CITATION REPORT List of articles citing

Gene expression profiling predicts clinical outcome of breast cancer

DOI: 10.1038/415530a Nature, 2002, 415, 530-6.

Source: https://exaly.com/paper-pdf/34729237/citation-report.pdf

Version: 2024-04-09

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

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

| # | Paper | IF | Citations |
|------|--|----|-----------|
| 2209 | | | |
| 2208 | p-Medicine: From data sharing and integration via VPH models to personalized medicine. 2011 , 5, 218 | | 12 |
| 2207 | Integrated gene expression analysis of multiple microarray data sets based on a normalization technique and on adaptive connectionist model. | | 1 |
| 2206 | Adrenocortical function in epilepsy: II. The role of corticosterone in the mechanism and management of epilepsy. 1961 , 11, 246-246 | | 2 |
| 2205 | The interaction of bovine erythrocyte superoxide dismutase with hydrogen peroxide: inactivation of the enzyme. 1975 , 14, 5294-9 | | 686 |
| 2204 | Triple-negative breast cancer types exhibit a distinct poor clinical characteristic in lymph node-negative Chinese patients. 1994 , 20, 987 | | 1 |
| 2203 | Gene expression profiling can distinguish tumor subclasses of breast carcinomas. 2001 , 132-161 | | 1 |
| 2202 | Technique of microarrays: microarray platforms. 2001 , 8-26 | | |
| 2201 | Prediction of response and resistance to treatment by gene expression profiling. 2001 , 212-237 | | |
| 2200 | Hypertension, angiotensin II, and oxidative stress. 2002 , 346, 1999-2001 | | 180 |
| 2199 | Gene expression studies using microarrays: principles, problems, and prospects. 2002 , 26, 256-70 | | 114 |
| 2198 | SELDI ProteinChip array in oncoproteomic research. 2002 , 1, 273-80 | | 68 |
| 2197 | A senescence rescue screen identifies BCL6 as an inhibitor of anti-proliferative p19(ARF)-p53 signaling. 2002 , 16, 681-6 | | 119 |
| 2196 | Progress in the treatment of breast cancer in the elderly. 2002 , 13 Suppl 4, 207-10 | | 9 |
| 2195 | Pre-validation and inference in microarrays. 2002, 1, Article1 | | 81 |
| 2194 | Yellow pages to the transcriptome. 2002 , 3, 791-807 | | 24 |
| 2193 | A common reference for cDNA microarray hybridizations. 2002 , 30, e116 | | 57 |

| 2192 Analyzing array data using supervised methods. 2002 , 3, 403-15 | 59 |
|--|--------------|
| 2191 Phenomenology and scientific progress. 2002 , 1, 436-7 | 36 |
| 2190 Information management systems for pharmacogenomics. 2002 , 3, 651-67 | 6 |
| 2189 Classification and prediction in pharmacogeneticscontext, construction and validation. 2002 , 3, 157-60 | O |
| 2188 Radiotherapy for breast cancer. 2002 , 346, 862-4 | 4 |
| 2187 Molecular signatures of breast cancerpredicting the future. 2002 , 347, 2067-8 | 22 |
| 2186 Molecular characteristics of diffuse large-B-cell lymphoma. 2002 , 346, 1998-9 | 8 |
| [Function and responsibility of an interdisciplinary tumor center. Need for a "cancer center" for multimodal therapy concepts]. 2002 , 127, 901-6 | |
| 2184 Application of toxicogenomics to drug development. 2002 , 2, 337-45 | 11 |
| | |
| 2183 Chapter 23. Tumor classification for tailored cancer therapy. 2002 , 37, 225-236 | |
| 2183 Chapter 23. Tumor classification for tailored cancer therapy. 2002 , 37, 225-236 2182 Practical approaches to analyzing results of microarray experiments. 2002 , 27, 125-32 | 76 |
| | 76 3 |
| 2182 Practical approaches to analyzing results of microarray experiments. 2002 , 27, 125-32 | , |
| 2182 Practical approaches to analyzing results of microarray experiments. 2002 , 27, 125-32 2181 Gene expression analysis using cDNA microarrays. 2002 , Chapter 4, Unit 4.28 | 3 |
| 2182 Practical approaches to analyzing results of microarray experiments. 2002, 27, 125-32 2181 Gene expression analysis using cDNA microarrays. 2002, Chapter 4, Unit 4.28 2180 Genomic approaches to the pathogenesis and treatment of acute lymphoblastic leukemias. 2002, 9, 339-44 Global gene expression changes during neoadjuvant chemotherapy for human breast cancer. 2002, | 3 |
| 2182 Practical approaches to analyzing results of microarray experiments. 2002, 27, 125-32 2181 Gene expression analysis using cDNA microarrays. 2002, Chapter 4, Unit 4.28 2180 Genomic approaches to the pathogenesis and treatment of acute lymphoblastic leukemias. 2002, 9, 339-44 Clobal gene expression changes during neoadjuvant chemotherapy for human breast cancer. 2002, 8, 461-8 DNA microarrays: a bridge between genome sequence information and biological understanding. | 3 8 75 |
| 2182 Practical approaches to analyzing results of microarray experiments. 2002, 27, 125-32 2181 Gene expression analysis using cDNA microarrays. 2002, Chapter 4, Unit 4.28 2180 Genomic approaches to the pathogenesis and treatment of acute lymphoblastic leukemias. 2002, 9, 339-44 2179 Global gene expression changes during neoadjuvant chemotherapy for human breast cancer. 2002, 8, 461-8 2178 DNA microarrays: a bridge between genome sequence information and biological understanding. 2002, 10, 389-408 | 3 8 75 |

| 2174 | Gene expression profiles of mouse submandibular gland development: FGFR1 regulates branching morphogenesis in vitro through BMP- and FGF-dependent mechanisms. 2002 , 129, 5767-78 | 160 |
|------|---|------|
| 2173 | Gene expression signatures may predict clinical outcome. 2002 , 4, 1 | |
| 2172 | Perspective: prostate cancer susceptibility genes. 2002 , 143, 2029-40 | 37 |
| 2171 | The pathology of inherited breast cancer. 2002 , 34, 309-14 | 45 |
| 2170 | Distinct and complementary information provided by use of tissue and DNA microarrays in the study of breast tumor markers. 2002 , 161, 1223-33 | 133 |
| 2169 | Genes involved in breast cancer progression: analysis of global changes in gene expression or retroviral tagging?. 2002 , 161, 1973-7 | 2 |
| 2168 | Editorial radiotherapy and oncology 2002: predictive assays for normal tissue damage. 2002 , 64, 125-9 | 39 |
| 2167 | Time-resolved fluorescence imaging in biology and medicine. 2002 , 35, R61-R76 | 164 |
| 2166 | Microarrays in pharmacogenomicsadvances and future promise. 2002 , 3, 589-601 | 37 |
| 2165 | A gene-expression signature as a predictor of survival in breast cancer. 2002 , 347, 1999-2009 | 5020 |
| 2164 | Algorithms in Bioinformatics. 2002, | 3 |
| 2163 | Expression profiling predicts outcome in breast cancer. 2003 , 5, 57-8 | 123 |
| 2162 | Expression profiling to predict outcome in breast cancer: the influence of sample selection. 2003, 5, 23-6 | 32 |
| 2161 | Mutations in DNA damage response genes and breast cancer susceptibility. 2002 , 4, 1 | 2 |
| 2160 | Defining the galaxy of gene expression in breast cancer. 2002 , 4, 141-4 | 13 |
| 2159 | Microarrays and molecular markers for tumor classification. 2002 , 3, comment2005 | 12 |
| 2158 | Baclofen: possible therapy for gastro-oesophageal reflux?. 2002 , &NA, 17 | |
| 2157 | Biomedical imaging in the postgenomic era: opportunities and challenges. 2002 , 9, 999-1003 | 7 |

(2002-2002)

| 2156 | Perspective: microarray technology, seeing more than spots. 2002 , 143, 1983-9 | 43 |
|------|---|------|
| 2155 | Toxicogenomics: an opportunity to optimise drug development and safety evaluation. 2002 , 1, 275-86 | 28 |
| 2154 | Gene-expression profiling and identification of patients at high risk of breast cancer. 2002 , 360, 173-4; author reply 174 | 11 |
| 2153 | BRCA1: mechanisms of inactivation and implications for management of patients. 2002 , 360, 1007-14 | 99 |
| 2152 | Identification of genes regulating colorectal carcinogenesis by using the algorithm for diagnosing malignant state method. 2002 , 296, 497-506 | 12 |
| 2151 | Identification of genes induced by BRCA1 in breast cancer cells. 2002 , 299, 839-46 | 188 |
| 2150 | Impact of the Human Genome Project on the clinical management of sporadic cancers. 2002 , 3, 349-56 | 11 |
| 2149 | Applications of microarrays in the pharmaceutical industry. 2002 , 2, 551-4 | 18 |
| 2148 | The promise of biomarkers in cancer screening and detection. 2002 , 8, 288-93 | 82 |
| 2147 | Gene Expression Patterns in Breast Cancer May Identify Specific Tumor Phenotypes and Predict Disease Outcome. 2002 , 3, 240-242 | |
| 2146 | Functional genomics and the breast cancer problem. 2002 , 1, 15-7 | 17 |
| 2145 | Gene expression correlates of clinical prostate cancer behavior. 2002 , 1, 203-9 | 1829 |
| 2144 | Focus on breast cancer. 2002 , 1, 319-22 | 76 |
| 2143 | Recent developments in DNA microarrays. 2002 , 5, 334-7 | 68 |
| 2142 | Combination of taxanes and anthracyclines in first-line chemotherapy of metastatic breast cancer: an interim report. 2002 , 38, 1730-8 | 15 |
| 2141 | Dietary protein quantity and quality affect rat hepatic gene expression. 2002 , 132, 3632-7 | 71 |
| 2140 | Endostatin: are the 2 years up yet?. 2002 , 20, 3758-60 | 13 |
| 2139 | Status of lymph node staging. 2002 , 91, 263-7 | 3 |

| 2138 | HER-2/Neu signaling and therapeutic approaches in breast cancer. 2002 , 15, 13-24 | 7 |
|--------------------------------------|---|-----------------------|
| 2137 | The Future of Cancer Research. 2002 , 17, 38-40 | |
| 2136 | Breast cancer 2002: where do we stand?. 2002 , 52, 253-5 | 3 |
| 2135 | Optimization and evaluation of T7 based RNA linear amplification protocols for cDNA microarray analysis. 2002 , 3, 31 | 105 |
| 2134 | Molecular markers in the diagnosis and staging of breast cancer. 2002 , 12, 305-18 | 5 |
| 2133 | Percutaneous stereotactic en bloc excision of nonpalpable breast carcinoma: a step in the direction of supraconservative surgery. 2002 , 11, 501-8 | 2 |
| 2132 | Genotype-phenotype mapping: genes as computer programs. 2002 , 18, 555-9 | 57 |
| 2131 | Turning quantity into quality: novel quality assurance strategies for data produced by high-throughput genomics technologies. 2002 , 1, 139-146 | 2 |
| 2130 | Computational selection of distinct class- and subclass-specific gene expression signatures. 2002 , 35, 160-70 | 45 |
| | | |
| 2129 | Altered methylation patterns in cancer cell genomes: cause or consequence?. 2002 , 1, 299-305 | 243 |
| 2129 | Altered methylation patterns in cancer cell genomes: cause or consequence?. 2002 , 1, 299-305 Optimal gene expression analysis by microarrays. 2002 , 2, 353-61 | 128 |
| 2128 | | |
| 2128 | Optimal gene expression analysis by microarrays. 2002 , 2, 353-61 | 128 |
| 2128 | Optimal gene expression analysis by microarrays. 2002 , 2, 353-61 Applications of antisense and siRNAs during preclinical drug development. 2002 , 7, 912-7 | 128 |
| 2128 2127 2126 | Optimal gene expression analysis by microarrays. 2002, 2, 353-61 Applications of antisense and siRNAs during preclinical drug development. 2002, 7, 912-7 mRNA differential display of gene expression in colonic carcinoma. 2002, 23, 1667-76 | 128 40 23 |
| 2128 2127 2126 2125 | Optimal gene expression analysis by microarrays. 2002, 2, 353-61 Applications of antisense and siRNAs during preclinical drug development. 2002, 7, 912-7 mRNA differential display of gene expression in colonic carcinoma. 2002, 23, 1667-76 Highlight: BRCA1 and BRCA2 proteins in breast cancer. 2002, 59, 68-83 | 128 40 23 11 |
| 2128 2127 2126 2125 2124 | Optimal gene expression analysis by microarrays. 2002, 2, 353-61 Applications of antisense and siRNAs during preclinical drug development. 2002, 7, 912-7 mRNA differential display of gene expression in colonic carcinoma. 2002, 23, 1667-76 Highlight: BRCA1 and BRCA2 proteins in breast cancer. 2002, 59, 68-83 Current Awareness on Comparative and Functional Genomics. 2002, 3, 293-304 Non-palpable breast carcinomas: correlation of mammographically detected malignant-appearing | 128 40 23 11 |

| 2120 A | study of estrogen signaling using DNA microarray in human breast cancer. 2002 , 9, 308-11 | | 15 |
|-----------------|--|------|-----|
| 2119 G e | enetische Risikofaktoren des Mammakarzinoms. 2002 , 35, 527-536 | | 4 |
| 2118 M | olekulare Frauenheilkunde. 2002 , 35, 872-880 | | 2 |
| 2117 M | ammakarzinom - prognostische und präiktive Faktoren. 2002 , 8, 808-816 | | 2 |
| 2116 Sy | mposium 1: Everything you want to know about molecular pathology. 2002 , 41, 1-11 | | 2 |
| 2115 Sy | mposium 15: Expression and profiling in surgical pathology. 2002 , 41, 249-262 | | O |
| | zzy neural network applied to gene expression profiling for predicting the prognosis of diffuse ge B-cell lymphoma. 2002 , 93, 1207-12 | | 40 |
| 2113 DN | NA methylation analysis: a powerful new tool for lung cancer diagnosis. 2002 , 21, 5450-61 | | 243 |
| 2112 Co | ontrol of the centriole and centrosome cycles by ubiquitination enzymes. 2002 , 21, 6209-21 | | 17 |
| | creased CpG methylation of the estrogen receptor gene in BRCA1-linked estrogen ceptor-negative breast cancers. 2002 , 21, 7034-41 | | 34 |
| | oviral activation of the tumor suppressor E2a contributes to T cell lymphomagenesis in EmuMyc ansgenic mice. 2002 , 21, 6559-66 | | 15 |
| | creased incidence of ERBB2 overexpression and TP53 mutation in inflammatory breast cancer. 102, 21, 7593-7 | | 68 |
| 2108 Th | e cancer connection: BRCA1 and BRCA2 tumor suppression in mice and humans. 2002 , 21, 8994-9007 | | 99 |
| | togenetic alterations and cytokeratin expression patterns in breast cancer: integrating a new odel of breast differentiation into cytogenetic pathways of breast carcinogenesis. 2002 , 82, 1525-33 | | 194 |
| 2106 Th | ne molecular outlook. <i>Nature</i> , 2002 , 415, 484-5 | 50.4 | 76 |
| 2105 Or | n the offensive. <i>Nature</i> , 2002 , 416, 470-4 | 50.4 | 14 |
| 2104 Pi | cture this. <i>Nature</i> , 2002 , 418, 11-3 | 50.4 | 15 |
| 2103 E2 | F-dependent accumulation of hEmi1 regulates S phase entry by inhibiting APC(Cdh1). 2002 , 4, 358-66 | | 274 |

| 2102 Medical applications of microarray technologies: a regulatory science perspective. 2002 , 32 Suppl, 474-9 | 191 |
|---|------|
| 2101 Options availablefrom start to finishfor obtaining data from DNA microarrays II. 2002 , 32 Suppl, 481-9 | 221 |
| 2100 From patterns to pathways: gene expression data analysis comes of age. 2002 , 32 Suppl, 502-8 | 444 |
| 2099 Molecular portraits and the family tree of cancer. 2002 , 32 Suppl, 533-40 | 223 |
| 2098 Dancing the two-step. 2002 , 2, 156-156 | |
| 2097 Tailor-made therapy. 2002 , 2, 157-157 | |
| 2096 Epithelial-mesenchymal transitions in tumour progression. 2002 , 2, 442-54 | 5249 |
| 2095 The fundamental role of epigenetic events in cancer. 2002 , 3, 415-28 | 4311 |
| 2094 Design issues for cDNA microarray experiments. 2002 , 3, 579-88 | 583 |
| 2093 Prognosis of breast cancer and gene expression profiling using DNA arrays. 2002 , 975, 217-31 | 31 |
| 2092 RNA expression profiling as prognostic tool in renal patients: toward nephrogenomics. 2002 , 62, 1125-35 | 27 |
| Gene expression profiling: methodological challenges, results, and prospects for addiction research. 2002 , 121, 241-56 | 41 |
| Economics and quality of care for patients with acute coronary syndromes: the impending crisis. 2002 , 25, I9-15 | |
| [New aspects of molecular biology diagnosis. Array technology and expression profile for characterization of rheumatic diseases]. 2002 , 61, 396-404 | 1 |
| 2088 Associations between gene expressions in breast cancer and patient survival. 2002 , 111, 411-20 | 72 |
| $_{2087}$ Validated genomic approach to study differentially expressed genes in complex tissues. 2002 , 27, 1027-33 | 34 |
| Expression profiling with oligonucleotide arrays: technologies and applications for neurobiology. 2002 , 27, 1005-26 | 8 |
| 2085 Application of DNA microarrays in pharmacogenomics and toxicogenomics. 2002 , 19, 1773-8 | 45 |

| 2084 | Can metabolomics be used for assessing nutritive-dependent human diseases?. 2002 , 1, 223-230 | 2 |
|------|---|-----|
| 2083 | NF-kappaB and breast cancer. 2002 , 26, 282-309 | 57 |
| 2082 | Molecular genetic alterations in adrenal and extra-adrenal pheochromocytomas and paragangliomas. 2003 , 14, 329-50 | 21 |
| 2081 | p53 inactivation is a rare event in familial breast tumors negative for BRCA1 and BRCA2 mutations. 2003 , 82, 1-9 | 14 |
| 2080 | Expression profiling of human breast cancers and gene regulation by progesterone receptors. 2003 , 8, 257-68 | 44 |
| 2079 | Interrogating mouse mammary cancer models: insights from gene expression profiling. 2003, 8, 321-34 | 10 |
| 2078 | Laser capture microdissection and advanced molecular analysis of human breast cancer. 2003 , 8, 335-45 | 37 |
| 2077 | Expression profiling in multistage hepatocarcinogenesis: identification of HSP70 as a molecular marker of early hepatocellular carcinoma. 2003 , 37, 198-207 | 228 |
| 2076 | General keynote: hereditary cancer: lessons from Li-Fraumeni syndrome. 2003 , 88, S4-7; discussion S11-3 | 16 |
| 2075 | Prognostic factors and risk-based therapy in pediatric acute myeloid leukemia. 2003 , 5, 489-97 | 12 |
| 2074 | Pharmacogenomic applications in clinical drug development. 2003 , 52 Suppl 1, S57-60 | 5 |
| 2073 | Genexpressionsmuster als Prognoseindikator bei Brustkrebs. 2003 , 36, 1011-1015 | 1 |
| 2072 | Differential gene expression in the periprosthetic membrane: lubricin as a new possible pathogenetic factor in prosthesis loosening. 2003 , 443, 57-66 | 22 |
| 2071 | Gene expression profiles of microdissected pancreatic ductal adenocarcinoma. 2003, 443, 508-17 | 93 |
| 2070 | DNA microarrays in clinical practice: past, present, and future. 2003 , 3, 1-3 | 16 |
| 2069 | Profiling cancer. 2003 , 15, 213-20 | 12 |
| 2068 | New data on chemotherapy in the adjuvant setting. 2003 , 12, 373-8 | 12 |
| 2067 | Histopathology of primary breast cancer 2003. 2003 , 12, 391-6 | 8 |
| | | |

| | Best use of adjuvant systemic therapies II, chemotherapy aspects: dose of chemotherapy-cytotoxicity, duration and responsiveness. 2003 , 12, 529-37 | 7 |
|--------------------------------------|--|----------------------|
| 2065 | Inhibition of FLT3 in MLL. Validation of a therapeutic target identified by gene expression based classification. 2003 , 3, 173-83 | 353 |
| 2064 | FANCF methylation contributes to chemoselectivity in ovarian cancer. 2003 , 3, 417-20 | 64 |
| 2063 | A multigenic program mediating breast cancer metastasis to bone. 2003 , 3, 537-49 | 2050 |
| 2062 | Prostate-specific deletion of the murine Pten tumor suppressor gene leads to metastatic prostate cancer. 2003 , 4, 209-21 | 852 |
| 2061 | Biomarker Discovery by Tissue Microdissectionand ProteinChip Array Analysis. 2003, 27, 79-84 | 1 |
| 2060 | Microarrays: the use of oligonucleotides and cDNA for the analysis of gene expression. 2003, 8, 134-41 | 106 |
| 2059 | Drug sensitivity and resistance genes in cancer chemotherapy: a chemogenomics approach. 2003, 8, 356-63 | 40 |
| 2058 | The use of gene-specific IgY antibodies for drug target discovery. 2003 , 8, 364-71 | 73 |
| 2057 | Tumor markers: discovery to practice. 2003 , 8, 441-3 | 1 |
| | | |
| 2056 | Cancer pharmacogenomics: current and future applications. 2003 , 1603, 99-111 | 37 |
| 2056 2055 | Cancer pharmacogenomics: current and future applications. 2003, 1603, 99-111 Direct comparison of microarray gene expression profiles between non-amplification and a modified cDNA amplification procedure applicable for needle biopsy tissues. 2003, 27, 405-11 | 37 |
| | Direct comparison of microarray gene expression profiles between non-amplification and a | |
| 2055 | Direct comparison of microarray gene expression profiles between non-amplification and a modified cDNA amplification procedure applicable for needle biopsy tissues. 2003 , 27, 405-11 Epidemiology, cancer genetics and microarrays: making correct inferences, using appropriate | 14 |
| 2055 | Direct comparison of microarray gene expression profiles between non-amplification and a modified cDNA amplification procedure applicable for needle biopsy tissues. 2003, 27, 405-11 Epidemiology, cancer genetics and microarrays: making correct inferences, using appropriate designs. 2003, 19, 690-5 Neural network analysis of lymphoma microarray data: prognosis and diagnosis near-perfect. 2003, | 40 |
| 2055 2054 2053 | Direct comparison of microarray gene expression profiles between non-amplification and a modified cDNA amplification procedure applicable for needle biopsy tissues. 2003, 27, 405-11 Epidemiology, cancer genetics and microarrays: making correct inferences, using appropriate designs. 2003, 19, 690-5 Neural network analysis of lymphoma microarray data: prognosis and diagnosis near-perfect. 2003, 4, 13 Expression profiling of blood samples from an SU5416 Phase III metastatic colorectal cancer clinical trial: a novel strategy for biomarker identification. 2003, 3, 3 | 14 40 54 |
| 2055 2054 2053 2052 2051 | Direct comparison of microarray gene expression profiles between non-amplification and a modified cDNA amplification procedure applicable for needle biopsy tissues. 2003, 27, 405-11 Epidemiology, cancer genetics and microarrays: making correct inferences, using appropriate designs. 2003, 19, 690-5 Neural network analysis of lymphoma microarray data: prognosis and diagnosis near-perfect. 2003, 4, 13 Expression profiling of blood samples from an SU5416 Phase III metastatic colorectal cancer clinical trial: a novel strategy for biomarker identification. 2003, 3, 3 | 14 40 54 73 |

| 2048 | The relevance of alternative RNA splicing to pharmacogenomics. 2003, 21, 346-53 | 71 |
|------|---|-----|
| 2047 | Expression profiling targeting chromosomes for tumor classification and prediction of clinical behavior. 2003 , 38, 207-14 | 16 |
| 2046 | Review of proteomics with applications to genetic epidemiology. 2003 , 24, 83-98 | 51 |
| 2045 | Total RNA yield and microarray gene expression profiles from fine-needle aspiration biopsy and core-needle biopsy samples of breast carcinoma. 2003 , 97, 2960-71 | 157 |
| 2044 | Insights into the mechanisms of lymph node metastasis. 2003 , 98, 413-23 | 321 |
| 2043 | Author reply. 2003 , 98, 1326-1327 | 4 |
| 2042 | Weekly vinorelbine is an effective palliative regimen after failure with anthracyclines and taxanes in metastatic breast carcinoma. 2003 , 98, 1325-6; author reply 1326-7 | 7 |
| 2041 | The biology of breast carcinoma. 2003 , 98, 1327-8; author 1328-9 | 1 |
| 2040 | Author reply. 2003 , 98, 1328-1329 | 7 |
| 2039 | Disruption of the expected positive correlation between breast tumor size and lymph node status in BRCA1-related breast carcinoma. 2003 , 98, 1569-77 | 92 |
| 2038 | Breast cancer revisited using DNA array-based gene expression profiling. 2003, 103, 565-71 | 46 |
| 2037 | Tenascin-C upregulates matrix metalloproteinase-9 in breast cancer cells: direct and synergistic effects with transforming growth factor beta1. 2003 , 105, 53-60 | 84 |
| 2036 | Prognostic significance of reduced expression of beta-N-acetylgalactosaminylated N-linked oligosaccharides in human breast cancer. 2003 , 105, 533-41 | 23 |
| 2035 | Chromosomal region 15q21.1 is a frequent target of allelic imbalance in advanced breast carcinomas. 2003 , 106, 74-7 | 17 |
| 2034 | Loss of FHIT protein expression is a marker of adverse evolution in good prognosis localized breast cancer. 2003 , 107, 854-62 | 16 |
| 2033 | BRCA1 splice variants exhibit overlapping and distinct transcriptional transactivation activities. 2003 , 89, 120-32 | 7 |
| 2032 | BRCA1 gene in breast cancer. 2003 , 196, 19-41 | 191 |
| 2031 | Validation of consensus between proteomic and clinical chemistry datasets by applying a new randomisation F-test for generalised procrustes analysis. 2003 , 490, 365-378 | 5 |

| 2030 | The myelodysplastic syndrome(s): a perspective and review highlighting current controversies. 2003 , 27, 95-120 | | 125 |
|------|--|------|------|
| 2029 | Simultaneous classification and relevant feature identification in high-dimensional spaces: application to molecular profiling data. 2003 , 83, 729-743 | | 50 |
| 2028 | Cancer classification using gene expression data. 2003 , 28, 243-268 | | 160 |
| 2027 | Interdisciplinary sciences in the 21st century. 2003 , 14, 328-31 | | 7 |
| 2026 | Current and potential uses for DNA microarrays in transplantation medicine: lessons from other disciplines. 2003 , 62, 93-103 | | 2 |
| 2025 | Aspects of cancer immunotherapy. 2003 , 81, 79-85 | | 8 |
| 2024 | Beyond Herceptin and Gleevec. 2003 , 7, 490-5 | | 81 |
| 2023 | Oligodeoxyribonucleotide probe accessibility on a three-dimensional DNA microarray surface and the effect of hybridization time on the accuracy of expression ratios. 2003 , 3, 6 | | 47 |
| 2022 | Prognostic indicators for gastrointestinal stromal tumours: a clinicopathological and immunohistochemical study of 108 resected cases of the stomach. 2003 , 43, 118-26 | | 113 |
| 2021 | Stem cells in normal breast development and breast cancer. 2003 , 36 Suppl 1, 59-72 | | 444 |
| 2020 | Bignal Transduction and Commmunication in Cancer Cells[]117th Advanced Course of the International School of Medical Science. 2003 , 3, NA-NA | | |
| 2019 | Application of differential display, with in situ hybridization verification, to microscopic samples of breast cancer tissue. 2003 , 84, 207-12 | | 5 |
| 2018 | Marker genes for circulating tumour cells predict survival in metastasized breast cancer patients. 2003 , 88, 1091-4 | | 73 |
| 2017 | Overexpression of a set of genes, including WISP-1, common to pulmonary metastases of both mouse D122 Lewis lung carcinoma and B16-F10.9 melanoma cell lines. 2003 , 89, 314-9 | | 36 |
| 2016 | Toxicity of the high-dose chemotherapy CTC regimen (cyclophosphamide, thiotepa, carboplatin): the Netherlands Cancer Institute experience. 2003 , 88, 1831-8 | | 17 |
| 2015 | Glomeruloid microvascular proliferation is associated with p53 expression, germline BRCA1 mutations and an adverse outcome following breast cancer. 2003 , 89, 1031-4 | | 43 |
| 2014 | Genetics of gene expression surveyed in maize, mouse and man. <i>Nature</i> , 2003 , 422, 297-302 | 50.4 | 1244 |
| 2013 | Cyclin E overexpression enhances cytokine-mediated apoptosis in MCF7 breast cancer cells. 2003 , 4, 336-42 | | 10 |

