regulations in cancer. **2013**, 6 Suppl 3, S1	4
979	DNA repair gene patterns as prognostic and predictive factors in molecular breast cancer subtypes. **2013**, 18, 1063-73	64
978	PAM50 proliferation score as a predictor of weekly paclitaxel benefit in breast cancer. **2013**, 138, 457-66	78
977	Agreement for tumor grade of ovarian carcinoma: analysis of archival tissues from the surveillance, epidemiology, and end results residual tissue repository. **2013**, 24, 749-57	23
976	Symbolic data analysis to defy low signal-to-noise ratio in microarray data for breast cancer prognosis. **2013**, 20, 610-20	4
975	Grading breast cancer tissues using molecular portraits. **2013**, 12, 3612-23	25
974	Multigene Assays for Classification, Prognosis, and Prediction in Breast Cancer: a Critical Review on the Background and Clinical Utility. **2013**, 73, 932-940	46
973	[Personalized medicine and breast cancer: anticipatory medicine, prognostic evaluation and therapeutic targeting]. **2013**, 100, 1295-310	3
972	Differences in degradation lead to asynchronous expression of cyclin E1 and cyclin E2 in cancer cells. **2013**, 12, 596-605	28
971	Gene expression profile analysis of t1 and t2 breast cancer reveals different activation pathways. **2013**, 2013, 924971	2
970	Biomolecular events in cancer revealed by attractor metagenes. **2013**, 9, e1002920	78
969	Integrative analysis of cancer-related signaling pathways. **2013**, 4, 124	9
968	Overview of diagnostic/targeted treatment combinations in personalized medicine for breast cancer patients. **2013**, 7, 1-19	8

967   Genomic grade adds prognostic value in invasive lobular carcinoma. **2013**, 24, 377-384   35

966   Classification of tumor samples from expression data using decision trunks. **2013**, 12, 53-66   3

965   Significance analysis of prognostic signatures. **2013**, 9, e1002875   22

964   Prognostic discrimination using a 70-gene signature among patients with estrogen receptor-positive breast cancer and an intermediate 21-gene recurrence score. **2013**, 14, 23685-99   13

963   Genome-wide reprogramming of the chromatin landscape underlies endocrine therapy resistance in breast cancer. **2013**, 110, E1490-9   120

962   Utility of prognostic genomic tests in breast cancer practice: The IMPAKT 2012 Working Group Consensus Statement. **2013**, 24, 647-54   96

961   Progression of Early Breast Cancer to an Invasive Phenotype. **2013**, 143-159   0

960   Comparison of the prognostic value of genomic grade index, Ki67 expression and mitotic activity index in early node-positive breast cancer patients. **2013**, 24, 625-32   26

959   Breast Cancer Genomics: From Portraits to Landscapes. **2013**, 255-294

958   GDNF-RET signaling in ER-positive breast cancers is a key determinant of response and resistance to aromatase inhibitors. **2013**, 73, 3783-95   74

957   In silico discovery of mitosis regulation networks associated with early distant metastases in estrogen receptor positive breast cancers. **2013**, 12, 31-51   13

956   From High-Throughput Microarray-Based Screening to Clinical Application: The Development of a Second Generation Multigene Test for Breast Cancer Prognosis. **2013**, 2, 243-64   4

955   Combined analysis of vascular invasion, grade, HER2 and Ki67 expression identifies early breast cancer patients with questionable benefit of systemic adjuvant therapy. **2013**, 52, 91-101   18

954   Improving Pathological Assessment of Breast Cancer by Employing Array-Based Transcriptome Analysis. **2013**, 2, 228-42   20

953   Genomic approaches in breast cancer research. **2013**, 12, 391-6   13

952   Treatment of estrogen receptor-positive breast cancer. **2013**, 20, 596-604   142

951   Genomic profiling in luminal breast cancer. **2013**, 8, 414-22   10

950   Low cdc27 and high securin expression predict short survival for breast cancer patients. **2013**, 121, 945-53   15

949	Omnibus risk assessment via accelerated failure time kernel machine modeling. **2013**, 69, 861-73	6
948	Clinical and pathologic risk factors of tumor recurrence in patients with node-negative early breast cancer after mastectomy. **2013**, 108, 352-7	12
947	Identification of p130Cas/ErbB2-dependent invasive signatures in transformed mammary epithelial cells. **2013**, 12, 2409-22	17
946	Prognostic microRNA/mRNA signature from the integrated analysis of patients with invasive breast cancer. **2013**, 110, 7413-7	128
945	Development of a prognostic model for breast cancer survival in an open challenge environment. **2013**, 5, 181ra50	91
944	Sparse latent factor models with interactions: Analysis of gene expression data. **2013**, 7,	10
943	An optimized five-gene multi-platform predictor of hormone receptor negative and triple negative breast cancer metastatic risk. **2013**, 15, R103	25
942	Determining epithelial contribution to in vivo mesenchymal tumour expression signature using species-specific microarray profiling analysis of xenografts. **2013**, 95, 14-29	2
941	Architecture of epigenetic reprogramming following Twist1-mediated epithelial-mesenchymal transition. **2013**, 14, R144	63
940	How useful are molecular assays in breast cancer in the elderly?. **2013**, 9, 291-305	1
939	Biological NetworksâBased Analysis of Gene Expression Signatures. **2013**, 495-506	
938	[Simplified, low-cost gene expression profiling for the prediction of outcome in breast cancer based on routine histologic specimens]. **2013**, 154, 627-32	
937	Proliferation and estrogen signaling can distinguish patients at risk for early versus late relapse among estrogen receptor positive breast cancers. **2013**, 15, R86	33
936	Modeling precision treatment of breast cancer. **2013**, 14, R110	204
935	Expression of VEGF and semaphorin genes define subgroups of triple negative breast cancer. **2013**, 8, e61788	53
934	A data similarity-based strategy for meta-analysis of transcriptional profiles in cancer. **2013**, 8, e54979	4
933	Long-term prognostic performance of Ki67 rate in early stage, pT1-pT2, pN0, invasive breast carcinoma. **2013**, 8, e55901	25
932	Neoplastic and stromal cells contribute to an extracellular matrix gene expression profile defining a breast cancer subtype likely to progress. **2013**, 8, e56761	38

| 931 | Decreased FOXF2 mRNA expression indicates early-onset metastasis and poor prognosis for breast cancer patients with histological grade II tumor. **2013**, 8, e61591 | 38 |

| 930 | Association between SPARC mRNA expression, prognosis and response to neoadjuvant chemotherapy in early breast cancer: a pooled in-silico analysis. **2013**, 8, e62451 | 23 |

| 929 | Genomic Grade Index (GGI): feasibility in routine practice and impact on treatment decisions in early breast cancer. **2013**, 8, e66848 | 13 |

| 928 | Wnt pathway activity in breast cancer sub-types and stem-like cells. **2013**, 8, e67811 | 106 |

| 927 | Dual-color fluorescence in situ hybridization reveals an association of chromosome 8q22 but not 8p21 imbalance with high grade invasive breast carcinoma. **2013**, 8, e70790 | 9 |

| 926 | Molecular phenotypes in triple negative breast cancer from African American patients suggest targets for therapy. **2013**, 8, e71915 | 49 |

| 925 | Infrequent loss of luminal differentiation in ductal breast cancer metastasis. **2013**, 8, e78097 | 5 |

| 924 | . **2013**, | 0 |

| 923 | Molecular profiling and therapeutic decision-making: the promise of personalized medicine. 929-935 | |

| 922 | Adjuvant chemotherapy: which patient? What regimen?. **2013**, 3-8 | 3 |

| 921 | A core invasiveness gene signature reflects epithelial-to-mesenchymal transition but not metastatic potential in breast cancer cell lines and tissue samples. **2014**, 9, e89262 | 9 |

| 920 | Gasdermin-B promotes invasion and metastasis in breast cancer cells. **2014**, 9, e90099 | 67 |

| 919 | Integration of mRNA expression profile, copy number alterations, and microRNA expression levels in breast cancer to improve grade definition. **2014**, 9, e97681 | 46 |

| 918 | Systematic pathway enrichment analysis of a genome-wide association study on breast cancer survival reveals an influence of genes involved in cell adhesion and calcium signaling on the patients' clinical outcome. **2014**, 9, e98229 | 14 |

| 917 | Increased macroH2A1.1 expression correlates with poor survival of triple-negative breast cancer patients. **2014**, 9, e98930 | 16 |

| 916 | Do breast cancer cell lines provide a relevant model of the patient tumor methylome?. **2014**, 9, e105545 | 15 |

| 915 | Functional analysis of prognostic gene expression network genes in metastatic breast cancer models. **2014**, 9, e111813 | 10 |

| 914 | RRHGE: a novel approach to classify the estrogen receptor based breast cancer subtypes. **2014**, 2014, 362141 | 3 |

913	Endocrine Resistance in Breast Cancer. **2014**, 2014, 1-27		40
912	Breast cancer prognosis risk estimation using integrated gene expression and clinical data. **2014**, 2014, 459203		5
911	Overexpression of Raf-1 in basal-like carcinoma of the breast: correlation with clinicopathology and prognosis. **2014**, 18, 391-5		1
910	Hypoxia-inducible factor 1 mediates TAZ expression and nuclear localization to induce the breast cancer stem cell phenotype. **2014**, 5, 12509-27		83
909	Computational drug designing of fungal pigments as potential aromatase inhibitors. **2014**, 9,		5
908	Ceramide kinase promotes tumor cell survival and mammary tumor recurrence. **2014**, 74, 6352-63		46
907	Microarray big data integrated analysis to identify robust diagnostic signature for triple negative breast cancer. **2014**,		1
906	Meta-analysis of the global gene expression profile of triple-negative breast cancer identifies genes for the prognostication and treatment of aggressive breast cancer. **2014**, 3, e100		45
905	Invasive Breast Carcinoma. **2014**, 934-951		3
904	Outcomes of HER2-positive early breast cancer patients in the pre-trastuzumab and trastuzumab eras: a real-world multicenter observational analysis. The RETROHER study. **2014**, 147, 599-607		32
903	PRMT2 and ROR expression are associated with breast cancer survival outcomes. **2014**, 28, 1166-85		36
902	Construction and investigation of breast-cancer-specific ceRNA network based on the mRNA and miRNA expression data. **2014**, 8, 96-103		58
901	Frequent MYC coamplification and DNA hypomethylation of multiple genes on 8q in 8p11-p12-amplified breast carcinomas. **2014**, 3, e95		48
900	Identification and validation of an anthracycline/cyclophosphamide-based chemotherapy response assay in breast cancer. *Journal of the National Cancer Institute*, **2014**, 106, djt335	9.7	73
899	Breast Cancer Survival Defined by the ER/PR/HER2 Subtypes and a Surrogate Classification according to Tumor Grade and Immunohistochemical Biomarkers. **2014**, 2014, 469251		128
898	Current Clinical Role of Genetic Profiling in Breast Cancer. **2014**, 15-34		
897	The critical role of the pathologist in determining eligibility for active surveillance as a management option in patients with prostate cancer: consensus statement with recommendations supported by the College of American Pathologists, International Society of Urological Pathology, Association of Directors of Anatomic and Surgical Pathology, the New Zealand Society of		99
896	Integrated microarray analytics for the discovery of gene signatures for triple-negative breast cancer. **2014**,		1

895   The Coxlogit model: Feature selection from survival and classification data. **2014**,

894   omniClassifier: a Desktop Grid Computing System for Big Data Prediction Modeling. **2014**, 2014, 514-523   2

893   Multigene Assays for Classification, Prognosis, and Prediction in Breast Cancer: a Critical Review on the Background and Clinical Utility. **2014**, 11, 153-161

892   Pathway-based expression profile for breast cancer diagnoses. **2014**, 2014, 1151-4   3

891   Construction of novel immune-related signature for prediction of pathological complete response to neoadjuvant chemotherapy in human breast cancer. **2014**, 25, 100-6   26

890   Additive effect of the AZGP1, PIP, S100A8 and UBE2C molecular biomarkers improves outcome prediction in breast carcinoma. **2014**, 134, 1617-29   43

889   Molecular phenotype of the foci in multifocal invasive breast carcinomas: intertumoral heterogeneity is related to shorter survival and may influence the choice of therapy. **2014**, 120, 26-34   30

888   Raf kinase inhibitory protein role in the molecular subtyping of breast cancer. **2014**, 115, 488-97   9

887   The cyclin D1-CDK4 oncogenic interactome enables identification of potential novel oncogenes and clinical prognosis. **2014**, 13, 2889-900   23

886   Validation of the prognostic gene portfolio, ClinicoMolecular Triad Classification, using an independent prospective breast cancer cohort and external patient populations. **2014**, 16, R71   6

885   TheHOXB13:IL17BRbiomarker: prognostic for late recurrence and predictive for ?benefit from endocrine therapy. **2014**, 3, 155-163

884   Transfer of clinically relevant gene expression signatures in breast cancer: from Affymetrix microarray to Illumina RNA-Sequencing technology. **2014**, 15, 1008   45

883   Prognostic and therapeutic significance of ribonucleotide reductase small subunit M2 in estrogen-negative breast cancers. **2014**, 14, 664   31

882   Estrogen independent gene expression defines clinically relevant subgroups of estrogen receptor positive breast cancer. **2014**, 14, 871   2

881   Claudin-low breast cancers: clinical, pathological, molecular and prognostic characterization. **2014**, 13, 228   73

880   When is a vesicle not just a vesicle: mitochondrial spheroids and mitochondrial autophagosomes. **2014**, 4, 66   6

879   Pathway activity inference for multiclass disease classification through a mathematical programming optimisation framework. **2014**, 15, 390   4