(2003-2003)

| Expression profiles of non-small cell lung cancers on cDNA microarrays: identification of genes for prediction of lymph-node metastasis and sensitivity to anti-cancer drugs. 2003 , 22, 2192-205 | 277 |
|--|-------------|
| 2011 Genomic profiling of gastric cancer predicts lymph node status and survival. 2003 , 22, 1872-9 | 95 |
| 2010 Effects of methylation on expression of TMS1/ASC in human breast cancer cells. 2003 , 22, 3475-88 | 53 |
| 2009 Gene-expression profiling in human cutaneous melanoma. 2003 , 22, 3076-80 | 97 |
| 2008 Chronic myelogenous leukemia molecular signature. 2003 , 22, 3952-63 | 101 |
| 2007 BCL-6 is expressed in breast cancer and prevents mammary epithelial differentiation. 2003 , 22, 5572-8 | 65 |
| 2006 Biologic and therapeutic role of HER2 in cancer. 2003 , 22, 6570-8 | 304 |
| 2005 Advantages and limitations of microarray technology in human cancer. 2003 , 22, 6497-507 | 204 |
| 2004 Expression profiling of epithelial plasticity in tumor progression. 2003 , 22, 7155-69 | 249 |
| 2003 Molecular analysis of transitional cell carcinoma using cDNA microarray. 2003 , 22, 7702-10 | 42 |
| 2002 Survivin, versatile modulation of cell division and apoptosis in cancer. 2003 , 22, 8581-9 | 756 |
| 2001 DNA arrays in clinical oncology: promises and challenges. 2003 , 83, 305-16 | 32 |
| Genetic background is an important determinant of metastatic potential. 2003 , 34, 23-4; author reply 25 | 88 |
| | |
| 1999 A molecular signature of metastasis in primary solid tumors. 2003 , 33, 49-54 | 1973 |
| | 1973 401 |
| 1999 A molecular signature of metastasis in primary solid tumors. 2003 , 33, 49-54 | |
| A molecular signature of metastasis in primary solid tumors. 2003 , 33, 49-54 1998 Identifying distinct classes of bladder carcinoma using microarrays. 2003 , 33, 90-6 | 401 |

| 1994 Predicting the future of breast cancer. 2003 , 9, 16-8 | 18 |
|---|-----|
| 1993 Myelin management. 2003 , 9, 18-18 | |
| 1992 Road map to metastasis. 2003 , 9, 999-1000 | 83 |
| 1991 Prediction power. 2003 , 3, 82-82 | |
| 1990 Ovarian cancer: strategies for overcoming resistance to chemotherapy. 2003 , 3, 502-16 | 883 |
| 1989 Cancer pharmacogenetics: polymorphisms, pathways and beyond. 2003 , 3, 912-20 | 160 |
| 1988 Issues and progress with protein kinase inhibitors for cancer treatment. 2003 , 2, 296-313 | 410 |
| 1987 Is proteomics heading in the wrong direction?. 2003 , 4, 74-80 | 107 |
| 1986 Application of microarray technology in environmental and comparative physiology. 2003 , 65, 231-59 | 141 |
| [Sentinel lymph node versus functional genomics for prognosis and treatment of breast cancer]. 2003 , 120, 414-6 | |
| 1984 Microarray analysis in the clinical management of cancer. 2003 , 17, 377-87 | 14 |
| 1983 Primer on medical genomics. Part VI: Genomics and molecular genetics in clinical practice. 2003 , 78, 307-17 | 20 |
| 1982 Use of Metabolomics to Discover Metabolic Patterns Associated with Human Diseases. 2003 , 199-215 | 3 |
| Classification of bladder cancer by microarray expression profiling: towards a general clinical use of microarrays in cancer diagnostics. 2003 , 3, 635-47 | 32 |
| 1980 Toxicogenomics: challenges and opportunities. 2003 , 140-141, 145-8 | 28 |
| 1979 From peas to "chips" - the new millennium of molecular biology: a primer for the surgeon. 2003 , 1, 21 | 3 |
| 1978 Spectral biclustering of microarray data: coclustering genes and conditions. 2003 , 13, 703-16 | 401 |
| High-throughput analysis of total RNA expression profiles by capillary gel electrophoresis. 2003 , 75, 4415-22 | 12 |

| 1976 | Tissue microarray study for classification of breast tumors. 2003 , 73, 3189-99 | 31 |
|------|---|-----|
| 1975 | Bax inhibitor-1 is overexpressed in prostate cancer and its specific down-regulation by RNA interference leads to cell death in human prostate carcinoma cells. 2003 , 163, 543-52 | 76 |
| 1974 | Multicolor deconvolution microscopy of thick biological specimens. 2003 , 162, 373-9 | 12 |
| 1973 | The molecular detection of micrometastatic breast cancer. 2003 , 186, 351-8 | 20 |
| 1972 | From the messenger RNA saga to the transcriptome era. 2003 , 326, 893-900 | 5 |
| 1971 | Gene expression profiling of breast carcinomas using nylon DNA arrays. 2003 , 326, 1031-9 | 3 |
| 1970 | Molecular diagnostics: an FDA perspective. 2003 , 3, 129-40 | 10 |
| 1969 | Diagnosing male factor infertility using microarrays. 2003 , 24, 783-9 | 32 |
| 1968 | Targeted therapy in non-small cell lung cancer: myth or reality. 2003, 41 Suppl 1, S3-8 | 29 |
| 1967 | Prognostic factors in ovarian cancer: current evidence and future prospects. 2003 , 1, 127-145 | 14 |
| 1966 | Gene expression monitoring accurately predicts medulloblastoma positive and negative clinical outcomes. 2003 , 533, 110-4 | 8 |
| 1965 | Component plane presentation integrated self-organizing map for microarray data analysis. 2003 , 538, 117-24 | 47 |
| 1964 | Integration and cross-validation of high-throughput gene expression data: comparing heterogeneous data sets. 2003 , 546, 98-102 | 26 |
| 1963 | Schizosaccharomyces pombe Int6 and Ras homologs regulate cell division and mitotic fidelity via the proteasome. 2003 , 112, 207-17 | 74 |
| 1962 | MTA3, a Mi-2/NuRD complex subunit, regulates an invasive growth pathway in breast cancer. 2003 , 113, 207-19 | 426 |
| 1961 | Metastatic potential: generic predisposition of the primary tumor or rare, metastatic variants-or both?. 2003 , 113, 821-3 | 139 |
| 1960 | A mechanism of cyclin D1 action encoded in the patterns of gene expression in human cancer. 2003 , 114, 323-34 | 353 |
| 1959 | Gene expression predictors of breast cancer outcomes. 2003 , 361, 1590-6 | 509 |

| 1958 DNA microarrays in breast cancer: the promise of personalised medicine. 2003 , 361, 1576-7 | 47 |
|--|---------------------|
| 1957 New biology of the oestrogen receptor. 2003 , 362, 260-2 | 12 |
| 1956 Child survival: a global health challenge. 2003 , 362, 262 | 33 |
| Gene expression profiling for the prediction of therapeutic response to docetaxel in patients breast cancer. 2003 , 362, 362-9 | s with 708 |
| 1954 The ErbB receptors and their role in cancer progression. 2003 , 284, 99-110 | 516 |
| 1953 Towards genetic prediction of radiation responses: ESTRO's GENEPI project. 2003 , 69, 121-5 | 71 |
| 1952 Epigenetic gene silencing in cancer initiation and progression. 2003 , 190, 125-33 | 141 |
| 1951 Differentially expressed genes in gastric tumors identified by cDNA array. 2003 , 190, 199-211 | 1 22 |
| Allelic diversity in the host genetic background may be an important determinant in tumor metastatic dissemination. 2003 , 200, 97-105 | 36 |
| Repeated observation of breast tumor subtypes in independent gene expression data sets. 2^{1949} 100, 8418-23 | 2 003 , 4262 |
| 1948 Germline BRCA1 mutations and a basal epithelial phenotype in breast cancer. 2003 , 95, 1482- | -5 737 |
| 1947 Pitfalls in the use of DNA microarray data for diagnostic and prognostic classification. 2003 , 9 | 95, 14-8 837 |
| 1946 Classification of cancers by expression profiling. 2003 , 13, 97-103 | 50 |
| Can patient-, treatment- and pathology-related characteristics explain the high local recurrer rate following breast-conserving therapy in young patients?. 2003 , 39, 932-44 | nce 145 |
| 1944 Global functional profiling of gene expression. 2003 , 81, 98-104 | 479 |
| 1943 Cancer diagnosis and microarrays. 2003 , 35, 119-24 | 30 |
| 1942 Study of suboptimum treatment response: lessons from breast cancer. 2003 , 4, 177-85 | 49 |
| 1941 Classifying human cancer by analysis of gene expression. 2003 , 9, 5-10 | 21 |

| 1940 Estro <u>c</u> | gen and growth factor signaling pathway: basic approaches for clinical application. 2003 , 86, 433-42 | 12 |
|------------------------------|---|-----|
| | ljuvant comparisons of aromatase inhibitors and tamoxifen: pretreatment determinants of nse and on-treatment effect. 2003 , 86, 301-7 | 38 |
| 1938 Nuclei | c acid microarrays: an overview. 2003 , 9, 155-158 | 6 |
| 1937 Bioinf | ormatics: Organisms from Venus, Technology from Jupiter, Algorithms from Mars. 2003 , 9, 237-278 | 8 |
| 1936 The Er | bB receptors and their role in cancer progression. 2003 , 103-114 | 1 |
| 1935 Micro a | arrays bring new insights into understanding of breast cancer metastasis to bone. 2004 , 6, 61-4 | 31 |
| | agnosis and management of pre-invasive breast disease: promise of new technologies in standing pre-invasive breast lesions. 2003 , 5, 320-8 | 18 |
| 1022 | array technology and its effect on breast cancer (re)classification and prediction of outcome. 5, 303-4 | 13 |
| 1932 June 2 | can Society for Clinical Oncology 39th Annual Meeting, Chicago, Illinois, USA, 31 May to 3 2003: breast cancer neoadjuvant and adjuvant chemotherapyprognostic and predictive rs. 2003 , 5, 289-93 | 1 |
| 1931 The fu | ture of cytotoxic therapy: selective cytotoxicity based on biology is the key. 2003 , 5, 154-9 | 32 |
| | nicroenvironment in breast cancer development: epithelial-mesenchymal transition in breast development. 2003 , 5, 101-6 | 169 |
| Multic 1929 2003 , | lass classification of microarray data with repeated measurements: application to cancer. 4, R83 | 90 |
| 1928 Cluste | ring gene-expression data with repeated measurements. 2003 , 4, R34 | 132 |
| | fication of expressed genes linked to malignancy of human colorectal carcinoma by etric clustering of quantitative expression data. 2003 , 4, R21 | 50 |
| 1926 Gene | orofiling for defining targets for new therapeutics in autoimmune diseases. 2003 , 5, 47-50 | 4 |
| 1925 Lookir | ng beyond morphology: cancer gene expression profiling using DNA microarrays. 2003 , 21, 937-49 | 38 |
| | atent disseminated cells to overt metastasis: genetic analysis of systemic breast cancer ession. 2003 , 100, 7737-42 | 517 |
| 1923 Identi | fication of a gene expression signature associated with pediatric AML prognosis. 2003 , 102, 1849-56 | 151 |

| 1922 | Breast and ovarian cancer. 2003 , 348, 2339-47 | 446 |
|------|--|------|
| 1921 | Molecular Diagnosis of Infectious Diseases. 2003, | 1 |
| 1920 | PATHOGENESIS OF RESPIRATORY DISEASES: NEW SOLUTIONS TO OLD PROBLEMS?. 2003 , 29, 3-92 | |
| 1919 | Proteomic prediction of disease outcome in cancer: clinical framework and current status. 2003, 3, 107-15 | 6 |
| 1918 | Breast cancer classification and prognosis based on gene expression profiles from a population-based study. 2003 , 100, 10393-8 | 1562 |
| 1917 | Profiling of estrogen up- and down-regulated gene expression in human breast cancer cells: insights into gene networks and pathways underlying estrogenic control of proliferation and cell phenotype. 2003 , 144, 4562-74 | 806 |
| 1916 | Biomarker discovery and identification in laser microdissected head and neck squamous cell carcinoma with ProteinChip technology, two-dimensional gel electrophoresis, tandem mass spectrometry, and immunohistochemistry. 2003 , 2, 443-52 | 69 |
| 1915 | Clinical application of cDNA microarrays in oncology. 2003 , 8, 252-8 | 64 |
| 1914 | Using gene expression ratios to predict outcome among patients with mesothelioma. 2003 , 95, 598-605 | 151 |
| 1913 | Hereditary breast-ovarian cancer at the bedside: role of the medical oncologist. 2003 , 21, 740-53 | 51 |
| 1912 | Gene expression profiles of primary breast tumors maintained in distant metastases. 2003 , 100, 15901-5 | 367 |
| 1911 | New approaches to cancer therapy. 2003 , 14, 813-6 | 5 |
| 1910 | Ligand-independent activation of estrogen receptor alpha by XBP-1. 2003 , 31, 5266-74 | 102 |
| 1909 | In situ-synthesized novel microarray optimized for mouse stem cell and early developmental expression profiling. 2003 , 13, 1011-21 | 91 |
| 1908 | Variation in gene expression patterns in human gastric cancers. 2003 , 14, 3208-15 | 253 |
| 1907 | Microarray technologies 2003 an overview. 2003 , 4, 251-6 | 17 |
| 1906 | Molecular diagnostics by microelectronic microchips. 2003 , 41, 462-7 | 13 |
| 1905 | Classifying the estrogen receptor status of breast cancers by expression profiles reveals a poor prognosis subpopulation exhibiting high expression of the ERBB2 receptor. 2003 , 12, 3245-58 | 39 |

| 1904 Gene-expression signatures in breast cancer. 2003 , 348, 1715-7; author reply 1715-7 | 16 |
|---|-----------------|
| 1903 A neural survival factor is a candidate oncogene in breast cancer. 2003 , 100, 10931-6 | 100 |
| EZH2 is a marker of aggressive breast cancer and promotes neoplastic transformation of breast epithelial cells. 2003 , 100, 11606-11 | 1295 |
| Biomarker Discovery by Tissue Microdissection and ProteinChip Array Analysis/Identifizierung von Biomarkern ber Gewebemikrodissektion und ProteinChip Array Analyse. 2003 , 27, 79-84 | |
| Towards integrated clinico-genomic models for personalized medicine: combining gene expression signatures and clinical factors in breast cancer outcomes prediction. 2003 , 12 Spec No 2, R153-7 | 103 |
| 1899 Multistep Carcinogenesis: A Chain Reaction of Aneuploidizations. 2003 , 2, 201-209 | 122 |
| 1898 Microarray data analysis and mining. 2004 , 94, 67-90 | 7 |
| Gene Selection and Sample Classification Using a Genetic Algorithm and k-Nearest Neighbor Method. 2003 , 216-229 | 4 |
| Diagnostic and prognostic prediction using gene expression profiles in high-dimensional microarray data. 2003 , 89, 1599-604 | 131 |
| 1895 Applications of array technology: identification of molecular targets in bladder cancer. 2003 , 89, 2172-7 | 46 |
| 1894 A Bayesian missing value estimation method for gene expression profile data. 2003 , 19, 2088-96 | 47 ¹ |
| 1893 Molecular classification of familial non-BRCA1/BRCA2 breast cancer. 2003 , 100, 2532-7 | 157 |
| 1892 Prostate cancer susceptibility genes: lessons learned and challenges posed. 2003 , 10, 225-59 | 71 |
| 1891 Anthracyclines: is more, better and/or more dangerous?. 2003 , 14, 663-5 | 4 |
| 1890 Extending the utility of gene profiling data by bridging microarray platforms. 2003 , 100, 10585-7 | 12 |
| 1889 DNA arrays: applications and implications for circadian biology. 2003 , 18, 96-105 | 29 |
| 1888 Gene expression profiles of human breast cancer progression. 2003 , 100, 5974-9 | 722 |
| 1887 Irruption of genomics in the search for disease related genes. 2003 , 52 Suppl 2, ii1-5 | 1 |

| 1886 | Onto-Tools, the toolkit of the modern biologist: Onto-Express, Onto-Compare, Onto-Design and Onto-Translate. 2003 , 31, 3775-81 | 280 |
|------|--|-----|
| 1885 | The systemic progression of human cancer: a focus on the individual disseminated cancer cellthe unit of selection. 2003 , 89, 35-67 | 48 |
| 1884 | Idiopathic Pulmonary Fibrosis. Proceedings of the 1st Annual Pittsburgh International Lung Conference. October 2002. 2003 , 29, S1-105 | 28 |
| 1883 | MODEL-BASED CLUSTERING IN GENE EXPRESSION MICROARRAYS: AN APPLICATION TO BREAST CANCER DATA. 2003 , 13, 579-592 | 13 |
| 1882 | Gene expression patterns in ovarian carcinomas. 2003 , 14, 4376-86 | 273 |
| 1881 | Comprehensive proteomic profiling identifies serum proteomic signatures for detection of hepatocellular carcinoma and its subtypes. 2003 , 49, 752-60 | 208 |
| 1880 | In Reply:. 2003 , 21, 3180-3180 | |
| 1879 | Representational oligonucleotide microarray analysis: a high-resolution method to detect genome copy number variation. 2003 , 13, 2291-305 | 317 |
| 1878 | Specificity of short interfering RNA determined through gene expression signatures. 2003, 100, 6347-52 | 426 |
| 1877 | Mechanisms of Toxicity, Carcinogenesis, Cancer Prevention and Cancer Therapy: July 1416, 2002, The Gant Conference Center, Aspen, Colorado. 2003 , 31, 140-170 | 1 |
| 1876 | Handbook of Proteomic Methods. 2003, | |
| 1875 | Detection of isolated tumor cells in bone marrow is an independent prognostic factor in breast cancer. 2003 , 21, 3469-78 | 387 |
| 1874 | Customized molecular phenotyping by quantitative gene expression and pattern recognition analysis. 2003 , 13, 1719-27 | 87 |
| 1873 | Microarray standard data set and figures of merit for comparing data processing methods and experiment designs. 2003 , 19, 956-65 | 76 |
| 1872 | Multivariate curve resolution for hyperspectral image analysis: applications to microarray technology. 2003 , 4959, 55 | 16 |
| 1871 | HIN-1 and the nosology of breast cancer. 2003 , 2, 564-5 | 1 |
| 1870 | INT6: A Link Between the Proteasome and Tumorigenesis. 2003 , 2, 80-82 | 11 |
| 1869 | Differential chemokine, chemokine receptor, cytokine and cytokine receptor expression in pulmonary adenocarcinoma: Diffuse down-regulation is associated with immune evasion and brain metastasis. 2003 , 23, 965 | 2 |

(2003-2003)

| Gene expression phenotypes of Arabidopsis associated with sensitivity to low temperatures. 2003 , 132, 893-906 | 120 |
|---|-----|
| 1867 SEP: score for expression profile-a novel method for predicting clinical outcome in breast cancer. | 1 |
| 1866 [Gene expression analysis using DNA microarrays in soft tissue and bone tumors]. 2003 , 128, 2030-6 | |
| The insulin-like growth factors and insulin-signalling systems: an appealing target for breast cancer therapy?. 2003 , 35, 857-71 | 23 |
| Pharmacogenomics: implications and considerations for pharmacists. 2003 , 4, 321-30 | 16 |
| 1863 Genomic & proteomic technological advances in cancer research. 2003, 4, 245-9 | 6 |
| Noninvasive molecular detection of cancer the bench and the bedside. 2003 , 10, 691-706 | 17 |
| Differential expression, class discovery and class prediction using S-PLUS and S+ArrayAnalyzer. 2003, 5, 38-47 | 2 |
| 1860 The Emergence of Pharmacogenomics. 2003 , 33, 133-137 | 2 |
| 1859 Nuclear factor-kappa B as a predictor of treatment response in breast cancer. 2003 , 15, 405-11 | 25 |
| 1858 Physiopathology of liver metastasis. 2003 , 103, 444-7 | 1 |
| Tissue-specific gene expression of head and neck squamous cell carcinoma in vivo by complementary DNA microarray analysis. 2003 , 129, 760-70 | 43 |
| Conservation therapy in T1-T2 breast cancer: past, current issues, and future challenges and opportunities. 2003 , 9, 442-53 | 18 |
| 1855 . 2003 , 237, 474-482 | 16 |
| 1854 Molecular classification of breast carcinomas using tissue microarrays. 2003 , 12, 27-34 | 142 |
| 1853 CHIPing soft tissue tumors: will the paradigms be changed?. 2003 , 10, 1-7 | 4 |
| Beta defensin-1, parvalbumin, and vimentin: a panel of diagnostic immunohistochemical markers for renal tumors derived from gene expression profiling studies using cDNA microarrays. 2003 , 27, 199-205 | 96 |
| DNA expression analysis: serial analysis of gene expression, microarrays and kidney disease. 2003 , 12, 407-14 | 12 |

| 1850 | Gene-expression profiles and breast-cancer prognosis. 2003 , 10, 338-46 | 1 |
|------|--|-----|
| 1849 | Estimation of population effects in synchronized budding yeast experiments. 2003, | 3 |
| 1848 | Global Functional Profiling of Gene Expression Data. 2003 , 306-325 | 4 |
| 1847 | Molecular mechanisms of bone metastasis and therapeutic implications. 2003, S100-4 | 30 |
| 1846 | Rating the risk factors for breast cancer. 2003 , 237, 474-82 | 155 |
| 1845 | Early prognosis of the development of renal chronic allograft rejection by gene expression profiling of human protocol biopsies. 2003 , 75, 1323-30 | 83 |
| 1844 | Current World Literature. 2003 , 12, 463-482 | |
| 1843 | Supervised analysis when the number of candidate features (p) greatly exceeds the number of cases (n). 2003 , 5, 31-36 | 52 |
| 1842 | Identification of endothelial cell genes by combined database mining and microarray analysis. 2003 , 13, 249-62 | 99 |
| 1841 | HER-2/neu testing in breast cancer. 2003 , 120 Suppl, S53-71 | 19 |
| 1840 | Gene expression profiling of multiple myeloma reveals molecular portraits in relation to the pathogenesis of the disease. 2003 , 101, 4998-5006 | 109 |
| 1839 | Supervised classification for gene network reconstruction. 2003 , 31, 1497-502 | 15 |
| 1838 | Demystifiedtissue microarray technology. 2003 , 56, 198-204 | 93 |
| 1837 | Functional Relationship and Gene Ontology Classification of Breast Cancer Biomarkers. 2003 , 18, 241-272 | 16 |
| 1836 | Molecular Characterization of Breast Cancer Aggressiveness. 2003 , 18, 36-39 | |
| 1835 | Genetic Profiling of Breast Cancer: From Molecular Portraits to Clinical Utility. 2003, 18, 54-56 | 2 |
| 1834 | The clinical geneticist and the "new genetics". 2003 , 178, 458-62 | 14 |
| 1833 | Informatics United. 2003 , 42, 126-133 | 10 |

| 1832 | Using DNA microarrays for diagnostic and prognostic prediction. 2003 , 3, 587-95 | 31 |
|--------------|---|-----|
| 1831 | Poster Sessions. 2003 , 25, 249-307 | 78 |
| 1830 | Quantitative Real-Time RT-PCR Analysis of Eight Novel Estrogen-Regulated Genes in Breast Cancer. 2003, 18, 123-129 | 13 |
| 1829 | BRCA1 and estrogen signaling in breast cancer. 2003 , 18, 11-20 | 4 |
| 1828 | Microarray of recombinant antibodies using a streptavidin sensor surface self-assembled onto a gold layer. 2003 , 34, 124-30 | 37 |
| 1827 | Optimizing stringency for expression microarrays. 2003 , 35, 828-35 | 13 |
| 1826 | Microarray-Based Cancer Diagnosis with Artificial Neural Networks. 2003 , 34, S30-S35 | 28 |
| 1825 | Open Source Software for the Analysis of Microarray Data. 2003 , 34, S45-S51 | 172 |
| 1824 | Gene Expression Databases and Data Mining. 2003 , 34, S36-S44 | 14 |
| 1823 | Application of DNA array analyses in the management of gastrointestinal cancer patients. 2003 , 21, 309-14 | 4 |
| 1822 | Clinical relevance of prognostic factors in axillary node-negative breast cancer. 2003 , 26, 438-45 | 7 |
| 1821 | Gene expression profiling of breast cancers with emphasis of beta-catenin regulation. 2004 , 19, 275-82 | 22 |
| 1820 | Combining nearest neighbor classifiers versus cross-validation selection. 2004 , 3, Article12 | 9 |
| 181 <i>9</i> | Universal mouse reference RNA derived from neonatal mice. 2004 , 37, 464-8 | 11 |
| 1818 | Large-scale transcriptional profiling of murine mammary development. 2004 , 19, 47-57 | 2 |
| 1817 | Rational surveillance programs for early stage breast cancer patients after primary treatment. 2004 , 21, 47-54 | 9 |
| 1816 | 5 Invasive growth: a genetic program. 2004 , 48, 451-6 | 31 |
| 1815 | Curated databases and their role in clinical bioinformatics. 2004 , 13, 121-136 | |
| | | |

| 1814 | Genomic approaches to identifying breast cancer susceptibility factors. 2004 , 19, 3-9 | 5 |
|------|---|-----|
| 1813 | . 2004, | 4 |
| 1812 | . 2004, | 107 |
| 1811 | Novel technologies and recent advances in metastasis research. 2004 , 48, 573-81 | 27 |
| 1810 | . 2004, | 46 |
| 1809 | . 2004, | 7 |
| 1808 | Bibliography. 2004 , 251-258 | |
| 1807 | Expression profiling and breast cancer biology. 2004 , 19, 29-34 | 1 |
| 1806 | Genomic approaches to understanding and treating breast cancer. 2004 , 19, 35-46 | 4 |
| 1805 | Seeing the unseen: Microarray-based gene expression profiling in vision. 2004 , 45, 2457-62 | 6 |
| 1804 | Gene Microarray Technologies for Cancer Drug Discovery and Development. 2004 , 141-186 | |
| 1803 | Pathobiology of Human Cerebrovascular Malformations: Basic Mechanisms and Clinical Relevance. 2004 , | 54 |
| 1802 | Gene expression profiling in breast cancer research. 2004 , 19, 23-7 | 1 |
| 1801 | Transcriptional profiling reveals coordinated up-regulation of oxidative metabolism genes in thyroid oncocytic tumors. 2004 , 89, 994-1005 | 68 |
| 1800 | Analysis of DNA microarray data. 2004 , 4, 1357-70 | 22 |
| 1799 | Microarray analysis of human nervous system gene expression in neurological disease. 2004 , 60, 135-51 | 1 |
| 1798 | Adjustment of systematic microarray data biases. 2004 , 20, 105-14 | 313 |
| 1797 | Research issues and strategies for genomic and proteomic biomarker discovery and validation: a statistical perspective. 2004 , 5, 709-19 | 99 |

| 1796 | Novel strategies in cancer therapeutics: targeting enzymes involved in cell cycle regulation and cellular proliferation. 2004 , 4, 403-24 | 19 |
|------|--|-----|
| 1795 | Hematopoietic Growth Factors in Oncology. 2004 , | |
| 1794 | Gene microarray analysis of peripheral blood cells in pulmonary arterial hypertension. 2004 , 170, 911-9 | 131 |
| 1793 | Classification of cDNA array genes that have a highly significant discriminative power due to their unique distribution in four brain regions. 2004 , 23, 661-74 | 4 |
| 1792 | Principles of Molecular Oncology. 2004, | 6 |
| 1791 | A Bayesian network classification methodology for gene expression data. 2004 , 11, 581-615 | 39 |
| 1790 | Signature of a silent killer: expression profiling in epithelial ovarian cancer. 2004 , 4, 157-67 | 25 |
| 1789 | Extreme value distribution based gene selection criteria for discriminant microarray data analysis using logistic regression. 2004 , 11, 215-26 | 18 |
| 1788 | Identification of estrogen-responsive genes by complementary deoxyribonucleic acid microarray and characterization of a novel early estrogen-induced gene: EEIG1. 2004 , 18, 402-11 | 113 |
| 1787 | Treating brain metastases: current approaches and future directions. 2004 , 4, 1015-22 | 5 |
| 1786 | Large-scale meta-analysis of cancer microarray data identifies common transcriptional profiles of neoplastic transformation and progression. 2004 , 101, 9309-14 | 790 |
| 1785 | Identification of a transcriptional profile associated with in vitro invasion in non-small cell lung cancer cell lines. 2004 , 3, 624-31 | 12 |
| 1784 | siRNA-mediated gene silencing: a global genome view. 2004 , 32, 3836-45 | 53 |
| 1783 | CleanEx: a database of heterogeneous gene expression data based on a consistent gene nomenclature. 2004 , 32, D542-7 | 29 |
| 1782 | Immediate gene expression changes after the first course of neoadjuvant chemotherapy in patients with primary breast cancer disease. 2004 , 10, 6418-31 | 53 |
| 1781 | Decoding randomly ordered DNA arrays. 2004 , 14, 870-7 | 241 |
| 1780 | Validation of the 2001 St Gallen risk categories for node-negative breast cancer using a database from the Spanish Breast Cancer Research Group (GEICAM). 2004 , 22, 961-2 | 14 |
| 1779 | Hierarchical clustering analysis of tissue microarray immunostaining data identifies prognostically significant groups of breast carcinoma. 2004 , 10, 6143-51 | 175 |

| 1778 | Somatic mutation of p53 leads to estrogen receptor alpha-positive and -negative mouse mammary tumors with high frequency of metastasis. 2004 , 64, 3525-32 | 103 |
|------|---|-----|
| 1777 | Overexpression of the anti-adhesin podocalyxin is an independent predictor of breast cancer progression. 2004 , 64, 5068-73 | 124 |
| 1776 | Sequence-matched probes produce increased cross-platform consistency and more reproducible biological results in microarray-based gene expression measurements. 2004 , 32, e74 | 152 |
| 1775 | Broadly altered gene expression in blood leukocytes in essential hypertension is absent during treatment. 2004 , 43, 947-51 | 66 |
| 1774 | Clustering of gene hypermethylation associated with clinical risk groups in neuroblastoma. 2004 , 96, 1208-19 | 109 |
| 1773 | DNA amplification method tolerant to sample degradation. 2004 , 14, 2357-66 | 73 |
| 1772 | Pharmacogenomic analysis of cytogenetic response in chronic myeloid leukemia patients treated with imatinib. 2004 , 10, 155-65 | 73 |
| 1771 | Trawling for genes that predict response to breast cancer adjuvant therapy. 2004 , 22, 2267-9 | 13 |
| 1770 | Tissue-wide expression profiling using cDNA subtraction and microarrays to identify tumor-specific genes. 2004 , 64, 844-56 | 190 |
| 1769 | Microarrays as a tool to investigate the biology of aging: a retrospective and a look to the future. 2004 , 2004, re7 | 24 |
| 1768 | The 'subsequent artificial neural network' (SANN) approach might bring more classificatory power to ANN-based DNA microarray analyses. 2004 , 20, 3544-52 | 40 |
| 1767 | Session 1: Metastasis. 2004 , 32, 730-731 | |
| 1766 | Association of breast cancer DNA methylation profiles with hormone receptor status and response to tamoxifen. 2004 , 64, 3807-13 | 284 |
| 1765 | Reliability of gene expression ratios for cDNA microarrays in multiconditional experiments with a reference design. 2004 , 32, e29 | 28 |
| 1764 | RESPONSE: Re: Germline BRCA1 Mutations and a Basal Epithelial Phenotype in Breast Cancer. 2004 , 96, 714-714 | 1 |
| 1763 | Expression profiling of purified normal human luminal and myoepithelial breast cells: identification of novel prognostic markers for breast cancer. 2004 , 64, 3037-45 | 208 |
| 1762 | Prediction of clinical outcome using gene expression profiling and artificial neural networks for patients with neuroblastoma. 2004 , 64, 6883-91 | 165 |
| 1761 | A gene expression signature associated with metastatic outcome in human leiomyosarcomas. 2004 , 64, 7201-4 | 65 |

(2004-2004)

| 1760 | Gene expression profiles predict complete pathologic response to neoadjuvant paclitaxel and fluorouracil, doxorubicin, and cyclophosphamide chemotherapy in breast cancer. 2004 , 22, 2284-93 | 439 |
|------|---|-----|
| 1759 | RRE: a tool for the extraction of non-coding regions surrounding annotated genes from genomic datasets. 2004 , 20, 2848-50 | 12 |
| 1758 | Intracellular patterns of Her-2/neu, ras, and ploidy abnormalities in primary human breast cancers predict postoperative clinical disease-free survival. 2004 , 10, 3042-52 | 11 |
| 1757 | A molecular signature of the Nottingham prognostic index in breast cancer. 2004 , 64, 2962-8 | 55 |
| 1756 | Genomics and proteomics tools for compound mode-of-action studies in drug discovery. 2004 , 5, 395-404 | 11 |
| 1755 | An integrative genomics approach to the reconstruction of gene networks in segregating populations. 2004 , 105, 363-74 | 178 |
| 1754 | Universal RNA reference materials for gene expression. 2004 , 50, 1464-71 | 67 |
| 1753 | Cell-type-specific responses to chemotherapeutics in breast cancer. 2004 , 64, 4218-26 | 307 |
| 1752 | Profiling the evolution of human metastatic bladder cancer. 2004 , 64, 7813-21 | 82 |
| 1751 | Classification of human breast cancer using gene expression profiling as a component of the survival predictor algorithm. 2004 , 10, 2272-83 | 58 |
| 1750 | The prognostic value of BCAR1 in patients with primary breast cancer. 2004 , 10, 6194-202 | 47 |
| 1749 | Identification and validation of cell surface antigens for antibody targeting in oncology. 2004 , 11, 659-87 | 91 |
| 1748 | Design of a real time quantitative PCR assay to assess global mRNA amplification of small size specimens for microarray hybridisation. 2004 , 57, 1278-87 | 4 |
| 1747 | BRCA1 functions as a breast stem cell regulator. 2004 , 41, 1-5 | 122 |
| 1746 | Curcumin Derivatives: Potential for Prostate Cancer Management: ADDANKI P. KUMAR, GRETCHEN E. GARCIA, RITA GHOSH, RAJENDRAN V. RAJNARAYANAN,1 WILLIAM L. ALWORTH,1 AND THOMAS J. SLAGA, Center for Cancer Causation and Prevention, AMC Cancer Research Center and University | |
| 1745 | Gene Expression Profiling of Node-Negative Breast Tumors Reveals Metastatic Recurrence Risk: ANAND IMMANENI, ANNA TSIMELZON, SUSAN G. HILSENBECK, CRAIG ALLRED, PETER O'CONNELL, AND WILLIAM R. BRINKLEY, Breast Center, Department of Molecular and Cellular Biology, | |
| 1744 | Intensity-based analysis of two-colour microarrays enables efficient and flexible hybridization designs. 2004 , 32, e41 | 31 |
| 1743 | Integrated modeling of clinical and gene expression information for personalized prediction of disease outcomes. 2004 , 101, 8431-6 | 174 |

| 1742 | Signal transducer and activator of transcription-5 activation and breast cancer prognosis. 2004 , 22, 2053-60 | 185 |
|------|---|-----|
| 1741 | Multigene reverse transcription-PCR profiling of circulating tumor cells in hormone-refractory prostate cancer. 2004 , 50, 826-35 | 61 |
| 1740 | Effects of hemolysis on the Roche ammonia method for Hitachi analyzers. 2004 , 50, 976-7 | 19 |
| 1739 | Ontogeny and oncogenesis balance the transcriptional profile of renal cell cancer. 2004 , 64, 7279-87 | 28 |
| 1738 | A statistical method for identifying differential gene-gene co-expression patterns. 2004 , 20, 3146-55 | 121 |
| 1737 | MYC is amplified in BRCA1-associated breast cancers. 2004 , 10, 499-507 | 71 |
| 1736 | Gene expression profiles of epithelial cells microscopically isolated from a breast-invasive ductal carcinoma and a nodal metastasis. 2004 , 101, 18147-52 | 90 |
| 1735 | Identification and testing of a gene expression signature of invasive carcinoma cells within primary mammary tumors. 2004 , 64, 8585-94 | 365 |
| 1734 | [Neoadjuvant therapy of breast cancer]. 2004 , 44, 92-101 | 4 |
| 1733 | The Microrevolution: Applications and impacts of microarray technology on molecular biology and medicine (Review). 2004 , 13, 483 | 1 |
| 1732 | Tissue microarrays - big potential from small samples (Review). 2004 , 25, 167 | |
| 1731 | A close association between alteration in growth kinetics by neoadjuvant chemotherapy and survival outcome in primary breast cancer. 2004 , 25, 397 | 1 |
| 1730 | Proteomic profiling in microdissected hepatocellular carcinoma tissue using ProteinChip[] technology. 2004 , 24, 885 | 2 |
| 1729 | Basal and luminal breast cancers: Basic or luminous? (Review). 2004 , 25, 249 | 4 |
| 1728 | Finding the bEST routes to cancer. 2004 , 3, 1090-1 | 7 |
| 1727 | Survivin' cancer. 2004 , 3, 180-3 | 6 |
| 1726 | Aneuploidy Approaching a Perfect Score in Predicting and Preventing Cancer: Highlights from a Conference Held in Oakland, CA in January, 2004. 2004 , 3, 821-826 | 20 |
| 1725 | Metastasizing and non-metastasizing tumors likely evolve from DNA phenotypes via independent pathways. 2004 , 3, 1250-1 | 3 |

| 1724 | Hard Wired Genotype in Metastatic Breast Cancer. 2004 , 3, 754-755 | 14 |
|------|---|-----|
| 1723 | Using microarrays to predict resistance to chemotherapy in cancer patients. 2004 , 5, 611-25 | 13 |
| 1722 | How to understand a complex reality: statistical issues in microarray experiments. Interview by Nadine Lemmens. 2004 , 5, 9-13 | |
| 1721 | A technical triade for proteomic identification and characterization of cancer biomarkers. 2004 , 64, 4099-104 | 91 |
| 1720 | New challenges in gene expression data analysis and the extended GEPAS. 2004 , 32, W485-91 | 44 |
| 1719 | Genetic epidemiology of BRCA1. 2004 , 3, 509-14 | 19 |
| 1718 | Gene Expression Signatures, Cancer Cell Evolution and Metastatic Progression. 2004 , 3, 28-30 | 20 |
| 1717 | Gene expression profiling for molecular characterization of inflammatory breast cancer and prediction of response to chemotherapy. 2004 , 64, 8558-65 | 155 |
| 1716 | Functional characterization of BRCA1 sequence variants using a yeast small colony phenotype assay. 2004 , 3, 453-7 | 37 |
| 1715 | Systematic benchmarking of microarray data classification: assessing the role of non-linearity and dimensionality reduction. 2004 , 20, 3185-95 | 190 |
| 1714 | Gene expression profiling after radiation-induced DNA damage is strongly predictive of BRCA1 mutation carrier status. 2004 , 10, 958-63 | 36 |
| 1713 | Epidermal growth factor receptor stimulation activates the RNA binding protein CUG-BP1 and increases expression of C/EBPbeta-LIP in mammary epithelial cells. 2004 , 24, 3682-91 | 66 |
| 1712 | Using protein expressions to predict survival in clear cell renal carcinoma. 2004 , 10, 5464-71 | 188 |
| 1711 | Acquired expression of periostin by human breast cancers promotes tumor angiogenesis through up-regulation of vascular endothelial growth factor receptor 2 expression. 2004 , 24, 3992-4003 | 260 |
| 1710 | Ten-year outcomes in a population-based cohort of node-negative, lymphatic, and vascular invasion-negative early breast cancers without adjuvant systemic therapies. 2004 , 22, 1630-7 | 117 |
| 1709 | Requirement for Arf6 in breast cancer invasive activities. 2004 , 101, 6647-52 | 213 |
| 1708 | Prognostic significance of E-cadherin protein expression in pathological stage I-III endometrial cancer. 2004 , 10, 5546-53 | 61 |
| 1707 | Membrane-associated and secreted genes in breast cancer. 2004 , 64, 8682-7 | 17 |

| 1706 | Microarrays in veterinary diagnostics. 2004 , 5, 249-55 | 9 |
|------------------------------|--|-----------------------|
| 1705 | Proteinase K added to the extraction procedure markedly increases RNA yield from primary breast tumors for use in microarray studies. 2004 , 50, 975-6 | 22 |
| 1704 | Selective estrogen receptor modulators: discrimination of agonistic versus antagonistic activities by gene expression profiling in breast cancer cells. 2004 , 64, 1522-33 | 279 |
| 1703 | Activation of the MDR1 upstream promoter in breast carcinoma as a surrogate for metastatic invasion. 2004 , 10, 2776-83 | 40 |
| 1702 | A novel, high-performance random array platform for quantitative gene expression profiling. 2004 , 14, 2347-56 | 150 |
| 1701 | Coexpression analysis of human genes across many microarray data sets. 2004 , 14, 1085-94 | 571 |
| 1700 | Metastatic cancer DNA phenotype identified in normal tissues surrounding metastasizing prostate carcinomas. 2004 , 101, 11428-31 | 41 |
| 1699 | Detection of metastases in sentinel lymph nodes of breast cancer patients by multiple mRNA markers. 2004 , 90, 1531-7 | 56 |
| 1698 | New chondrocyte genes discovered by representational difference analysis of chondroinduced human fibroblasts. 2004 , 176, 41-53 | 21 |
| | | |
| 1697 | Differential gene-expression profiles associated with gastric adenoma. 2004 , 90, 216-23 | 23 |
| 1697 1696 | Differential gene-expression profiles associated with gastric adenoma. 2004, 90, 216-23 Zymographic detection and clinical correlations of MMP-2 and MMP-9 in breast cancer sera. 2004, 90, 1414-21 | 139 |
| , | Zymographic detection and clinical correlations of MMP-2 and MMP-9 in breast cancer sera. 2004 , 90, 1414-21 | |
| 1696 1695 | Zymographic detection and clinical correlations of MMP-2 and MMP-9 in breast cancer sera. 2004 , 90, 1414-21 Cellular responses to ErbB-2 overexpression in human mammary luminal epithelial cells: | 139 |
| 1696 1695 | Zymographic detection and clinical correlations of MMP-2 and MMP-9 in breast cancer sera. 2004, 90, 1414-21 Cellular responses to ErbB-2 overexpression in human mammary luminal epithelial cells: comparison of mRNA and protein expression. 2004, 90, 173-81 | 139 37 |
| 1696 1695 1694 | Zymographic detection and clinical correlations of MMP-2 and MMP-9 in breast cancer sera. 2004, 90, 1414-21 Cellular responses to ErbB-2 overexpression in human mammary luminal epithelial cells: comparison of mRNA and protein expression. 2004, 90, 173-81 A prognostic index for operable, node-negative breast cancer. 2004, 90, 1933-41 DNA microarray time series analysis: automated statistical assessment of circadian rhythms in gene expression patterning. 2004, 383, 149-66 | 139 37 16 |
| 1696 1695 1694 1693 | Zymographic detection and clinical correlations of MMP-2 and MMP-9 in breast cancer sera. 2004, 90, 1414-21 Cellular responses to ErbB-2 overexpression in human mammary luminal epithelial cells: comparison of mRNA and protein expression. 2004, 90, 173-81 A prognostic index for operable, node-negative breast cancer. 2004, 90, 1933-41 DNA microarray time series analysis: automated statistical assessment of circadian rhythms in gene expression patterning. 2004, 383, 149-66 | 139 37 16 97 |
| 1696 1695 1694 1693 | Zymographic detection and clinical correlations of MMP-2 and MMP-9 in breast cancer sera. 2004, 90, 1414-21 Cellular responses to ErbB-2 overexpression in human mammary luminal epithelial cells: comparison of mRNA and protein expression. 2004, 90, 173-81 A prognostic index for operable, node-negative breast cancer. 2004, 90, 1933-41 DNA microarray time series analysis: automated statistical assessment of circadian rhythms in gene expression patterning. 2004, 383, 149-66 DNA Repair in Cancer Therapy. 2004, Gold nanoparticle probe-based gene expression analysis with unamplified total human RNA. 2004, | 139 37 16 97 |

(2004-2004)

| 1688 | Gene expression signature of fibroblast serum response predicts human cancer progression: similarities between tumors and wounds. 2004 , 2, E7 | 698 |
|------|---|-----|
| 1687 | Genomics and proteomics: expression arrays in clinical oncology. 2004 , 15 Suppl 4, iv163-5 | 4 |
| 1686 | Re: Germline BRCA1 mutations and a basal epithelial phenotype in breast cancer. 2004 , 96, 712-4; author reply 714 | 28 |
| 1685 | Dʃ vu for breast cancer two?. 2004 , 96, 497-9 | 3 |
| 1684 | Gene expression analysis on biochemical networks using the Potts spin model. 2004 , 20, 1500-5 | 12 |
| 1683 | Organ-selective chemoresistance in metastasis from human breast cancer cells: inhibition of apoptosis, genetic variability and microenvironment at the metastatic focus. 2004 , 25, 2293-301 | 23 |
| 1682 | Modeling metastasis in vivo. 2005 , 26, 513-23 | 330 |
| 1681 | Re: Germline BRCA1 mutations and a basal epithelial phenotype in breast cancer. 2004 , 96, 712-3; author reply 714 | 63 |
| 1680 | Impact of microarray technology in clinical oncology. 2004 , 22, 312-20 | 23 |
| 1679 | Genomic profiling of viable and proliferative micrometastatic cells from early-stage breast cancer patients. 2004 , 10, 3457-64 | 99 |
| 1678 | Molecular medicine: a clinician's primer on microarrays. 2004 , 34, 565-9 | 1 |
| 1677 | Molecular footprints of human lung cancer progression. 2004 , 95, 197-204 | 114 |
| 1676 | Expression profiling to predict postoperative prognosis for estrogen receptor-negative breast cancers by analysis of 25,344 genes on a cDNA microarray. 2004 , 95, 218-25 | 181 |
| 1675 | Prediction of prognosis of estrogen receptor-positive breast cancer with combination of selected estrogen-regulated genes. 2004 , 95, 496-502 | 68 |
| 1674 | Applications of microarrays to histopathology. 2004 , 44, 97-108 | 73 |
| 1673 | Analysing the platelet transcriptome. 2004 , 87 Suppl 2, 42-6 | 13 |
| 1672 | Histological quantitation of tumour angiogenesis. 2004 , 112, 413-30 | 123 |
| 1671 | Gene expression signatures in chronic and aggressive periodontitis: a pilot study. 2004 , 112, 216-23 | 31 |

| 1670 | Developing a classifier for the Habitats Directive grassland types in Denmark using species lists for prediction. 2004 , 7, 71-80 | 30 |
|------|--|------|
| 1669 | DNA microarray technology and its applications in dermatology. 2004 , 13, 593-606 | 37 |
| 1668 | Co-stimulation of human breast cancer cells with transforming growth factor-beta and tenascin-C enhances matrix metalloproteinase-9 expression and cancer cell invasion. 2004 , 85, 373-9 | 33 |
| 1667 | The analysis of placement values for evaluating discriminatory measures. 2004 , 60, 528-35 | 69 |
| 1666 | Rules of evidence for cancer molecular-marker discovery and validation. 2004 , 4, 309-14 | 415 |
| 1665 | Dissecting the metastatic cascade. 2004 , 4, 448-56 | 1026 |
| 1664 | BRCA1 and BRCA2: 1994 and beyond. 2004 , 4, 665-76 | 694 |
| 1663 | Hallmarks of 'BRCAness' in sporadic cancers. 2004 , 4, 814-9 | 1268 |
| 1662 | Gene expression profiling of colon cancer by DNA microarrays and correlation with histoclinical parameters. 2004 , 23, 1377-91 | 265 |
| 1661 | Identification of genes associated with tumorigenesis and metastatic potential of hypopharyngeal cancer by microarray analysis. 2004 , 23, 2484-98 | 220 |
| 1660 | Identification and validation of an ERBB2 gene expression signature in breast cancers. 2004, 23, 2564-75 | 101 |
| 1659 | Ubiquitin and breast cancer. 2004 , 23, 2079-88 | 98 |
| 1658 | Modeling of lung cancer by an orthotopically growing H460SM variant cell line reveals novel candidate genes for systemic metastasis. 2004 , 23, 6316-24 | 29 |
| 1657 | Antisense intronic non-coding RNA levels correlate to the degree of tumor differentiation in prostate cancer. 2004 , 23, 6684-92 | 132 |
| 1656 | Mutation of GATA3 in human breast tumors. 2004 , 23, 7669-78 | 209 |
| 1655 | Prediction of high risk Ewing's sarcoma by gene expression profiling. 2004 , 23, 8997-9006 | 84 |
| 1654 | Host genetics and tumour metastasis. 2004 , 90, 752-5 | 76 |
| 1653 | Deciphering a subgroup of breast carcinomas with putative progression of grade during carcinogenesis revealed by comparative genomic hybridisation (CGH) and immunohistochemistry. 2004 90 1422-8 | 30 |

| 1652 | Molecular profiling of breast cancer: clinical implications. 2004 , 90, 1120-4 | | 77 |
|------|--|------|-----|
| 1651 | Balancing false positives and false negatives for the detection of differential expression in malignancies. 2004 , 91, 1160-5 | | 12 |
| 1650 | Real-time RT-PCR correlates with immunocytochemistry for the detection of disseminated epithelial cells in bone marrow aspirates of patients with breast cancer. 2004 , 91, 1813-20 | | 44 |
| 1649 | A distinct phenotype characterizes tumors from a putative genetic trait involving chondrosarcoma and breast cancer occurring in the same patient. 2004 , 84, 191-202 | | 9 |
| 1648 | Utilizing Nottingham Prognostic Index in microarray gene expression profiling of breast carcinomas. 2004 , 17, 756-64 | | 28 |
| 1647 | Novel endothelial cell markers in hepatocellular carcinoma. 2004 , 17, 1198-210 | | 69 |
| 1646 | Rb inactivation promotes genomic instability by uncoupling cell cycle progression from mitotic control. <i>Nature</i> , 2004 , 430, 797-802 | 50.4 | 457 |
| 1645 | Earth science: putting the squeeze on oxidation. <i>Nature</i> , 2004 , 428, 379 | 50.4 | 1 |
| 1644 | Medicine: profile of a tumour. <i>Nature</i> , 2004 , 428, 379-82 | 50.4 | 19 |
| 1643 | Comparison of different isolation techniques prior gene expression profiling of blood derived cells: impact on physiological responses, on overall expression and the role of different cell types. 2004 , 4, 193-207 | | 178 |
| 1642 | Pharmacogenetics in the treatment of breast cancer. 2004 , 4, 143-53 | | 48 |
| 1641 | DNA microarrays and data analysis: an overview. 2004 , 136, 500-3 | | 13 |
| 1640 | Genomic approaches in cancer biology. 2004 , 136, 511-8 | | 3 |
| 1639 | Application of microarray profiling to clinical trials in cancer. 2004 , 136, 519-23 | | 13 |
| 1638 | Prognostic predictor with multiple fuzzy neural models using expression profiles from DNA microarray for metastases of breast cancer. 2004 , 98, 193-9 | | 22 |
| 1637 | Metadherin, a cell surface protein in breast tumors that mediates lung metastasis. 2004, 5, 365-74 | | 316 |
| 1636 | Molecular classification of head and neck squamous cell carcinomas using patterns of gene expression. 2004 , 5, 489-500 | | 516 |
| 1635 | [Colorectal cancer: prognostic molecular markers]. 2004 , 28, 21-32 | | 5 |

| 1634 | Apoptosis in cancerimplications for therapy. 2004 , 31, 90-119 | 120 |
|------|--|-----|
| 1633 | Therapeutic targeting in the estrogen receptor hormonal pathway. 2004 , 31, 28-38 | 81 |
| 1632 | Improving patient care through molecular diagnostics. 2004 , 31, 14-20 | 21 |
| 1631 | Lymphangiogenesis is pivotal to the trials of a successful cancer metastasis. 2004 , 135, 121-4 | 17 |
| 1630 | Gene expression profiling in human endometrial cancer tissue samples: utility and diagnostic value. 2004 , 93, 292-300 | 13 |
| 1629 | A combinational feature selection and ensemble neural network method for classification of gene expression data. 2004 , 5, 136 | 77 |
| 1628 | Combining gene expression data from different generations of oligonucleotide arrays. 2004 , 5, 159 | 42 |
| 1627 | Comparing functional annotation analyses with Catmap. 2004 , 5, 193 | 67 |
| 1626 | Systematic analysis of T7 RNA polymerase based in vitro linear RNA amplification for use in microarray experiments. 2004 , 5, 29 | 66 |
| 1625 | A molecular 'signature' of primary breast cancer cultures; patterns resembling tumor tissue. 2004 , 5, 47 | 43 |
| 1624 | Expression microarray reproducibility is improved by optimising purification steps in RNA amplification and labelling. 2004 , 5, 9 | 40 |
| 1623 | Prognostic meta-signature of breast cancer developed by two-stage mixture modeling of microarray data. 2004 , 5, 94 | 87 |
| 1622 | Preoperative chemotherapy and endocrine therapy in patients with breast cancer. 2004 , 5, 198-207 | 5 |
| 1621 | Urokinase-type plasminogen activator and its inhibitor type 1 predict disease outcome and therapy response in primary breast cancer. 2004 , 5, 348-52 | 81 |
| 1620 | Potential predictive value of Bcl-2 for response to tamoxifen in the adjuvant setting of node-positive breast cancer. 2004 , 5, 364-9 | 12 |
| 1619 | A primer on gene expression and microarrays for machine learning researchers. 2004 , 37, 293-303 | 24 |
| 1618 | Mapping high-dimensional data onto a relative distance planean exact method for visualizing and characterizing high-dimensional patterns. 2004 , 37, 366-79 | 28 |
| 1617 | Soy isoflavone phyto-pharmaceuticals in interleukin-6 affections. Multi-purpose nutraceuticals at the crossroad of hormone replacement, anti-cancer and anti-inflammatory therapy. 2004 , 68, 1171-85 | 97 |

| 1616 | Radioresistance in carcinoma of the breast. 2004 , 13, 452-60 | 85 |
|------|--|------|
| 1615 | Aneuploidies, deletion, and overexpression of TP53 gene in intestinal metaplasia of patients without gastric cancer. 2004 , 153, 127-32 | 18 |
| 1614 | Prediction of chemotherapeutic response in ovarian cancer with DNA microarray expression profiling. 2004 , 154, 63-6 | 47 |
| 1613 | Genomic organization of the 8p11-p12 amplicon in three breast cancer cell lines. 2004 , 155, 57-62 | 29 |
| 1612 | A two-gene expression ratio predicts clinical outcome in breast cancer patients treated with tamoxifen. 2004 , 5, 607-16 | 774 |
| 1611 | Tamoxifen resistance by a conformational arrest of the estrogen receptor alpha after PKA activation in breast cancer. 2004 , 5, 597-605 | 218 |
| 1610 | Molecular characterization of the tumor microenvironment in breast cancer. 2004 , 6, 17-32 | 1038 |
| 1609 | Aneuploidy, the primary cause of the multilateral genomic instability of neoplastic and preneoplastic cells. 2004 , 56, 65-81 | 115 |
| 1608 | TMS1/ASC: the cancer connection. 2004 , 9, 5-18 | 72 |
| 1607 | BAX Inhibitor-1, an ancient cell death suppressor in animals and plants with prokaryotic relatives. 2004 , 9, 299-307 | 144 |
| 1606 | Relevance of breast cancer cell lines as models for breast tumours: an update. 2004 , 83, 249-89 | 602 |
| 1605 | Gene expression profiling: from microarrays to medicine. 2004 , 24, 213-24 | 38 |
| 1604 | Breast cancer biomarkers and molecular medicine: part II. 2004 , 4, 169-88 | 35 |
| 1603 | Diagnostic classification of cancer using DNA microarrays and artificial intelligence. 2004 , 1020, 49-66 | 28 |
| 1602 | Data-driven computer simulation of human cancer cell. 2004 , 1020, 132-53 | 76 |
| 1601 | Gene expression profiling of human cancers. 2004 , 1028, 28-37 | 44 |
| 1600 | Recent progress in predictive biomarkers for metastatic recurrence of human hepatocellular carcinoma: a review of the literature. 2004 , 130, 497-513 | 160 |
| 1599 | Gene expression patterns as marker for 5-year postoperative prognosis of primary breast cancers. 2004 , 130, 537-45 | 14 |

| 1598 | Microarray-based gene expression profiling in pancreatic ductal carcinoma: status quo and perspectives. 2004 , 19, 401-13 | 21 |
|------|--|-----|
| 1597 | Das Chip-Zeitaltergegenwftiger Stand der Technik und Einsatzmglichkeiten der Chip-Technologie in der Onkologie. 2004 , 10, 7-19 | |
| 1596 | Les banques de tissus tumoraux appliquès au cancer du sein : pourquoi? Comment?. 2004 , 6, 93-98 | 1 |
| 1595 | Traitement adjuvant du cancer du sein, aujourdBui et demain: « Carte » ou « Menu »?. 2004 , 6, 99-106 | |
| 1594 | Een introductie in de genetica van complexe ziekten. 2004 , 72, 53-58 | 1 |
| 1593 | Gene expression profiling in breast cancer: from molecular portraits to personalized medicine. 2004 , 6, 192-202 | 1 |
| 1592 | DNA microarraystechniques and applications in microbial systems. 2004 , 49, 635-64 | 16 |
| 1591 | Current progress in the prediction of chemosensitivity for breast cancer. 2004 , 11, 42-8 | 12 |
| 1590 | Where next with preoperative radiation therapy for rectal cancer?. 2004 , 58, 597-602 | 33 |
| 1589 | In situ hybridization in the pathology laboratory: general principles, automation, and emerging research applications for tissue-based studies of gene expression. 2004 , 35, 595-601 | 9 |
| 1588 | Estrogen and progesterone receptor isoforms: clinical significance in breast cancer. 2004 , 87 Suppl 1, S3-10 | 28 |
| 1587 | The scientific value of preoperative studies and how they can be used. 2004 , 87 Suppl 1, S19-26 | 26 |
| 1586 | Designing the future shape of breast cancer diagnosis, prognosis and treatment. 2004 , 87 Suppl 1, S27-9 | 4 |
| 1585 | [Microarrays]. 2004 , 43, 653-8 | 4 |
| 1584 | Biomolecular features of clinical relevance in breast cancer. 2004 , 31 Suppl 1, S3-14 | 8 |
| 1583 | Analysis of gastric cancer with cDNA microarray. 2004 , 54 Suppl 1, S21-4 | 4 |
| 1582 | Role of HER2/neu in tumor progression and therapy. 2004 , 61, 2965-78 | 110 |
| 1581 | Genchipdiagnostik. 2004 , 37, 203-209 | |

| 1580 | Statistics in clinical trials. 2004 , 6, 36-41 | 3 |
|------|---|-----------------|
| 1579 | Inhibition of proliferation of human breast cancer MCF-7 cells by small interference RNA against LRP16 gene. 2004 , 16, 239-245 | 2 |
| 1578 | Are tumours angiogenesis-dependent?. 2004 , 202, 5-13 | 103 |
| 1577 | Surgical margin and Gleason score as predictors of postoperative recurrence in prostate cancer with or without chromosome 8p allelic imbalance. 2004 , 61, 81-91 | 8 |
| 1576 | Proteomic signature of human cancer cells. 2004 , 4, 2776-88 | 63 |
| 1575 | Gene expression profiling for prognosis using Cox regression. 2004 , 23, 1767-80 | 22 |
| 1574 | Proteomics: beginning to realize its promise?. 2004 , 50, 3741-4 | 9 |
| 1573 | In situ synthesis of oligonucleotide microarrays. 2004 , 73, 579-96 | 178 |
| 1572 | A new way to look at liver cancer. 2004 , 40, 521-3 | 8 |
| 1571 | Classification and prediction of survival in hepatocellular carcinoma by gene expression profiling. 2004 , 40, 667-76 | 69 7 |
| 1570 | Germ-line mutations in BRCA1 or BRCA2 in the normal breast are associated with altered expression of estrogen-responsive proteins and the predominance of progesterone receptor A. 2004 , 39, 236-48 | 72 |
| 1569 | Prognostic classification of relapsing favorable histology Wilms tumor using cDNA microarray expression profiling and support vector machines. 2004 , 41, 65-79 | 42 |
| 1568 | Diminished transcription of chromosome arm 4q is inversely related to local spreading of hepatocellular carcinoma. 2004 , 41, 390-4 | 5 |
| 1567 | Immunohistochemically detected tumor cells in the sentinel lymph nodes of patients with breast carcinoma: biologic metastasis or procedural artifact?. 2004 , 100, 929-34 | 88 |
| 1566 | alphaB-crystallin as a marker of lymph node involvement in breast carcinoma. 2004, 100, 2543-8 | 60 |
| 1565 | Getting the right cells to the array: Gene expression microarray analysis of cell mixtures and sorted cells. 2004 , 59, 191-202 | 54 |
| 1564 | The role of functional genomics in selecting disease targets for antibody-based therapy. 2004 , 61, 155-171 | 1 |
| 1563 | Application of expression genomics in drug development and genomic medicine. 2004 , 62, 124-133 | 4 |

| 1562 | Expression genomics and cancer drug development. 2004 , 62, 295-302 | 2 |
|------|---|-----|
| 1561 | Immunohistochemical analysis of NAD(P)H:quinone oxidoreductase and NADPH cytochrome P450 reductase in human superficial bladder tumours: relationship between tumour enzymology and clinical outcome following intravesical mitomycin C therapy. 2004 , 109, 703-9 | 24 |
| 1560 | Gene expression profiles in breast tumors regarding the presence or absence of estrogen and progesterone receptors. 2004 , 111, 892-9 | 20 |
| 1559 | Molecular circuits of apoptosis regulation and cell division control: the survivin paradigm. 2004 , 92, 656-63 | 120 |
| 1558 | Molecular identification of ERalpha-positive breast cancer cells by the expression profile of an intrinsic set of estrogen regulated genes. 2004 , 200, 440-50 | 39 |
| 1557 | Finding predictive gene groups from microarray data. 2004 , 90, 106-131 | 80 |
| 1556 | A Bayesian approach to nonlinear probit gene selection and classification. 2004 , 341, 137-156 | 18 |
| 1555 | State of the science: molecular classifications of breast cancer for clinical diagnostics. 2004 , 37, 572-8 | 13 |
| 1554 | Predicting drug response based on gene expression. 2004 , 51, 205-27 | 14 |
| 1553 | Identifying multiple tumor-specific epitopes from large-scale screening for overexpressed mRNA. 2004 , 16, 137-42 | 8 |
| 1552 | Statistical analysis of global gene expression data: some practical considerations. 2004 , 15, 52-7 | 24 |
| 1551 | Hypermethylation in histologically distinct classes of breast cancer. 2004 , 10, 5998-6005 | 102 |
| 1550 | Hypermethylation of CpG islands in primary and metastatic human prostate cancer. 2004 , 64, 1975-86 | 416 |
| 1549 | Development of a knowledge-based-multi-scheme cancer microarray data analysis system. | 1 |
| 1548 | A variant of SVM-RFE for gene selection in cancer classification with expression data. | 10 |
| 1547 | The role of cost-effectiveness analysis in the era of pharmacogenomics. 2004 , 22, 481-93 | 82 |
| 1546 | Cross-validation for linear model with unequal variances in genomic analysis. 2004 , 14, 723-39 | 4 |
| 1545 | Multiclass Decision Foresta novel pattern recognition method for multiclass classification in microarray data analysis. 2004 , 23, 685-94 | 33 |