878   Predicting breast cancer using an expression values weighted clinical classifier. **2014**, 15, 411   8

| 877 | HeatmapGenerator: high performance RNAseq and microarray visualization software suite to examine differential gene expression levels using an R and C++ hybrid computational pipeline. **2014**, 9, 30 | 32 |

| 876 | Identification by array comparative genomic hybridization of a new amplicon on chromosome 17q highly recurrent in BRCA1 mutated triple negative breast cancer. **2014**, 16, 466 | 24 |

| 875 | E2F4 regulatory program predicts patient survival prognosis in breast cancer. **2014**, 16, 486 | 39 |

| 874 | Cancer progression modeling using static sample data. **2014**, 15, 440 | 18 |

| 873 | Effect of aromatase inhibition on functional gene modules in estrogen receptor-positive breast cancer and their relationship with antiproliferative response. **2014**, 20, 2485-94 | 34 |

| 872 | Chromosomal instability selects gene copy-number variants encoding core regulators of proliferation in ER+ breast cancer. **2014**, 74, 4853-4863 | 42 |

| 871 | Cross-study validation for the assessment of prediction algorithms. **2014**, 30, i105-12 | 44 |

| 870 | The PAM50 risk-of-recurrence score predicts risk for late distant recurrence after endocrine therapy in postmenopausal women with endocrine-responsive early breast cancer. **2014**, 20, 1298-305 | 144 |

| 869 | Association of H3K9me3 and H3K27me3 repressive histone marks with breast cancer subtypes in the Nurses' Health Study. **2014**, 147, 639-51 | 37 |

| 868 | Omics Approaches in Breast Cancer. **2014**, | 8 |

| 867 | Breast Cancer Genomics. **2014**, 53-103 | |

| 866 | Early invasive cancer and partial intraoperative electron radiation therapy of the breast: experience of the jules bordet institute. **2014**, 2014, 627352 | 10 |

| 865 | Mining genome sequencing data to identify the genomic features linked to breast cancer histopathology. **2014**, 5, 3 | 19 |

| 864 | Age-specific changes in intrinsic breast cancer subtypes: a focus on older women. **2014**, 19, 1076-83 | 85 |

| 863 | Using molecular profiles to tailor treatment in breast cancer: are they ready for prime time?. **2014**, 26, 21-6 | 1 |

| 862 | Más-o-menos: a simple sign averaging method for discrimination in genomic data analysis. **2014**, 30, 3062-9 | 29 |

| 861 | Global gene expression changes induced by prolonged cold ischemic stress and preservation method of breast cancer tissue. **2014**, 8, 717-27 | 21 |

| 860 | TP53 mutation-correlated genes predict the risk of tumor relapse and identify MPS1 as a potential therapeutic kinase in TP53-mutated breast cancers. **2014**, 8, 508-19 | 49 |

841   Maximum Likelihood Estimation of GEVD: Applications in Bioinformatics. **2014**, 11, 673-80   1

840   Infrared imaging in breast cancer: automated tissue component recognition and spectral characterization of breast cancer cells as well as the tumor microenvironment. **2014**, 139, 1044-56   55

839   The cell cycle profiling-risk score based on CDK1 and 2 predicts early recurrence in node-negative, hormone receptor-positive breast cancer treated with endocrine therapy. **2014**, 355, 217-23   12

838   Invasive lobular breast cancer and its variants: how special are they for systemic therapy decisions?. **2014**, 92, 235-57   51

837   On integrating multi-experiment microarray data. **2014**, 372, 20130136   5

836   Development of a prediction model for lymph node metastasis in luminal A subtype breast cancer: the possibility to omit sentinel lymph node biopsy. **2014**, 353, 52-8   9

835   Cell type-restricted activity of hnRNPM promotes breast cancer metastasis via regulating alternative splicing. **2014**, 28, 1191-203   143

834   Circulating tumor cell clusters are oligoclonal precursors of breast cancer metastasis. **2014**, 158, 1110-1122   1420

833   Luminal B breast cancer: molecular characterization, clinical management, and future perspectives. **2014**, 32, 2794-803   197

832   Selection of personalized patient therapy through the use of knowledge-based computational models that identify tumor-driving signal transduction pathways. **2014**, 74, 2936-45   51

831   Gene expression analysis in RA: towards personalized medicine. **2014**, 14, 93-106   50

830   Ensemble analyses improve signatures of tumour hypoxia and reveal inter-platform differences. **2014**, 15, 170   19

829   A computational model to predict bone metastasis in breast cancer by integrating the dysregulated pathways. **2014**, 14, 618   12

828   A program to identify prognostic and predictive gene signatures. **2014**, 7, 546   1

827   Refinement of breast cancer risk prediction with concordant leading edge subsets from prognostic gene signatures. **2014**, 147, 353-70   2

826   Prognostic and biological significance of proliferation and HER2 expression in the luminal class of breast cancer. **2014**, 145, 317-30   10

825   Karyopherin a2 and chromosome region maintenance protein 1 expression in meningiomas: novel biomarkers for recurrence and malignant progression. **2014**, 118, 289-296   8

824   Clinical drug response can be predicted using baseline gene expression levels and in vitro drug sensitivity in cell lines. **2014**, 15, R47   297

805	Next generation sequencing profiling identifies miR-574-3p and miR-660-5p as potential novel prognostic markers for breast cancer. **2015**, 16, 735	64
804	Appraisal of the technologies and review of the genomic landscape of ductal carcinoma in situ of the breast. **2015**, 17, 80	5
803	Delineating transcriptional networks of prognostic gene signatures refines treatment recommendations for lymph node-negative breast cancer patients. **2015**, 282, 3455-73	9
802	Dynamic classification using case-specific training cohorts outperforms static gene expression signatures in breast cancer. **2015**, 136, 2091-8	8
801	The importance of molecular markers for diagnosis and selection of targeted treatments in patients with cancer. **2015**, 278, 545-70	38
800	Offline Kernel Analysis. **2015**, 41-68	
799	Bayesian factor models for the detection of coherent patterns in gene expression data. **2015**, 29,	4
798	Urokinase plasminogen activator (uPA) and plasminogen activator inhibitor type-1 (PAI-1) in breast cancer - correlation with traditional prognostic factors. **2015**, 49, 357-64	23
797	Derivation of a fifteen gene prognostic panel for six cancers. **2015**, 5, 13248	19
796	Systems biology approach to studying proliferation-dependent prognostic subnetworks in breast cancer. **2015**, 5, 12981	11
795	Long-term outcomes among breast cancer patients with extensive regional lymph node involvement: implications for locoregional management. **2015**, 154, 633-9	2
794	Mechanistic-enriched models: integrating transcription factor networks and metabolic deregulation in cancer. **2015**, 12, 16	1
793	Extensive rewiring of epithelial-stromal co-expression networks in breast cancer. **2015**, 16, 128	31
792	A balanced hazard ratio for risk group evaluation from survival data. **2015**, 34, 2528-43	2
791	Integrating genetics and epigenetics in breast cancer: biological insights, experimental, computational methods and therapeutic potential. **2015**, 9, 62	34
790	Advances in the Molecular Analysis of Breast Cancer: Pathway Toward Personalized Medicine. **2015**, 22, 211-9	21
789	Association of molecular subtypes with breast cancer risk factors: a case-only analysis. **2015**, 24, 484-90	11
788	CCR 20th Anniversary Commentary: Gene-Expression Signature in Breast Cancer--Where Did It Start and Where Are We Now?. **2015**, 21, 4743-6	18

| 769 | Pathologic diagnosis, immunohistochemistry, multigene assays and breast cancer treatment: progress toward "precision" cancer therapy. **2015**, 90, 81-92 | 11 |

| 768 | miR-214 as a key hub that controls cancer networks: small player, multiple functions. **2015**, 135, 960-969 | 131 |

| 767 | Gene expression-based prognostic and predictive tools in breast cancer. **2015**, 22, 245-52 | 10 |

| 766 | Gene expression abnormalities in histologically normal breast epithelium from patients with luminal type of breast cancer. **2015**, 42, 977-88 | 20 |

| 765 | Mining cancer gene expression databases for latent information on intronic microRNAs. **2015**, 9, 473-87 | 4 |

| 764 | APOBEC3B expression in breast cancer reflects cellular proliferation, while a deletion polymorphism is associated with immune activation. **2015**, 112, 2841-6 | 95 |

| 763 | Multigene prognostic tests in breast cancer: past, present, future. **2015**, 17, 11 | 173 |

| 762 | Genomic predictor of residual risk of recurrence after adjuvant chemotherapy and endocrine therapy in high risk estrogen receptor-positive breast cancers. **2015**, 149, 789-97 | 4 |

| 761 | Gene-Expression-Based Predictors for Breast Cancer. **2015**, 22, 3418-32 | 19 |

| 760 | KPNA2 is a nuclear export protein that contributes to aberrant localisation of key proteins and poor prognosis of breast cancer. **2015**, 112, 1929-37 | 43 |

| 759 | [Molecular taxonomy of luminal breast cancer in 2015]. **2015**, 102, S34-46 | 5 |

| 758 | Has the time come for genomic tests to guide the use of adjuvant chemotherapy in node-positive breast cancer?. **2015**, 26, 1521-3 | 1 |

| 757 | Presence of insulin-like growth factor binding proteins correlates with tumor-promoting effects of matrix metalloproteinase 9 in breast cancer. **2015**, 17, 421-33 | 18 |

| 756 | Intra-tumour signalling entropy determines clinical outcome in breast and lung cancer. **2015**, 11, e1004115 | 33 |

| 755 | Multiscale characterization of ageing and cancer progression by a novel network entropy measure. **2015**, 11, 1824-31 | 14 |

| 754 | Commercialized biomarkers: new horizons in prostate cancer diagnostics. **2015**, 15, 491-503 | 10 |

| 753 | Fuzzy logic selection as a new reliable tool to identify molecular grade signatures in breast cancer--the INNODIAG study. **2015**, 8, 3 | 8 |

| 752 | Integrative analysis of survival-associated gene sets in breast cancer. **2015**, 8, 11 | 15 |

733   Transcriptional master regulator analysis in breast cancer genetic networks. **2015**, 59 Pt B, 67-77   39

732   Prediction of Clinical Drug Response Based on Differential Gene Expression Levels. **2015**, 480-488

731   LINC00472 expression is regulated by promoter methylation and associated with disease-free survival in patients with grade 2 breast cancer. **2015**, 154, 473-82   49

730   The role of cytokines in breast cancer development and progression. **2015**, 35, 1-16   256

729   Pathway-level disease data mining through hyper-box principles. **2015**, 260, 25-34   5

728   Molecular markers for breast cancer diagnosis, prognosis and targeted therapy. **2015**, 111, 81-90   23

727   Annotation enrichment analysis: an alternative method for evaluating the functional properties of gene sets. **2014**, 4, 4191   44

726   NF-B signaling is required for XBP1 (unspliced and spliced)-mediated effects on antiestrogen responsiveness and cell fate decisions in breast cancer. **2015**, 35, 379-90   54

725   Genomic Applications in Pathology. **2015**,

724   Double-edged role of G protein-coupled estrogen receptor 1 in breast cancer prognosis: an analysis of 167 breast cancer samples and online data sets. **2016**, 9, 6407-6415   4

723   Targeting the chromatin remodeling enzyme BRG1 increases the efficacy of chemotherapy drugs in breast cancer cells. **2016**, 7, 27158-75   37

722   Retrospective analysis of efficacy of trastuzumab in adjuvant treatment of HER 2 positive early breast cancer - single institution experience. **2016**, 63, 761-7   3

721   Tailoring Chemotherapy in Early-Stage Breast Cancer: Based on Tumor Biology or Tumor Burden?. **2016**, 35, e31-8   5

720   Histone deacetylase 9 regulates breast cancer cell proliferation and the response to histone deacetylase inhibitors. **2016**, 7, 19693-708   35

719   A Systematic Framework for Drug Repositioning from Integrated Omics and Drug Phenotype Profiles Using Pathway-Drug Network. **2016**, 2016, 7147039   24

718   Identifying the role of Wilms tumor 1 associated protein in cancer prediction using integrative genomic analyses. **2016**, 14, 2823-31   8

717   Microenvironmental Heterogeneity Parallels Breast Cancer Progression: A Histology-Genomic Integration Analysis. **2016**, 13, e1001961   74

716   Transcriptional Network Architecture of Breast Cancer Molecular Subtypes. **2016**, 7, 568   25

697 Biomarker assessment and molecular testing for prognostication in breast cancer. **2016**, 68, 70-85 | 44

696 Molecular Cytopathology. **2016**, | 1

695 Occurrence and outcome of de novo metastatic breast cancer by subtype in a large, diverse population. **2016**, 27, 1127-38 | 34

694 Tumour sampling method can significantly influence gene expression profiles derived from neoadjuvant window studies. **2016**, 6, 29434 | 11

693 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

692 CGDM: collaborative genomic data model for molecular profiling data using NoSQL. **2016**, 32, 3654-3660 | 3

691 Bagging survival tree procedure for variable selection and prediction in the presence of nonsusceptible patients. **2016**, 17, 230 | 6

690 [Non-metastatic triple-negative breast cancer in 2016: Definitions and management]. **2016**, 44, 492-504 | 2

689 A microscopic landscape of the invasive breast cancer genome. **2016**, 6, 27545 | 19

688 Breast cancer subtype predictors revisited: from consensus to concordance?. **2016**, 9, 26 | 4

687 Comprehensive Gene Mutation Profiling of Breast Tumors: Is It Ready for Prime Time Use?. **2016**, 8, 53-59

686 Protein interaction network (PIN)-based breast cancer subsystem identification and activation measurement for prognostic modeling. **2016**, 110, 81-89 | 12

685 The Nuclear Receptor, ROR Regulates Pathways Necessary for Breast Cancer Metastasis. **2016**, 6, 59-72 | 29

684 ATP-Dependent Lon Protease Contributes to Helicobacter pylori-Induced Gastric Carcinogenesis. **2016**, 18, 242-52 | 12

683 Assessment of the prognostic and predictive utility of the Breast Cancer Index (BCI): an NCIC CTG MA.14 study. **2016**, 18, 1 | 55

682 Determining breast cancer histological grade from RNA-sequencing data. **2016**, 18, 48 | 21

681 Novel effects of sphingosylphosphorylcholine on invasion of breast cancer: Involvement of matrix metalloproteinase-3 secretion leading to WNT activation. **2016**, 1862, 1533-43 | 8

680 PRRX2 as a novel TGF-Induced factor enhances invasion and migration in mammary epithelial cell and correlates with poor prognosis in breast cancer. **2016**, 55, 2247-2259 | 18