| 1544 | Comparative study of microarray data for cancer research. 2004 , 2004, 2960-3 | 1 |
|------|--|------|
| 1543 | Systematic analysis and nomenclature of mammalian F-box proteins. 2004 , 18, 2573-80 | 503 |
| 1542 | Immunohistochemical and clinical characterization of the basal-like subtype of invasive breast carcinoma. 2004 , 10, 5367-74 | 2156 |
| 1541 | Gene expression profiles and molecular markers to predict recurrence of Dukes' B colon cancer. 2004 , 22, 1564-71 | 381 |
| 1540 | Gene expression in the urinary bladder: a common carcinoma in situ gene expression signature exists disregarding histopathological classification. 2004 , 64, 4040-8 | 351 |
| 1539 | Predictive models for breast cancer susceptibility from multiple single nucleotide polymorphisms. 2004 , 10, 2725-37 | 131 |
| 1538 | Expression and motogenic activity of TFF2 in human breast cancer cells. 2004 , 25, 865-865 | |
| 1537 | Using molecular markers to predict outcome. 2004 , 172, S18-21; discussion S21-2 | 12 |
| 1536 | DNA microarray analysis of pancreatic malignancies. 2004 , 4, 587-97 | 36 |
| 1535 | The prognostic implication of the basal-like (cyclin E high/p27 low/p53+/glomeruloid-microvascular-proliferation+) phenotype of BRCA1-related breast cancer. 2004 , 64, 830-5 | 307 |
| 1534 | Breast Cancer Prognostic and Predictive Factors. 2004 , 7, 91-100 | |
| 1533 | Predicting prostate cancer behavior using transcript profiles. 2004 , 172, S28-32; discussion S33 | 36 |
| 1532 | Gene expression profiling of microdissected pancreatic ductal carcinomas using high-density DNA microarrays. 2004 , 6, 611-22 | 156 |
| 1531 | Expression profiling identifies chemokine (C-C motif) ligand 18 as an independent prognostic indicator in gastric cancer. 2004 , 127, 457-69 | 81 |
| 1530 | Genome-scale profiling of gene expression in hepatocellular carcinoma: classification, survival prediction, and identification of therapeutic targets. 2004 , 127, S51-5 | 143 |
| 1529 | E15. Use of micro-array analysis to predict outcome and response in breast cancer patients. 2004 , 2, 49-50 | |
| 1528 | Locked nucleic acid: a potent nucleic acid analog in therapeutics and biotechnology. 2004, 14, 130-46 | 162 |
| 1527 | Microarray platformscomparisons and contrasts. 2004 , 5, 487-502 | 151 |

| 1526 | DNA microarrays and pharmacogenomics. 2004 , 49, 303-8 | 15 |
|------|---|------|
| 1525 | Genome-wide screening for prognosis-predicting genes in early-stage non-small-cell lung cancer. 2004 , 45 Suppl 2, S145-50 | 26 |
| 1524 | Adjuvant therapy in elderly patients with breast cancer. 2004 , 5, 188-95; discussion 196-7 | 15 |
| 1523 | An unsupervised approach to identify molecular phenotypic components influencing breast cancer features. 2004 , 64, 1584-8 | 19 |
| 1522 | Expression of S100A4 and Met: potential predictors for metastasis and survival in early-stage breast cancer. 2004 , 66, 429-38 | 72 |
| 1521 | Genetic alteration and gene expression modulation during cancer progression. 2004 , 3, 9 | 70 |
| 1520 | Methods to find out the expression of activated genes. 2004 , 2, 68 | 5 |
| 1519 | Optimizing treatment for cervical cancer. 2004 , 3, 215-227 | 4 |
| 1518 | Phenotype characterisation using integrated gene transcript, protein and metabolite profiling. 2004 , 3, 205-17 | 55 |
| 1517 | caGEDA: a web application for the integrated analysis of global gene expression patterns in cancer. 2004 , 3, 49-62 | 71 |
| 1516 | Use of gene-expression profiling to identify prognostic subclasses in adult acute myeloid leukemia. 2004 , 350, 1605-16 | 822 |
| 1515 | Creation of the whole human genome microarray. 2004 , 1, 19-28 | 27 |
| 1514 | CNS metastases in breast cancer. 2004 , 22, 3608-17 | 526 |
| 1513 | Thoracic manifestations of common nonpulmonary malignancies of women. 2004 , 25, 379-90 | 10 |
| 1512 | A multigene assay to predict recurrence of tamoxifen-treated, node-negative breast cancer. 2004 , 351, 2817-26 | 4778 |
| 1511 | A compendium to ensure computational reproducibility in high-dimensional classification tasks. 2004 , 3, Article37 | 61 |
| 1510 | Breast cancer oestrogen independence mediated by BCAR1 or BCAR3 genes is transmitted through mechanisms distinct from the oestrogen receptor signalling pathway or the epidermal growth factor receptor signalling pathway. 2005 , 7, R82-92 | 24 |
| 1509 | Recent translational research: microarray expression profiling of breast cancerbeyond classification and prognostic markers?. 2004 , 6, 192-200 | 18 |

| 1508 | A multigene RT-PCR assay used to predict recurrence in early breast cancer: two presentations with contradictory results. 2004 , 6, 185-7 | 2 |
|------------------------------|---|----------------------------|
| 1507 | Prognostic molecular markers in early breast cancer. 2004 , 6, 109-18 | 156 |
| 1506 | Multistep tumorigenesis and the microenvironment. 2004 , 6, 93-101 | 74 |
| 1505 | Intratumoural mRNA expression of genes from the oestradiol metabolic pathway and clinical and histopathological parameters of breast cancer. 2004 , 6, R46-55 | 35 |
| 1504 | Discovery of estrogen receptor alpha target genes and response elements in breast tumor cells. 2004 , 5, R66 | 213 |
| 1503 | Molecular tumor profiling: translating genomic insights into clinical advances. 2004 , 5, 113 | 2 |
| 1502 | Common ground in the transcriptional profiles of wounds and tumors. 2004 , 5, 228 | 10 |
| 1501 | Perspectives and limitations of gene expression profiling in rheumatology: new molecular strategies. 2004 , 6, 140-6 | 12 |
| 1500 | ?Good Old? clinical markers have similar power in breast cancer prognosis as microarray gene expression profilers*1. 2004 , | |
| | | |
| 1499 | Critical Review of European Experience with Neoadjuvant Therapy. 2004 , 7, 113-121 | 1 |
| 177 | ONCOMINE: a cancer microarray database and integrated data-mining platform. 2004 , 6, 1-6 | 2548 |
| 1498 | | |
| 1498 | ONCOMINE: a cancer microarray database and integrated data-mining platform. 2004 , 6, 1-6 | 2548 |
| 1498 | ONCOMINE: a cancer microarray database and integrated data-mining platform. 2004 , 6, 1-6 Twist, a master regulator of morphogenesis, plays an essential role in tumor metastasis. 2004 , 117, 927-39 | 2548 2996 |
| 1498 1497 1496 | ONCOMINE: a cancer microarray database and integrated data-mining platform. 2004 , 6, 1-6 Twist, a master regulator of morphogenesis, plays an essential role in tumor metastasis. 2004 , 117, 927-39 Epithelial-mesenchymal transitions: twist in development and metastasis. 2004 , 118, 277-9 | 2548 2996 1198 |
| 1498 1497 1496 | ONCOMINE: a cancer microarray database and integrated data-mining platform. 2004, 6, 1-6 Twist, a master regulator of morphogenesis, plays an essential role in tumor metastasis. 2004, 117, 927-39 Epithelial-mesenchymal transitions: twist in development and metastasis. 2004, 118, 277-9 Genomics in the immune system. 2004, 111, 175-85 | 2548 2996 1198 |
| 1498 1497 1496 1495 | ONCOMINE: a cancer microarray database and integrated data-mining platform. 2004, 6, 1-6 Twist, a master regulator of morphogenesis, plays an essential role in tumor metastasis. 2004, 117, 927-39 Epithelial-mesenchymal transitions: twist in development and metastasis. 2004, 118, 277-9 Genomics in the immune system. 2004, 111, 175-85 Prediction of hormone sensitivity by DNA microarray. 2004, 58, 1-9 | 2548 2996 1198 22 |

| 1490 | "Good Old" clinical markers have similar power in breast cancer prognosis as microarray gene expression profilers. 2004 , 40, 1837-41 | 130 |
|------|--|-----|
| 1489 | Old and new markers for breast cancer prognosis: the need for integrated research on quantitative issues. 2004 , 40, 1803-6 | 9 |
| 1488 | Genomic and proteomic technologies for individualisation and improvement of cancer treatment. 2004 , 40, 2623-32 | 77 |
| 1487 | Biomarkers of ovarian tumours. 2004 , 40, 2604-12 | 68 |
| 1486 | Understanding cancer at the chromosome level: 40 years of progress. 2004 , 40, 1960-7 | 6 |
| 1485 | Gene expression microarray technologies in the development of new therapeutic agents. 2004 , 40, 2560-91 | 70 |
| 1484 | Molecular portraits of breast cancer: tumour subtypes as distinct disease entities. 2004 , 40, 2667-75 | 267 |
| 1483 | Highly specific marker genes for detecting minimal gastric cancer cells in cytology negative peritoneal washings. 2004 , 313, 931-7 | 28 |
| 1482 | Clinico-molecular study of dedifferentiation in well-differentiated liposarcoma. 2004 , 314, 1133-40 | 24 |
| 1481 | XBP-1 increases ERalpha transcriptional activity through regulation of large-scale chromatin unfolding. 2004 , 323, 269-74 | 26 |
| 1480 | Heterogeneity within and between primary colorectal carcinomas and matched metastases as revealed by analysis of Ki-ras and p53 mutations. 2004 , 325, 784-91 | 78 |
| 1479 | Loss of annexin A1 expression in human breast cancer detected by multiple high-throughput analyses. 2005 , 326, 218-27 | 59 |
| 1478 | Individual-specific variation of gene expression in peripheral blood leukocytes. 2004 , 83, 980-8 | 119 |
| 1477 | Expression and motogenic activity of TFF2 in human breast cancer cells. 2004 , 25, 865-72 | 22 |
| 1476 | Phenotypic and microarray gene expression analysis of tri-dimensional raft-modeled human head and neck squamous cell carcinoma. 2004 , 131, 577-84 | 3 |
| 1475 | Multi-platform, multi-site, microarray-based human tumor classification. 2004 , 164, 9-16 | 178 |
| 1474 | Whole genome amplification of DNA from laser capture-microdissected tissue for high-throughput single nucleotide polymorphism and short tandem repeat genotyping. 2004 , 164, 23-33 | 83 |
| 1473 | Measurement of gene expression in archival paraffin-embedded tissues: development and performance of a 92-gene reverse transcriptase-polymerase chain reaction assay. 2004 , 164, 35-42 | 469 |

(2004-2004)

| 1472 | Single-channel quantitative multiplex reverse transcriptase-polymerase chain reaction for large numbers of gene products differentiates nondemented from neuropathological Alzheimer's disease. 2004 , 164, 795-806 | 4 |
|------|---|-----|
| 1471 | Gene expression profiling identifies genes associated with invasive intraductal papillary mucinous neoplasms of the pancreas. 2004 , 164, 903-14 | 176 |
| 1470 | It's the matrix! ECM, proteases, and cancer. 2004 , 164, 1141-2 | 23 |
| 1469 | Quantitative gene expression profiling in formalin-fixed, paraffin-embedded tissues using universal bead arrays. 2004 , 165, 1799-807 | 138 |
| 1468 | Biologie molĉulaire des cancers. 2004 , 19, 13-22 | 2 |
| 1467 | Identification of a host gene subset related to disease prognosis of HIV-1 infected individuals. 2004 , 4, 1829-36 | 14 |
| 1466 | Molecular classification of nemaline myopathies: "nontyping" specimens exhibit unique patterns of gene expression. 2004 , 15, 590-600 | 11 |
| 1465 | Quantitative T1 mapping and absolute water content measurement using MRI. 2004, 1265, 113-123 | 8 |
| 1464 | Oncogenic pathways in hereditary and sporadic breast cancer. 2004 , 49, 34-43 | 38 |
| 1463 | About GATA3, HNF3A, and XBP1, three genes co-expressed with the oestrogen receptor-alpha gene (ESR1) in breast cancer. 2004 , 219, 1-7 | 114 |
| 1462 | Prediction of lymph node metastasis and perineural invasion of biliary tract cancer by selected features from cDNA array data. 2004 , 122, 184-94 | 25 |
| 1461 | A gene-expression signature can quantify the degree of hepatic fibrosis in the rat. 2004 , 41, 399-406 | 29 |
| 1460 | Telomere maintenance in clinical medicine. 2004 , 117, 262-9 | 21 |
| 1459 | Identification of differentially expressed genes in salivary gland tumors with cDNA microarray. 2004 , 31, 261-8 | 4 |
| 1458 | Gene expression studies in lung development and lung stem cell biology. 2004 , 64, 57-71 | 4 |
| 1457 | Comparative value of tumour grade, hormonal receptors, Ki-67, HER-2 and topoisomerase II alpha status as predictive markers in breast cancer patients treated with neoadjuvant anthracycline-based chemotherapy. 2004 , 40, 205-11 | 204 |
| 1456 | [The genetics of glioma: molecular classification]. 2004 , 33, 1268-73 | 1 |
| 1455 | Dissecting the molecular mechanisms of human cancer: translating laboratory advances into clinical practice. 2004 , 2, 1-6 | 1 |

1454 E4. Gene expression profiles: What the clinicians need to know. **2004**, 2, 10-11

| | f human colon xenograft tumors following treatment with SU11 | 248, a 45 |
|--|--|------------------|
| multitargeted tyrosine kina | se inhibitor. 2004 , 23, 1618-26 | 7.7 |
| 1452 Oncogenic aberrations of co | ullin-dependent ubiquitin ligases. 2004 , 23, 2037-49 | 67 |
| 1451 Biomedical marker moleculo | es for cancer Œurrent status and perspectives. 2004 , 3, 228-237 | 6 |
| 1450 Genetic inheritance of gene | e expression in human cell lines. 2004 , 75, 1094-105 | 304 |
| 1449 Shaping the future: training | of professionals for radiotherapy in Europe. 2004 , 70, 103-5 | 5 |
| 1448 Injury research in the genon | nic era. 2004 , 363, 2076-83 | 101 |
| 1447 Exceptional matters. 2004, 3 | 364, 2142-51 | 12 |
| Genomic and expression and 64, 40-7 | alysis of the 8p11-12 amplicon in human breast cancer cell lines. | 2004, |
| 1445 Sophisticated radiotherapy | with optimal surgery is the way forward. 2004 , 16, 529-35 | |
| Ensemble Recordings Of Hu 1444 Brain-Machine Interface. 20 | uman Subcortical Neurons as a Source Of Motor Control Signals F 1 04 , 55, 27-38 | For a 155 |
| 1443 Molecular Analysis and Gen | ome Discovery. 2004 , 5, 609-610 | |
| 1442 Expression genomics and ca | ancer biology. 2004 , 5, 1117-28 | 4 |
| 1441 Challenges in breast cancer | clinical trial design in the postgenomic era. 2004 , 16, 536-41 | 13 |
| Distinctive gene expression of the endometrium. 2004 , | profiles by cDNA microarrays in endometrioid and serous carcin 23, 321-9 | omas 34 |
| 1439 Pharmacogenomics. 2004 , 1 | 11, 211-20 | 32 |
| 1438 Exceptional matters: clinical | l research from bedside to bench. 2004 , 4, 551-66 | 9 |
| A three-layer multidatabase results. 2004 , 2004, 2805-8 | e system for functional statistical analyses of microarray experim | ent |

| 1436 | Predicting drug response based on gene expression. 2004 , 51, 205-227 | 26 |
|------|---|-----|
| 1435 | Gene expression patterns, prognostic and diagnostic markers, and lung cancer biology. 2004 , 125, 111S-5S | 13 |
| 1434 | GOAL: automated Gene Ontology analysis of expression profiles. 2004 , 32, W492-9 | 36 |
| 1433 | Review of: Classification of human breast cancer using gene expression profiling as a component of the survival predictor algorithm. 2004 , 7, | 1 |
| 1432 | Gene expression analysis of human renal biopsies: recent developments towards molecular diagnosis of kidney disease. 2004 , 13, 313-8 | 16 |
| 1431 | Genetic, genomic, and bioinformatic tools for studying breast cancer progression. 2004 , 19, 83-91 | 1 |
| 1430 | Gene expression profiles predict complete pathologic response to neoadjuvant paclitaxel and fluorouracil, doxorubicin, and cyclophosphamide chemotherapy in breast cancer. 2004 , 4, 211-213 | 1 |
| 1429 | Application of proteomics in the study of tumor metastasis. 2004 , 2, 152-66 | 22 |
| 1428 | Genomic and proteomic approaches for studying human cancer: prospects for true patient-tailored therapy. 2004 , 1, 134-40 | 49 |
| 1427 | The pathology of hereditary breast cancer. 2004 , 2, 131-8 | 16 |
| 1426 | Increased measurement accuracy for sequence-verified microarray probes. 2004, 18, 308-15 | 67 |
| 1425 | A comparison of oligonucleotide and cDNA-based microarray systems. 2004 , 16, 361-70 | 97 |
| 1424 | Proteomic analysis of pulmonary edema fluid and plasma in patients with acute lung injury. 2004 , 286, L1095-104 | 73 |
| 1423 | Genomics and clinical medicine: rationale for creating and effectively evaluating animal models. 2004 , 229, 866-75 | 33 |
| 1422 | The Use of a Compendium of Expression Profiles for Mechanism of Toxicity Predictions. 2005 , 215-233 | |
| 1421 | A Short Introduction to the Expression Profile Toolbox. 2005 , 45-53 | |
| 1420 | Statistics for Toxicogenomics. 2005 , 115-145 | |
| 1419 | Gene expression profiling allows distinction between primary and metastatic squamous cell carcinomas in the lung. 2005 , 65, 3063-71 | 122 |

| 1418 | The Mark Coventry Award: white blood cell gene expression: a new approach toward the study and diagnosis of infection. 2005 , 440, 38-44 | 47 |
|------|---|----|
| 1417 | Functional profiling: from microarrays via cell-based assays to novel tumor relevant modulators of the cell cycle. 2005 , 65, 7733-42 | 18 |
| 1416 | Linking transcriptional elongation and messenger RNA export to metastatic breast cancers. 2005 , 65, 3011-6 | 49 |
| 1415 | Tumor heterogeneity affects the precision of microarray analysis. 2005 , 14, 65-71 | 14 |
| 1414 | Gene expression analysis using filter cDNA microarrays. 2006 , 120, 415-24 | 2 |
| 1413 | High-throughput scanning with single-molecule sensitivity. 2005 , 5699, 202 | 6 |
| 1412 | Identifying site-specific metastasis genes and functions. 2005 , 70, 149-58 | 79 |
| 1411 | Genomics and circulating tumor cells: promising tools for choosing and monitoring adjuvant therapy in patients with early breast cancer?. 2005 , 17, 551-8 | 19 |
| 1410 | Expression profiling of colon cancer cell lines and colon biopsies: towards a screening system for potential cancer-preventive compounds. 2005 , 14, 439-57 | 9 |
| 1409 | Quantitative in situ cancer proteomics: molecular pathology comes of age with automated tissue microarray analysis. 2005 , 2, 291-300 | 2 |
| 1408 | Specialized DNA arrays for the differentiation of pancreatic tumors. 2005 , 11, 8048-54 | 41 |
| 1407 | Clinical application of molecular profiling in breast cancer. 2005 , 1, 485-96 | 11 |
| 1406 | Emerging approaches in molecular profiling affecting oncology drug discovery. 2005 , 70, 445-8 | 3 |
| 1405 | Dose-dense primary systemic chemotherapy with gemcitabine plus epirubicin sequentially followed by docetaxel for early breast cancer: final results of a phase I/II trial. 2005 , 16, 1023-8 | 11 |
| 1404 | Gene expression profiling of primary tumor cell populations using laser capture microdissection, RNA transcript amplification, and GeneChip microarrays. 2005 , 293, 187-207 | 15 |
| 1403 | Systems Biology: Applications in Drug Discovery. 2005 , 123-183 | 14 |
| 1402 | Integration of Microarray Data for a Comparative Study of Classifiers and Identification of Marker Genes. 2005 , 147-162 | |
| 1401 | 1 Identification of Tumor-Specific Genes. 2005 , 3-21 | 1 |

| Dissecting tBHQ induced ARE-driven gene expression through long and short oligonucleotide arrays. 2005 , 21, 43-58 | 14 |
|---|---------|
| 1399 Genomics-based prognosis and therapeutic prediction in breast cancer. 2005 , 3, 291-300 | 47 |
| 1398 The potential of microarrays to assist shrimp breeding and production: a review. 2005 , 45, 901 | 4 |
| 1397 Statistical methods for gene expression analysis. 2005 , | |
| 1396 Tailored therapy of colorectal cancer: results, challenges and future directions. 2005 , 11, 175-88 | 3 |
| 1395 Bioinformatics Challenges and Opportunities. 2005 , 63-94 | 1 |
| Gene expression profiling in follicular lymphoma to assess clinical aggressiveness and to guide the choice of treatment. 2005 , 105, 301-7 | 183 |
| 1393 High Sensitivity Expression Profiling. 2005 , 229-250 | 1 |
| 1392 Apports des puces ^ADN dans la comprhension de la polyarthrite rhumatoffe. 2005 , 72, 281-286 | |
| Locoregional recurrence rates and prognostic factors for failure in node-negative patients treated with mastectomy: implications for postmastectomy radiation. 2005 , 62, 1035-9 | 126 |
| cRNA target preparation for microarrays: comparison of gene expression profiles generated with different amplification procedures. 2005 , 344, 92-101 | 24 |
| Population pharmacokinetics of CCI-779: correlations to safety and pharmacogenomic responses in patients with advanced renal cancer. 2005 , 77, 76-89 | 68 |
| 1388 Exploiting scale-free information from expression data for cancer classification. 2005 , 29, 288-93 | 3 |
| | |
| 1387 GeneMCL in microarray analysis. 2005 , 29, 354-9 | 10 |
| GeneMCL in microarray analysis. 2005, 29, 354-9 1386 Application of expression genomics for predicting treatment response in cancer. 2005, 1058, 186-95 | 10 9 |
| | |
| 1386 Application of expression genomics for predicting treatment response in cancer. 2005 , 1058, 186-95 | 9 |

| 1382 | Diet induction of monocyte chemoattractant protein-1 and its impact on obesity. 2005 , 13, 1311-20 | 170 |
|------|---|------|
| 1381 | Genomic approaches in the management and treatment of breast cancer. 2005 , 92, 618-24 | 26 |
| 1380 | Histopathologic indicators of breast cancer biology: insights from population mammographic screening. 2005 , 92, 1366-71 | 12 |
| 1379 | Primary chemotherapy with gemcitabine, epirubicin and taxol (GET) in operable breast cancer: a phase II study. 2005 , 93, 406-11 | 15 |
| 1378 | No common denominator for breast cancer lymph node metastasis. 2005 , 93, 924-32 | 78 |
| 1377 | Probabilistic model of the human protein-protein interaction network. 2005 , 23, 951-9 | 338 |
| 1376 | An expression profile for diagnosis of lymph node metastases from primary head and neck squamous cell carcinomas. 2005 , 37, 182-6 | 346 |
| 1375 | Integrative analysis of the cancer transcriptome. 2005 , 37 Suppl, S31-7 | 385 |
| 1374 | An integrative genomics approach to infer causal associations between gene expression and disease. 2005 , 37, 710-7 | 820 |
| 1373 | Control of DNA replication and its potential clinical exploitation. 2005 , 5, 135-41 | 136 |
| 1372 | The promise of genetically engineered mice for cancer prevention studies. 2005 , 5, 184-98 | 57 |
| 1371 | Ovarian cancer metastasis: integrating insights from disparate model organisms. 2005 , 5, 355-66 | 427 |
| 1370 | Breast cancer metastasis: markers and models. 2005 , 5, 591-602 | 1591 |
| 1369 | Opinion: emerging mechanisms of tumour lymphangiogenesis and lymphatic metastasis. 2005 , 5, 735-43 | 249 |
| 1368 | On the road to cancer: aneuploidy and the mitotic checkpoint. 2005 , 5, 773-85 | 903 |
| 1367 | Biomarkers in cancer staging, prognosis and treatment selection. 2005 , 5, 845-56 | 1278 |
| 1366 | How molecular profiling could revolutionize drug discovery. 2005 , 4, 345-50 | 104 |
| 1365 | An array of problems. 2005 , 4, 362-3 | 57 |

| 1364 | Expression of AMAP1, an ArfGAP, provides novel targets to inhibit breast cancer invasive activities. 2005 , 24, 963-73 | | 131 |
|------|--|------|------|
| 1363 | Peripheral blood gene expression profiling in rheumatoid arthritis. 2005 , 6, 388-97 | | 131 |
| 1362 | A network of clinically and functionally relevant genes is involved in the reversion of the tumorigenic phenotype of MDA-MB-231 breast cancer cells after transfer of human chromosome 8. 2005 , 24, 869-79 | | 7 |
| 1361 | Gene expression signature predicts lymphatic metastasis in squamous cell carcinoma of the oral cavity. 2005 , 24, 1244-51 | | 154 |
| 1360 | Identification of molecular apocrine breast tumours by microarray analysis. 2005, 24, 4660-71 | | 594 |
| 1359 | Gene expression analysis reveals a strong signature of an interferon-induced pathway in childhood lymphoblastic leukemia as well as in breast and ovarian cancer. 2005 , 24, 6367-75 | | 61 |
| 1358 | Induction of heat shock proteins by heregulin beta1 leads to protection from apoptosis and anchorage-independent growth. 2005 , 24, 6564-73 | | 98 |
| 1357 | Identification of a proliferation gene cluster associated with HPV E6/E7 expression level and viral DNA load in invasive cervical carcinoma. 2005 , 24, 7094-104 | | 110 |
| 1356 | Colon cancer prognosis prediction by gene expression profiling. 2005 , 24, 6155-64 | | 83 |
| 1355 | A quantitative genomic expression analysis platform for multiplexed in vitro prediction of drug action. 2005 , 5, 126-34 | | 17 |
| 1354 | Candidate-based proteomics in the search for biomarkers of cardiovascular disease. 2005 , 563, 23-60 | | 298 |
| 1353 | Reliable gene expression measurements from degraded RNA by quantitative real-time PCR depend on short amplicons and a proper normalization. 2005 , 85, 1040-50 | | 177 |
| 1352 | Beta4 integrin subunit gene expression correlates with tumor size and nuclear grade in early breast cancer. 2005 , 18, 1165-75 | | 57 |
| 1351 | The molecular pathology of hereditary breast cancer: genetic testing and therapeutic implications. 2005 , 18, 1305-20 | | 125 |
| 1350 | Genes that mediate breast cancer metastasis to lung. <i>Nature</i> , 2005 , 436, 518-24 | 50.4 | 2242 |
| 1349 | Utilizing logical relationships in genomic data to decipher cellular processes. 2005 , 272, 5110-8 | | 32 |
| 1348 | The interface of genomic technologies and nursing. 2005 , 37, 111-9 | | 16 |
| 1347 | Gene expression profiling of breast cancer in ethnic populations: an aid to gene discovery for the benefit of all. 2005 , 11, 89-91 | | 3 |

| 1346 | Chromosomal alterations cause the high rates and wide ranges of drug resistance in cancer cells. 2005 , 163, 44-56 | 49 |
|------|--|------|
| 1345 | Expression profiling using a tumor-specific cDNA microarray predicts the prognosis of intermediate risk neuroblastomas. 2005 , 7, 337-50 | 131 |
| 1344 | The transcriptional repressor Snail promotes mammary tumor recurrence. 2005 , 8, 197-209 | 585 |
| 1343 | Integrative genomic and proteomic analysis of prostate cancer reveals signatures of metastatic progression. 2005 , 8, 393-406 | 625 |
| 1342 | Analysis of paired primary lung and lymph node tumor cells: a model of metastatic potential by multiple genetic programs. 2005 , 29, 509-17 | 17 |
| 1341 | Molecular requirements for epithelial-mesenchymal transition during tumor progression. 2005 , 17, 548-58 | 1505 |
| 1340 | An automated procedure to properly handle digital images in large scale tissue microarray experiments. 2005 , 79, 197-208 | 13 |
| 1339 | Gelatinase-mediated migration and invasion of cancer cells. 2005 , 1755, 37-69 | 269 |
| 1338 | The oligometastatic state in breast cancer: hypothesis or reality. 2005 , 14, 87-93 | 50 |
| 1337 | Histopathology of primary breast cancer 2005. 2005 , 14, 487-92 | 15 |
| 1336 | Preoperative (neoadjuvant) systemic treatment of breast cancer. 2005 , 14, 576-81 | 29 |
| 1335 | When will more useful predictive factors be ready for use?. 2005 , 14, 617-23 | 16 |
| 1334 | Adjuvant chemotherapy for breast cancer"one fits all"?. 2005 , 14, 564-9 | 7 |
| 1333 | Prognostic and predictive factors revisited. 2005 , 14, 493-9 | 85 |
| 1332 | Determination of tumour marker genes from gene expression data. 2005 , 10, 429-37 | 27 |
| 1331 | The transcriptome's drugable frequenters. 2005 , 10, 857-64 | 13 |
| 1330 | Gene Expression Profiling Predicts Therapeutic Response and Prognosis in Patients with Breast Cancer. 2005 , 6, 199-201 | |
| 1329 | Surgical application of cDNA microarray technique. 2005 , 138, 399-403 | |