679 Multi-gene classifiers for prediction of recurrence in breast cancer patients. **2016**, 23, 12-18 29

678 Assessing the evidentiary value of smokeless powder comparisons. **2016**, 259, 179-87 17

677 An Endothelial Gene Signature Score Predicts Poor Outcome in Patients with Endocrine-Treated, Low Genomic Grade Breast Tumors. **2016**, 22, 2417-26 7

676 Comprehensive Transcriptome Profiling Reveals Multigene Signatures in Triple-Negative Breast Cancer. **2016**, 22, 1653-62 53

675 ASXL2 promotes proliferation of breast cancer cells by linking ER to histone methylation. **2016**, 35, 3742-52 27

674 Ductal carcinoma in situ - update on risk assessment and management. **2016**, 68, 96-109 34

673 G0S2 Suppresses Oncogenic Transformation by Repressing a MYC-Regulated Transcriptional Program. **2016**, 76, 1204-13 26

672 c-Met and ER expression differences in basal-like and non-basal-like triple-negative breast cancer. **2016**, 37, 11385-95 8

671 Subtype-Specific Metagene-Based Prediction of Outcome after Neoadjuvant and Adjuvant Treatment in Breast Cancer. **2016**, 22, 337-45 43

670 Comparative study of joint analysis of microarray gene expression data in survival prediction and risk assessment of breast cancer patients. **2016**, 17, 771-85 11

669 Comprehensive profiling of biological processes reveals two major prognostic subtypes in breast cancer. **2016**, 37, 3365-70

668 Hybrid Mixture Model for Subpopulation Identification. **2016**, 8, 28-42

667 KRT19 directly interacts with catenin/RAC1 complex to regulate NUMB-dependent NOTCH signaling pathway and breast cancer properties. **2017**, 36, 332-349 59

666 Breast carcinoma subtypes show different patterns of metastatic behavior. **2017**, 470, 275-283 41

665 A novel non-parametric method for uncertainty evaluation of correlation-based molecular signatures: its application on PAM50 algorithm. **2017**, 33, 693-700 10

664 Polymeric immunoglobulin receptor promotes tumor growth in hepatocellular carcinoma. **2017**, 65, 1948-1962 28

663 Genomic pathways modulated by Twist in breast cancer. **2017**, 17, 52 13

662 The critical role of the ZNF217 oncogene in promoting breast cancer metastasis to the bone. **2017**, 242, 73-89 28

661 Annexin A1 influences in breast cancer: Controversies on contributions to tumour, host and immunoediting processes. **2017**, 119, 278-288 | 16

660 Transposon insertional mutagenesis in mice identifies human breast cancer susceptibility genes and signatures for stratification. **2017**, 114, E2215-E2224 | 24

659 The transcription factor MAFK induces EMT and malignant progression of triple-negative breast cancer cells through its target GPNMB. **2017**, 10, | 35

658 Transcriptomic and genomic features of invasive lobular breast cancer. **2017**, 44, 98-105 | 20

657 Improving accuracy of RNA-based diagnosis and prognosis of oral cancer by using noninvasive methods. **2017**, 69, 62-67 | 11

656 miR-424(322)/503 is a breast cancer tumor suppressor whose loss promotes resistance to chemotherapy. **2017**, 31, 553-566 | 62

655 Mutational signatures and mutable motifs in cancer genomes. **2018**, 19, 1085-1101 | 25

654 ADAM12 induction by Twist1 promotes tumor invasion and metastasis via regulation of invadopodia and focal adhesions. **2017**, 130, 2036-2048 | 26

653 Validity and reliability of Ki-67 assessment in oestrogen receptor positive breast cancer. **2017**, 49, 371-378 | 3

652 MiSTIC, an integrated platform for the analysis of heterogeneity in large tumour transcriptome datasets. **2017**, 45, e122 | 12

651 Classification et signatures molĉulaires des cancers du sein en 2017. **2017**, 19, 64-70 | 1

650 Personalized Prognostic Prediction Models for Breast Cancer Recurrence and Survival Incorporating Multidimensional Data. *Journal of the National Cancer Institute*, **2017**, 109, | 9.7 | 23

649 The Advantage of Discordance: An Example Using the Highly Subjective Nuclear Grading of Breast Cancer. **2017**, 41, 1105-1111 | 8

648 Interaction of mammographic breast density with menopausal status and postmenopausal hormone use in relation to the risk of aggressive breast cancer subtypes. **2017**, 165, 421-431 | 9

647 Clinical utility of gene-expression signatures in early stage breast cancer. **2017**, 14, 595-610 | 127

646 CDK4 phosphorylation status and a linked gene expression profile predict sensitivity to palbociclib. **2017**, 9, 1052-1066 | 53

645 Computational approach for deriving cancer progression roadmaps from static sample data. **2017**, 45, e69 | 8

644 A 3q gene signature associated with triple negative breast cancer organ specific metastasis and response to neoadjuvant chemotherapy. **2017**, 7, 45828 | 17

643   Pathologic diagnosis of breast cancer patients: evolution of the traditional clinical-pathologic paradigm toward "precision" cancer therapy. **2017**, 92, 175-200   8

642   The Prognostic Role of Androgen Receptor in Patients with Early-Stage Breast Cancer: A Meta-analysis of Clinical and Gene Expression Data. **2017**, 23, 2702-2712   51

641   MicroRNA-567 dysregulation contributes to carcinogenesis of breast cancer, targeting tumor cell proliferation, and migration. **2017**, 161, 605-616   25

640   Molecular classification of breast cancer: what the pathologist needs to know. **2017**, 49, 111-119   54

639   Molecular Classification and Testing of Breast Carcinoma. **2017**, 215-231

638   Discerning Clinical Responses in Breast Cancer Based On Molecular Signatures. **2017**, 187, 2199-2207   12

637   G0S2 represses PI3K/mTOR signaling and increases sensitivity to PI3K/mTOR pathway inhibitors in breast cancer. **2017**, 16, 2146-2155   12

636   A Novel 18-Marker Panel Predicting Clinical Outcome in Breast Cancer. **2017**, 26, 1619-1628   1

635   Prognostic and functional role of subtype-specific tumor-stroma interaction in breast cancer. **2017**, 11, 1399-1412   3

634   Dissecting the Biological Heterogeneity within Hormone Receptor Positive HER2 Negative Breast Cancer by Gene Expression Markers Identifies Indolent Tumors within Late Stage Disease. **2017**, 10, 699-706   4

633   Improved prediction of breast cancer outcome by identifying heterogeneous biomarkers. **2017**, 33, 3619-3626   28

632   Identification of a Human Airway Epithelial Cell Subpopulation with Altered Biophysical, Molecular, and Metastatic Properties. **2017**, 10, 514-524   6

631   Assessment of Ki67 expression for breast cancer subtype classification and prognosis in the Nurses' Health Study. **2017**, 166, 613-622   20

630   Premalignant and Pre-invasive Lesions of the Breast. **2017**, 103-120   1

629   Prognostic and Predictive Role of Genetic Signatures. **2017**, 121-131

628   Ridle for sparse regression with mandatory covariates with application to the genetic assessment of histologic grades of breast cancer. **2017**, 17, 12   1

627   Molecular signatures in breast cancer. **2017**, 131, 135-146   32

626   The molecular basis of breast cancer pathological phenotypes. **2017**, 241, 375-391   62

625	Pathology and Molecular Pathology of Breast Cancer. **2017**, 173-231		0
624	Effects of In Utero Exposure to Ethinyl Estradiol on Tamoxifen Resistance and Breast Cancer Recurrence in a Preclinical Model. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	18
623	RNA Sequencing to Predict Response to Neoadjuvant Anti-HER2 Therapy: A Secondary Analysis of the NeoALTTO Randomized Clinical Trial. **2017**, 3, 227-234		79
622	Promoting similarity of model sparsity structures in integrative analysis of cancer genetic data. **2017**, 36, 509-559		8
621	Breast Pathology. **2017**,		1
620	A Bayesian hidden Markov mixture model to detect overexpressed chromosome regions. **2017**, 66, 387-412		1
619	Novel biomarkers in cancer: The whole is greater than the sum of its parts. **2017**, 45, 50-57		6
618	Identification of prognostic signature in cancer based on DNA methylation interaction network. **2017**, 10, 63		15
617	Comparison of Oncotype DX With Modified Magee Equation Recurrence Scores in Low-Grade Invasive Carcinoma of Breast. **2017**, 148, 167-172		14
616	Network Modularity in Breast Cancer Molecular Subtypes. **2017**, 8, 915		22
615	Gene Expression Meta-Analysis of Potential Metastatic Breast Cancer Markers. **2017**, 17, 200-210		30
614	The landscape of DNA methylation-mediated regulation of long non-coding RNAs in breast cancer. **2017**, 8, 51134-51150		9
613	Evolutionary Origins of Cancer Driver Genes and Implications for Cancer Prognosis. **2017**, 8,		12
612	Tumor Heterogeneity in Breast Cancer. **2017**, 4, 227		211
611	Osteoclast proton pump regulator Atp6v1c1 enhances breast cancer growth by activating the mTORC1 pathway and bone metastasis by increasing V-ATPase activity. **2017**, 8, 47675-47690		24
610	Genome-wide identification of key modulators of gene-gene interaction networks in breast cancer. **2017**, 18, 679		2
609	Distance in cancer gene expression from stem cells predicts patient survival. **2017**, 12, e0173589		7
608	Intra-tumor heterogeneity in breast cancer has limited impact on transcriptomic-based molecular profiling. **2017**, 17, 802		5

607 Gene expression modules in primary breast cancers as risk factors for organotropic patterns of first metastatic spread: a case control study. **2017**, 19, 113   3

606 Pathway-based classification of breast cancer subtypes. **2017**, 22, 1697-1712   11

605 Clinical utility of multigene profiling assays in early-stage breast cancer. **2017**, 24, e403-e422   14

604 Depletion of TFAP2E attenuates adriamycin-mediated apoptosis in human neuroblastoma cells. **2017**, 37, 2459-2464   5

603 Molecular Testing in Breast Cancer. **2017**, 257-269

602 Pathway aggregation for survival prediction via multiple kernel learning. **2018**, 37, 2501-2515   4

601 Tumor metabolism assessed by FDG-PET/CT and tumor proliferation assessed by genomic grade index to predict response to neoadjuvant chemotherapy in triple negative breast cancer. **2018**, 45, 1279-1288   12

600 Subtype classification and heterogeneous prognosis model construction in precision medicine. **2018**, 74, 814-822   3

599 XIAP Regulation by MNK Links MAPK and NFB Signaling to Determine an Aggressive Breast Cancer Phenotype. **2018**, 78, 1726-1738   29

598 Genes and functions from breast cancer signatures. **2018**, 18, 473   13

597 Breast cancer in Ethiopia: evidence for geographic difference in the distribution of molecular subtypes in Africa. **2018**, 18, 40   32

596 Tumor infiltrating lymphocytes in early breast cancer. **2018**, 37, 207-214   64

595 The Genomic Grade Index predicts postoperative clinical outcome in patients with soft-tissue sarcoma. **2018**, 29, 459-465   16

594 Gene expression profiling of brain metastatic cell from triple negative breast cancer: Understanding the molecular events. **2018**, 640, 21-27   8

593 Digital image analysis of Ki67 in hot spots is superior to both manual Ki67 and mitotic counts in breast cancer. **2018**, 72, 974-989   44

592 The GDNF Family: A Role in Cancer?. **2018**, 20, 99-117   34

591 Comparison of Receptor-Defined Breast Cancer Subtypes Between German and Sudanese Women: A Facility-Based Cohort Study. **2018**, 4, 1-12   4

590 Clinical Value of RNA Sequencing-Based Classifiers for Prediction of the Five Conventional Breast Cancer Biomarkers: A Report From the Population-Based Multicenter Sweden Cancerome Analysis Network-Breast Initiative. **2018**, 2,   45

589   Breast cancer vaccination comes to age: impacts of bioinformatics. **2018**, 8, 223-235   17

588   Signal translational efficiency between mRNA expression and antibody-based protein expression for breast cancer and its subtypes from cell lines to tissue. **2018**, 11, 67   0

587   Aplicaciĩ de tres modelos pronĨticos en cĩcer de mama precoz. **2018**, 70, 212-217

586   Expression-based analyses indicate a central role for hypoxia in driving tumor plasticity through microenvironment remodeling and chromosomal instability. **2018**, 4, 38   4

585   Gene Expression Analyses in Breast Cancer: Sample Matters. **2018**, 2, pky019

584   Atypical Ductal Lesions of the Breast: Criteria, Significance, and Laboratory Updates. **2018**, 142, 1182-1185   6

583   LEM4 confers tamoxifen resistance to breast cancer cells by activating cyclin D-CDK4/6-Rb and ERﬂ pathway. **2018**, 9, 4180   29

582   Signature miRNAs in peripheral blood monocytes of patients with gastric or breast cancers. **2018**, 8,   7

581   Prediction of early breast cancer patient survival using ensembles of hypoxia signatures. **2018**, 13, e0204123   7

580   Tumor grade and progesterone receptor status predict 21-gene recurrence score in early stage invasive breast carcinoma. **2018**, 172, 671-677   13

579   Targeting invadopodia for blocking breast cancer metastasis. **2018**, 39, 1-17   47

578   Molecular Biology of Breast Cancer. **2018**, 569-588   3

577   Breast cancer development and progression: Risk factors, cancer stem cells, signaling pathways, genomics, and molecular pathogenesis. **2018**, 5, 77-106   288

576   Clinical and molecular aspects of breast cancer: Targets and therapies. **2018**, 106, 14-34   33

575   CSF-1/CSF-1R axis is associated with epithelial/mesenchymal hybrid phenotype in epithelial-like inflammatory breast cancer. **2018**, 8, 9427   16

574   Long noncoding RNA signature in predicting metastasis following tamoxifen treatment for ER-positive breast cancer. **2018**,   6

573   Impact of breast cancer grade discordance on prediction of outcome. **2018**, 73, 904-915   15

572   Construction of a novel multi-gene assay (42-gene classifier) for prediction of late recurrence in ER-positive breast cancer patients. **2018**, 171, 33-41   3

571   Impact of subtypes and comorbidities on breast cancer relapse and survival in population-based studies. **2018**, 41, 151-158   9

570   Graphene oxide-hydroxyapatite nanocomposites effectively deliver HSV-TK suicide gene to inhibit human breast cancer growth. **2018**, 33, 216-226   13

569   Boosting support vector machines for cancer discrimination tasks. **2018**, 101, 236-249   23

568   Expressional analysis of MLH1 and MSH2 in breast cancer. **2019**, 43, 97-105   12

567   A Feature Sampling Strategy for Analysis of High Dimensional Genomic Data. **2019**, 16, 434-441   3

566   A novel assessing system for predicting the prognosis of gastric cancer. **2019**, 11, 1251-1266   1

565   Uncovering the signaling landscape controlling breast cancer cell migration identifies novel metastasis driver genes. **2019**, 10, 2983   29

564   A multiple breast cancer stem cell model to predict recurrence of T, N breast cancer. **2019**, 19, 729   5

563   DNA Methylation Module Network-Based Prognosis and Molecular Typing of Cancer. **2019**, 10,   8

562   LobSig is a multigene predictor of outcome in invasive lobular carcinoma. **2019**, 5, 18   19

561   Graph Theoretic and Pearson Correlation-Based Discovery of Network Biomarkers for Cancer. **2019**, 4, 81   3

560   Reprogramming of Amino Acid Transporters to Support Aspartate and Glutamate Dependency Sustains Endocrine Resistance in Breast Cancer. **2019**, 28, 104-118.e8   40

559   CapG promotes resistance to paclitaxel in breast cancer through transactivation of PIK3R1/P50. **2019**, 9, 6840-6855   19

558   Breast Cancer Metastasis and Drug Resistance. **2019**,   13

557   Breast Cancer Heterogeneity in Primary and Metastatic Disease. **2019**, 1152, 75-104   13

556   Combining the Hough Transform with MLP for Identifying Cashmere and Wool Fibers. **2019**,   0

555   An integrative view on breast cancer signature panels. **2019**, 19, 715-724   1

554   Cross comparison and prognostic assessment of breast cancer multigene signatures in a large population-based contemporary clinical series. **2019**, 9, 12184   17

553 Cancer-associated fibroblast-derived Gremlin 1 promotes breast cancer progression. **2019**, 21, 109   42

552 Association of breast cancer grade with response to neoadjuvant chemotherapy assessed postoperatively. **2019**, 70, 91-99   6

551 Bayesian Inference Identifies Combination Therapeutic Targets in Breast Cancer. **2019**, 66, 2684-2692   18

550 pAKT pathway activation is associated with mutations and good prognosis in luminal breast cancer in contrast to p-mTOR pathway activation. **2019**, 5, 7   15

549 Exploring Collagen Parameters in Pure Special Types of Invasive Breast Cancer. **2019**, 9, 7715   12

548 SIGN: similarity identification in gene expression. **2019**, 35, 4830-4833   1

547 MetaGxData: Clinically Annotated Breast, Ovarian and Pancreatic Cancer Datasets and their Use in Generating a Multi-Cancer Gene Signature. **2019**, 9, 8770   15

546 Characterization of molecular scores and gene expression signatures in primary breast cancer, local recurrences and brain metastases. **2019**, 19, 549   5

545 A novel risk score system for assessment of ovarian cancer based on co-expression network analysis and expression level of five lncRNAs. **2019**, 20, 103   26

544 LncRNA Profile Study Reveals a Three-LncRNA Signature Associated With the Pathological Complete Response Following Neoadjuvant Chemotherapy in Breast Cancer. **2019**, 10, 574   12

543 Risk stratification of ER-positive breast cancer patients: A multi-institutional validation and outcome study of the Rochester Modified Magee algorithm (RoMMa) and prediction of an Oncotype DX recurrence score . **2019**, 8, 4176-4188   11

542 A key genomic subtype associated with lymphovascular invasion in invasive breast cancer. **2019**, 120, 1129-1136   12

541 An Ensemble Strategy to Predict Prognosis in Ovarian Cancer Based on Gene Modules. **2019**, 10, 366   2

540 aFold - using polynomial uncertainty modelling for differential gene expression estimation from RNA sequencing data. **2019**, 20, 364   2

539 Parsimonious Gene Correlation Network Analysis (PGCNA): a tool to define modular gene co-expression for refined molecular stratification in cancer. **2019**, 5, 13   10

538 In silico markers: an evolutionary and statistical approach to select informative genes of human breast cancer subtypes. **2019**, 41, 1371-1382   2

537 The biological characteristics of transcription factors AP-2α and AP-2γ and their importance in various types of cancers. **2019**, 39,   21

536 Tumor Microenvironment Characterization in Gastric Cancer Identifies Prognostic and Immunotherapeutically Relevant Gene Signatures. **2019**, 7, 737-750   301

535   Identification of Cancer Hallmarks Based on the Gene Co-expression Networks of Seven Cancers. **2019**, 10, 99   4

534   Atypical ductal hyperplasia is a multipotent precursor of breast carcinoma. **2019**, 248, 326-338   12

533   Six novel immunoglobulin genes as biomarkers for better prognosis in triple-negative breast cancer by gene co-expression network analysis. **2019**, 9, 4484   18

532   Prognostic effect of Ki-67 in common clinical subgroups of patients with HER2-negative, hormone receptor-positive early breast cancer. **2019**, 175, 617-625   20

531   Breast Disease. **2019**,

530   Seeking for Correlative Genes and Signaling Pathways With Bone Metastasis From Breast Cancer by Integrated Analysis. **2019**, 9, 138   29

529   Epigenetic Regulation of by Drives Metastatic Progression in Triple-Negative Breast Cancer. **2019**, 79, 3347-3359   62

528   Identifying cancer prognostic modules by module network analysis. **2019**, 20, 85   3

527   OSbrca: A Web Server for Breast Cancer Prognostic Biomarker Investigation With Massive Data From Tens of Cohorts. **2019**, 9, 1349   15

526   Differential impact of classical and non-canonical NF-B pathway-related gene expression on the survival of breast cancer patients. **2019**, 10, 5191-5211   11

525   Harmonizing gene signatures to predict benefit from adjuvant chemotherapy in early breast cancer. **2019**, 31, 472-479   2

524   Identification of Distinct Prognostic Groups: Implications for Patient Selection to Targeted Therapies Among Anti-Endocrine Therapy-Resistant Early Breast Cancers.. **2019**, 3, 1-13

523   Recent advances in breast cancer research impacting clinical diagnostic practice. **2019**, 247, 552-562   21

522   Prognostic values of F-box members in breast cancer: an online database analysis and literature review. **2019**, 39,   11

521   Discrepancy in risk assessment of hormone receptor positive early-stage breast cancer patients using breast cancer index and recurrence score. **2019**, 173, 375-383   1

520   Antrocin, a bioactive component from Antrodia cinnamomea, suppresses breast carcinogenesis and stemness via downregulation of Latenin/Notch1/Akt signaling. **2019**, 52, 70-78   9

519   Molecular subtyping of cancer: current status and moving toward clinical applications. **2019**, 20, 572-584   35

518   Deep-learning approach to identifying cancer subtypes using high-dimensional genomic data. **2020**, 36, 1476-1483   39

| 517 | Integrative Analysis of Multi-Genomic Data for Kidney Renal Cell Carcinoma. **2020**, 12, 12-23 | 3 |

| 516 | BRAF/MEK Pathway is Associated With Breast Cancer in ER-dependent Mode and Improves ER Status-based Cancer Recurrence Prediction. **2020**, 20, 41-50.e8 | 3 |

| 515 | Clonality, Antigen Recognition, and Suppression of CD8 T Cells Differentially Affect Prognosis of Breast Cancer Subtypes. **2020**, 26, 505-517 | 13 |

| 514 | Validation of the OncoMasTR Risk Score in Estrogen Receptor-Positive/HER2-Negative Patients: A TransATAC study. **2020**, 26, 623-631 | 6 |

| 513 | The Impact of Stroma Admixture on Molecular Subtypes and Prognostic Gene Signatures in Serous Ovarian Cancer. **2020**, 29, 509-519 | 17 |

| 512 | Molecular Classification of Breast Cancer. **2020**, 27, 27-35 | 101 |

| 511 | Grading Ductal Carcinoma In Situ (DCIS) of the Breast - What's Wrong with It?. **2020**, 26, 665-671 | 11 |

| 510 | Using hidden Markov model to predict recurrence of breast cancer based on sequential patterns in gene expression profiles. **2020**, 111, 103570 | 5 |

| 509 | Clustering non-linear interactions in factor analysis. **2020**, 78, 329-352 | |

| 508 | Characterization of the Immune Cell Infiltration Landscape in Head and Neck Squamous Cell Carcinoma to Aid Immunotherapy. **2020**, 22, 298-309 | 70 |

| 507 | Involved microRNAs in alternative polyadenylation intervene in breast cancer via regulation of cleavage factor "CFIm25". **2020**, 10, 11608 | 8 |

| 506 | Gene signature-based prediction of triple-negative breast cancer patient response to Neoadjuvant chemotherapy. **2020**, 9, 6281-6295 | 9 |

| 505 | High formin binding protein 17 (FBP17) expression indicates poor differentiation and invasiveness of ductal carcinomas. **2020**, 10, 11543 | 4 |

| 504 | Construction and optimization of gene expression signatures for prediction of survival in two-arm clinical trials. **2020**, 21, 333 | |

| 503 | A Prognostic Model Based on the Immune-related Genes in Colon Adenocarcinoma. **2020**, 17, 1879-1896 | 7 |

| 502 | BRAF drives dedifferentiation in small intestinal and colonic organoids and cooperates with mutant p53 and Apc loss in transformation. **2020**, 39, 6053-6070 | 6 |

| 501 | Emerging Roles of SRSF3 as a Therapeutic Target for Cancer. **2020**, 10, 577636 | 13 |

| 500 | A Five-Gene-Pair-Based Prognostic Signature for Predicting the Relapse Risk of Early Stage ER+ Breast Cancer. **2020**, 11, 566928 | 1 |

499   Revisiting the Concept of Stress in the Prognosis of Solid Tumors: A Role for Stress Granules Proteins?. **2020**, 12,   5

498   Breast cancer survival in Nordic BRCA2 mutation carriers-unconventional association with oestrogen receptor status. **2020**, 123, 1608-1615   1

497   A novel single-cell based method for breast cancer prognosis. **2020**, 16, e1008133   7

496   Association of an anaplastic lymphoma kinase pathway signature with cell de-differentiation, neoadjuvant chemotherapy response, and recurrence risk in breast cancer. **2020**, 40, 422-434   3

495   High Levels of Chromosomal Copy Number Alterations and TP53 Mutations Correlate with Poor Outcome in Younger Breast Cancer Patients. **2020**, 190, 1643-1656   4

494   Correlation-centred variable selection of a gene expression signature to predict breast cancer metastasis. **2020**, 10, 7923   4

493   BIK drives an aggressive breast cancer phenotype through sublethal apoptosis and predicts poor prognosis of ER-positive breast cancer. **2020**, 11, 448   10

492   Gene-signature-derived ICs/ECs reflect the potency of causative upstream targets and downstream phenotypes. **2020**, 10, 9670   2

491   Overview of Breast Cancer and Implications of Overtreatment of Early-Stage Breast Cancer: An Indian Perspective. **2020**, 6, 789-798   12

490   The therapeutic response of ER+/HER2- breast cancers differs according to the molecular Basal or Luminal subtype. **2020**, 6, 8   14

489   Tumor Microenvironment. **2020**,   6

488   Comprehensive Transcriptomic Profiling Identifies Breast Cancer Patients Who May Be Spared Adjuvant Systemic Therapy. **2020**, 26, 171-182   4

487   mA regulator-mediated methylation modification patterns and tumor microenvironment infiltration characterization in gastric cancer. **2020**, 19, 53   272

486   Prognostic and Predictive Impact of Beta-2 Adrenergic Receptor Expression in HER2-Positive Breast Cancer. **2020**, 20, 262-273.e7   5

485   Perturbations of pathway co-expression network identify a core network in metastatic breast cancer. **2020**, 87, 107313   3

484   Identification of a prognostic LncRNA signature for ER-positive, ER-negative and triple-negative breast cancers. **2020**, 183, 95-105   5

483   A novel signature based on microvascular invasion predicts the recurrence of HCC. **2020**, 18, 272   5

482   Visual histological assessment of morphological features reflects the underlying molecular profile in invasive breast cancer: a morphomolecular study. **2020**, 77, 631-645   4

481	Identification of GSN and LAMC2 as Key Prognostic Genes of Bladder Cancer by Integrated Bioinformatics Analysis. **2020**, 12,	10
480	Methylation signature genes identification of cancers occurrence and pattern recognition. **2020**, 85, 107198	1
479	Network modeling of patients' biomolecular profiles for clinical phenotype/outcome prediction. **2020**, 10, 3612	4
478	MAGI1, a New Potential Tumor Suppressor Gene in Estrogen Receptor Positive Breast Cancer. **2020**, 12,	11
477	Expression and clinicopathological significance of lipin-1 in human breast cancer and its association with p53 tumor suppressor gene. **2020**, 235, 5835-5846	10
476	A qualitative transcriptional signature to reclassify histological grade of ER-positive breast cancer patients. **2020**, 21, 283	1
475	TIE2 Induces Breast Cancer Cell Dormancy and Inhibits the Development of Osteolytic Bone Metastases. **2020**, 12,	3
474	Heterogeneous multiple kernel learning for breast cancer outcome evaluation. **2020**, 21, 155	1
473	MiR-891a-5p as a prognostic marker and therapeutic target for hormone receptor-positive breast cancer. **2020**, 11, 3771-3782	11
472	Tumor microenvironment characterization identifies two lung adenocarcinoma subtypes with specific immune and metabolic state. **2020**, 111, 1876-1886	7
471	Pharmacogenetics of Breast Cancer. **2020**,	
470	Identification of a Prognostic Signature Based on the Expression of Genes Related to the Insulin Pathway in Early Breast Cancer. **2021**, 16, 299-306	0
469	Computational Studies in Breast Cancer. **2021**, 106-126	1
468	Graph and Heterogeneous Network Transformations. **2021**, 107-142	
467	Identified the novel resistant biomarkers for taxane-based therapy for triple-negative breast cancer. **2021**, 18, 2521-2531	1
466	Analysis of the Immunoexpression of Opioid Receptors and their Correlation with Markers of Angiogenesis, Cell Proliferation and Apoptosis in Breast Cancer. **2021**, 22, 633-640	2
465	mA modification patterns and tumor immune landscape in clear cell renal carcinoma. **2021**, 9,	19
464	NCAPG upregulation mediated by four microRNAs combined with activation of the p53 signaling pathway is a predictor of poor prognosis in patients with breast cancer. **2021**, 21, 323	7