1328 Hypothesis Flact or Fiction?. **2005**, 138, 403

| 1327 Molecular changes in prostatic cancer. 2005 , 14, 91-104 | 10 |
|--|-----|
| 1326 Tumor cells caught in the act of invading: their strategy for enhanced cell motility. 2005 , 15, 138-45 | 224 |
| 1325 Breast cancer: integrating the patient with her genome. 2005 , 23, 3-5 | |
| Comparison of supervised clustering methods to discriminate genotoxic from non-genotoxic carcinogens by gene expression profiling. 2005 , 575, 17-33 | 51 |
| 1323 In pursuit of effective toxicogenomics. 2005 , 575, 4-16 | 14 |
| 1322 Cancer: undifferentiation or specialization?. 2005 , 41, 655-6 | |
| 1321 Bringing molecular prognosis and prediction to the clinic. 2005 , 6, 61-76 | 30 |
| Predictive value of biologic parameters for primary chemotherapy in operable breast cancer. 2005 , 6, 315-24 | 6 |
| 1319 Signal transduction pathway profiling of individual tumor samples. 2005 , 6, 163 | 31 |
| 1318 Storing, linking, and mining microarray databases using SRS. 2005 , 6, 192 | 10 |
| 1317 stama Bioconductor compliant R package for structured analysis of microarray data. 2005 , 6, 211 | 2 |
| Cross-platform analysis of cancer microarray data improves gene expression based classification of phenotypes. 2005 , 6, 265 | 146 |
| 1315 In silico microdissection of microarray data from heterogeneous cell populations. 2005 , 6, 54 | 60 |
| An integrated approach of immunogenomics and bioinformatics to identify new Tumor Associated Antigens (TAA) for mammary cancer immunological prevention. 2005 , 6 Suppl 4, S7 | 25 |
| 1313 Gene expression signature of estrogen receptor alpha status in breast cancer. 2005 , 6, 37 | 114 |
| 1312 Three microarray platforms: an analysis of their concordance in profiling gene expression. 2005 , 6, 63 | 83 |
| 1311 Numbers of mutations to different types of colorectal cancer. 2005 , 5, 126 | 12 |

| 1310 | Differences in gene expression in prostate cancer, normal appearing prostate tissue adjacent to cancer and prostate tissue from cancer free organ donors. 2005 , 5, 45 | 113 |
|------|---|-----|
| 1309 | Distinction between serous tumors of low malignant potential and serous carcinomas based on global mRNA expression profiling. 2005 , 96, 684-94 | 93 |
| 1308 | Downregulation of metastasis suppressor genes in malignant pheochromocytoma. 2005 , 114, 139-43 | 87 |
| 1307 | Prediction of recurrence in advanced gastric cancer patients after curative resection by gene expression profiling. 2005 , 114, 963-8 | 30 |
| 1306 | High-throughput protein expression analysis using tissue microarray technology of a large well-characterised series identifies biologically distinct classes of breast cancer confirming recent cDNA expression analyses. 2005 , 116, 340-50 | 443 |
| 1305 | Expression levels of the putative zinc transporter LIV-1 are associated with a better outcome of breast cancer patients. 2005 , 117, 961-73 | 62 |
| 1304 | Expression of RPIP9 (Rap2 interacting protein 9) is activated in breast carcinoma and correlates with a poor prognosis. 2005 , 117, 934-41 | 14 |
| 1303 | The persistence of isolated tumor cells in bone marrow from patients with breast carcinoma predicts an increased risk for recurrence. 2005 , 103, 884-91 | 146 |
| 1302 | Microarray technology for surgeons. 2005 , 92, 387-8 | 1 |
| 1301 | Overview of Microarrays in Genomic Analysis. 2005 , 127-165 | |
| 1300 | Introduction to DNA Microarray Technology. 2005 , 1-15 | |
| 1299 | References. 2005 , 152-182 | |
| 1298 | Lymph node staging surgery and breast cancer: potholes in the fast lane from more to less. 2005 , 89, 53-60 | 3 |
| 1297 | Contemporary management of penile squamous cell carcinoma. 2005 , 89, 43-50 | 51 |
| 1296 | Follicular thyroid lesions, elements that affect both diagnosis and prognosis. 2005, 89, 108-13 | 36 |
| 1295 | Estrogen signaling and prediction of endocrine therapy. 2005 , 56 Suppl 1, 27-31 | 12 |
| 1294 | Modifiers of mammary tumor progression and metastasis on mouse chromosomes 7, 9, and 17. 2005 , 16, 120-6 | 33 |
| 1293 | Adaptor-tagged competitive polymerase chain reaction: amplification bias and quantified gene expression levels. 2005 , 339, 15-28 | 7 |

| The coefficient of intrinsic dependence (feature selection using el CID). 2005 , 38, 623-636 | 17 |
|--|-----|
| Gene expression profiling of nonneoplastic mucosa may predict clinical outcome of colon cancer patients. 2005 , 48, 2238-48 | 25 |
| p63, cytokeratin 5, and P-cadherin: three molecular markers to distinguish basal phenotype in breast carcinomas. 2005 , 447, 688-94 | 177 |
| 1289 «Cancers du sein». 2005 , 7, 342-379 | 12 |
| 1288 Protocole temporaire de traitement Trastuzumab (Herceptin) en situation adjuvante. 2005 , 7, s86-s99 | |
| Lymphatic staging in colorectal cancer: pathologic, molecular, and sentinel node techniques. 2005 , 48, 371-83 | 15 |
| 1286 MammakarzinomBtandards der Versorgung heute und morgen. 2005, 11, 265-272 | 1 |
| Internationale Konferenz St. Gallen 2609.01.2005: B rimary Therapy of Early Breast Cancer 2005 , 11, 446-456 | |
| 1284 Molekulare Diagnostik bei nicht-hähatologischen malignen Erkrankungen. 2005 , 11, 873-888 | |
| 1283 Vers de nouveaux tests biologiques pour prdire le potentiel mtastatique dun cancer. 2005 , 17, 30-33 | |
| 1282 Utilizing prognostic and predictive factors in breast cancer. 2005 , 6, 147-59 | 47 |
| 1281 Gene expression profiling of primary breast cancer. 2005 , 7, 38-44 | 15 |
| 1280 Maintenance of cell type diversification in the human breast. 2005 , 10, 61-74 | 13 |
| Non-angiogenic functions of VEGF in breast cancer. 2005 , 10, 283-90 | 63 |
| 1278 Analysis of target genes induced by IL-13 cytotoxin in human glioblastoma cells. 2005 , 72, 35-46 | 9 |
| 1277 Prognostic factors affecting the natural history of node-negative breast cancer. 2005 , 89, 35-45 | 38 |
| Phenotypic characterization of BRCA1 and BRCA2 tumors based in a tissue microarray study with 37 immunohistochemical markers. 2005 , 90, 5-14 | 135 |
| Histone deacetylase-1 and -3 protein expression in human breast cancer: a tissue microarray | 180 |

| 1274 | The "portrait" of hereditary breast cancer. 2005 , 89, 297-304 | 42 |
|--------------------------------------|---|----------------------|
| 1273 | BRCA1 promoter methylation in sporadic breast tumors: relationship to gene expression profiles. 2005 , 91, 179-86 | 143 |
| 1272 | The future of breast cancer: the role of prognostic factors. 2005 , 89 Suppl 1, S17-26 | 25 |
| 1271 | Morphologic and immunophenotypic markers as surrogate endpoints of tamoxifen effect for prevention of breast cancer. 2005 , 94, 205-11 | 14 |
| 1270 | Abstracts of the 10th International Congress of the Metastasis Research Society, Genoa, Italy, 17월0 September 2004. 2005 , 21, 599-662 | |
| 1269 | Metastasis predictive signature profiles pre-exist in normal tissues. 2005 , 22, 593-603 | 94 |
| 1268 | A simplified immunoprecipitation method for quantitatively measuring antibody responses in clinical sera samples by using mammalian-produced Renilla luciferase-antigen fusion proteins. 2005 , 5, 22 | 87 |
| 1267 | Prognostic index in lobular breast cancer. 2005 , 10, 165-172 | 1 |
| 1266 | Molecular evolution of breast cancer. 2005 , 205, 248-54 | 391 |
| | | |
| 1265 | Hunting the primary: novel strategies for defining the origin of tumours. 2005 , 205, 236-47 | 22 |
| 1265 1264 | Hunting the primary: novel strategies for defining the origin of tumours. 2005 , 205, 236-47 Cell-cycle-dependent regulation of DNA replication and its relevance to cancer pathology. 2005 , 205, 123-9 | 115 |
| | Cell-cycle-dependent regulation of DNA replication and its relevance to cancer pathology. 2005 , | |
| 1264 | Cell-cycle-dependent regulation of DNA replication and its relevance to cancer pathology. 2005 , 205, 123-9 TP53 mutations are associated with a particular pattern of genomic imbalances in breast carcinomas. 2005 , 207, 14-9 | |
| 1264 | Cell-cycle-dependent regulation of DNA replication and its relevance to cancer pathology. 2005 , 205, 123-9 TP53 mutations are associated with a particular pattern of genomic imbalances in breast carcinomas. 2005 , 207, 14-9 | 115 7 |
| 1264 1263 1262 | Cell-cycle-dependent regulation of DNA replication and its relevance to cancer pathology. 2005, 205, 123-9 TP53 mutations are associated with a particular pattern of genomic imbalances in breast carcinomas. 2005, 207, 14-9 FDR-controlling testing procedures and sample size determination for microarrays. 2005, 24, 2267-80 BeadArray-based solutions for enabling the promise of pharmacogenomics. 2005, 39, S583-8 | 115 7 46 |
| 1264 1263 1262 1261 | Cell-cycle-dependent regulation of DNA replication and its relevance to cancer pathology. 2005, 205, 123-9 TP53 mutations are associated with a particular pattern of genomic imbalances in breast carcinomas. 2005, 207, 14-9 FDR-controlling testing procedures and sample size determination for microarrays. 2005, 24, 2267-80 BeadArray-based solutions for enabling the promise of pharmacogenomics. 2005, 39, S583-8 | 115 7 46 23 |
| 1264 1263 1262 1261 1260 | Cell-cycle-dependent regulation of DNA replication and its relevance to cancer pathology. 2005, 205, 123-9 TP53 mutations are associated with a particular pattern of genomic imbalances in breast carcinomas. 2005, 207, 14-9 FDR-controlling testing procedures and sample size determination for microarrays. 2005, 24, 2267-80 BeadArray-based solutions for enabling the promise of pharmacogenomics. 2005, 39, S583-8 Classification and selection of biomarkers in genomic data using LASSO. 2005, 2005, 147-54 Analysis of Neural Precursor Cells in the Context of Origin of Brain Tumors, Their Treatment, and | 115 7 46 23 |

| 1256 | DNA array-based gene profiling: from surgical specimen to the molecular portrait of cancer. 2005 , 241, 16-26 | 29 |
|------|--|-----|
| 1255 | Strategy for gene expression-based biomarker discovery. 2005 , Suppl, 25-9 | 3 |
| 1254 | . 2005, | 3 |
| 1253 | Expression Profiling of Breast Cancer: From Molecular Portraits to Clinical Utility. 2005 , 77-100 | 1 |
| 1252 | References. 2005 , 145-164 | |
| 1251 | Integrating genotypic, molecular profiling, and clinical data to elucidate common human diseases. 2005 , | |
| 1250 | Microarray CGH. 2005 , | |
| 1249 | Microarray analysis and RNA silencing to determine genes functionally important in mesothelioma. 2005 , 447-469 | |
| 1248 | Clinomics: Postgenomic Cancer Care. 2005 , 341-358 | |
| 1247 | Technologies for systematic analysis of eukaryotic transcriptomes. 2005, | |
| 1246 | Gene Expression Data and Survival Analysis. 2005 , 21-34 | 2 |
| 1245 | Use of extreme patient samples for outcome prediction from gene expression data. 2005, 21, 3377-84 | 23 |
| 1244 | Gene expression profile predicts patient survival of gastric cancer after surgical resection. 2005 , 23, 7286-95 | 111 |
| 1243 | Distinct molecular portraits of human failing hearts identified by dedicated cDNA microarrays. 2005 , 7, 157-65 | 27 |
| 1242 | Identification of a novel c-Myc protein interactor, JPO2, with transforming activity in medulloblastoma cells. 2005 , 65, 5607-19 | 64 |
| 1241 | DNA microarrays in clinical cancer research. 2005 , 5, 111-20 | 42 |
| 1240 | Gene profile and response to treatment. 2005 , 16 Suppl 2, ii195-202 | 11 |
| | | |

| 1238 | Analysis of recursive gene selection approaches from microarray data. 2005 , 21, 3741-7 | 77 |
|------|---|-----|
| 1237 | Gene expression profiling of the irinotecan pathway in colorectal cancer. 2005 , 11, 2053-62 | 52 |
| 1236 | From traditional biomarkers to transcriptome analysis in drug development. 2005 , 5, 29-38 | 34 |
| 1235 | Clinical pharmacogenomics and transcriptional profiling in early phase oncology clinical trials. 2005 , 5, 83-102 | 31 |
| 1234 | Discovering molecular functions significantly related to phenotypes by combining gene expression data and biological information. 2005 , 21, 2988-93 | 90 |
| 1233 | Mammary cancer and social interactions: identifying multiple environments that regulate gene expression throughout the life span. 2005 , 60 Spec No 1, 32-41 | 65 |
| 1232 | Comparative functional genomics for identifying models of human cancer. 2005 , 26, 1013-20 | 51 |
| 1231 | Personalized diagnostic and therapeutic strategies in oncology. 2005 , 2, 97-110 | 1 |
| 1230 | Gene expression profiling and breast cancer care: what are the potential benefits and policy implications?. 2005 , 7, 380-9 | 57 |
| 1229 | Functional genomic analysis of cancer metastasis: biologic insights and clinical implications. 2005 , 5, 385-95 | 25 |
| 1228 | New developments in the treatment of metastatic breast cancer: from chemotherapy to biological therapy. 2005 , 16 Suppl 2, ii191-4 | 21 |
| 1227 | Hotelling's T2 multivariate profiling for detecting differential expression in microarrays. 2005 , 21, 3105-13 | 75 |
| 1226 | Survivin, other IAPs, Smac/Diablo, and Omi/Htra2 [Modulation of the Advancing Apoptotic Process. 2005 , 137-155 | 1 |
| 1225 | Predicting cancer susceptibility from single-nucleotide polymorphism data. 2005, | 28 |
| 1224 | Gene expression profiles in paraffin-embedded core biopsy tissue predict response to chemotherapy in women with locally advanced breast cancer. 2005 , 23, 7265-77 | 461 |
| 1223 | Tumor gene expression and prognosis in breast cancer patients with 10 or more positive lymph nodes. 2005 , 11, 8623-31 | 173 |
| 1222 | Changes in gene expression associated with response to neoadjuvant chemotherapy in breast cancer. 2005 , 23, 3331-42 | 138 |
| 1221 | A cell proliferation signature is a marker of extremely poor outcome in a subpopulation of breast cancer patients. 2005 , 65, 4059-66 | 212 |

| 1220 | BRCA1 promoter methylation in sporadic breast cancer is associated with reduced BRCA1 copy number and chromosome 17 aneusomy. 2005 , 65, 10692-9 | 157 |
|--------------|---|-----|
| 1219 | Galectin-9 as a prognostic factor with antimetastatic potential in breast cancer. 2005 , 11, 2962-8 | 141 |
| 1218 | From the Cover: Location analysis of estrogen receptor alpha target promoters reveals that FOXA1 defines a domain of the estrogen response. 2005 , 102, 11651-6 | 306 |
| 1217 | Ensemble dependence model for classification and prediction of cancer and normal gene expression data. 2005 , 21, 3114-21 | 28 |
| 1216 | A basal epithelial phenotype is more frequent in interval breast cancers compared with screen detected tumors. 2005 , 14, 1108-12 | 159 |
| 1215 | An expression signature for p53 status in human breast cancer predicts mutation status, transcriptional effects, and patient survival. 2005 , 102, 13550-5 | 999 |
| 1214 | Bayesian model averaging: development of an improved multi-class, gene selection and classification tool for microarray data. 2005 , 21, 2394-402 | 203 |
| 1213 | DIGa system for gene annotation and functional discovery. 2005 , 21, 2957-9 | 1 |
| 1212 | Brain Tumors. 2005, | 9 |
| 1211 | How many samples are needed to build a classifier: a general sequential approach. 2005 , 21, 63-70 | 22 |
| 121 0 | Gene expression profiling of breast cancer: a new tumor marker. 2005 , 23, 1631-5 | 126 |
| 1209 | Copy number aberrations in mouse breast tumors reveal loci and genes important in tumorigenic receptor tyrosine kinase signaling. 2005 , 65, 9695-704 | 46 |
| 1208 | Molecular decomposition of complex clinical phenotypes using biologically structured analysis of microarray data. 2005 , 21, 1971-8 | 34 |
| 1207 | Distinct hypermethylation profile of primary breast cancer is associated with sentinel lymph node metastasis. 2005 , 11, 2156-62 | 132 |
| 1206 | Circulating and disseminated tumor cells. 2005 , 23, 1623-6 | 107 |
| 1205 | Estimating misclassification error with small samples via bootstrap cross-validation. 2005 , 21, 1979-86 | 102 |
| 1204 | The intersection of inheritance and metastasis: the role and implications of germline polymorphism in tumor dissemination. 2005 , 4, 1719-21 | 10 |
| 1203 | Progesterone-independent effects of human progesterone receptors (PRs) in estrogen receptor-positive breast cancer: PR isoform-specific gene regulation and tumor biology. 2005 , 19, 574-87 | 107 |

| 1202 | Gene expression profiling in human cardiovascular disease. 2005 , 43, 696-701 | 11 |
|--------------|--|-----|
| 1201 | Identification of GATA3 as a breast cancer prognostic marker by global gene expression meta-analysis. 2005 , 65, 11259-64 | 221 |
| 12 00 | Tumor markers in breast cancer- European Group on Tumor Markers recommendations. 2005 , 26, 281-93 | 246 |
| 1199 | Microarray Technology and Its Applications. 2005, | 30 |
| 1198 | Biochemical and molecular markers in renal cell carcinoma: an update and future prospects. 2005 , 10, 258-94 | 35 |
| 1197 | Contralateral breast cancer: where does it all begin?. 2005 , 23, 4585-7 | 6 |
| 1196 | Testing association of a pathway with survival using gene expression data. 2005 , 21, 1950-7 | 122 |
| 1195 | Identification of T cell-restricted genes, and signatures for different T cell responses, using a comprehensive collection of microarray datasets. 2005 , 175, 7837-47 | 95 |
| 1194 | Gene expression profiling of NMU-induced rat mammary tumors: cross species comparison with human breast cancer. 2005 , 26, 1343-53 | 91 |
| 1193 | The sensitivity and specificity of markers for event times. 2006 , 7, 182-97 | 51 |
| 1192 | [Treatment results following breast-conserving therapy in primary breast cancer]. 2005, 127, 31-6 | |
| 1191 | Microarrays: applications and pitfalls. 2005 , 62, 1669-72 | 23 |
| 1190 | Cell cycle progression stimulated by tamoxifen-bound estrogen receptor-alpha and promoter-specific effects in breast cancer cells deficient in N-CoR and SMRT. 2005 , 19, 1543-54 | 93 |
| 1189 | A variational Bayesian mixture modelling framework for cluster analysis of gene-expression data. 2005 , 21, 3025-33 | 58 |
| 1188 | A protocol for building and evaluating predictors of disease state based on microarray data. 2005 , 21, 3755-62 | 111 |
| 1187 | Screening of tissue microarrays for ubiquitin proteasome system components in tumors. 2005 , 399, 334-55 | 5 |
| 1186 | Breast cancer gene expression profiling: clinical trial and practice implications. 2005 , 6, 49-58 | 10 |
| 1185 | Prognostic factors for breast cancer and their use in the clinical setting. 2005 , 5, 269-81 | 7 |

| 1184 | Case records of the Massachusetts General Hospital. Case 24-2005. A 58-year-old woman with early-stage estrogen-receptor-positive breast cancer. 2005 , 353, 617-22 | 2 |
|------|--|-----|
| 1183 | Inhibition of angiogenesis in cancer patients. 2005 , 10, 403-12 | 16 |
| 1182 | Prognostic relevance of basal cytokeratin expression in operable breast cancer. 2005 , 69, 478-85 | 83 |
| 1181 | Genetic profiling of human hepatocellular carcinoma. 2005 , 25, 125-32 | 46 |
| 1180 | Gene expression profiling for pharmaceutical safety assessment. 2005 , 1, 247-60 | 9 |
| 1179 | Gene expression profiling to characterize anticancer drug sensitivity. 2005 , 111, 197-231 | |
| 1178 | Optimized Kernel Machines for Cancer Classification Using Gene Expression Data. 2005, | О |
| 1177 | GAVis: a Tool for Visualization and Control of Genetic Algorithms for -omic Data Analysis. 2005 , 2005, 2855-8 | |
| 1176 | Modern approaches to age-old questions about thyroid tumors. 2005 , 15, 575-82 | 7 |
| 1175 | Advancing the molecular diagnosis of thyroid nodules: defining benign lesions by molecular profiling. 2005 , 15, 562-8 | 29 |
| 1174 | Application of DNA microarray technology in determining breast cancer prognosis and therapeutic response. 2005 , 5, 1069-83 | 44 |
| 1173 | Utility of high dimensional genomic composite biomarkers in therapeutic and/or diagnostic development. | 1 |
| 1172 | Death-from-cancer signatures and stem cell contribution to metastatic cancer. 2005 , 4, 1171-5 | 98 |
| 1171 | TGF-beta and the Smad signaling pathway support transcriptomic reprogramming during epithelial-mesenchymal cell transition. 2005 , 16, 1987-2002 | 460 |
| 1170 | Discovery of highly differentiative gene groups from microarray gene expression data using the gene club approach. 2005 , 3, 1263-80 | 16 |
| 1169 | Epidemiology informing clinical practice: from bills of mortality to population laboratories. 2005 , 2, 625-34 | 16 |
| 1168 | Differential gene expression profiles in stage I primary biliary cirrhosis. 2005 , 100, 2019-30 | 24 |
| 1167 | Apoptotic Pathways as Targets for Novel Therapies in Cancer and Other Diseases. 2005, | 5 |

| 1166 | A role for Erbin in the regulation of Nod2-dependent NF-kappaB signaling. 2005 , 280, 40301-9 | 147 |
|------|--|-----|
| 1165 | Prediction of docetaxel response in human breast cancer by gene expression profiling. 2005 , 23, 422-31 | 237 |
| 1164 | Targeted drug delivery in cancer therapy. 2005 , 4, 363-74 | 214 |
| 1163 | SPBP is a phosphoserine-specific repressor of estrogen receptor alpha. 2005 , 25, 3421-30 | 34 |
| 1162 | Limits of predictive models using microarray data for breast cancer clinical treatment outcome. 2005 , 97, 927-30 | 104 |
| 1161 | Validation of microarray data by quantitative reverse-transcriptase polymerase chain reaction. 2005 , 23, 9439-40; author reply 9440 | 5 |
| 1160 | Integrative genomics revealed RAI3 is a cell growth-promoting gene and a novel P53 transcriptional target. 2005 , 280, 12935-43 | 35 |
| 1159 | Placental cadherin and the basal epithelial phenotype of BRCA1-related breast cancer. 2005 , 11, 4003-11 | 143 |
| 1158 | GEPAS, an experiment-oriented pipeline for the analysis of microarray gene expression data. 2005 , 33, W616-20 | 79 |
| 1157 | Transcriptional programs following genetic alterations in p53, INK4A, and H-Ras genes along defined stages of malignant transformation. 2005 , 65, 4530-43 | 49 |
| 1156 | Mice expressing a mammary gland-specific R270H mutation in the p53 tumor suppressor gene mimic human breast cancer development. 2005 , 65, 8166-73 | 52 |
| 1155 | Prediction of radiation sensitivity using a gene expression classifier. 2005 , 65, 7169-76 | 155 |
| 1154 | Robustness, scalability, and integration of a wound-response gene expression signature in predicting breast cancer survival. 2005 , 102, 3738-43 | 823 |
| 1153 | Gene expression profiling of chemically induced rat mammary gland cancer. 2005 , 26, 503-9 | 21 |
| 1152 | Robust Ensemble Learning for Cancer Diagnosis Based on Microarray Data Classification. 2005 , 564-574 | 1 |
| 1151 | Gene expression profiling in acute myeloid leukemia. 2005 , 23, 6296-305 | 84 |
| 1150 | Suppression of RAD21 gene expression decreases cell growth and enhances cytotoxicity of etoposide and bleomycin in human breast cancer cells. 2005 , 4, 361-8 | 76 |
| 1149 | Optimal number of features as a function of sample size for various classification rules. 2005 , 21, 1509-15 | 220 |

| 1148 | A weighted nearest mean classifier for sparse subspaces. | 2 |
|--------------------------------------|--|--|
| 1147 | An Introduction to MAMA (Meta-Analysis of MicroArray data) System. 2005 , 2005, 7730-3 | 4 |
| 1146 | Genomic profiling of cancer: what next?. 2005 , 23, 7253-6 | 10 |
| 1145 | Molecular classification of tamoxifen-resistant breast carcinomas by gene expression profiling. 2005 , 23, 732-40 | 283 |
| 1144 | Somatic induction of Pten loss in a preclinical astrocytoma model reveals major roles in disease progression and avenues for target discovery and validation. 2005 , 65, 5172-80 | 73 |
| 1143 | A molecular signature in superficial bladder carcinoma predicts clinical outcome. 2005 , 11, 4029-36 | 123 |
| 1142 | Down-regulation and growth inhibitory role of C/EBPalpha in breast cancer. 2005 , 11, 3184-90 | 74 |
| 1141 | Letrozole-, anastrozole-, and tamoxifen-responsive genes in MCF-7aro cells: a microarray approach. 2005 , 3, 203-18 | 68 |
| 1140 | An integrated feature selection and classification method to select minimum number of variables on the case study of gene expression data. 2005 , 3, 1107-36 | 9 |
| | The state of the s | |
| 1139 | Tissue inhibitor of metalloproteinases-1 in breast cancer. 2005 , 12, 215-27 | 95 |
| 1139 | Identification of RAI3 as a therapeutic target for breast cancer. 2005 , 12, 215-27 | 9537 |
| 1138 | | |
| 1138 | Identification of RAI3 as a therapeutic target for breast cancer. 2005 , 12, 65-73 | 37 |
| 1138 | Identification of RAI3 as a therapeutic target for breast cancer. 2005 , 12, 65-73 Bladder cancer outcome and subtype classification by gene expression. 2005 , 11, 4044-55 Allelic imbalance in primary breast carcinomas and metastatic tumors of the axillary lymph nodes. | 37 266 |
| 1138 1137 1136 | Identification of RAI3 as a therapeutic target for breast cancer. 2005 , 12, 65-73 Bladder cancer outcome and subtype classification by gene expression. 2005 , 11, 4044-55 Allelic imbalance in primary breast carcinomas and metastatic tumors of the axillary lymph nodes. 2005 , 3, 71-7 Mitotic index and benefit of adjuvant anthracycline-based chemotherapy in patients with early | 37 266 22 |
| 1138 1137 1136 1135 | Identification of RAI3 as a therapeutic target for breast cancer. 2005, 12, 65-73 Bladder cancer outcome and subtype classification by gene expression. 2005, 11, 4044-55 Allelic imbalance in primary breast carcinomas and metastatic tumors of the axillary lymph nodes. 2005, 3, 71-7 Mitotic index and benefit of adjuvant anthracycline-based chemotherapy in patients with early breast cancer. 2005, 23, 2996-3000 DNA Microarray-Based Gene Expression Profiling in Cancer: Aiding Cancer Diagnosis, Assessing | 37 266 22 27 |
| 1138 1137 1136 1135 1134 | Identification of RAI3 as a therapeutic target for breast cancer. 2005, 12, 65-73 Bladder cancer outcome and subtype classification by gene expression. 2005, 11, 4044-55 Allelic imbalance in primary breast carcinomas and metastatic tumors of the axillary lymph nodes. 2005, 3, 71-7 Mitotic index and benefit of adjuvant anthracycline-based chemotherapy in patients with early breast cancer. 2005, 23, 2996-3000 DNA Microarray-Based Gene Expression Profiling in Cancer: Aiding Cancer Diagnosis, Assessing Prognosis and Predicting Response to Therapy. 2005, 3, 289-304 | 3726622278 |

| 1130 | Cyclin E expression in breast cancer: predicting germline BRCA1 mutations, prognosis and response to treatment. 2005 , 16, 735-42 | 43 |
|--------------------------------------|--|------------------|
| 1129 | Effects of threshold choice on biological conclusions reached during analysis of gene expression by DNA microarrays. 2005 , 102, 8961-5 | 83 |
| 1128 | Superior feature-set ranking for small samples using bolstered error estimation. 2005, 21, 1046-54 | 37 |
| 1127 | M@CBETH: a microarray classification benchmarking tool. 2005 , 21, 3185-6 | 13 |
| 1126 | Evolving understanding of growth regulation in human breast cancer: interactions of the steroid and peptide growth regulatory pathways. 2005 , 97, 1238-9 | 12 |
| 1125 | Effects of RNA degradation on gene expression analysis of human postmortem tissues. 2005 , 19, 1356-8 | 90 |
| 1124 | Gene-expression profiling and the future of adjuvant therapy. 2005 , 10 Suppl 2, 30-4 | 53 |
| 1123 | A unique gene expression signature discriminates familial Alzheimer's disease mutation carriers from their wild-type siblings. 2005 , 102, 14854-9 | 39 |
| 1122 | Visualizing chromosomes as transcriptome correlation maps: evidence of chromosomal domains containing co-expressed genesa study of 130 invasive ductal breast carcinomas. 2005 , 65, 1376-83 | 58 |
| | | |
| 1121 | Heat shock proteins in cancer: diagnostic, prognostic, predictive, and treatment implications. 2005 , 10, 86-103 | 1001 |
| 1121 1120 | 10, 86-103 | 1001 |
| 1120 | 10, 86-103 | |
| 1120 | 10, 86-103 SVM ensembles for selecting the relevant feature subsets. | 1 |
| 1120 1119 | 10, 86-103 SVM ensembles for selecting the relevant feature subsets. Tumor profiling turmoil. 2005, 4, 659-60 In silico identification of breast cancer genes by combined multiple high throughput analyses. 2005, | 1 |
| 1120 1119 1118 | SVM ensembles for selecting the relevant feature subsets. Tumor profiling turmoil. 2005, 4, 659-60 In silico identification of breast cancer genes by combined multiple high throughput analyses. 2005, 15, 205 Gene expression profiles in prostate cancer: Association with patient subgroups and tumour differentiation. 2005, 26, 329 Aberrant expressions of annexin A10 short isoform, osteopontin and Fetoprotein at chromosome | 1 6 0 |
| 1120 1119 1118 1117 | SVM ensembles for selecting the relevant feature subsets. Tumor profiling turmoil. 2005, 4, 659-60 In silico identification of breast cancer genes by combined multiple high throughput analyses. 2005, 15, 205 Gene expression profiles in prostate cancer: Association with patient subgroups and tumour differentiation. 2005, 26, 329 Aberrant expressions of annexin A10 short isoform, osteopontin and Fetoprotein at chromosome 4q cooperatively contribute to progression and poor prognosis of hepatocellular carcinoma. 2005, | 1 6 0 |
| 1120 1119 1118 1117 1116 | SVM ensembles for selecting the relevant feature subsets. Tumor profiling turmoil. 2005, 4, 659-60 In silico identification of breast cancer genes by combined multiple high throughput analyses. 2005, 15, 205 Gene expression profiles in prostate cancer: Association with patient subgroups and tumour differentiation. 2005, 26, 329 Aberrant expressions of annexin A10 short isoform, osteopontin and Eetoprotein at chromosome 4q cooperatively contribute to progression and poor prognosis of hepatocellular carcinoma. 2005, 26, 1053 Prediction of chemosensitivity of colorectal cancer to 5-fluorouracil by gene expression profiling | 1 6 0 4 |