463	A variable selection approach for highly correlated predictors in high-dimensional genomic data. **2021**,	0
462	Cross-talk of four types of RNA modification writers defines tumor microenvironment and pharmacogenomic landscape in colorectal cancer. **2021**, 20, 29	42
461	In modern times, how important are breast cancer stage, grade and receptor subtype for survival: a population-based cohort study. **2021**, 23, 17	5
460	Genomic Assays in Node Positive Breast Cancer Patients: A Review. **2020**, 10, 609100	5
459	A Clinical Decision Support System for Predicting Invasive Breast Cancer Recurrence: Preliminary Results. **2021**, 11, 576007	3
458	Genetic co-expression networks contribute to creating predictive model and exploring novel biomarkers for the prognosis of breast cancer. **2021**, 11, 7268	1
457	Development and Validation of a Prognostic Signature Based on Immune Genes in Cervical Cancer. **2021**, 11, 616530	4
456	Predictive and prognostic transcriptomic biomarkers in soft tissue sarcomas. **2021**, 5, 17	6
455	Tumor Microenvironment Analysis Identified Subtypes Associated With the Prognosis and the Tumor Response to Immunotherapy in Bladder Cancer. **2021**, 12, 551605	5
454	NIBNA: A network-based node importance approach for identifying breast cancer drivers. **2021**,	1
453	Variability in Breast Cancer Biomarker Assessment and the Effect on Oncological Treatment Decisions: A Nationwide 5-Year Population-Based Study. **2021**, 13,	5
452	Inferring latent temporal progression and regulatory networks from cross-sectional transcriptomic data of cancer samples. **2021**, 17, e1008379	0
451	Radioproteomics in Breast Cancer: Prediction of Ki-67 Expression With MRI-based Radiomic Models. **2021**,	4
450	Complexity index in sarcoma and genomic grade index gene signatures in rhabdomyosarcoma of pediatric and adult ages. **2021**, 68, e28987	0
449	Integrated Analysis of Immune Infiltration Features for Cervical Carcinoma and Their Associated Immunotherapeutic Responses. **2021**, 9, 573497	7
448	Tumor microenvironment characterization in cervical cancer identifies prognostic relevant gene signatures. **2021**, 16, e0249374	4
447	Tumor Immune Microenvironment Characterization Identifies Prognosis and Immunotherapy-Related Gene Signatures in Melanoma. **2021**, 12, 663495	10
446	A Pipeline for Integrated Theory and Data-Driven Modeling of Biomedical Data. **2021**, 18, 811-822	1

445   Globaltest confidence regions and their application to ridge regression. **2021**, 63, 1351-1365   1

444   Characterization of the Immune Cell Infiltration Profile in Pancreatic Carcinoma to Aid in Immunotherapy. **2021**, 11, 677609   4

443   Tumor Microenvironment Characteristics of Pancreatic Cancer to Determine Prognosis and Immune-Related Gene Signatures. **2021**, 8, 645024   2

442   Uncovering the roles of microRNAs/lncRNAs in characterising breast cancer subtypes and prognosis. **2021**, 22, 300   0

441   DNA methylation regulator-mediated modification patterns and tumor microenvironment characterization in gastric cancer. **2021**, 24, 695-710   6

440   Evaluation of tumor immune contexture among intrinsic molecular subtypes helps to predict outcome in early breast cancer. **2021**, 9,   1

439   Expression of X-Linked Inhibitor of Apoptosis Protein (XIAP) in Breast Cancer Is Associated with Shorter Survival and Resistance to Chemotherapy. **2021**, 13,   4

438   Cancer Grade Model: a multi-gene machine learning-based risk classification for improving prognosis in breast cancer. **2021**, 125, 748-758   1

437   Cellular dormancy in minimal residual disease following targeted therapy. **2021**, 23, 63   4

436   Integrated multi-omics profiling of high-grade estrogen receptor-positive, HER2-negative breast cancer. **2021**,

435   Identification of CXCL10-Relevant Tumor Microenvironment Characterization and Clinical Outcome in Ovarian Cancer. **2021**, 12, 678747   2

434   Analyzing the characteristics of immune cell infiltration in lung adenocarcinoma via bioinformatics to predict the effect of immunotherapy. **2021**, 73, 369-380   13

433   Prognostic value of tumor immune cell infiltration patterns in colon adenocarcinoma based on systematic bioinformatics analysis. **2021**, 21, 344   2

432   Graphene-based nanomaterials for breast cancer treatment: promising therapeutic strategies. **2021**, 19, 211   6

431   Identification of Immune-Related Subtypes and Characterization of Tumor Microenvironment Infiltration in Bladder Cancer. **2021**, 9, 723817   3

430   Establishment of a Prognostic Prediction and Drug Selection Model for Patients with Clear Cell Renal Cell Carcinoma by Multi-Omics Data Analysis.   1

429   Immune Infiltrating Cells-Derived Risk Signature Based on Large-scale Analysis Defines Immune Landscape and Predicts Immunotherapy Responses in Glioma Tumor Microenvironment. **2021**, 12, 691811   12

428   A quantitative score of immune cell infiltration predicts the prognosis in pancreatic ductal adenocarcinoma. **2021**, 98, 107890   0

427   Characterization of the immune cell infiltration landscape in bladder cancer to aid immunotherapy. **2021**, 708, 108950   1

426   Spatial immunophenotypes predict response to anti-PD1 treatment and capture distinct paths of T cell evasion in triple negative breast cancer. **2021**, 12, 5668   7

425   The Impact of m1A Methylation Modification Patterns on Tumor Immune Microenvironment and Prognosis in Oral Squamous Cell Carcinoma. **2021**, 22,   1

424   Identification of Five Hub Genes as Key Prognostic Biomarkers in Liver Cancer via Integrated Bioinformatics Analysis. **2021**, 10,   3

423   Improved breast cancer histological grading using deep learning. **2021**,   5

422   Stable breast cancer prognosis.

421   Genomic analysis uncovers prognostic and immunogenic characteristics of ferroptosis for clear cell renal cell carcinoma. **2021**, 25, 186-197   10

420   DNA Methylation Regulator-Meditated Modification Patterns Define the Distinct Tumor Microenvironment in Lung Adenocarcinoma. **2021**, 11, 734873

419   mA Methylation Modification Patterns and Tumor Microenvironment Infiltration Characterization in Pancreatic Cancer. **2021**, 12, 739768   2

418   Expression of Ferroptosis-Related Genes Shapes Tumor Microenvironment and Pharmacological Profile in Gastric Cancer. **2021**, 9, 694003   0

417   Basal-like breast cancer with low TGFβ and high TNFα pathway activity is rich in activated memory CD4 T cells and has a good prognosis. **2021**, 17, 670-682   4

416   Multi-omics Analysis of Ferroptosis Regulation Patterns and Characterization of Tumor Microenvironment in Patients with Oral Squamous Cell Carcinoma. **2021**, 17, 3476-3492   4

415   Improved Prediction of Cancer Outcome Using Graph-Embedded Generative Adversarial Networks. **2021**, 9, 20076-20088   1

414   New tools for assessing breast cancer recurrence. **2008**, 141, 99-118   2

413   Prognostic and predictive factors. **2009**, 151, 13-30   2

412   Cell cycle machinery: links with genesis and treatment of breast cancer. **2008**, 630, 189-205   46

411   Breast. **2010**, 347-376   27

410   Understanding Tamoxifen Resistance of Breast Cancer Based on Integrative Bioinformatics Approaches. **2013**, 249-260   1

| 409 | Biomarkers in breast cancer. **2010**, 593, 137-56 | 6 |

| 408 | Heterogeneity of Breast Cancer: Gene Signatures and Beyond. **2012**, 13-25 | 2 |

| 407 | Integrative Functional Analysis Improves Information Retrieval in Breast Cancer. **2015**, 43-50 | 1 |

| 406 | Grading of Invasive Carcinoma. **2017**, 87-95 | 1 |

| 405 | Independent Component Analysis to Remove Batch Effects from Merged Microarray Datasets. **2016**, 281-292 | 4 |

| 404 | Supporting Breast Cancer Diagnosis with Multi-objective Genetic Algorithm for Outlier Detection. **2018**, 304-315 | 5 |

| 403 | Integrative Visual Data Mining of Biomedical Data: Investigating Cases in Chronic Fatigue Syndrome and Acute Lymphoblastic Leukaemia. **2008**, 367-388 | 1 |

| 402 | Detecting Disease-Specific Dysregulated Pathways Via Analysis of Clinical Expression Profiles. **2008**, 347-359 | 34 |

| 401 | Coupling Regulatory Networks and Microarays: Revealing Molecular Regulations of Breast Cancer Treatment Responses. **2012**, 239-246 | 8 |

| 400 | Tumors of the Breast. **2013**, 131-143 | 1 |

| 399 | Systems Biology and Integrative Omics in Breast Cancer. **2014**, 333-352 | 2 |

| 398 | The Molecular Evolution of Breast Cancer Precursors and Risk Indicators. **2011**, 89-117 | 3 |

| 397 | Immunohistochemistry and Molecular Biology of Breast Cancers: Old and New Prognostic Factors. **2011**, 119-148 | 3 |

| 396 | Molecular Profiling of Breast Cancer in Clinical Trials: A Perspective. **2020**, 313-332 | 4 |

| 395 | Molecular-based Testing in Breast Disease for Therapeutic Decisions. **2012**, 173-188 | 1 |

| 394 | Gene expression signatures: A tool for analysis of breast cancer prognosis and therapy. **2020**, 151, 102964 | 13 |

| 393 | Network-Based Biomarkers Enable Cross-Disease Biomarker Discovery. | 1 |

| 392 | Defining common principles of gene co-expression refines molecular stratification in cancer. | 0 |

391   Uncovering the signaling landscape controlling breast cancer cell migration identifies splicing factor PRPF4B as a metastasis driver.   1

390   SLCs contribute to endocrine resistance in breast cancer: role of SLC7A5 (LAT1).   4

389   DNA methylation and upregulation of ΔNp73 are associated with an adverse prognosis in breast cancer. **2018**, 71, 52-58   7

388   The retinoblastoma tumor suppressor modifies the therapeutic response of breast cancer. **2007**, 117, 218-28   152

387   RCP is a human breast cancer-promoting gene with Ras-activating function. **2009**, 119, 2171-83   89

386   Thioredoxin-like 2 regulates human cancer cell growth and metastasis via redox homeostasis and NF-κB signaling. **2011**, 121, 212-25   102

385   Identification of human triple-negative breast cancer subtypes and preclinical models for selection of targeted therapies. **2011**, 121, 2750-67   3125

384   CD4+ follicular helper T cell infiltration predicts breast cancer survival. **2013**, 123, 2873-92   554

383   Notch promotes recurrence of dormant tumor cells following HER2/neu-targeted therapy. **2015**, 125, 2484-96   78

382   MammaPrint® Translating Research into a Diagnostic Test. **2010**, 165-184   3

381   Molecular Biological Features of Nottingham Histological Grade 3 Breast Cancers. **2020**, 27, 4475-4485   24

380   Special AT-rich Sequence Binding-Protein 1 (SATB1) Correlates with Immune Infiltration in Breast, Head and Neck, and Prostate Cancer. **2020**, 26, e923208   2

379   Lactic acidosis triggers starvation response with paradoxical induction of TXNIP through MondoA. **2010**, 6, e1001093   88

378   Heterologous tissue culture expression signature predicts human breast cancer prognosis. **2007**, 2, e145   6

377   Inhibition of proliferation by PERK regulates mammary acinar morphogenesis and tumor formation. **2007**, 2, e615   59

376   Prognostic breast cancer signature identified from 3D culture model accurately predicts clinical outcome across independent datasets. **2008**, 3, e2994   170

375   The neurotensin receptor-1 pathway contributes to human ductal breast cancer progression. **2009**, 4, e4223   65

374   Meta-analysis and gene set enrichment relative to er status reveal elevated activity of MYC and E2F in the "basal" breast cancer subgroup. **2009**, 4, e4710   74

373	Comparison of prognostic gene profiles using qRT-PCR in paraffin samples: a retrospective study in patients with early breast cancer. **2009**, 4, e5911	14
372	Can survival prediction be improved by merging gene expression data sets?. **2009**, 4, e7431	32
371	Improved microarray-based decision support with graph encoded interactome data. **2010**, 5, e10225	5
370	Minimising immunohistochemical false negative ER classification using a complementary 23 gene expression signature of ER status. **2010**, 5, e15031	24
369	Gene expression profiles from formalin fixed paraffin embedded breast cancer tissue are largely comparable to fresh frozen matched tissue. **2011**, 6, e17163	118
368	Do two machine-learning based prognostic signatures for breast cancer capture the same biological processes?. **2011**, 6, e17795	29
367	Global microRNA expression profiling identifies MiR-210 associated with tumor proliferation, invasion and poor clinical outcome in breast cancer. **2011**, 6, e20980	175
366	An evaluation protocol for subtype-specific breast cancer event prediction. **2011**, 6, e21681	6
365	Microarray-based oncogenic pathway profiling in advanced serous papillary ovarian carcinoma. **2011**, 6, e22469	19
364	The influence of feature selection methods on accuracy, stability and interpretability of molecular signatures. **2011**, 6, e28210	226
363	Shortening of 3'UTRs correlates with poor prognosis in breast and lung cancer. **2012**, 7, e31129	73
362	Respective prognostic value of genomic grade and histological proliferation markers in early stage (pN0) breast carcinoma. **2012**, 7, e35184	17
361	How reliable is Ki-67 immunohistochemistry in grade 2 breast carcinomas? A QA study of the Swiss Working Group of Breast- and Gynecopathologists. **2012**, 7, e37379	150
360	Stromal genes add prognostic information to proliferation and histoclinical markers: a basis for the next generation of breast cancer gene signatures. **2012**, 7, e37646	15
359	Integration of clinical and gene expression data has a synergetic effect on predicting breast cancer outcome. **2012**, 7, e40358	30
358	The role of master regulators in the metabolic/transcriptional coupling in breast carcinomas. **2012**, 7, e42678	18
357	Overexpression of karyopherin 2 in human ovarian malignant germ cell tumor correlates with poor prognosis. **2012**, 7, e42992	18
356	Doubly Optimized Calibrated Support Vector Machine (DOC-SVM): an algorithm for joint optimization of discrimination and calibration. **2012**, 7, e48823	7

355	A systematic evaluation of multi-gene predictors for the pathological response of breast cancer patients to chemotherapy. **2012**, 7, e49529	11
354	Identifying in-trans process associated genes in breast cancer by integrated analysis of copy number and expression data. **2013**, 8, e53014	41
353	The CIN4 chromosomal instability qPCR classifier defines tumor aneuploidy and stratifies outcome in grade 2 breast cancer. **2013**, 8, e56707	23
352	E47 and Id1 interplay in epithelial-mesenchymal transition. **2013**, 8, e59948	39
351	A prognosis classifier for breast cancer based on conserved gene regulation between mammary gland development and tumorigenesis: a multiscale statistical model. **2013**, 8, e60131	3
350	Genomic instability: a stronger prognostic marker than proliferation for early stage luminal breast carcinomas. **2013**, 8, e76496	16
349	Post-mastectomy radiotherapy for breast cancer patients with t1-t2 and 1-3 positive lymph nodes: a meta-analysis. **2013**, 8, e81765	24
348	The prognostic value of mitotic activity index (MAI), phosphohistone H3 (PPH3), cyclin B1, cyclin A, and Ki67, alone and in combinations, in node-negative premenopausal breast cancer. **2013**, 8, e81902	22
347	Inferring gene dependency network specific to phenotypic alteration based on gene expression data and clinical information of breast cancer. **2014**, 9, e92023	7
346	Use of formalin-fixed paraffin-embedded samples for gene expression studies in breast cancer patients. **2015**, 10, e0123194	9
345	A ranking-based meta-analysis reveals let-7 family as a meta-signature for grade classification in breast cancer. **2015**, 10, e0126837	14
344	Promoter Methylation Status Modulate the Expression of Tumor Suppressor (RbL2/p130) Gene in Breast Cancer. **2015**, 10, e0134687	11
343	Identification of Gene-Expression Signatures and Protein Markers for Breast Cancer Grading and Staging. **2015**, 10, e0138213	20
342	Beyond Axillary Lymph Node Metastasis, BMI and Menopausal Status Are Prognostic Determinants for Triple-Negative Breast Cancer Treated by Neoadjuvant Chemotherapy. **2015**, 10, e0144359	18
341	Estrogen-Receptor, Progesterone-Receptor and HER2 Status Determination in Invasive Breast Cancer. Concordance between Immuno-Histochemistry and MapQuantâMicroarray Based Assay. **2016**, 11, e0146474	27
340	Low Concordance between Gene Expression Signatures in ER Positive HER2 Negative Breast Carcinoma Could Impair Their Clinical Application. **2016**, 11, e0148957	7
339	Tumor tissue protein signatures reflect histological grade of breast cancer. **2017**, 12, e0179775	6
338	The mutational landscape of the SCAN-B real-world primary breast cancer transcriptome. **2020**, 12, e12118	11

| 337 | [Modern pathologic diagnostics in breast cancer]. **2012**, 153, 22-30 | 3 |

| 336 | The 3'UTR signature defines a highly metastatic subgroup of triple-negative breast cancer. **2016**, 7, 59834-59844 | 16 |

| 335 | Overexpression of POLQ confers a poor prognosis in early breast cancer patients. **2010**, 1, 175-84 | 74 |

| 334 | Identifying prognostic signature in ovarian cancer using DirGenerank. **2017**, 8, 46398-46413 | 9 |

| 333 | Secretory leukocyte protease inhibitor (SLPI) as a potential target for inhibiting metastasis of triple-negative breast cancers. **2017**, 8, 108292-108302 | 11 |

| 332 | FDG-PET/CT and molecular markers to predict response to neoadjuvant chemotherapy and outcome in HER2-negative advanced luminal breast cancers patients. **2018**, 9, 16343-16353 | 8 |

| 331 | Genome-wide multi-omics profiling of the 8p11-p12 amplicon in breast carcinoma. **2018**, 9, 24140-24154 | 12 |

| 330 | A breast cancer meta-analysis of two expression measures of chromosomal instability reveals a relationship with younger age at diagnosis and high risk histopathological variables. **2011**, 2, 529-37 | 7 |

| 329 | Identification and evaluation of network modules for the prognosis of basal-like breast cancer. **2015**, 6, 17713-24 | 3 |

| 328 | A novel HMGA1-CCNE2-YAP axis regulates breast cancer aggressiveness. **2015**, 6, 19087-101 | 49 |

| 327 | MiR-26b/KPNA2 axis inhibits epithelial ovarian carcinoma proliferation and metastasis through downregulating OCT4. **2015**, 6, 23793-806 | 46 |

| 326 | Genome and transcriptome delineation of two major oncogenic pathways governing invasive ductal breast cancer development. **2015**, 6, 36652-74 | 12 |

| 325 | Tamoxifen therapy benefit predictive signature coupled with prognostic signature of post-operative recurrent risk for early stage ER+ breast cancer. **2015**, 6, 44593-608 | 15 |

| 324 | Histone H3 lysine 4 acetylation and methylation dynamics define breast cancer subtypes. **2016**, 7, 5094-109 | 66 |

| 323 | Trastuzumab plus adjuvant chemotherapy for human epidermal growth factor receptor 2 (HER2)-positive early-stage breast cancer: A real-world retrospective study in Chinese patients. **2019**, 31, 759-770 | 3 |

| 322 | Gene Expression Assay in the Management of Early Breast Cancer. **2020**, 27, 2826-2839 | 5 |

| 321 | OPTIMA prelim: a randomised feasibility study of personalised care in the treatment of women with early breast cancer. **2016**, 20, xxiii-xxix, 1-201 | 42 |

| 320 | Microenvironment Analysis of Prognosis and Molecular Signature of Immune-Related Genes in Lung Adenocarcinoma. **2021**, 28, 561-578 | 6 |

319   A Critical Evaluation of Analytic Aspects of Gene Expression Profiling in Lymphoid Leukemias with Broad Applications to Cancer Genomics. **2016**, 3, 248-271   1

318   Should Histologic Grade Be Incorporated into the TNM Classification System for Small (T1, T2) Node-Negative Breast Adenocarcinomas?. **2010**, 2011, 825627   2

317   Histopathological and genomic grading provide complementary prognostic information in breast cancer: a study on publicly available datasets. **2011**, 2011, 890938   3

316   Which patients might benefit from postmastectomy radiotherapy in breast cancer patients with t1-2 tumor and 1-3 axillary lymph nodes metastasis?. **2013**, 45, 103-11   13

315   Biological subtypes of breast cancer: Prognostic and therapeutic implications. **2014**, 5, 412-24   390

314   Basal-like breast carcinoma: from expression profiling to routine practice. **2009**, 133, 860-8   58

313   Hub-Based Reliable Gene Expression Algorithm toClassify ER+ and ER- Breast Cancer Subtypes. **2013**, 20-26   1

312   IHC-based Ki67 as response biomarker to tamoxifen in breast cancer window trials enrolling premenopausal women. **2021**, 7, 138

311   Identification and quantification of immune infiltration landscape on therapy and prognosis in left- and right-sided colon cancer. **2021**, 1   2

310   Immune Signatures Combined With BRCA1-Associated Protein 1 Mutations Predict Prognosis and Immunotherapy Efficacy in Clear Cell Renal Cell Carcinoma. **2021**, 9, 747985   0

309   Overview of Human HtrA Family Proteases and Their Distinctive Physiological Roles and Unique Involvement in Diseases, Especially Cancer and Pregnancy Complications. **2021**, 22,   0

308   Radiogenomics Map Reveals the Landscape of m6A Methylation Modification Pattern in Bladder Cancer. **2021**, 12, 722642   5

307   Development and Validation of Gene Expression Profile Signatures in Early-Stage Breast Cancer. **2007**, 121-136

306   Estrogen receptor phenotypes defined by gene expression profiling. **2009**, 147, 1-18

305   Molecular Tools, Expression Profiling. **2009**, 299-311

304   New perspectives for therapy choice. **2009**, 151, 31-40

303   Investigational Molecular Prognostic Factors for Breast Carcinoma. **2009**, 463-475

302   Tumor Biology and Pathology. **2010**, 21-35

301   [Gene expression based multigene prognostic and predictive tests in breast cancer]. **2009**, 53, 351-9

300   Breast. **2010**, 419-460

299   The 2010 Signal Separation Evaluation Campaign (SiSEC2010): Biomedical Source Separation. **2010**, 123-130   2

298   Learning Network from High-Dimensional Array Data. **2010**, 133-156

297   Le phħomħe mħastatique. Paramħres pronostiques et prħictifs. Intħt ħventuel des signatures molħulaires. **2010**, 13-22

296   Sequential Application of Feature Selection and Extraction for Predicting Breast Cancer Aggressiveness. **2010**, 46-57

295   Introduction to Gene Expression Profiling in Breast Cancer. **2010**, 295-314

294   Prognostische und prħiktive Faktoren (unter Berħksichtigung von Genexpressionsanalysen). **2010**, 98-108

293   Personalizing Treatment Selection for Breast Cancer. **2010**, 297-323

292   Nuances and Details of the Pathology Report. **2011**, 63-75

291   Evaluating Oncopathological Studies: The Need to Evaluate the Internal and External Validity of Study Results. **2011**, 121-140

290   Histologic Grade. **2011**, 260-271

289   Linking Interactome to Disease. **2011**, 406-427   1

288   Diagnostic and Prognostic Cancer Biomarkers: From Traditional to Systems Approaches. **2011**, 329-366

287   Introduction on Genome-wide Expression Profiling from Formalin-Fixed Paraffin-Embedded Tissues Using Microarrays. **2011**, 233-237

286   Le cancer du sein localisħ **2011**, 175-184

285   Molecular Gene-Signatures and Cancer Clinical Trials. **2012**, 139-155

284   The prognostic and predictive value of gene expression signatures in breast cancer. **2011**, 4-12

283   Invasive Ductal Carcinoma of No Special Type and Histologic Grade. **2012**, 429-445   1

282   The 2011 Signal Separation Evaluation Campaign (SiSEC2011): - Biomedical Data Analysis -. **2012**, 423-429   0

281   Biological Knowledge Integration in DNA Microarray Gene Expression Classification Based on Rough Set Theory. **2012**, 53-61   1

280   Molecular Classification of Breast Carcinoma. **2012**, 365-379

279   Analysis of Array Data and Clinical Validation of Array-Based Assays. **2012**, 171-210

278   Systemic hormonal therapies for early-stage breast cancer. **2013**, 463-477

277   Dfinition biologique de lâggressivit'tumorale : les signatures biologiques peuvent-elles t're utilisès en pratique clinique ?. **2013**, 72-78

276   Signaling Networks of Activated Oncogenic and Altered Tumor Suppressor Genes in Head and Neck Cancer. **2013**, Suppl 7, 4   4

275   Supervised Normalization of Large-Scale Omic Datasets Using Blind Source Separation. **2014**, 465-497

274   A Differential Approach for Identifying Important Student Learning Behavior Patterns with Evolving Usage over Time. **2014**, 281-292

273   Molecular Testing in Breast Cancer. **2014**, 169-188

272   Genomic Applications in Breast Carcinoma. **2015**, 359-382

271   Early Biomarkers in Breast Cancer. **2015**, 61-142

270   Factor Analysis with Mixture Modeling to Evaluate Coherent Patterns in Microarray Data. **2015**, 185-195

269   When will RNA-based tests similar to Oncotype DX be used for oral cancer?. **2015**, 4, 121

268   Molecular Prognostic and Predictive Assays in Breast Cancer. **2016**, 21, 4-10

267   Dfinition du pronostic des cancers du sein aujourd'hui : intġration de l'anatomie et de la biologie. **2016**, 189-195

266   Molecular Analysis of Breast Cancer in Cytology Samples. **2016**, 139-152

265 Future Role of Molecular Profiling in Small Breast Samples and Personalised Medicine. **2016**, 803-817

264 Biology and Genetics of Breast Cancer. **2016**, 145-160   1

263 Prognostic and Predictive Gene Expression Signatures in Breast Cancer. **2016**, 269-281

262 Adjuvant Systemic Chemotherapy for HER2-Negative Disease. **2016**, 131-187

261 Nouveaux marqueurs pronostiques et ́prd́ictifs dans les ́cancers luminaux (HER2 nǵatifs) ́: signatures et tests multiparamt̀riques. **2016**, 109-116

260 Gene Expression Analysis: Applications. **2016**, 137-149

259 Molecular Classification of Breast Cancer. **2016**, 203-219   0

258 Premalignant and Malignant Breast Pathology. **2016**, 179-194

257 Gene modules associated with breast cancer distant metastasis-free survival in the PAM50 molecular subtypes. **2016**, 7, 21686-98   2

256 MetaGxData: Clinically Annotated Breast, Ovarian and Pancreatic Cancer Datasets and their Use in Generating a Multi-Cancer Gene Signature.