Time-dependent RNA degradation affecting cDNA array quality in spontaneous canine tumours sampled using standard surgical procedures. **2005**, 16, 979

| 1111 | Embracing complexity, inching closer to reality. 2005 , 2005, pe40 | 35 |
|------|--|------|
| 1110 | Gene expression patterns and profile changes pre- and post-erlotinib treatment in patients with metastatic breast cancer. 2005 , 11, 6226-32 | 32 |
| 1109 | Prediction of cancer outcome with microarrays: a multiple random validation strategy. 2005 , 365, 488-92 | 815 |
| 1108 | Gene-expression profiles to predict distant metastasis of lymph-node-negative primary breast cancer. 2005 , 365, 671-9 | 2172 |
| 1107 | Gene-expression profiling in breast cancer. 2005 , 365, 634-5 | 31 |
| 1106 | Prediction of cancer outcome with microarrays. 2005 , 365, 1683; author reply 1684-5 | 12 |
| 1105 | Breast cancer. 2005 , 365, 1727-41 | 346 |
| 1104 | Macrodissection versus microdissection of rectal carcinoma: minor influence of stroma cells to tumor cell gene expression profiles. 2005 , 6, 142 | 35 |
| 1103 | Current and future pathological examination in breast cancer. 2005 , 3, 121-130 | |
| 1102 | Gene Array Technologies in Biological Investigations. 2005 , 93, 737-749 | 2 |
| 1101 | Bioinformatics in otolaryngology. 2005 , 38, 321-32, vii | 1 |
| 1100 | Voltage-gated sodium channel expression and potentiation of human breast cancer metastasis. 2005 , 11, 5381-9 | 340 |
| 1099 | Molecular classification and molecular forecasting of breast cancer: ready for clinical application?. 2005 , 23, 7350-60 | 696 |
| 1098 | The Importance of Validation in Genomic Studies of Breast Cancer. 2005 , 16, 16-19 | |
| 1097 | Beyond lymph node staging: molecular predictors of outcome in breast cancer. 2005 , 14, 69-84, vi | 1 |
| 1096 | Transcript AA454543 is a novel prognostic marker for hepatocellular carcinoma after curative partial hepatectomy. 2005 , 7, 91-8 | 9 |
| 1095 | Advances in Bioinformatics and Computational Biology. 2005, | 3 |

| 1094 | Medical Biomethods Handbook. 2005 , | 2 |
|------|--|-----|
| 1093 | Molecular targets of growth, differentiation, tissue integrity, and ectopic cell death in cancer cells. 2005 , 20, 579-88 | 9 |
| 1092 | Survival trees for analyzing clinical outcome in lung adenocarcinomas based on gene expression profiles: identification of neogenin and diacylglycerol kinase alpha expression as critical factors. 2005 , 12, 534-44 | 24 |
| 1091 | Adoption of array technologies into the clinical laboratory. 2005 , 5, 409-20 | 18 |
| 1090 | Molecular portraits and 70-gene prognosis signature are preserved throughout the metastatic process of breast cancer. 2005 , 65, 9155-8 | 264 |
| 1089 | A Genetic Algorithm Approach for Discovering Diagnostic Patterns in Molecular Measurement Data. 2005 , | 7 |
| 1088 | Gene Selection via a Spectral Approach. | |
| 1087 | Pathology of the Future: Molecular Profiling for Targeted Therapy. 2005 , 23, 36-46 | 58 |
| 1086 | Microarrays and Crohn's disease: collecting reliable information. 2005 , 40, 369-77 | 8 |
| 1085 | Identifying simple discriminatory gene vectors with an information theory approach. 2005, 13-24 | 2 |
| 1084 | Mining the tumor phosphoproteome for cancer markers. 2005 , 11, 3163-9 | 74 |
| 1083 | Multivariate gene selection: does it help?. | |
| 1082 | Platelet genomics and proteomics in human health and disease. 2005 , 115, 3370-7 | 120 |
| 1081 | Technology insight: Application of molecular techniques to formalin-fixed paraffin-embedded tissues from breast cancer. 2005 , 2, 246-54 | 77 |
| 1080 | Discovery of gene expression patterns across multiple cancer types. | |
| 1079 | Characterization of pepsinogen C as a potential biomarker for gastric cancer using a histo-proteomic approach. 2005 , 4, 1799-804 | 56 |
| 1078 | Molecular staging for survival prediction of colorectal cancer patients. 2005 , 23, 3526-35 | 285 |
| 1077 | Genomic medicine: genetic variation and its impact on the future of health care. 2005 , 360, 1543-50 | 50 |

| 1076 Efficiently searching the important input variables using Bayesian discriminant. 2005 , 52, 785-793 | 11 |
|---|---------|
| 1075 Global protein shotgun expression profiling of proliferating mcf-7 breast cancer cells. 2005 , 4, 674-89 | 31 |
| Missing value estimation for DNA microarray gene expression data: local least squares imputation. 2005 , 21, 187-98 | 314 |
| 1073 Cancer epigenetics. 2005 , 14 Spec No 1, R65-76 | 384 |
| 1072 Advances in toxicogenomics. 2005 , 18, 403-14 | 50 |
| Scaling of True and Apparent ROC AUC with Number of Observations and Number of Variables. 2005 , 34, 771-781 | 5 |
| 1070 Outcome signature genes in breast cancer: is there a unique set?. 2005 , 21, 171-8 | 622 |
| 1069 The evolving portrait of cancer metastasis. 2005 , 70, 291-7 | 70 |
| 1068 Advances in Targeted Cancer Therapy. 2005, | |
| | |
| 1067 A history of microarrays in biomedicine. 2005 , 5, 315-28 | 26 |
| A history of microarrays in biomedicine. 2005 , 5, 315-28 Improved representation of gene markers on microarray by PCR-Select subtracted cDNA targets. 2005 , 137, 110-8 | 26 4 |
| Improved representation of gene markers on microarray by PCR-Select subtracted cDNA targets. | |
| Improved representation of gene markers on microarray by PCR-Select subtracted cDNA targets. 2005 , 137, 110-8 | |
| Improved representation of gene markers on microarray by PCR-Select subtracted cDNA targets. 2005, 137, 110-8 Investigations into the molecular background of endometrial cancer. 2005, 1279, 149-153 Logical networks inferred from highly specific discovery of transcriptionally regulated genes | 4 |
| Improved representation of gene markers on microarray by PCR-Select subtracted cDNA targets. 2005, 137, 110-8 Investigations into the molecular background of endometrial cancer. 2005, 1279, 149-153 Logical networks inferred from highly specific discovery of transcriptionally regulated genes predict protein states in cultured gliomas. 2005, 336, 1278-84 | 7 |
| Improved representation of gene markers on microarray by PCR-Select subtracted cDNA targets. 2005, 137, 110-8 Investigations into the molecular background of endometrial cancer. 2005, 1279, 149-153 Logical networks inferred from highly specific discovery of transcriptionally regulated genes predict protein states in cultured gliomas. 2005, 336, 1278-84 Mechanisms of cancer cell invasion. 2005, 15, 87-96 | 7 388 |
| Improved representation of gene markers on microarray by PCR-Select subtracted cDNA targets. 2005, 137, 110-8 Investigations into the molecular background of endometrial cancer. 2005, 1279, 149-153 Logical networks inferred from highly specific discovery of transcriptionally regulated genes predict protein states in cultured gliomas. 2005, 336, 1278-84 Mechanisms of cancer cell invasion. 2005, 15, 87-96 Central high-grade osteosarcoma of bone: Diagnostic and genetic considerations. 2005, 11, 390-399 PAR1 is a matrix metalloprotease-1 receptor that promotes invasion and tumorigenesis of breast | 7 388 |

| 1058 Endostatin: the logic of antiangiogenic therapy. 2005 , 8 , 59-74 | 91 |
|---|--------|
| 1057 Metastases and their microenvironments: linking pathogenesis and therapy. 2005 , 8, 247-57 | 24 |
| 1056 Tailoring Ras-pathwayinhibitor combinations for cancer therapy. 2005 , 8, 369-80 | 50 |
| 1055 Molecular markers of prostate cancer outcome. 2005 , 41, 858-87 | 153 |
| Prognostic relevance of uPAR-del4/5 and TIMP-3 mRNA expression levels in breast cancer. 2005 , 41, 2760-8 | 37 |
| $_{1053}$ Growth factors and their relationship to neoplastic and paraneoplastic disease. 2005 , 16, 83-94 | 3 |
| Gelatinases (MMP-2 and -9) and their natural inhibitors as prognostic indicators in solid cancers. 2005 , 87, 287-97 | 225 |
| Bcl-x(L)-mediated changes in metabolic pathways of breast cancer cells: from survival in the bloo stream to organ-specific metastasis. 2005 , 167, 1125-37 | od 27 |
| Gene expression analysis of immune-mediated arrest of tumorigenesis in a transgenic mouse model of HER-2/neu-positive basal-like mammary carcinoma. 2005 , 166, 1205-16 | 41 |
| Interpreting expression profiles of cancers by genome-wide survey of breadth of expression in normal tissues. 2005 , 86, 127-41 | 218 |
| 1048 [Molecular alterations in breast cancer: clinical implications and new analytical tools]. 2005 , 26, 4 | 70-8 3 |
| | |
| 1047 The Oncogenetic Basis of Breast Cancer. 2005 , 15-26 | |
| The Oncogenetic Basis of Breast Cancer. 2005 , 15-26 1046 Molecular, Cellular, and Developmental Biology of Breast Cancer. 2005 , 27-41 | |
| | |
| 1046 Molecular, Cellular, and Developmental Biology of Breast Cancer. 2005 , 27-41 | 11 |
| Molecular, Cellular, and Developmental Biology of Breast Cancer. 2005 , 27-41 Molecular Pathology Assays for Breast Cancer. 2005 , 145-168 | 11 |
| Molecular, Cellular, and Developmental Biology of Breast Cancer. 2005, 27-41 Molecular Pathology Assays for Breast Cancer. 2005, 145-168 Discovering causes and cures for cancer from gene expression analysis. 2005, 4, 548-63 Predictors of primary breast cancers responsiveness to preoperative epirubicin/cyclophosphamide-based chemotherapy: translation of microarray data into clinically | |

| 1040 Variance in the expression of 5-Fluorouracil pathway genes in colorectal cancer. 2005 , 11, 2612-9 | 57 |
|--|-----------------|
| 1039 Roadmap for developing and validating therapeutically relevant genomic classifiers. 2005 , 23, 7332-41 | 324 |
| 1038 Applications of DNA microarrays in biology. 2005 , 74, 53-82 | 309 |
| 1037 cDNA Microarrays. 2005 , 255-271 | |
| 1036 RFID Technology and Electronic Tags to Identify Cryopreserved Materials. 2005 , 3, 112-115 | 6 |
| Discovery and identification of alpha-defensins as low abundant, tumor-derived serum markers in colorectal cancer. 2005 , 129, 66-73 | 110 |
| Microarray profiles of human basal cell carcinoma: insights into tumor growth and behavior. 2005 , 39, 39-51 | 31 |
| 1033 Genome-wide views of cancer metastasis. 2005 , 2, 165-169 | 4 |
| 1032 Models of epithelialthesenchymal transition. 2005 , 2, 57-63 | 24 |
| | |
| 1031 Utility of microarrays in the management of breast cancer patients. 2005 , 2, 307-311 | |
| Utility of microarrays in the management of breast cancer patients. 2005, 2, 307-311 Molecular approaches to the identification of biomarkers of exposure and effectreport of an expert meeting organized by COST Action B15. November 28, 2003. 2005, 156, 227-40 | 23 |
| Molecular approaches to the identification of biomarkers of exposure and effectreport of an | 23 |
| Molecular approaches to the identification of biomarkers of exposure and effectreport of an expert meeting organized by COST Action B15. November 28, 2003. 2005 , 156, 227-40 A novel method for generation of signature networks as biomarkers from complex high throughput | |
| Molecular approaches to the identification of biomarkers of exposure and effectreport of an expert meeting organized by COST Action B15. November 28, 2003. 2005, 156, 227-40 A novel method for generation of signature networks as biomarkers from complex high throughput data. 2005, 158, 20-9 Methylation of estrogen receptor beta promoter correlates with loss of ER-beta expression in | 120 |
| Molecular approaches to the identification of biomarkers of exposure and effectreport of an expert meeting organized by COST Action B15. November 28, 2003. 2005, 156, 227-40 A novel method for generation of signature networks as biomarkers from complex high throughput data. 2005, 158, 20-9 Methylation of estrogen receptor beta promoter correlates with loss of ER-beta expression in mammary carcinoma and is an early indication marker in premalignant lesions. 2005, 12, 903-16 Complex diseases in gastroenterology and hepatology: GERD, Barrett's, and esophageal | 120 65 |
| Molecular approaches to the identification of biomarkers of exposure and effectreport of an expert meeting organized by COST Action B15. November 28, 2003. 2005, 156, 227-40 A novel method for generation of signature networks as biomarkers from complex high throughput data. 2005, 158, 20-9 Methylation of estrogen receptor beta promoter correlates with loss of ER-beta expression in mammary carcinoma and is an early indication marker in premalignant lesions. 2005, 12, 903-16 Complex diseases in gastroenterology and hepatology: GERD, Barrett's, and esophageal adenocarcinoma. 2005, 3, 529-37 | 120 65 |
| Molecular approaches to the identification of biomarkers of exposure and effectreport of an expert meeting organized by COST Action B15. November 28, 2003. 2005, 156, 227-40 A novel method for generation of signature networks as biomarkers from complex high throughput data. 2005, 158, 20-9 Methylation of estrogen receptor beta promoter correlates with loss of ER-beta expression in mammary carcinoma and is an early indication marker in premalignant lesions. 2005, 12, 903-16 Complex diseases in gastroenterology and hepatology: GERD, Barrett's, and esophageal adenocarcinoma. 2005, 3, 529-37 The promise of gene signatures in cancer diagnosis and prognosis. 2005, | 120 65 21 |

| 1022 | Breast cancer biomarkers. 2005 , 40, 99-125 | 17 |
|------|--|-----|
| 1021 | Molecular Biology of Human Cancers. 2005, | 4 |
| 1020 | Molecular mechanisms in gliomagenesis. 2005 , 94, 1-27 | 55 |
| 1019 | Laser Capture Microdissection. 2005 , | 11 |
| 1018 | Mutation analysis of FANCD2, BRIP1/BACH1, LMO4 and SFN in familial breast cancer. 2005 , 7, R1005-16 | 38 |
| 1017 | High resolution genomic analysis of sporadic breast cancer using array-based comparative genomic hybridization. 2005 , 7, R1186-98 | 164 |
| 1016 | Gene expression profiling spares early breast cancer patients from adjuvant therapy: derived and validated in two population-based cohorts. 2005 , 7, R953-64 | 597 |
| 1015 | Early detection of breast cancer based on gene-expression patterns in peripheral blood cells. 2005 , 7, R634-44 | 93 |
| 1014 | The promise of microarrays in the management and treatment of breast cancer. 2005, 7, 100-4 | 20 |
| 1013 | Microarrays and breast cancer clinical studies: forgetting what we have not yet learnt. 2005 , 7, 96-9 | 22 |
| 1012 | Show me the genes - I will tell you who/how to treat!. 2005 , 7, 77-9 | 5 |
| 1011 | Outcome signature genes in breast cancer: is there a unique set?. 2005 , 7, 1 | 5 |
| 1010 | Role of translational studies in optimizing palliative chemotherapy. 2005 , 7, 1 | 1 |
| 1009 | Classical versus new prognostic factors for adjuvant treatment selection based on line software to estimate risk and benefit. 2005 , 7, 1 | 78 |
| 1008 | The role of Xeloda in metastasic breast cancer. 2005 , 7, 1 | 78 |
| 1007 | SOLTI (Solid Tumor Intensification) Group experience with high-dose chemotherapy treatment for early breast carcinoma. 2005 , 7, 1 | 78 |
| 1006 | New agents for bone metastasis. 2005 , 7, 1 | 78 |
| 1005 | Predictors of positive axillary lymph nodes in breast cancer patients with metastatic sentinel lymph node. 2005 , 7, 1 | 78 |

| 1004 | Clinical profile and management of bilateral breast cancer. 2005 , 7, 1 | 2 |
|------|---|----|
| 1003 | Nanoparticulate paclitaxel loaded into sterically stabilized mixed phospholipid micelles to improve chemotherapy of breast cancer. 2005 , 7, 1 | 1 |
| 1002 | Breast cancer-screening programme amongst unpriviledged women in Charleroi (Hainaut), Belgium. 2005 , 7, 1 | 78 |
| 1001 | The role of gene expression profiling by microarray analysis for prognostic classification of breast cancer. 2005 , 7, 1 | 2 |
| 1000 | A phase II randomized trial of doxorubicin (DXR) and gemcitabine (GMZ) administered in patients with metastatic breast cancer (MBC). 2005 , 7, 1 | 78 |
| 999 | Methods for gene expression profiling in clinical trials for breast cancer. 2005 , 7, 1 | 78 |
| 998 | Expression of c-met gene in invasive ductal carcinomas. 2005 , 7, 1 | 78 |
| 997 | Simultaneous breast reconstruction. 2005 , 7, 1 | 78 |
| 996 | Chemoprevention: beyond tamoxifen. 2005 , 7, 1 | 78 |
| 995 | Tamoxifen resistance and adjuvant hormone therapy. 2005 , 7, 1 | 78 |
| 994 | Adjuvant chemotherapy for operable breast cancer: old vs new schema. 2005, 7, 1 | 78 |
| 993 | Letrozole efficacy is related to human aromatase CYP19 single nucleotide polymorphisms (SNPs) in metastatic breast cancer. 2005 , 7, 1 | 78 |
| 992 | Cyclo-oxygenase-2 expression is associated with poor clinical outcome after doxorubicin-based chemotherapy in node-positive breast cancer: integration of tissue microarray. 2005 , 7, 1 | 78 |
| 991 | Fibroadenoma of breast in Iranian women between 1994 and 2004. 2005 , 7, 1 | 78 |
| 990 | Adjuvant radiotherapy after surgery in breast cancer: evaluation of acute toxicity. 2005, 7, 1 | 78 |
| 989 | 6-(1-oxobutyl)-5,8-dimetoxy-1,4-naphthoquinone inhibits the growth of MCF-7 cells via inhibition of angiogenesis and hypoxia inducible factor alpha. 2005 , 7, 1 | 1 |
| 988 | A performance study of different soft-computing procedures for automatic detection of breast cancer malignancy. 2005 , 7, 1 | 78 |
| 987 | Gene expression profiles and molecular classification to predict distant metastasis and tamoxifen-resistant breast cancer. 2005 , 7, 1 | 2 |
| | | |

| 986 | The role of magnetic resonance imaging as an imaging tool to assess disease status and residual disease in locally advanced breast cancer. 2005 , 7, 1 | 78 |
|-----|---|----|
| 985 | The axillary study with ultrasound and cytological puncture with fine needle in invasive breast cancer 2005 , 7, 1 | 78 |
| 984 | Gene expression profile-based predictors of response to chemotherapy. 2005 , 7, 1 | 78 |
| 983 | Minimal residual disease (MRD) in the bone marrow in ER-positive primary breast cancer patients. 2005 , 7, 1 | 78 |
| 982 | [ASCRIT] Antisense chemoradioimmunotherapy consisting of anti-POEM (Arg-Gly-Asp) scFv linked onto high-energy radioisotopes, vinorelbine-tartrate and 21-nucleotide double-stranded siRNA targeted to DNMT1 induce apoptosis in metastatic breast cancer (MBC) characterized by | 78 |
| 981 | hypermethylated p53, p16, RASSF1A, RAR-b2, BRCA2, H1C1, ESRI1, CDH1, Trbeta1, GSTP1, CCND2 and overexpression of bcl-2, cdc25c, Paf-1 and Ril integrin, 2005, 7, 1 Simultaneous reconstructive surgery for radical mastectomy. 2005, 7, 1 | 78 |
| 980 | Preoperative hormonal therapy: results and implications. 2005 , 7, 1 | 1 |
| 979 | Radiotherapy in early stage invasive breast cancer: current tendencies. 2005 , 7, 1 | 1 |
| 978 | Neoadjuvant treatment: the MD Anderson experience. 2005 , 7, 1 | 78 |
| 977 | Prognostic studies in patients with high-risk primary breast cancer (HRPBC) receiving high-dose chemotherapy (HDC). 2005 , 7, 1 | 78 |
| 976 | The roles of PET and CT/PET as preoperative studies. 2005 , 7, 1 | 78 |
| 975 | Present situation and future of genetic profiling for prognosis and treatment. 2005 , 7, 1 | 78 |
| 974 | Circulating tumor cells and novel biomarkers for prognostic and biological of breast cancer. 2005 , 7, 1 | 1 |
| 973 | Sentinel node biopsy versus conventional axillary dissection in clinically node-negative breast cancer patients. 2005 , 7, 1 | 78 |
| 972 | Primary chemotherapy for operable breast cancer: the NSABP experience. 2005 , 7, 1 | 4 |
| 971 | Efficacy of high-dose alkylating chemotherapy in the adjuvant treatment of HER2/neu-negative primary breast cancer: update of the Dutch randomized trial. 2005 , 7, 1 | 78 |
| 970 | Targeting the right chemotherapy for the right patient. 2005 , 7, 1 | 1 |
| 969 | Oral vinorelbine in metastatic breast cancer. 2005 , 7, 1 | 2 |

| 968 | Partial breast irradiation: why and how. 2005 , 7, 1 | 6 |
|-----|---|-----|
| 967 | Erratum to: Multiclass classification of microarray data with repeated measurements: application to cancer. 2005 , 6, 405 | 2 |
| 966 | Predicting the sites of metastases. 2005 , 6, 241 | 8 |
| 965 | L2L: a simple tool for discovering the hidden significance in microarray expression data. 2005 , 6, R81 | 101 |
| 964 | A DNA microarray survey of gene expression in normal human tissues. 2005 , 6, R22 | 172 |
| 963 | Genomic analysis of early murine mammary gland development using novel probe-level algorithms. 2005 , 6, R20 | 17 |
| 962 | Measuring proliferation in breast cancer: practicalities and applications. 2006 , 8, 216 | 139 |
| 961 | GATA3 protein as a MUC1 transcriptional regulator in breast cancer cells. 2006 , 8, R64 | 24 |
| 960 | Molecular subtypes of breast cancer in relation to paclitaxel response and outcomes in women with metastatic disease: results from CALGB 9342. 2006 , 8, R66 | 108 |
| 959 | CD44+/CD24- breast cancer cells exhibit enhanced invasive properties: an early step necessary for metastasis. 2006 , 8, R59 | 716 |
| 958 | Gene expression signatures of morphologically normal breast tissue identify basal-like tumors. 2006 , 8, R58 | 107 |
| 957 | Predicting a local recurrence after breast-conserving therapy by gene expression profiling. 2006, 8, R62 | 163 |
| 956 | Classification of ductal carcinoma in situ by gene expression profiling. 2006, 8, R61 | 128 |
| 955 | When will tumor gene expression profiling be incorporated into clinical breast cancer decision making?. 2006 , 8, 302 | 1 |
| 954 | Breast cancer prognosis by combinatorial analysis of gene expression data. 2006 , 8, R41 | 49 |
| 953 | Epigenetic silencing and deletion of the BRCA1 gene in sporadic breast cancer. 2006 , 8, R38 | 179 |
| 952 | Comparison of gene expression profiles in core biopsies and corresponding surgical breast cancer samples. 2006 , 8, R51 | 14 |
| 951 | Array-CGH and breast cancer. 2006 , 8, 210 | 62 |

| 950 | The effect of the stromal component of breast tumours on prediction of clinical outcome using gene expression microarray analysis. 2006 , 8, R32 | 56 |
|-----|--|-----|
| 949 | A population-based study of tumor gene expression and risk of breast cancer death among lymph node-negative patients. 2006 , 8, R25 | 387 |
| 948 | Classification and risk stratification of invasive breast carcinomas using a real-time quantitative RT-PCR assay. 2006 , 8, R23 | 150 |
| 947 | Dissection of a metastatic gene expression signature into distinct components. 2006 , 7, R117 | 34 |
| 946 | Classification methods for the development of genomic signatures from high-dimensional data. 2006 , 7, R121 | 17 |
| 945 | A consensus prognostic gene expression classifier for ER positive breast cancer. 2006 , 7, R101 | 75 |
| 944 | Genes regulated by estrogen in breast tumor cells in vitro are similarly regulated in vivo in tumor xenografts and human breast tumors. 2006 , 7, R28 | 98 |
| 943 | Variability in synovial inflammation in rheumatoid arthritis investigated by microarray technology. 2006 , 8, R47 | 39 |
| 942 | Nutrient-gene interactions and their role in complex diseases in dogs. 2006 , 228, 1513-20 | 4 |
| 941 | Bioinformatics and Drug Discovery. 2006 , | 1 |
| 940 | Evolving Intelligent Systems: Methods, Learning, & Applications. 2006, | 27 |
| 939 | Improving Treatment of Early Breast Cancer. 2006 , 4, 14-16 | |
| 938 | Cancer du sein. 2006 , | |
| 937 | Breast Cancer and Molecular Medicine. 2006, | 2 |
| 936 | Breast Cancer Research Protocols. 2006 , | 2 |
| 935 | Biomarkers in Breast Cancer. 2006 , | 3 |
| 934 | Global expression-based classification of lymph node metastasis and extracapsular spread of oral tongue squamous cell carcinoma. 2006 , 8, 925-32 | 86 |
| 933 | Histopathologic and Metabolic Criteria for Assessment of Treatment Response in Breast Cancer. 2006 , 1, 83-94 | |

| 932 | Cancer Drug Resistance. 2006 , | 17 |
|-----|---|-----|
| 931 | Biomarqueurs tissulaires tumoraux. Cancer du sein. Facteurs pronostiques, facteurs prdictifs. Quels standards en 2005 ?. 2006 , 83-130 | |
| 930 | Beyond linker histones and high mobility group proteins: global profiling of perchloric acid soluble proteins. 2006 , 5, 925-34 | 17 |
| 929 | Profils daxpression ghique et Puces ^ADN dans le cancer du sein : choix du patient, choix du protocole. 2006 , 267-276 | |
| 928 | DNA repair pathway profiling and microsatellite instability in colorectal cancer. 2006, 12, 5104-11 | 31 |
| 927 | Cancer survivorshipgenetic susceptibility and second primary cancers: research strategies and recommendations. 2006 , 98, 15-25 | 233 |
| 926 | Detection of circulating tumour cells in blood by quantitative real-time RT-PCR: effect of pre-analytical time. 2006 , 44, 1082-7 | 25 |
| 925 | Microarray Gene Expression Classification Based on Supervised Learning and Similarity Measures. 2006 , | 1 |
| 924 | Significance of gene ranking for classification of microarray samples. 2006 , 3, 312-20 | 37 |
| 923 | Advances in Health care Technology Care Shaping the Future of Medical. 2006, | 7 |
| 922 | Prevention and Treatment of Age-related Diseases. 2006, | 2 |
| 921 | Locoregional therapy of breast cancer: maximizing control, minimizing morbidity. 2006 , 6, 1281-99 | 1 |
| 920 | 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 |
| 919 | ITTACA: a new database for integrated tumor transcriptome array and clinical data analysis. 2006 , 34, D613-6 | 47 |
| 918 | Fast and sensitive analysis of DNA hybridization in a PDMS micro-fluidic channel using fluorescence resonance energy transfer. 2006 , 1509-11 | 29 |
| 917 | Mechanisms of transcoelomic metastasis in ovarian cancer. 2006 , 7, 925-34 | 320 |
| 916 | Adenopatâ axilar de primario oculto. Manejo clâico. 2006 , 49, 316-328 | 1 |
| 915 | Molecular classification of breast tumors: toward improved diagnostics and treatments. 2007 , 360, 91-114 | 50 |

| 914 | The Connectivity Map: using gene-expression signatures to connect small molecules, genes, and disease. 2006 , 313, 1929-35 | 3392 |
|-----|---|------|
| 913 | Molecular biology of bladder cancer: prognostic and clinical implications. 2006 , 5, 67-77 | 43 |
| 912 | Gene expression profiling in breast cancer: understanding the molecular basis of histologic grade to improve prognosis. 2006 , 98, 262-72 | 1485 |
| 911 | Expression profiling and prediction of distant metastases in head and neck squamous cell carcinoma. 2006 , 59, 1254-60 | 34 |
| 910 | Current and future directions for adjuvant chemotherapy in early-stage breast cancer. 2006 , 4, 14-20 | 1 |
| 909 | Conclusions. 2006 , 4, 21-23 | |
| 908 | Current and future directions in early breast cancer therapy. 2006 , 4, 12-16 | |
| 907 | Host genetics influence tumour metastasis. 2006 , 6, 141-6 | 105 |
| 906 | . 2006 , 94, 692-709 | 5 |
| 905 | Fully-automated detection of cerebral water content changes: study of age- and gender-related H2O patterns with quantitative MRI. 2006 , 29, 910-22 | 92 |
| 904 | Exploring the human genome in cancer with genomic approaches. 2006 , 17, 1225-33 | 6 |
| 903 | Diverse gene expression and DNA methylation profiles correlate with differential adaptation of breast cancer cells to the antiestrogens tamoxifen and fulvestrant. 2006 , 66, 11954-66 | 197 |
| 902 | The molecular biology of pulmonary metastasis. 2006 , 16, 115-24 | 23 |
| 901 | A Molecular Profiling of Breast Cancer. 2006 , 9, 19-24 | 2 |
| 900 | Gene expression profile assays as predictors of recurrence-free survival in early-stage breast cancer: a metaanalysis. 2006 , 7, 372-9 | 24 |
| 899 | Heterogeneity of mammary lesions represent molecular differences. 2006 , 6, 275 | 29 |
| 898 | A systems approach to clinical oncology: focus on breast cancer. 2006 , 4, 5 | 37 |
| 897 | Prognostic factors in prostate cancer. 2006 , 1, 4 | 56 |