255 Prediction of early breast cancer patient survival using ensembles of hypoxia signatures.

254 Prognostic and Predictive Factors in Breast Carcinoma. **2018**, 327-356   1

253 Expression-based analyses indicate a central role for hypoxia in driving tumor plasticity through microenvironment remodeling and chromosomal instability.

252 The impact of stroma on the discovery of molecular subtypes and prognostic gene signatures in serous ovarian cancer.   1

251 Adjuvant Systemic Chemotherapy for HER2-Negative Disease. **2019**, 129-171

250 Gene Arrays, Prognosis, and Therapeutic Interventions. **2019**, 173-189

249 Biology and Genetics of Breast Cancer. **2019**, 125-142

248 Deep Learning Approach to Identifying Breast Cancer Subtypes Using High-Dimensional Genomic Data.   2

247   Gene-signatures predict biologically relevant dose-response potencies in phenotypic assays.

246   m6A-Mediated Tumor Invasion and Methylation Modification in Breast Cancer Microenvironment. **2021**, 2021, 9987376   3

245   Comprehensive of N1-Methyladenosine Modifications Patterns and Immunological Characteristics in Ovarian Cancer. **2021**, 12, 746647   3

244   Characterization of the Immune Cell Infiltration Landscape of Thyroid Cancer for Improved Immunotherapy. **2021**, 8, 714053   1

243   A qualitative transcriptional signature to reclassify histological grade of ER-positive breast cancer patients.

242   Correlation between MR Image-Based Radiomics Features and Risk Scores Associated with Gene Expression Profiles in Breast Cancer. **2020**, 81, 632

241   The Mutational Landscape of the SCAN-B Real-World Primary Breast Cancer Transcriptome.   0

240   The Immune Landscape in Women Cancers. **2020**, 180, 215-249   1

239   A qualitative transcriptional signature to reclassify histological grade of ER-positive breast cancer patients.

238   A novel single-cell based method for breast cancer prognosis.

237   Construction of an Immune Cell Infiltration Score to Evaluate the Prognosis and Therapeutic Efficacy of Ovarian Cancer Patients. **2021**, 12, 751594   3

236   Wound-like tumor periphery in human breast cancer predicts a convergent drug nonresponse.   0

235   Immune Cell Infiltration Landscape of Ovarian Cancer to Identify Prognosis and Immunotherapy-Related Genes to Aid Immunotherapy. **2021**, 9, 749157   2

234   Postpartum breast cancer has a distinct molecular profile that predicts poor outcomes. **2021**, 12, 6341   3

233   mC Regulator-Mediated Methylation Modification Patterns and Tumor Microenvironment Infiltration Characterization in Papillary Thyroid Carcinoma. **2021**, 11, 729887   5

232   Linking Interactome to Disease. 151-172

231   Classification molťulaire des cancers du sein. Implications pratiques. **2007**, 289-295

230   Analysis of Array Data and Clinical Validation of Array-Based Assays. **2012**, 171-210   0

| 229 | Expression Profiling for Diagnostics. **2012**, 21-27 | 0 |

| 228 | Effect of data combination on predictive modeling: a study using gene expression data. **2010**, 2010, 567-71 | 7 |

| 227 | Gene expression profiling in breast cancer. **2013**, 5, 132-8 | 9 |

| 226 | Hybrid method for prediction of metastasis in breast cancer patients using gene expression signals. **2013**, 3, 79-86 | 4 |

| 225 | Modern Risk Assessment for Individualizing Treatment Concepts in Early-stage Breast Cancer. **2013**, 6, 165-73 | 3 |

| 224 | T-ReCS: stable selection of dynamically formed groups of features with application to prediction of clinical outcomes. **2015**, 431-42 | 8 |

| 223 | FOXA1 positively regulates gene expression by changing gene methylation status in human breast cancer MCF-7 cells. **2015**, 8, 96-106 | 9 |

| 222 | Breast cancer intrinsic subtype classification, clinical use and future trends. **2015**, 5, 2929-43 | 296 |

| 221 | Prognostic signatures of breast cancer: Perou's molecular subtypes and Schmidt's metagenes. **2012**, 11, 204-7 | 4 |

| 220 | Medullary Breast Carcinoma and Invasive Ductal Carcinoma: A Review Study. **2018**, 43, 365-371 | 10 |

| 219 | Comprehensive characterization of the tumor microenvironment for assessing immunotherapy outcome in patients with head and neck squamous cell carcinoma. **2020**, 12, 22509-22526 | 4 |

| 218 | Transcription factor NF-B, interleukin-1and interleukin-8 expression and its association with tobacco smoking and severity in chronic obstructive pulmonary disease. **2022**, 26, 101453 | |

| 217 | Analysis of Multi-Layer RNA Modification Patterns for the Characterization of Tumor Immune Microenvironment in Hepatocellular Carcinoma. **2021**, 9, 761391 | 0 |

| 216 | 5mC regulator-mediated molecular subtypes depict the hallmarks of the tumor microenvironment and guide precision medicine in bladder cancer. **2021**, 19, 289 | 5 |

| 215 | Mammary collagen is under reproductive control with implications for breast cancer. **2021**, 105, 104-104 | 1 |

| 214 | Pyroptosis-Mediated Molecular Subtypes and Tumor Microenvironment Infiltration Characterization in Colon Cancer. **2021**, 9, 766503 | 1 |

| 213 | Metabolic characterization and metabolism-score of tumor to predict the prognosis in prostate cancer. **2021**, 11, 22486 | 1 |

| 212 | mA Regulator-Mediated Methylation Modification Patterns and Characteristics of Immunity in Blood Leukocytes of COVID-19 Patients.. **2021**, 12, 774776 | 1 |

193	Pyroptosis Regulators and Tumor Microenvironment Infiltration Characterization in Clear Cell Renal Cell Carcinoma.. **2021**, 11, 774279	1
192	ErbB2 promotes breast cancer metastatic potential via HSF1/LDHA axis-mediated glycolysis.. **2022**, 39, 45	0
191	Analysis of N6-Methyladenosine Modification Patterns and Tumor Immune Microenvironment in Pancreatic Adenocarcinoma.. **2021**, 12, 752025	0
190	Crosstalk Between Four Types of RNA Modification Writers Characterizes the Tumor Immune Microenvironment Infiltration Patterns in Skin Cutaneous Melanoma.. **2022**, 10, 821678	
189	The Identification of Two RNA Modification Patterns and Tumor Microenvironment Infiltration Characterization of Lung Adenocarcinoma.. **2022**, 13, 761681	
188	Immunogenomic Landscape in Breast Cancer Reveals Immunotherapeutically Relevant Gene Signatures.. **2022**, 13, 805184	0
187	Analysis of m6A Methylation Modification Patterns and Tumor Immune Microenvironment in Breast Cancer.. **2022**, 10, 785058	0
186	Ferroptosis-associated molecular classification characterized by distinct tumor microenvironment profiles in colorectal cancer.. **2022**, 18, 1773-1794	1
185	Development of Gene Expression-Based Random Forest Model for Predicting Neoadjuvant Chemotherapy Response in Triple-Negative Breast Cancer.. **2022**, 14,	1
184	Exploration of Potential Integrated Models of N6-Methyladenosine Immunity in Systemic Lupus Erythematosus by Bioinformatic Analyses.. **2021**, 12, 752736	2
183	Characterization of Two Ferroptosis Subtypes With Distinct Immune Infiltration and Gender Difference in Gastric Cancer.. **2021**, 8, 756193	2
182	Multi-omic machine learning predictor of breast cancer therapy response. **2021**,	15
181	Comprehensive Characterization of Metabolism-Associated Subtypes of Renal Cell Carcinoma to Aid Clinical Therapy.. **2022**, 2022, 9039732	
180	Pyroptosis patterns and immune infiltrates characterization in head and neck squamous cell carcinoma.. **2022**, e24292	1
179	Identification of the Expression Patterns and Potential Prognostic Role of 5-Methylcytosine Regulators in Hepatocellular Carcinoma.. **2022**, 10, 842220	0
178	The Role of m6A Regulator-Mediated Methylation Modification and Tumor Microenvironment Infiltration in Glioblastoma Multiforme.. **2022**, 10, 842835	0
177	RNA modification writers influence tumor microenvironment in gastric cancer and prospects of targeted drug therapy.. **2022**, 2250004	
176	The Heterogeneity of Immune Cell Infiltration Landscape and Its Immunotherapeutic Implications in Hepatocellular Carcinoma.. **2022**, 13, 861525	1

175 — Identification of New mA Methylation Modification Patterns and Tumor Microenvironment Infiltration Landscape that Predict Clinical Outcomes for Papillary Renal Cell Carcinoma Patients.. **2022**, 10, 818194

174 — Two Pyroptosis-Related Subtypes with Distinct Immune Microenvironment Characteristics and a Novel Signature for Predicting Immunotherapy Response and Prognosis in Uveal Melanoma.. **2022**, 1-14

173 — A novel prognostic signature in osteosarcoma characterised from the perspective of unfolded protein response.. **2022**, 12, e750 — 1

172 — Chemokines in Triple-Negative Breast Cancer Heterogeneity: New Challenges for Clinical Implications.. **2022**, — 7

171 — Autophagy characteristics and establishment of autophagy prognostic models in lung adenocarcinoma and lung squamous cell carcinoma.. **2022**, 17, e0266070 — 0

170 — The Expression Pattern of Ferroptosis-Related Genes in Colon Adenocarcinoma: Highly Correlated to Tumor Microenvironment Characteristics.. **2022**, 13, 837941

169 — Comprehensive analysis of pyroptosis regulation patterns and their influence on tumor immune microenvironment and patient prognosis in glioma.. **2022**, 13, 13 — 0

168 — mA Regulator-Mediated Methylation Modification Patterns and Characterisation of Tumour Microenvironment Infiltration in Non-Small Cell Lung Cancer.. **2022**, 15, 1969-1989 — 1

167 — Modeling survival response using a parametric approach in the presence of multicollinearity. 1-10

166 — Tyrosine Phosphatase PTPRO Deficiency in ERBB2-Positive Breast Cancer Contributes to Poor Prognosis and Lapatinib Resistance.. **2022**, 13, 838171 — 1

165 — Anlotinib inhibits the proliferation, migration and invasion, and induces apoptosis of breast cancer cells by downregulating TFAP2C.. **2022**, 23, 46 — 0

164 — RNA Sequencing-Based Single Sample Predictors of Molecular Subtype and Risk of Recurrence for Clinical Assessment of Early-Stage Breast Cancer.

163 — Combined mRNAs and clinical factors model on predicting prognosis in patients with triple-negative breast cancer.. **2021**, 16, e0260811

162 — Transcriptomic and Metabolomic Profiling in Induced Gastric Cancer Identified Prognosis- and Immunotherapy-Relevant Gene Signatures.. **2021**, 9, 769409 — 0

161 — Identification of HCC Subtypes With Different Prognosis and Metabolic Patterns Based on Mitophagy.. **2021**, 9, 799507 — 0

160 — Projection of High-Dimensional Genome-Wide Expression on SOM Transcriptome Landscapes. **2022**, 2, 62-76 — 0

159 — COSMONET: An R Package for Survival Analysis Using Screening-Network Methods. **2021**, 9, 3262 — 1

158 — Definition of High-Risk Early Hormone-Positive HER2-Negative Breast Cancer: A Consensus Review.. **2022**, 14, — 1

157	Molecular Characteristics of m6A Regulators and Tumor Microenvironment Infiltration in Soft Tissue Sarcoma: A Gene-Based Study.. **2022**, 10, 846812	0
156	Improving ovarian cancer treatment decision using a novel risk predictive tool.. **2022**, 14,	0
155	Table_11.DOCX. **2020**,	
154	Table_2.DOCX. **2020**,	
153	Table_3.XLSX. **2020**,	
152	Table_4.XLSX. **2020**,	
151	Table_5.XLSX. **2020**,	
150	Table_6.XLSX. **2020**,	
149	Table_7.DOCX. **2020**,	
148	Table_8.DOCX. **2020**,	
147	Table_9.DOCX. **2020**,	
146	Data_Sheet_1.docx. **2019**,	
145	Table_1.XLSX. **2019**,	
144	Table_2.XLSX. **2019**,	
143	Table_3.XLSX. **2019**,	
142	Table_4.XLSX. **2019**,	
141	Table_5.XLSX. **2019**,	
140	Table_6.XLSX. **2019**,	

139   Table_7.XLSX. **2019,**

138   Table_8.XLSX. **2019,**

137   Table_9.XLSX. **2019,**

136   Table_1.xlsx. **2019,**

135   Table_10.xlsx. **2019,**

134   Table_11.xlsx. **2019,**

133   Table_12.xlsx. **2019,**

132   Table_13.xlsx. **2019,**

131   Table_14.xlsx. **2019,**

130   Table_15.xlsx. **2019,**

129   Table_2.xlsx. **2019,**

128   Table_3.xlsx. **2019,**

127   Table_4.xlsx. **2019,**

126   Table_5.xlsx. **2019,**

125   Table_6.xlsx. **2019,**

124   Table_7.xlsx. **2019,**

123   Table_8.xlsx. **2019,**

122   Table_9.xlsx. **2019,**

121   Image_1.TIF. **2020**,

120   Image_2.TIF. **2020**,

119   Image_3.TIF. **2020**,

118   Image_4.TIF. **2020**,

117   Image_5.TIF. **2020**,

116   Image_6.TIF. **2020**,

115   Image_7.TIF. **2020**,

114   Image_8.TIF. **2020**,

113   Table_1.XLSX. **2020**,

112   Table_10.DOCX. **2020**,

111   Table_1.XLSX. **2019**,

110   Does focal heterogeneity affect survival in postoperative ipsilateral multifocal and multicentric breast cancers?. **2022**, 68, 405-412

109   Dynamic Risk Prediction via a Joint Frailty-Copula Model and IPD Meta-Analysis: Building Web Applications. **2022**, 24, 589   2

108   The Significance of Tumor Microenvironment Score for Breast Cancer Patients.. **2022**, 2022, 5673810   0

107   Genomic Analysis Reveals the Prognostic and Immunotherapeutic Response Characteristics of Ferroptosis in Lung Squamous Cell Carcinoma.. **2022**,   0

106   Association between tumor F-fluorodeoxyglucose metabolism and survival in women with estrogen receptor-positive, HER2-negative breast cancer.. **2022**, 12, 7858   0

105   Molecular Progression of Breast Cancer and Personalized Medicine in Terms of Clinical Trials. **2022**, 367-401

104   Comprehensive Genomic Characterization of Tumor Microenvironment and Relevant Signature in Clear Cell Renal Cell Carcinoma. **2022**, 12,

103	Construction of an immune infiltration landscape based on immune-related genes in cervical cancer. **2022**, 105638	0
102	Regression of Breast Cancer Metastases Following Treatment with Irradiated SV-BR-1-GM, a GM-CSF Overexpressing Breast Cancer Cell Line: Intellectual Property and Immune Markers of Response.. **2022**,	1
101	The Clinical Implication and Translational Research of OSCC Differentiation.	
100	Cancer cell cycle dystopia: heterogeneity, plasticity, and therapy. **2022**,	0
99	Characterization of the Immune Cell Infiltration Landscape Uncovers Prognostic and Immunogenic Characteristics in Lung Adenocarcinoma. 13,	1
98	Characterization of RNA modifications in gastric cancer to identify prognosis-relevant gene signatures.	
97	Characterization of Immune Microenvironment Infiltration and m ^{6}A Regulator-Mediated RNA Methylation Modification Patterns in Osteoarthritis.	
96	Predicting prognosis and clinical features of the tumor microenvironment based on ferroptosis score in patients with breast cancer. **2022**, 12,	2
95	N6-Methyladenosine Modification Patterns and Tumor Microenvironment Immune Characteristics Associated With Clinical Prognosis Analysis in Stomach Adenocarcinoma. 10,	1
94	A Novel Deep Feature Extraction Engineering for Subtypes of Breast Cancer Diagnosis: A Transfer Learning Approach. **2022**,	1
93	Metabolomic and Transcriptomic Profiling Identified Significant Genes in Thymic Epithelial Tumor. **2022**, 12, 567	0
92	scHumanNet: a single-cell network analysis platform for the study of cell-type specificity of disease genes.	
91	RNA modification patterns based on major RNA modifications define tumor microenvironment characteristics in glioblastoma. **2022**, 12,	0
90	Role of germline variants in the metastasis of breast carcinomas. **2022**, 13, 843-862	
89	Tumor Microenvironment Characterization in Breast Cancer and an Immune Cell Infiltration Score Development, Validation, and Application. 12,	
88	Molecular subtypes, prognostic and immunotherapeutic relevant gene signatures mediated by DNA methylation regulators in hepatocellular carcinoma. **2022**, 14, 5271-5291	0
87	Identification of mRNA vaccines and conserved ferroptosis related immune landscape for individual precision treatment in bladder cancer. **2022**, 9,	0
86	Deep survival forests for extremely high censored data.	

85	Genomic analysis quantifies pyroptosis in the immune microenvironment of HBV-related hepatocellular carcinoma. 13,	
84	The Multi-Omics Landscape and Clinical Relevance of the Immunological Signature of Phagocytosis Regulators: Implications for Risk Classification and Frontline Therapies in Skin Cutaneous Melanoma. **2022**, 14, 3582	
83	Stemness Analysis Uncovers That The Peroxisome Proliferator-Activated Receptor Signaling Pathway Can Mediate Fatty Acid Homeostasis In Sorafenib-Resistant Hepatocellular Carcinoma Cells. 12,	0
82	Machine learning models based on immunological genes to predict the response to neoadjuvant therapy in breast cancer patients. 13,	0
81	Novel insight into m6A regulator-mediated methylation modification patterns and immune characteristics in intracranial aneurysm. 14,	0
80	Molecular subtypes of osteosarcoma classified by cancer stem cell related genes define immunological cell infiltration and patient survival. 13,	0
79	RNA sequencing-based single sample predictors of molecular subtype and risk of recurrence for clinical assessment of early-stage breast cancer. **2022**, 8,	0
78	Lactate score predicts survival, immune cell infiltration and response to immunotherapy in breast cancer. 13,	
77	Utility of Genomic Platforms in Treatment Decisions in Axilla-Positive Breast Cancer. **2022**,	
76	Risk Stratification for Breast Cancer Patient by Simultaneous Learning of Molecular Subtype and Survival Outcome Using Genetic Algorithm-Based Gene Set Selection. **2022**, 14, 4120	
75	A Novel hepatocellular carcinoma specific hypoxic related signature for predicting prognosis and therapeutic responses. 13,	
74	An uncertainty-based interpretable deep learning framework for breast cancer outcomes prediction.	
73	The integrated landscape of eRNA in gastric cancer reveals distinct immune subtypes with prognostic and therapeutic relevance. **2022**, 25, 105075	0
72	Pyroptosis-related gene expression patterns and corresponding tumor microenvironment infiltration characterization in ovarian cancer. **2022**, 20, 5440-5452	0
71	Computational Studies in Breast Cancer. **2022**, 434-456	0
70	The Ferroptosis Molecular Subtype Reveals Characteristics of the Tumor Microenvironment, Immunotherapeutic Response, and Prognosis in Gastric Cancer. **2022**, 23, 9767	0
69	Rational Approach to Finding Genes Encoding Molecular Biomarkers: Focus on Breast Cancer. **2022**, 13, 1538	0
68	DNA methylation regulator-mediated modification patterns and tumor microenvironment characterization in glioma.	0

67	Multiplex immunohistochemistry and high-throughput image analysis for evaluation of spatial tumor immune cell markers in human breast cancer. **2022**, 1-14	1
66	Identification and validation of a prognostic risk model based on caveolin family genes for breast cancer. 10,	0
65	A novel cuproptosis-related molecular pattern and its tumor microenvironment characterization in colorectal cancer. 13,	0
64	Ferroptosis Related Gene Signature in T Cell-Mediated Rejection After Kidney Transplantation.	0
63	The effect of chemotherapy on survival in oldest old patients with nonmetastatic triple negative breast cancer: A populationbased observational study.	0
62	Molecular Classification of Breast Cancer. **2022**,	0
61	Integrated analysis of Helicobacter pylori-related prognostic gene modification patterns in the tumour microenvironment of gastric cancer. 9,	0
60	Analysis of N6-Methyladenosine RNA Methylation Regulators in Diagnosis and Distinct Molecular Subtypes of Ankylosing Spondylitis. **2022**, 2022, 1-23	0
59	The regulatory role of AP-2 in monoaminergic neurotransmitter systems: insights on its signalling pathway, linked disorders and theragnostic potential. **2022**, 12,	0
58	Comprehensive analysis of m7G modification patterns based on potential m7G regulators and tumor microenvironment infiltration characterization in lung adenocarcinoma. 13,	0
57	Genomic analysis of 5-methylcytosine-related molecular subtypes reveals the characterisation of prognosis and immunotherapy in lung squamous cell carcinoma.	0
56	Investigation on the regulatory T cells signature and relevant Foxp3/ STAT3 axis in esophageal cancer.	0
55	m7G regulator-mediated methylation modification patterns define immune cell infiltration and patient survival. 13,	0
54	A novel twelve-gene signature to predict neoadjuvant chemotherapy response and prognosis in breast cancer. 13,	0
53	Construction of an immune-related signature for predicting the ischemic events in patients undergoing carotid endarterectomy. 13,	0
52	Prediction of prognosis, immune infiltration and immunotherapy response with N6-methyladenosine-related lncRNA clustering patterns in cervical cancer. **2022**, 12,	0
51	A Robust Personalized Classification Method for Breast Cancer Metastasis Prediction. **2022**, 14, 5327	0
50	Comprehensive analysis of autoimmune-related genes in amyotrophic lateral sclerosis from the perspective of 3P medicine.	0

49	High levels of m6A methylation and histone acetylation modification patterns contribute to the survival of LUAD patients.	0
48	Severe testing with high-dimensional omics data for enhancing biomedical scientific discovery. **2022**, 8,	0
47	Significance of immunogenic cell death-related prognostic gene signature in cervical cancer prognosis and anti-tumor immunity.	0
46	Plectin as a putative novel biomarker for breast cancer: an in silico study. **2022**, 11,	0
45	DNA5mC Regulator-Mediated Molecular Clusters and Tumor Microenvironment Signatures in Glioblastoma. 10,	0
44	Analysis of m6A Methylation Patterns and Tumor Microenvironment in Endometrial Cancer. **2022**, 147052	0
43	Splicing factor SRSF3 represses translation of p21cip1/waf1 mRNA. **2022**, 13,	1
42	scHumanNet: a single-cell network analysis platform for the study of cell-type specificity of disease genes.	0
41	Novel Ferroptosis-related gene signature for predicting the prognosis of breast cancer.	0
40	Comprehensive analysis of cuproptosis-related lncRNAs to predict prognosis and immune infiltration characteristics in colorectal cancer. 13,	0
39	Future Role of Molecular Profiling in Small Breast Samples and Personalised Medicine. **2022**, 895-915	0
38	NUSAP1 and PCLAF (KIA0101) Downregulation by Neoadjuvant Therapy is Associated with Better Therapeutic Outcomes and Survival in Breast Cancer. **2022**, 2022, 1-14	0
37	Characterization of immune microenvironment infiltration and m6A regulator-mediated RNA methylation modification patterns in osteoarthritis. 13,	0
36	Cuprotosis Patterns Are Associated with Tumor Mutation Burden and Immune Landscape in Lung Adenocarcinoma. **2022**, 2022, 1-12	0
35	Novel insight of N6-methyladenosine modified subtypes in abdominal aortic aneurysm. 13,	0
34	A signal recognition particle-related joint model of LASSO regression, SVM-RFE and artificial neural network for the diagnosis of systemic sclerosis-associated pulmonary hypertension. 13,	0
33	Discovery and validation of Ferroptosis-related molecular patterns and immune characteristics in Alzheimerâ's disease. 14,	0
32	Use of Novel m6A Regulator-mediated Methylation Modification Patterns in Distinct Tumor Microenvironment Profiles to Identify and Predict Glioma Prognosis and Progression, T-cell Dysfunction, and Clinical Response to ICI Immunotherapy. **2022**, 29,	0

31	Delineating the molecular landscape of different histopathological growth patterns in colorectal cancer liver metastases. 13,	0
30	m6A regulators featured by tumor immune microenvironment landscapes and correlated with immunotherapy in non-small cell lung cancer (NSCLC). 12,	0
29	An MRI-based Radiomics Approach to Improve Breast Cancer Histological Grading. **2023**,	1
28	Immune microenvironment infiltration landscape and immune-related subtypes in prostate cancer. 13,	0
27	Modification of m5C regulators in sarcoma can guide different immune infiltrations as well as immunotherapy. 9,	0
26	Association of RNA-modification âwriterâ genes with prognosis and response to immunotherapy in patients with low-grade glioma. **2023**, 18, e0279119	0
25	5-Methylcytosine (m5C) Modification Patterns and Tumor Immune Infiltration Characteristics in Clear Cell Renal Cell Carcinoma. **2023**, 30, 559-574	0
24	Molecular Diagnostics. **2019**, 226-248	0
23	Identification of IRF-associated molecular subtypes in clear cell renal cell carcinoma to characterize immunological characteristics and guide therapy. 12,	0
22	Ferroptosis related gene signature in T cell-mediated rejection after kidney transplantation. **2023**, 16,	0
21	Assessment of stained direct cytology smears of breast cancer for whole transcriptome and targeted messenger RNA sequencing.	0
20	Searching for DNA methylation in patients triple-negative breast cancer: a liquid biopsy approach. **2023**, 23, 41-51	0
19	Tumor stemness score to estimate epithelial-to-mesenchymal transition (EMT) and cancer stem cells (CSCs) characterization and to predict the prognosis and immunotherapy response in bladder urothelial carcinoma. **2023**, 14,	0
18	Genomic analysis and filtration of novel prognostic biomarkers based on metabolic and immune subtypes in pancreatic cancer.	0
17	m5C related-regulator-mediated methylation modification patterns and prognostic significance in breast cancer.	0
16	Lessons from other fields of medicine, Part 1: Breast cancer. **2023**, 101-118	0
15	An immune cell infiltration landscape classification to predict prognosis and immunotherapy effect in oral squamous cell carcinoma. 1-13	0
14	Clinically relevant gene signatures provide independent prognostic information in older breast cancer patients.	0

13	Differential Expression of AP-2 Transcription Factors Family in Lung Adenocarcinoma and Lung Squamous Cell Carcinomaâ€A Bioinformatics Study. **2023**, 12, 667	0
12	Cuproptosis-related classification and personalized treatment in lower-grade gliomas to prompt precise oncology.	0
11	Anterior gradient-2 regulates cell communication by coordinating cytokineâ€chemokine signaling and immune infiltration in breast cancer.	0
10	Breast cancer prediction and categorization in the molecular era of histologic grade.	0
9	Sensitivity Analysis for Survival Prognostic Prediction with Gene Selection: A Copula Method for Dependent Censoring. **2023**, 11, 797	0
8	Identification of the Expression Patterns and Potential Prognostic Role of m6A-RNA Methylation Regulators in Wilms Tumor.	0
7	Signatures of immune cell infiltration for predicting immune escape and immunotherapy in cervical cancer.	0
6	Integrative analysis revealed that distinct cuprotosis patterns reshaped tumor microenvironment and responses to immunotherapy of colorectal cancer. 14,	0
5	Comprehensive characterization of ferroptosis in hepatocellular carcinoma revealing the association with prognosis and tumor immune microenvironment. 13,	0
4	Molecular breast cancer subtype identification using photoacoustic spectral analysis and machine learning at the biomacromolecular level. **2023**, 30, 100483	0
3	Cuproptosis-related molecular subtypes direct T cell exhaustion phenotypes and therapeutic strategies for patients with lung adenocarcinoma. 14,	0
2	Ferroptosis-Related Molecular Clusters and Diagnostic Model in Rheumatoid Arthritis. **2023**, 24, 7342	0
1	Prognostic model development for classification of colorectal adenocarcinoma by using machine learning model based on feature selection technique boruta. **2023**, 13,	0