(2006-2006)

| 896 | Molecular markers of multiple drug resistance in breast cancer. 2006 , 52, 125-9 | 24 |
|-----|---|------|
| 895 | Lycopene. 2006 , 51, 99-164 | 156 |
| 894 | Identification of prognostic signatures in breast cancer microarray data using Bayesian techniques. 2006 , 3, 367-81 | 12 |
| 893 | Concordance among gene-expression-based predictors for breast cancer. 2006 , 355, 560-9 | 1071 |
| 892 | Affymetrix GeneChip system: moving from research to the clinic. 2006 , 6, 145-52 | 31 |
| 891 | Parallel analysis of transcript and translation profiles: identification of metastasis-related signal pathways differentially regulated by drug and genetic modifications. 2006 , 5, 1555-67 | 9 |
| 890 | Gene expression profiling and clinical outcome in breast cancer. 2006 , 10, 429-43 | 47 |
| 889 | Interpreting Microarray Data and Related Applications Using Nonlinear System Identification. 25-53 | |
| 888 | Integration of gene functional diversity for effective cancer detection. 2006, 37, 931-938 | 3 |
| 887 | Technology Insight: tuning into the genetic orchestra using microarrayslimitations of DNA microarrays in clinical practice. 2006 , 3, 501-16 | 63 |
| 886 | Microarray analysis and tumor classification. 2006 , 354, 2463-72 | 363 |
| 885 | Cancer biomarkersan invitation to the table. 2006 , 312, 1165-8 | 171 |
| 884 | Gene selection using support vector machines with non-convex penalty. 2006 , 22, 88-95 | 188 |
| 883 | Progression-specific genes identified by expression profiling of matched ductal carcinomas in situ and invasive breast tumors, combining laser capture microdissection and oligonucleotide microarray analysis. 2006 , 66, 5278-86 | 190 |
| 882 | Distinction between hereditary and sporadic breast cancer on the basis of clinicopathological data. 2006 , 59, 611-7 | 67 |
| 881 | Molecular pathology of breast apocrine carcinomas: a protein expression signature specific for benign apocrine metaplasia. 2006 , 580, 2935-44 | 41 |
| 880 | Gene expression analysis and clinical diagnosis. 2006 , 363, 157-64 | 26 |
| 879 | GATA-3 maintains the differentiation of the luminal cell fate in the mammary gland. 2006 , 127, 1041-55 | 479 |

| 878 | Elevated expression and potential roles of human Sp5, a member of Sp transcription factor family, in human cancers. 2006 , 340, 758-66 | 33 |
|-----|--|-----|
| 877 | Hhex is a direct repressor of endothelial cell-specific molecule 1 (ESM-1). 2006 , 346, 535-45 | 18 |
| 876 | [Elective radiotherapy of the regional lymph node areas in breast cancer]. 2006, 10, 343-8 | O |
| 875 | Molecular biology and clinical behavior of oral cancer. 2006 , 18, 483-91 | 3 |
| 874 | Expression profiling and individualisation of treatment for ovarian cancer. 2006 , 6, 345-9 | 14 |
| 873 | Systematic analysis of the transcriptional switch inducing migration of border cells. 2006 , 10, 497-508 | 65 |
| 872 | Identification of HNP3 as a tumour marker in CD4+ and CD4- lymphocytes of patients with cutaneous T-cell lymphoma. 2006 , 42, 249-55 | 30 |
| 871 | Linking survival of HER2-positive breast carcinoma patients with surgical invasiveness. 2006 , 42, 1057-61 | 7 |
| 870 | Prediction of peritoneal metastasis in advanced gastric cancer by gene expression profiling of the primary site. 2006 , 42, 1897-903 | 12 |
| 869 | What clinicians need to know about antioestrogen resistance in breast cancer therapy. 2006 , 42, 2692-705 | 43 |
| 868 | Gene expression profilers and conventional clinical markers to predict distant recurrences for premenopausal breast cancer patients after adjuvant chemotherapy. 2006 , 42, 2729-37 | 22 |
| 867 | Gene expression profile analysis of an isogenic tumour metastasis model reveals a functional role for oncogene AF1Q in breast cancer metastasis. 2006 , 42, 3274-86 | 55 |
| 866 | Constructing gene expression-based diagnostic rules for understanding individualized etiology of heart failure. 2006 , 1, 33-40 | 1 |
| 865 | [Primary systemic therapy in breast cancer: clinical and molecular factors predictors of outcome and response]. 2006 , 54, 209-14 | 2 |
| 864 | [DNA microarrays for gene expression profiling of breast cancer: principles and prognostic applications]. 2006 , 54, 49-54 | 1 |
| 863 | Clinical proteomics: searching for better tumour markers with SELDI-TOF mass spectrometry. 2006 , 27, 251-9 | 165 |
| 862 | Breast cancer. 2006 , 1, 187-210 | 2 |
| 861 | Single nucleotide polymorphisms: early diagnosis and risk assessment in genitourinary malignancy. 2006 , 24, 224-30 | |

| 860 | Stem cells in prostate and prostate cancer development. 2006 , 24, 131-40 | 30 |
|-----|---|-----|
| 859 | Genomic profiling in clinical oncology. The predictive value of genomic information in cancer management. 2006 , 119, 56-61 | 1 |
| 858 | Data Perturbation Independent Diagnosis and Validation of Breast Cancer Subtypes Using Clustering and Patterns. 2006 , 2, 117693510600200 | 10 |
| 857 | Detecting and profiling tissue-selective genes. 2006 , 26, 158-62 | 43 |
| 856 | The cell-specific activity of the estrogen receptor alpha may be fine-tuned by phosphorylation-induced structural gymnastics. 2006 , 4, e005 | 9 |
| 855 | Familial Breast Cancer, Prevention, Risk Factors and Genetics [Highlights from the San Antonio Breast Cancer Symposium (SABCS) Poster Presentations. 2006 , 1, 103-106 | |
| 854 | Section 7: Bioinformatics: Computational Approaches to Analysis of DNA Microarray Data. 2006 , 15, 91-103 | 4 |
| 853 | WISP-2 expression in human salivary gland tumors. 2006 , 17, 567 | 1 |
| 852 | Gene expression programs in response to hypoxia: cell type specificity and prognostic significance in human cancers. 2006 , 3, e47 | 476 |
| 851 | Identification and classification of differentially expressed genes in non-small cell lung cancer by expression profiling on a global human 59.620-element oligonucleotide array. 2006 , 16, 587 | 1 |
| 850 | Predictive and Prognostic Markers in Breast Cancer Treatment (Presentations at the 28th San Antonio Breast Cancer Symposium 2005. 2006 , 1, 118-122 | |
| 849 | Tumor Cell Dissemination and Metastasis in Breast Cancer: Selected Presentations at the 28th San Antonio Breast Cancer Symposium 2005. 2006 , 1, 113-116 | 1 |
| 848 | . 2006 , | 25 |
| 847 | References. 2006 , 401-449 | |
| 846 | Microarray-based Expression Profiling: From Technological Basics to Diagnostic Perspectives. 728-754 | |
| 845 | References. 275-380 | |
| 844 | . 2006, | 2 |
| 843 | New Technologies/New Markers/New Challenges. 2006 , 325-331 | |

| 842 | Profiling cancer expression. 2006 , 6, S22-S22 | |
|---|---|--------------|
| 841 | Gene expression profiles of small-cell lung cancers: Molecular signatures of lung cancer. 2006 , 29, 567 | 16 |
| 840 | Virology in the 21st century: finding function with functional genomics. 2006 , 1, 47-53 | 10 |
| 839 | Gene Expression Profiling with DNA Microarrays. 2006 , 47-61 | |
| 838 | Inference of Genetic Regulatory Networks via Best-Fit Extensions. 2006 , 259-278 | |
| 837 | Independent confirmation of a prognostic gene-expression signature in adult acute myeloid leukemia with a normal karyotype: a Cancer and Leukemia Group B study. 2006 , 108, 1677-83 | 108 |
| 836 | Molecular and cellular approaches to patient management in oncology. 2006 , 3, 299-310 | |
| 835 | Fast-Lane Evolution in the Tumor Microenvironment. 2006 , 317-329 | Ο |
| 834 | Microarray Bioinformatics. 2006, | |
| | | |
| 833 | DNA Chips and Microarrays. 2006, | |
| 833 | DNA Chips and Microarrays. 2006, Gene Expression Profiling in Hereditary, BRCA1-linked Breast Cancer: Preliminary Report. 2006, 4, 28-38 | 10 |
| | | 10 |
| 832 | Gene Expression Profiling in Hereditary, BRCA1-linked Breast Cancer: Preliminary Report. 2006 , 4, 28-38 Molecular profiling and personalized predictive pathology: challenge to the academic surgical | |
| 832 | Gene Expression Profiling in Hereditary, BRCA1-linked Breast Cancer: Preliminary Report. 2006 , 4, 28-38 Molecular profiling and personalized predictive pathology: challenge to the academic surgical pathology community. 2006 , 30, 402-4 | 6 |
| 832 831 830 | Gene Expression Profiling in Hereditary, BRCA1-linked Breast Cancer: Preliminary Report. 2006 , 4, 28-38 Molecular profiling and personalized predictive pathology: challenge to the academic surgical pathology community. 2006 , 30, 402-4 Genomic approach to biomarker identification and its recent applications. 2006 , 2, 103-33 | 6 |
| 8 ₃₂ 8 ₃₁ 8 ₃₀ 8 ₂₉ | Gene Expression Profiling in Hereditary, BRCA1-linked Breast Cancer: Preliminary Report. 2006, 4, 28-38 Molecular profiling and personalized predictive pathology: challenge to the academic surgical pathology community. 2006, 30, 402-4 Genomic approach to biomarker identification and its recent applications. 2006, 2, 103-33 INTEGRATION OF CLINICAL AND MICROARRAY DATA USING BAYESIAN NETWORKS. 2006, 39, 1174-1179 | 6 |
| 8 ₃₂ 8 ₃₁ 8 ₃₀ 8 ₂₉ 8 ₂₈ | Gene Expression Profiling in Hereditary, BRCA1-linked Breast Cancer: Preliminary Report. 2006, 4, 28-38 Molecular profiling and personalized predictive pathology: challenge to the academic surgical pathology community. 2006, 30, 402-4 Genomic approach to biomarker identification and its recent applications. 2006, 2, 103-33 INTEGRATION OF CLINICAL AND MICROARRAY DATA USING BAYESIAN NETWORKS. 2006, 39, 1174-1179 Targeting the Survivin Pathway for Rational Cancer Therapy. 427-442 | 6 31 2 |

(2006-2006)

| 824 | Review of: Gene expression profiling identifies molecular subtypes of inflammatory breast cancer. 2006 , 9, 1-3 | |
|-----|--|-----|
| 823 | Estrogen receptor alpha positive breast tumors and breast cancer cell lines share similarities in their transcriptome data structures. 2006 , 29, 1581 | 6 |
| 822 | Microarray Approaches to Gene Expression Analysis. 2006 , 121-148 | 1 |
| 821 | Laser capture microdissection of epithelial cancers guided by antibodies against fibroblast activation protein and endosialin. 2006 , 15, 35-42 | 29 |
| 820 | Factors that complicate the study of follicular variant of papillary thyroid cancer. 2006, 12, 250-2 | |
| 819 | Gene expression determinants of clinical outcome. 2006 , 18, 57-61 | 9 |
| 818 | Molecular profiling of breast cancer. 2006 , 18, 59-63 | 23 |
| 817 | Genetics and clinical characteristics to predict rheumatoid arthritis: where are we now and what are the future prospects?. 2006 , 1, 79-89 | 3 |
| 816 | Evaluation of HER-2/neu amplification and other biological markers as predictors of response to neoadjuvant anthracycline-based chemotherapy in primary breast cancer: the role of anthracycline dose intensity. 2006 , 29, 171-7 | 34 |
| 815 | Breast cancers with brain metastases are more likely to be estrogen receptor negative, express the basal cytokeratin CK5/6, and overexpress HER2 or EGFR. 2006 , 30, 1097-104 | 206 |
| 814 | Microarray expression technology: from start to finish. 2006 , 7, 123-34 | 24 |
| 813 | Gene Expression Profiles, Nonlinear System Identification In. 2006, | |
| 812 | DNA Chip Revolution. 2006, | |
| 811 | Gene expression profiling of lymph node metastasis by oligomicroarray analysis using laser microdissection in esophageal squamous cell carcinoma. 2006 , 29, 1337 | 1 |
| 810 | Learning Kernels from Distance Constraints. 2006 , 2, 441-451 | |
| 809 | Cross-validated Cox regression on microarray gene expression data. 2006 , 25, 3201-16 | 125 |
| 808 | Expression and functional analysis of Bax inhibitor-1 in human breast cancer cells. 2006 , 208, 340-9 | 54 |
| 807 | Quantitative analysis of allele imbalance supports atypical ductal hyperplasia lesions as direct breast cancer precursors. 2006 , 209, 307-16 | 47 |

| 806 | Identification of transmembrane proteins as potential prognostic markers and therapeutic targets in breast cancer by a screen for signal sequence encoding transcripts. 2006 , 210, 420-30 | 61 |
|-----|---|-----|
| 805 | Detection and identification of heat shock protein 10 as a biomarker in colorectal cancer by protein profiling. 2006 , 6, 2600-8 | 39 |
| 804 | Pathway alterations during glioma progression revealed by reverse phase protein lysate arrays. 2006 , 6, 2964-71 | 69 |
| 803 | Identification of breast cancer metastasis-associated proteins in an isogenic tumor metastasis model using two-dimensional gel electrophoresis and liquid chromatography-ion trap-mass spectrometry. 2006 , 6, 3352-68 | 124 |
| 802 | Expanding the protein catalogue in the proteome reference map of human breast cancer cells. 2006 , 6, 2609-25 | 35 |
| 801 | Computational exploration of the activated pathways associated with DNA damage response in breast cancer. 2006 , 65, 103-10 | 2 |
| 800 | Ascertaining prognosis for breast cancer in node-negative patients with innovative survival analysis. 2006 , 12, 37-47 | 16 |
| 799 | The challenging estrogen receptor-negative/progesterone receptor-negative/HER-2-negative patient: a promising candidate for epidermal growth factor receptor-targeted therapy?. 2006 , 12, 360-2 | 40 |
| 798 | Galectin-9, a novel prognostic factor with antimetastatic potential in breast cancer. 2006 , 12, S196-200 | 41 |
| 797 | Microarray analysis of gene expression associated with extrapulmonary dissemination of tuberculosis. 2006 , 11, 557-65 | 13 |
| 796 | Quality Management and Stimulation of Technology Transfer in a Research Institute. 2006, 15, 207-217 | 3 |
| 795 | Elucidating the murine brain transcriptional network in a segregating mouse population to identify core functional modules for obesity and diabetes. 2006 , 97 Suppl 1, 50-62 | 78 |
| 794 | Analysis of gene expression patterns of ovarian cancer cell lines with different metastatic potentials. 2006 , 16, 202-9 | 17 |
| 793 | Molecular prognostic markers in ovarian cancer: toward patient-tailored therapy. 2006 , 16 Suppl 1, 152-65 | 41 |
| 792 | Gene expression profiling of treatment resistance: hype or hope for therapeutic target identification. 2006 , 16 Suppl 2, 538-42 | 13 |
| 791 | Cytokeratin profiles of male breast cancers. 2006 , 49, 365-70 | 20 |
| 790 | Genetic regulators of large-scale transcriptional signatures in cancer. 2006 , 38, 421-30 | 185 |
| 789 | A signature of chromosomal instability inferred from gene expression profiles predicts clinical outcome in multiple human cancers. 2006 , 38, 1043-8 | 782 |

(2006-2006)

| 788 | Genome-wide analysis of estrogen receptor binding sites. 2006 , 38, 1289-97 | 1115 |
|-----------------|--|------|
| 787 | Where the chips fall. 2006 , 12, 158-9 | 5 |
| 786 | Acute lymphoblastic leukaemia: a model for the pharmacogenomics of cancer therapy. 2006 , 6, 117-29 | 180 |
| 785 | Common markers of proliferation. 2006 , 6, 99-106 | 402 |
| 784 | Tumour microenvironment - opinion: validating matrix metalloproteinases as drug targets and anti-targets for cancer therapy. 2006 , 6, 227-39 | 1005 |
| 783 | Linking oncogenic pathways with therapeutic opportunities. 2006 , 6, 735-41 | 139 |
| 782 | Polycomb silencers control cell fate, development and cancer. 2006 , 6, 846-56 | 1072 |
| 781 | Highly parallel genomic assays. 2006 , 7, 632-44 | 313 |
| 780 | Gene expression profiling of primary cultures of ovarian epithelial cells identifies novel molecular classifiers of ovarian cancer. 2006 , 94, 436-45 | 34 |
| 779 | Biobanking of fresh frozen tissue: RNA is stable in nonfixed surgical specimens. 2006 , 86, 202-11 | 171 |
| 778 | Phenotypic evaluation of the basal-like subtype of invasive breast carcinoma. 2006 , 19, 264-71 | 806 |
| 777 | mda-7 gene transfer sensitizes breast carcinoma cells to chemotherapy, biologic therapies and radiotherapy: correlation with expression of bcl-2 family members. 2006 , 13, 490-502 | 47 |
| 776 | Mutant Bik expression mediated by the enhanced minimal topoisomerase IIalpha promoter selectively suppressed breast tumors in an animal model. 2006 , 13, 706-19 | 14 |
| 775 | Cancer transcriptomics: modeling metastasis. 2006 , 14, 1-2 | 6 |
| 774 | Laser microdissection and microarray analysis of breast tumors reveal ER-alpha related genes and pathways. 2006 , 25, 1413-9 | 60 |
| 773 | BRCA1 and FOXA1 proteins coregulate the expression of the cell cycle-dependent kinase inhibitor p27(Kip1). 2006 , 25, 1391-9 | 55 |
| 77 ² | Gene expression signatures and biomarkers of noninvasive and invasive breast cancer cells: comprehensive profiles by representational difference analysis, microarrays and proteomics. 2006 , 25, 2328-38 | 156 |
| 771 | An estrogen receptor-negative breast cancer subset characterized by a hormonally regulated transcriptional program and response to androgen. 2006 , 25, 3994-4008 | 431 |

| 770 | Fate and characterization of circulating tumor cells in a NOD/SCID mouse model of human hepatocellular carcinoma. 2006 , 25, 4067-75 | 14 |
|-----|---|-----|
| 769 | Comparative and integrative functional genomics of HCC. 2006 , 25, 3801-9 | 96 |
| 768 | Identification of expressed genes characterizing long-term survival in malignant glioma patients. 2006 , 25, 5994-6002 | 85 |
| 767 | Induction of melanoma cell apoptosis and inhibition of tumor growth using a cell-permeable Survivin antagonist. 2006 , 25, 6968-74 | 46 |
| 766 | Pathology and gene expression of hereditary breast tumors associated with BRCA1, BRCA2 and CHEK2 gene mutations. 2006 , 25, 5837-45 | 87 |
| 765 | Use of genomic signatures in therapeutics development in oncology and other diseases. 2006 , 6, 166-73 | 118 |
| 764 | Is tailored therapy feasible in oncology?. 2006 , 57, 79-101 | 16 |
| 763 | Clinical trials design and treatment tailoring: general principles applied to breast cancer research. 2006 , 59, 98-105 | 12 |
| 762 | Histopathology of BRCA1- and BRCA2-associated breast cancer. 2006 , 59, 27-39 | 73 |
| 761 | Evolving clusters in gene-expression data. 2006 , 176, 1898-1927 | 92 |
| 760 | Profiling the breast cancer proteomethe new tool of the future?. 2006 , 18, 581-6 | 4 |
| 759 | A novel ensemble machine learning for robust microarray data classification. 2006 , 36, 553-73 | 91 |
| 758 | Genetic predictors of adverse radiotherapy effects: the Gene-PARE project. 2006 , 65, 646-55 | 98 |
| 757 | A prognostic scoring system for locoregional control in nasopharyngeal carcinoma following conformal radiotherapy. 2006 , 66, 992-1003 | 39 |
| 756 | Artifacts of Markov blanket filtering based on discretized features in small sample size applications. 2006 , 27, 709-714 | 5 |
| 755 | Random subspace method for multivariate feature selection. 2006 , 27, 1067-1076 | 129 |
| 754 | Stochastic dynamics of metastasis formation. 2006 , 240, 521-30 | 52 |
| 753 | PRAME is a membrane and cytoplasmic protein aberrantly expressed in chronic lymphocytic leukemia and mantle cell lymphoma. 2006 , 30, 1333-9 | 27 |

| 752 | DNA biosensor using fluorescence microscopy and impedance spectroscopy. 2006 , 118, 53-59 | 33 |
|-----|---|-----|
| 751 | Classification of gene-expression data: The manifold-based metric learning way. 2006 , 39, 2450-2463 | 20 |
| 75° | Selection bias in working with the top genes in supervised classification of tissue samples. 2006 , 3, 29-41 | 9 |
| 749 | Proteomic technology for biomarker profiling in cancer: an update. 2006 , 7, 411-20 | 37 |
| 748 | Gene expression profiling of breast cancer. 2006 , 13, 2-7 | 17 |
| 747 | Embracing the complexity of genomic data for personalized medicine. 2006 , 16, 559-66 | 103 |
| 746 | Genetic prognostic index influences patient outcome for node-positive breast cancer. 2006, 36, 793-801 | 22 |
| 745 | Expression of interleukin 11 and its receptor and their prognostic value in human breast cancer. 2006 , 13, 802-8 | 60 |
| 744 | A gene expression profile for vascular invasion can predict the recurrence after resection of hepatocellular carcinoma: a microarray approach. 2006 , 13, 1474-84 | 54 |
| 743 | A genetic signature can predict prognosis and response to therapy in breast cancer: Oncotype DX. 2006 , 6, 803-9 | 48 |
| 742 | High-dimensional biology in obstetrics and gynecology: functional genomics in microarray studies. 2006 , 195, 360-3 | 29 |
| 741 | BRCA1 and BRCA2: chemosensitivity, treatment outcomes and prognosis. 2006 , 5, 135-42 | 114 |
| 740 | cDNA microarray analysis of isogenic paclitaxel- and doxorubicin-resistant breast tumor cell lines reveals distinct drug-specific genetic signatures of resistance. 2006 , 96, 17-39 | 49 |
| 739 | Isolation and characterization of a breast progenitor epithelial cell line with robust DNA damage responses. 2006 , 98, 357-64 | 10 |
| 738 | Caveolin-1 expression is associated with a basal-like phenotype in sporadic and hereditary breast cancer. 2006 , 99, 85-90 | 111 |
| 737 | Degradomics: systems biology of the protease web. Pleiotropic roles of MMPs in cancer. 2006 , 25, 69-75 | 181 |
| 736 | Improving the prediction of the clinical outcome of breast cancer using evolutionary algorithms. 2006 , 10, 338-345 | 5 |
| 735 | Gene expression analyses reveal molecular relationships among 20 regions of the human CNS. 2006 , 7, 67-80 | 270 |

| 734 | Expression of cyclin-dependent kinases and CDC25a phosphatase is related with recurrences and survival in women with peri- and post-menopausal breast cancer. 2006 , 448, 539-44 | 19 |
|-----|---|-----|
| 733 | A clinical prognostic prediction of lymph node-negative breast cancer by gene expression profiles. 2006 , 132, 579-87 | 9 |
| 732 | [The significance of "normal tissue" in the development of breast cancer: new concepts of early carcinogenesis]. 2006 , 27, 319-25 | О |
| 731 | Metastasis: cell-autonomous mechanisms versus contributions by the tumor microenvironment. 2006 , 63, 449-68 | 190 |
| 730 | Genomic platforms for cancer research: potential diagnostic and prognostic applications in clinical oncology. 2006 , 8, 161-72 | 4 |
| 729 | Molecular biology of breast cancer. 2006 , 8, 7-14 | 22 |
| 728 | Bioinformatics and cancer: an essential alliance. 2006 , 8, 409-15 | 11 |
| 727 | Analysis of metastatic-related gene expression in gastric cancer by low-density cDNA microarrays. 2006 , 3, 77-82 | |
| 726 | Gene expression in breast cancer. 2006 , 7, 123-8 | 19 |
| 725 | Genomic signatures in non-small-cell lung cancer: targeting the targeted therapies. 2006 , 8, 252-7 | 5 |
| 724 | Molecular screening for breast cancer prevention, early detection, and treatment planning: combining biomarkers from DNA, RNA, and protein. 2006 , 8, 484-91 | 8 |
| 723 | Isolated tumor cells in bone marrow of early-stage breast cancer patients. 2006 , 203, 240-9; quiz A58-9 | 3 |
| 722 | X chromosomal abnormalities in basal-like human breast cancer. 2006 , 9, 121-32 | 649 |
| 721 | The challenges of gene expression microarrays for the study of human cancer. 2006 , 9, 333-9 | 80 |
| 720 | BRIT1 regulates early DNA damage response, chromosomal integrity, and cancer. 2006 , 10, 145-57 | 123 |
| 719 | ILEI: a cytokine essential for EMT, tumor formation, and late events in metastasis in epithelial cells. 2006 , 10, 227-39 | 136 |
| 718 | Gene expression-based chemical genomics identifies rapamycin as a modulator of MCL1 and glucocorticoid resistance. 2006 , 10, 331-42 | 422 |
| 717 | Somatic inactivation of E-cadherin and p53 in mice leads to metastatic lobular mammary carcinoma through induction of anoikis resistance and angiogenesis. 2006 , 10, 437-49 | 466 |

(2011-2006)

| 716 | Genomic and transcriptional aberrations linked to breast cancer pathophysiologies. 2006, 10, 529-41 | 998 |
|-----|---|------|
| 715 | Integrated breast cancer genomics. 2006 , 10, 453-4 | 3 |
| 714 | Endocan or endothelial cell specific molecule-1 (ESM-1): a potential novel endothelial cell marker and a new target for cancer therapy. 2006 , 1765, 25-37 | 144 |
| 713 | Inflammation and cancer: how hot is the link?. 2006 , 72, 1605-21 | 1039 |
| 712 | SAGE and related approaches for cancer target identification. 2006 , 11, 110-8 | 27 |
| 711 | Opening and introductory remarks. 2006 , 15, S1-S3 | |
| 710 | Axillary Dissection for Breast Cancer. 2006 , 8, 66-80 | 4 |
| 709 | Prognostische und präiktive Faktoren (unter Beräksichtigung von Genexpressionsanalysen). 2010 , 98-108 | |
| 708 | Evolutionary q-Gaussian Radial Basis Functions for Improving Prediction Accuracy of Gene Classification Using Feature Selection. 2010 , 327-336 | |
| 707 | An Introduction to Toxicogenomics. 1 | |
| 706 | Gene Expression Profiles as Preclinical and Clinical Cancer Biomarkers of Prognosis, Drug Response, and Drug Toxicity. 1 | |
| 705 | Genomics. 1 | |
| 704 | Biomarkers for Detection of Intra-epithelial Neoplasia. 2011 , 151-166 | |
| 703 | Preparation of 125. 2010 , 31, 2649-2655 | |
| 702 | Hereditary Breast Cancer Syndromes. 2011 , 51-104 | |
| 701 | Isolated Limb Perfusion for Melanoma. 2011 , 209-220 | |
| 700 | Classifying Data Considering Pairs of Patients in a Relational Space. 2011 , 132-140 | |
| 699 | The Comparison of Classification Model with Partial Least Square Based Dimension Reduction. 2011 , 173-180 | |

| 698 | Luolution dans le temps des mthodes diagnostiques et des thòries sur la carcinogente. 2011, 3-41 |
|-----|---|
| 697 | Linking Interactome to Disease. 2011 , 406-427 |
| 696 | Systemic Instigation: A Mouse Model to Study Breast Cancer as a Systemic Disease. 2011 , 145-162 |
| 695 | Analyses ghomiques pour la prise en charge du cancer du sein. 2011 , 81-83 |
| 694 | Cancer, Inflammasomes, and Adjuvanticity. 2011 , 151-163 |
| 693 | Prediction Analysis for Genomic and Proteomic Data: New Statistical Methods Based on Machine Learning. 2011 , 32, 49-73 |
| 692 | High-Throughput Genomic and Proteomic Technologies in the Post-genomic Era. 2011 , 1463-1477 |
| 691 | Experiment Specific Expression Patterns. 2011 , 339-354 |
| 690 | Kernel-Based Feature Selection with the Hilbert-Schmidt Independence Criterion. 2011 , 140-158 |
| 689 | The Design of Evolutionary Multiple Classifier System for the Classification of Microarray Data. 2011 , 513-522 |
| 688 | Introduction on Genome-wide Expression Profiling from Formalin-Fixed Paraffin-Embedded Tissues Using Microarrays. 2011 , 233-237 |
| 687 | Breast Cancer. 2011 , 169-176 |
| 686 | Systems Biology, Bioinformatics and Medicine Approaches to Cancer Progression Outcomes. 2011 , 297-307 |
| 685 | Transcriptomics and Cancer Risk Assessment. 195-205 |
| 684 | References. 2011 , 553-576 |
| 683 | Molecular Gene-Signatures and Cancer Clinical Trials. 2012 , 139-155 |
| 682 | Gene Signatures in CRC and Liver Metastasis. 2012, 27-33 |
| 681 | The prognostic and predictive value of gene expression signatures in breast cancer. 2011 , 4-12 |

| 680 | References. 189-196 | |
|-----|---|---|
| 679 | References. 2011 , 217-231 | |
| 678 | Origins of Metastasis-Initiating Cells. 2012 , 229-246 | |
| 677 | Cross Talk Between ER and Src Signaling and Its Relevance to ER Status and Hormone Responsiveness. 2012 , 61-78 | |
| 676 | Nucleic Acid Techniques. 2012 , 401-442 | |
| 675 | Meta-Analysis of High Throughput Oncology Data. 2012 , 67-95 | |
| 674 | Outils ghomiques du choix thrapeutique des cancers du sein. Quelles perspectives ^court et moyen terme sur le traitement locorgional. Opinion du radiothrapeute?. 2012 , 435-440 | |
| 673 | Facteurs de d'isions en radiothfapie. 2012 , 73-85 | |
| 672 | Breast Cancer: Role of Planar, SPECT and PET in Imaging Bone Metastases. 2012 , 661-689 | |
| 671 | Fusing Gene Interaction to Improve Disease Discrimination on Classification Analysis. 2012 , 1, 1000102 | 1 |
| 670 | A Method for the Detection of Meaningful and Reproducible Group Signatures from Gene Expression Profiles. 2012 , 387-401 | |
| 669 | Comparison of Data-Merging Methods with SVM Attribute Selection and Classification in Breast Cancer Gene Expression. 2012 , 498-507 | 4 |
| 668 | Tumor Markers. 2012 , 617-667 | 1 |
| 667 | Molecular Classification of Breast Carcinoma. 2012 , 365-379 | |
| 666 | Pattern Discovery from Biological Data. 2012 , 724-768 | |
| 665 | Random Walking on Functional Interaction Networks to Rank Genes Involved in Cancer. 2012 , 66-75 | 2 |
| 664 | Analysis of Array Data and Clinical Validation of Array-Based Assays. 2012 , 171-210 | |
| 663 | Molecular biology as applied to head and neck oncology. 2012 , 24-37 | |

| 662 | Prognostic Markers in Breast Cancer. 2013 , 25-42 | |
|-----|---|---|
| 661 | Novel Biclustering Methods for Re-ordering Data Matrices. 2013 , 1-39 | |
| 660 | Mathematical Models of Supervised Learning and Application to Medical Diagnosis. 2013, 67-81 | |
| 659 | Molecular Markers of Prostate Cancer Outcome. 2013 , 189-247 | |
| 658 | Role of IL-17 and IL-17 Family Cytokines on Tumor Development. 2013 , 219-230 | |
| 657 | Systems Biology Approaches in Breast Cancer Studies. 2013 , 329-340 | Ο |
| 656 | Molecular Classification. 2013 , 21-34 | |
| 655 | Molecular investigation of breast cancer. 2013 , 286-304 | |
| 654 | Pharmacogenomics in Acute Myeloid Leukemia. 2013 , 237-248 | 1 |
| 653 | MicroRNA Expression in Breast Cancer Revealed by Deep Sequencing Technology. 2013 , 233-261 | |
| 652 | Gene Selection for SRBCTs Subtype Classification Using Fuzzy Neural Network. 2013 , 1, 134-137 | 1 |
| 651 | Mechanisms of Metastasis. 2013 , 435-458 | 1 |
| 650 | Role of Stroma in Disease Progression. 2013 , 129-147 | |
| 649 | Next-Generation Sequencing for Cancer Genomics. 2013 , 55-74 | 1 |
| 648 | Is Tumor Dormancy Clinically Relevant?. 2013 , 7-21 | |
| 647 | Histological risk factors, prognostic indicators and staging. 2013 , 236-249 | |
| 646 | Innovative Technologies in the Molecular Characterization of Pancreatic Cancer. 2013, 209-228 | |
| 645 | An Incremental Linear Programming Based Tool for Analyzing Gene Expression Data. 2013 , 48-64 | |

Mutational Genomics for Cancer Pathway Discovery. 2013, 35-46 644 Dfinition biologique de lagressivit tumorale : les signatures biologiques peuvent-elles tre 643 utilisès en pratique clinique?. 2013, 72-78 Signaling Networks of Activated Oncogenic and Altered Tumor Suppressor Genes in Head and Neck 642 4 Cancer. **2013**, Suppl 7, 4 641 Introduction. 2013, 3-10 Facing a Shift in Paradigm at the Bedside?. 2013, 04, 35-40 640 - Spliceomics: The OMICS of RNA Splicing. 2013, 224-247 639 638 The effect of biology in the treatment of small breast tumors. 2013, 25-31 Ductal carcinoma in situ: how should we treat it?. 2013, 2, 245-256 637 Gene Expression Profiling in Melanoma. 2014, 529-545 636 MammaPrint for Individualized Recurrence Risk Assessment and Treatment Recommendations for 635 Early-Stage Breast Cancer Patients. 2013, 387-415 Reproductive System. 2014, 89-136 634 Metastasis. 2014, 211-272 633 632 Systemic Therapy. 2014, 381-420 Diagnostic and Therapeutic Mesenchymal Stem Cells for Breast Cancer Treatment. 145-158 631 Molecular Pathology and Diagnostics of Breast Cancer. 2014, 57-73 630 629 Molecular Pathology and Diagnostics of Pancreatic Endocrine Neoplasms. 2014, 423-448 miRNAs as Cancer Biomarkers. 2014, 97-124 628 Cancer Pathology. 2014, 21-34 627

| 626 | Integration of Clinico-Pathological and microRNA Data for Intelligent Breast Cancer Relapse Prediction Systems. 2014 , 178-193 | О |
|-----|--|---|
| 625 | Microarray-Based Investigations in Cancer. 2014 , 87-106 | |
| 624 | The role of adjuvant systemic therapy in patients with operable breast cancer. 2014 , 199-218 | |
| 623 | Metabolomics in Breast Cancer. 2014 , 211-224 | |
| 622 | Encyclopedia of Machine Learning and Data Mining. 2014 , 1-24 | |
| 621 | Omics Technologies Applied in Breast Cancer Research. 2014 , 3-15 | |
| 620 | Molekularbiologie und Genetik. 2014 , 101-115 | |
| 619 | Epirubicin/Cyclophosphamide followed by Docetaxel as Primary Systemic Therapy in Breast Cancer. 2014 , 22, 19-23 | |
| 618 | A Biclustering-Based Classification Framework for Microarray Analysis. 2014 , 429-440 | |
| 617 | CHAPTER 7:MS1 Label-free Quantification Using Ion Intensity Chromatograms in Skyline (Research and Clinical Applications). 2014 , 154-174 | Ο |
| 616 | Molecular Testing in Breast Cancer. 2014 , 169-188 | |
| 615 | Mining Diversified Shared Decision Tree Sets for Discovering Cross Domain Similarities. 2014, 534-547 | |
| 614 | Superresolution MUSIC Based on Maranko-Pastur Limit Distribution Reduces Uncertainty and | |
| | Improves DNA Gene Expression-Based Microarray Classification. 2014 , 194-209 | |
| 613 | Cancer After Metastasis: The Second Transformation. 2014 , 279-304 | |
| 613 | | |
| | Cancer After Metastasis: The Second Transformation. 2014 , 279-304 | |
| 612 | Cancer After Metastasis: The Second Transformation. 2014 , 279-304 A Genomic Analysis of Cellular Responses and Adaptions to Extracellular Acidosis. 2014 , 135-157 | |

Omics of Hereditary Breast Cancer. 2014, 17-40 608 Searching for Patterns in Imbalanced Data. 2014, 159-166 607 A Stable Instance Based Filter for Feature Selection in Small Sample Size Data Sets. 2014, 334-344 606 605 GENETICS FOR DIAGNOSTICS IN PREVENTIVE MEDICINE. 2014, 13, 75-80 Early Breast Cancers. 2015, 61-112 604 Genomic Applications in Breast Carcinoma. 2015, 359-382 603 Neural networks and Fuzzy clustering methods for assessing the efficacy of microarray based 602 intrinsic gene signatures in breast cancer classification and the character and relations of identified subtypes. 2015, 1260, 285-317 Analysis of AmpliSeq RNA-Sequencing Enrichment Panels. 2015, 495-500 601 Gene Selection Based On an Improved Iterative Feature Elimination Random Survival Forest. 2015, 600 2015, 124-129 Pharmacogenetics and Antineoplastic Therapies. 2015, 275-305 599 Gene Fusions in Prostate Cancer. 2015, 381-401 598 Systems Biology, Information Technology, and Cancer Research. 2015, 147-211 597 596 Current and Evolving Technologies. 2015, 11-34 Kinesin-8 Members and Their Potential as Biomarker or Therapeutic Target. 2015, 171-191 595 Cell-Specific Aptamers for Disease Profiling and Cell Sorting. 2015, 197-213 594 Feature Selection and Analysis of Gene Expression Data Using Low-Dimensional Linear 593 Programming. 2015, 235-264 Specimens for Molecular Testing in Breast Cancer. 2015, 317-327 592 Breast cancer and neutropenic sepsis. 2015, 1-10 591

| 590 | Tumors of the breast. 426-446 | |
|-----|---|--|
| 589 | From Gene Expression to Disease Phenotypes: Network-Based Approaches to Study Complex Human Diseases. 2016 , 115-140 | |
| 588 | Expression Profiling, MammaPrint Assay. 2016 , 482-483 | |
| 587 | The prognostic potential of alternative transcript isoforms across human tumors. | |
| 586 | Gene Expression Analysis: Current Methods. 2016 , 107-136 | |
| 585 | Gene Arrays, Prognosis, and Therapeutic Interventions. 2016 , 207-227 | |
| 584 | Genomic Markers in ER-Negative Breast Cancer. 2016 , 283-298 | |
| 583 | Personalisation of Radiotherapy for Breast Cancer. 2016 , 131-149 | |
| 582 | Construction of 3-Plex Barcodes for Differential Gene Expression Analysis with Pyrosequencing. 2016 , 217-230 | |
| 581 | Breast Cancer Molecular Testing for Prognosis and Prediction. 2016 , 195-202 | |
| 580 | Information Extraction from Microarray Data. 2016 , 1180-1211 | |
| 579 | Molecular Diagnostics: Translation from Discovery to Clinical Practice. 2016 , 1-26 | |
| 578 | Breast Cancer. 2016 , 433-446 | |
| 577 | How to Build Up Adequate Prognostic Markers in the Molecular Biology Context of Breast Cancer. 2016 , 149-181 | |
| 576 | Breast Cancer Molecular Subtypes Among Moroccan Women. 2016 , 3, 47-54 | |
| 575 | Prognostic and Predictive Gene Expression Signatures in Breast Cancer. 2016 , 269-281 | |
| 574 | A nonparametric Bayesian technique for high-dimensional regression. 2016 , 10, | |
| 573 | Comparative Gene Expression Analysis of Breast Cancer-Related Genes by Multiplex Pyrosequencing Coupled with Sequence Barcodes. 2016 , 315-325 | |

| 572 | Adjuvant Systemic Chemotherapy for HER2-Negative Disease. 2016 , 131-187 | |
|--------------------------|---|---|
| 571 | Gene Expression Analysis: Applications. 2016 , 137-149 | |
| 570 | Gene modules associated with breast cancer distant metastasis-free survival in the PAM50 molecular subtypes. 2016 , 7, 21686-98 | 2 |
| 569 | Mining Emerging Patterns for Activity Recognition. 2016 , 341-352 | |
| 568 | A comparative study of filter methods based on information entropy. 2016 , 40, 437-446 | 2 |
| 567 | Prognostic Value of SUVmax of ¹⁸F-FDG PET/CT in Early Stage Breast Cancer with No LN Metastasis. 2017 , 07, 112-123 | |
| 566 | Encyclopedia of Machine Learning and Data Mining. 2017 , 143-163 | |
| 565 | (L_1)-regularization Model Enriched with Biological Knowledge. 2017 , 579-590 | 2 |
| 564 | Bootstrap-Based LASSO-Type Selection to Build Generalized Additive Partially Linear Models for High-Dimensional Data. 2017 , 405-424 | |
| | | |
| 563 | Molecular Classification of Breast Cancer. 2017 , 1-22 | |
| 563 562 | Molecular Classification of Breast Cancer. 2017, 1-22 Big Data and DynamicsThe Mathematical Toolkit Towards Personalized Medicine. 2017, 338-369 | |
| | | O |
| 562 | B ig Data and DynamicsThe Mathematical Toolkit Towards Personalized Medicine. 2017 , 338-369 | O |
| 562 | Big Data and DynamicsThe Mathematical Toolkit Towards Personalized Medicine. 2017, 338-369 Survival-Expression Map and Essential Forms of Survival-Expression Relations for Genes. 2017, 641-649 | O |
| 562 561 560 | Big Data and DynamicsThe Mathematical Toolkit Towards Personalized Medicine. 2017, 338-369 Survival-Expression Map and Essential Forms of Survival-Expression Relations for Genes. 2017, 641-649 Prediction of Molecular Mechanisms of Breast Cancer Metastasis. Systems-level Analysis of 32 TCGA Cancers Reveals Disease-dependent tRNA Fragmentation | O |
| 562 561 560 | Big Data and DynamicsThe Mathematical Toolkit Towards Personalized Medicine. 2017, 338-369 Survival-Expression Map and Essential Forms of Survival-Expression Relations for Genes. 2017, 641-649 Prediction of Molecular Mechanisms of Breast Cancer Metastasis. Systems-level Analysis of 32 TCGA Cancers Reveals Disease-dependent tRNA Fragmentation Patterns and Very Selective Associations with Messenger RNAs and Repeat Elements. Reparameterization of PAM50 expression identifies novel breast tumor dimensions and leads to | O |
| 562 561 560 559 | Big Data and Dynamics he Mathematical Toolkit Towards Personalized Medicine. 2017, 338-369 Survival-Expression Map and Essential Forms of Survival-Expression Relations for Genes. 2017, 641-649 Prediction of Molecular Mechanisms of Breast Cancer Metastasis. Systems-level Analysis of 32 TCGA Cancers Reveals Disease-dependent tRNA Fragmentation Patterns and Very Selective Associations with Messenger RNAs and Repeat Elements. Reparameterization of PAM50 expression identifies novel breast tumor dimensions and leads to discovery of a breast cancer susceptibility locus at 12q15. A Nasal Brush-based Classifier of Asthma Identified by Machine Learning Analysis of Nasal RNA | 0 |

| 554 | A Biomaterial Screening Approach Reveals Microenvironmental Mechanisms of Drug Resistance. | 1 |
|---------------------------------|---|---|
| 553 | GAC: Gene Associations with Clinical, a web based application. 2017 , 6, 1039 | 1 |
| 552 | GAC: Gene Associations with Clinical, a web based application. 6, 1039 | |
| 551 | Identification of potential blood-derived extracellular vesicles biomarkers to diagnose and predict distant metastases in ER+ breast cancer patients. | 3 |
| 550 | PREVALENCE OF MOLECULAR SUBTYPES OF CARCINOMA OF BREAST- A STUDY FROM NORTH INDIA. 2017 , 6, 6204-6207 | 1 |
| 549 | CKS protein overexpression renders tumors susceptible to a chemotherapeutic strategy that protects normal tissues. 2017 , 8, 114911-114923 | |
| 548 | Competition and niche construction in a model of cancer metastasis. | |
| 547 | Microarray Bioinformatics. 1-7 | |
| 546 | The Spectrum of Risk Lesions in Breast Pathology: Risk Factors or Cancer Precursors?. 2018 , 1-19 | |
| | | |
| 545 | Encyclopedia of Signaling Molecules. 2018 , 4752-4756 | |
| 545 544 | Encyclopedia of Signaling Molecules. 2018, 4752-4756 Bi-objective Genetic Algorithm with Rough Set Theory for Important Gene Selection in Disease Diagnosis. 2018, 279-298 | |
| | Bi-objective Genetic Algorithm with Rough Set Theory for Important Gene Selection in Disease | O |
| 544 | Bi-objective Genetic Algorithm with Rough Set Theory for Important Gene Selection in Disease Diagnosis. 2018 , 279-298 A Visual Analytics Technique for Exploring Gene Expression in the Developing Mouse Embryo. 2018 | O |
| 544 | Bi-objective Genetic Algorithm with Rough Set Theory for Important Gene Selection in Disease Diagnosis. 2018, 279-298 A Visual Analytics Technique for Exploring Gene Expression in the Developing Mouse Embryo. 2018, 137-151 TuBA: Tunable Biclustering Algorithm Reveals Clinically Relevant Tumor Transcriptional Profiles in | O |
| 544 543 542 | Bi-objective Genetic Algorithm with Rough Set Theory for Important Gene Selection in Disease Diagnosis. 2018, 279-298 A Visual Analytics Technique for Exploring Gene Expression in the Developing Mouse Embryo. 2018, 137-151 TuBA: Tunable Biclustering Algorithm Reveals Clinically Relevant Tumor Transcriptional Profiles in Breast Cancer. | O |
| 544 543 542 541 | Bi-objective Genetic Algorithm with Rough Set Theory for Important Gene Selection in Disease Diagnosis. 2018, 279-298 A Visual Analytics Technique for Exploring Gene Expression in the Developing Mouse Embryo. 2018, 137-151 TuBA: Tunable Biclustering Algorithm Reveals Clinically Relevant Tumor Transcriptional Profiles in Breast Cancer. ANNC: AUC-Based Feature Selection by Maximizing Nearest Neighbor Complementarity. 2018, 772-785 | O |
| 544 543 542 541 540 | Bi-objective Genetic Algorithm with Rough Set Theory for Important Gene Selection in Disease Diagnosis. 2018, 279-298 A Visual Analytics Technique for Exploring Gene Expression in the Developing Mouse Embryo. 2018, 137-151 TuBA: Tunable Biclustering Algorithm Reveals Clinically Relevant Tumor Transcriptional Profiles in Breast Cancer. ANNC: AUC-Based Feature Selection by Maximizing Nearest Neighbor Complementarity. 2018, 772-785 GAC: Gene Associations with Clinical, a web based application. 6, 1039 A data-driven interactome of synergistic genes improves network based cancer outcome | O |

Migration.

Comprehensive Genomic Characterization of Breast Tumors with BRCA1 and BRCA2 Mutations. 536 Network-aware mutation clustering of cancer. 535 Prognostic and Predictive Factors. 2019, 171-186 534 A cross-cancer metastasis signature in the microRNA-mRNA axis of paired tissue samples. 533 EpiSmokEr: A robust classifier to determine smoking status from DNA methylation data. 532 Case Studies: Molecular Pathology Perspective and Impact on Oncologic Patients IManagement. 531 **2019**, 191-216 Frontiers in Precision Medicine IV: Artificial Intelligence, Assembling Large Cohorts, and the 530 Population Data Revolution. Research, Clinical Trials and Evidence-Based Medicine for Older Patients with Breast Cancer. 2019, 251-261 529 Clinical Application of Molecular Features in Therapeutic Selection and Drug Development. 2019, 137-166 528 7 The Anaphase Promoting Complex/Cyclosome (APC/C): A Versatile E3 Ubiquitin Ligase. 2019, 93, 539-623 527 Adjuvant Systemic Chemotherapy for HER2-Negative Disease. 2019, 129-171 526 Gene Arrays, Prognosis, and Therapeutic Interventions. 2019, 173-189 525 Molecular Pathway and Fluorescence In Situ Hybridization Testing of ERBB2 (HER2) Gene 524 Amplification in Invasive Ductal Carcinoma of Breast. 2019, 237-268 Prognostic and Predictive Factors. 2019, 163-172 523 APTER: Aggregated Prognosis Through Exponential Re-weighting. 2019, 425-436 522 521 Role of Heat Shock Protein 90 in Mammary Tumorigenesis. 2019, 103-124 Testing for dependence on tree structures. 520 Ο E2F1 Drives Breast Cancer Metastasis by Regulating the Target Gene FGF13 and Altering Cell 519

Ginecologâ endocrina: mtodos de determinaciti, exploraciti dintnica y molecular. **2019**, 55, 1-13

| 517 | Inferring Causal Associations between Genes and Disease via the Mapping of Expression Quantitative Trait Loci. 2019 , 697-38 | 1 |
|-----|---|---|
| 516 | Yeast Bax Inhibitor (Bxi1p/Ybh3p) is a Calcium Channel inE. coli. | |
| 515 | Early-life adversity is associated with differential gene expression in response to acute psychological stress: preliminary findings. | |
| 514 | Evaluating Ensemble Learning Impact on Gene Selection for Automated Cancer Diagnosis. 2020 , 183-186 | 1 |
| 513 | Maximizing the Reusability of Public Gene Expression Data by Predicting Missing Metadata. | |
| 512 | Determining Missing Key Elements in Oncology Information System to Improve Patient Experience and Clinical Care. 2020 , 567-586 | |
| 511 | Personalized single-cell networks: a framework to predict the response of any gene to any drug for any patient. | 2 |
| 510 | Prognosis and endocrine therapy selection for patients with low hormone receptor-positive breast cancer following neoadjuvant chemotherapy: A retrospective study of 570 patients in China. 2019 , 18, 6690-6696 | 3 |
| 509 | Molecular Profiles of Breast Cancer in Hispanic/Latina. 2020 , 103-109 | O |
| 508 | Multi-modal meta-analysis of cancer cell line omics profiles identifies ECHDC1 as a novel breast tumor suppressor. | 1 |
| 507 | Metformin Had Potential to Increase Endocan Levels in STZ-Induced Diabetic Mice. 2020 , 26, 133-141 | О |
| 506 | Challenges surrounding postoperative adjuvant chemotherapy for T2N0 gastric cancer. 2020 , 20, 126 | 2 |
| 505 | A Survey of Modern Gene Expression Based Techniques for Cancer Detection and Diagnosis. 2021 , 35-50 | 1 |
| 504 | Breast tumors escape endocrine therapy by ER-independent mechanisms triggered by the coordinated activities of HER2/HER3 and deacetylated FOXA1. | |
| 503 | Prognostic value of metabolic signature on 18F-FDGuptake in breast cancer patients after radiotherapy. 2021 , 23, 412-419 | O |
| 502 | Identification and characterization of a 25-lncRNA prognostic signature for early recurrence in hepatocellular carcinoma. 2021 , 21, 1165 | 0 |
| 501 | Molecular Basis of Breast Cancer. 2022 , 3-15 | |

(2020-2020)

| 500 | Construction and validation of a 6-gene nomogram discriminating lung metastasis risk of breast cancer patients. 2020 , 15, e0244693 | 1 |
|---------------------------------|---|--------|
| 499 | Association of mammography and ultrasound features with MammaPrint in patients with estrogen receptor-positive, HER2-negative, node-positive invasive breast cancer. 2021 , 62, 1592-1600 | O |
| 498 | CCDC170 affects breast cancer apoptosis through IRE1 pathway. 2020 , 13, 1332-1356 | 3 |
| 497 | In-silico analysis of differentially expressed genes and their regulating microRNA involved in lymph node metastasis in invasive breast carcinoma. | |
| 496 | Evaluation of primary breast cancers using dedicated breast PET and whole-body PET. 2020 , 10, 21930 | 2 |
| 495 | Summary Visualisations of Gene Ontology Terms with GO-Figure!. | O |
| 494 | A novel gene expression test method of minimizing breast cancer risk in reduced cost and time by improving SVM-RFE gene selection method combined with LASSO. 2020 , 18, 139-153 | 1 |
| 493 | Biomarkers in drug development. 2022 , 323-342 | 1 |
| 492 | CHAPTER 5:Big Data and Its Emerging Role in Precision Medicine and Therapeutic Response. 2020 , 88-116 | |
| | | |
| 491 | A Brief Overview on Intelligent Computing-Based Biological Data and Image Analysis. 2020 , 65-89 | |
| 491 490 | A Brief Overview on Intelligent Computing-Based Biological Data and Image Analysis. 2020 , 65-89 Carbonic Anhydrase Isozymes as Diagnostic Biomarkers and Therapeutic Targets. 2021 , 13-36 | |
| | | |
| 490 | Carbonic Anhydrase Isozymes as Diagnostic Biomarkers and Therapeutic Targets. 2021 , 13-36 | 2 |
| 490 489 | Carbonic Anhydrase Isozymes as Diagnostic Biomarkers and Therapeutic Targets. 2021 , 13-36 The Explanation Game: A Formal Framework for Interpretable Machine Learning. 2021 , 109-143 | 2 |
| 49° 489 488 | Carbonic Anhydrase Isozymes as Diagnostic Biomarkers and Therapeutic Targets. 2021, 13-36 The Explanation Game: A Formal Framework for Interpretable Machine Learning. 2021, 109-143 The Explanation Game: A Formal Framework for Interpretable Machine Learning. 2021, 185-219 | 2 |
| 49° 489 488 487 | Carbonic Anhydrase Isozymes as Diagnostic Biomarkers and Therapeutic Targets. 2021, 13-36 The Explanation Game: A Formal Framework for Interpretable Machine Learning. 2021, 109-143 The Explanation Game: A Formal Framework for Interpretable Machine Learning. 2021, 185-219 Biochips. 2021, 185-224 | 2 O |
| 490 489 488 487 486 | Carbonic Anhydrase Isozymes as Diagnostic Biomarkers and Therapeutic Targets. 2021, 13-36 The Explanation Game: A Formal Framework for Interpretable Machine Learning. 2021, 109-143 The Explanation Game: A Formal Framework for Interpretable Machine Learning. 2021, 185-219 Biochips. 2021, 185-224 Envisioning the Application of Systems Biology in Cancer Immunology. 2020, 599-624 The role of interactomic interactions in tamoxifen-resistant breast cancer: new approaches to | |

| 482 | Correlation between MR Image-Based Radiomics Features and Risk Scores Associated with Gene Expression Profiles in Breast Cancer. 2020 , 81, 632 | |
|-----|--|---|
| 481 | Systems Biology and Biomarkers in Necrotizing Soft Tissue Infections. 2020 , 1294, 167-186 | 1 |
| 480 | Decision Tree Model Based Gene Selection and Classification for Breast Cancer Risk Prediction. 2020 , 165-177 | |
| 479 | A novel single-cell based method for breast cancer prognosis. | |
| 478 | Targeted and systemic insights into the crosstalk between DNA-dependent protein kinase catalytic subunit and receptors of estrogen, progesterone and epidermal growth factor in the context of cancer. 2021 , 1 | 0 |
| 477 | Band-based similarity indices for gene expression classification and clustering. 2021 , 11, 21609 | |
| 476 | Nomogram for the personalisation of radiotherapy treatments in breast cancer patients. 2021 , 60, 255-262 | |
| 475 | Development and validation of a nomogram for predicting survival of breast cancer patients with ipsilateral supraclavicular lymph node metastasis. 2021 , 134, 2692-2699 | O |
| 474 | Präiktive und prognostische Faktoren in der Therapie des fräen Mammakarzinoms. 2021 , 27, 1175 | |
| 473 | PREDICTIVE IMMUNE CHECKPOINT BLOCKADE CLASSIFIERS DISTINGUISHING MONO- VERSUS COMBINATION THERAPY REQUIREMENT. | |
| 472 | Linking Interactome to Disease. 151-172 | |
| 471 | Machine Learning for Clinical Data Processing. 193-215 | Ο |
| 470 | Molecular markers in breast cancer: current practice and future possibilities. 2005, 563, 35-41 | O |
| 469 | Cancer Diagnosis. 427-447 | |
| 468 | Dynamic Nature of Tumour-Host Interactions Within the Tumor Microenvironment. 2005, 177-187 | |
| 467 | Gene Expression Signatures of TGF-//Smad-Induced Responses. 2006 , 335-360 | |
| 466 | Breast cancer with HER 2 overexpressed. From laboratory to clinical practice. 2006 , 205-220 | |
| 465 | Dawn of a new era in molecular cancer therapeutics. 2005 , 63, 1-17 | 1 |

| 464 | Heat Shock Proteins in the Progression of Cancer. 2007 , 422-450 |
|-----------------|--|
| 463 | Comparative Genomics of Tissue Specific Gene Expression. 2006 , 393-408 |
| 462 | Mining Interesting Clinico-Genomic Associations: The HealthObs Approach. 2007 , 137-145 |
| 461 | Systematic Validation of Breast Cancer Biomarkers Using Tissue Microarrays: From Construction to Image Analysis. 2008 , 235-250 |
| 460 | Lymph Node-Negative Breast Carcinoma: Assessment of HER-2/neu Gene Status as Prognostic Value. 2008 , 569-581 |
| 459 | Barrett® Esophagus. 2005 , 325-342 |
| 458 | Potential Use of Transgenic Mice in Chemoprevention Studies. 2005 , 47-55 |
| 457 | Molecular Biology Applications in Cardiovascular Medicine. 2005 , 11-43 |
| 456 | Molecular Profiling in Breast Cancer. 2006 , 559-576 |
| 455 | Considerations When Using Array Technologies for Male Factor Assessment. 2007 , 37-54 |
| 454 | Expression Profiling of Prostate Cancer Progression. 2007 , 247-267 |
| 453 | Microarray-based Gene Expression Analysis of Endocrine Systems: Principles of Experimental Design and Interpretation. 2008 , 3-22 |
| 452 | From Tissue Samples to Tumor Markers. 2007 , 17-28 |
| 45 ¹ | Targeted Therapy For Breast Cancer. 2008 , 309-342 |
| 450 | DNA and Tissue Microarrays. 2007 , 98-108 |
| 449 | Intft des nouvelles technologies de biologie dans le choix de la stratgie thfapeutique 2007. 2007 , 167-184 |
| 448 | Early Breast Cancer (Stage I and Stage II): Tailored Systemic Therapy for Endocrine-Responsive Breast Cancer. 2006 , 327-348 |
| 447 | Tailored Therapy for Breast Cancer in Very Young Women. 2006 , 349-374 |

| 446 | Genomic and Molecular Classification of Breast Cancer. 2006 , 595-621 | |
|-----|--|---|
| 445 | Biological Therapies for Metastatic Breast Cancer: Antiangiogenesis. 2006 , 671-704 | |
| 444 | Mechanisms of Resistance to Hormone Therapy. 2006 , 805-821 | |
| 443 | Clinical Trials in the Era of Treatment Tailoring. 2006 , 1007-1020 | |
| 442 | Genetische Verüderungen des sporadischen Mammakarzinoms. 2006 , 119-125 | |
| 441 | Prognostische und präiktive Faktoren bei Patientinnen mit Mammakarzinom. 2006 , 183-198 | |
| 440 | Biomarkers for Breast Cancer: Towards the Proposition of Clinically Relevant Tools. 2008, 15-32 | |
| 439 | Choices for surgery. 2007 , 175, 163-78 | |
| 438 | Resistance-associated signatures in breast cancer. 2007 , 176, 37-50 | |
| 437 | Boosting Threshold Classifiers for HighDimensional Data in Functional Genomics. 2008 , 147-156 | O |
| 436 | A Tree Index to Support Clustering Based Exploratory Data Analysis. 2008 , 1-15 | 1 |
| 435 | A Novel Relative Space Based Gene Feature Extraction and Cancer Recognition. 2007, 712-719 | 1 |
| 434 | The Synergy of Two Ovarian Hormone-induced Enzymes in Human Mammary Carcinogenesis. 2008 , 99-109 | |
| 433 | Informative Gene Selection and Tumor Classification by Null Space LDA for Microarray Data. 2007 , 435-446 | 5 |
| 432 | Cancer Identification Based on DNA Microarray Data. 2007 , 153-161 | 2 |
| 431 | Network-Based Inference of Cancer Progression from Microarray Data. 2008 , 268-279 | 1 |
| 430 | Analysis of Array Data and Clinical Validation of Array-Based Assays. 2012 , 171-210 | O |
| 429 | Molekularbiologie und Genetik. 2014 , 101-115 | O |

| 428 | Accurate Prediction of Breast Cancer Survival through Coherent Voting Networks with Gene Expression Profiling. | |
|---------------------------------|---|-------------------|
| 427 | Effects of underlying gene-regulation network structure on prediction accuracy in high-dimensional regression. | |
| 426 | Multi-Objective Approach for Identifying Cancer Subnetwork Markers. | |
| 425 | NeTFactor, a framework for identifying transcriptional regulators of gene expression-based biomarkers. 2020 , | 1 |
| 424 | Maximizing the reusability of gene expression data by predicting missing metadata. 2020 , 16, e1007450 | O |
| 423 | Kinase-substrate Edge Biomarkers Provide a More Accurate Prognostic Prediction in ER-negative Breast Cancer. 2020 , 18, 525-538 | |
| 422 | Clinical proteomics: present and future prospects. 2006 , 27, 99-116 | 50 |
| 421 | Mechanisms of oncogenic cooperation in cancer initiation and metastasis. 2006 , 79, 95-103 | 27 |
| 420 | Neutrophil gelatinase-associated lipocalin: new paths for an old shuttle. 2007 , 5, 463-470 | 49 |
| | | |
| 419 | Methods in molecular cardiology: microarray technology. 2003 , 11, 213-220 | |
| 419 | Methods in molecular cardiology: microarray technology. 2003, 11, 213-220 Statistical issues and analyses of in vivo and in vitro genomic data in order to identify clinically relevant profiles. 2007, 3, 231-43 | 1 |
| | Statistical issues and analyses of in vivo and in vitro genomic data in order to identify clinically | 1 |
| 418 | Statistical issues and analyses of in vivo and in vitro genomic data in order to identify clinically relevant profiles. 2007 , 3, 231-43 Genomancy: predicting tumour response to cancer therapy based on the oracle of genetics. 2009 , | |
| 418 | Statistical issues and analyses of in vivo and in vitro genomic data in order to identify clinically relevant profiles. 2007, 3, 231-43 Genomancy: predicting tumour response to cancer therapy based on the oracle of genetics. 2009, 16, 56-8 Clinical arrays of laboratory measures, or "clinarrays", built from an electronic health record enable | 4 |
| 418 417 416 | Statistical issues and analyses of in vivo and in vitro genomic data in order to identify clinically relevant profiles. 2007, 3, 231-43 Genomancy: predicting tumour response to cancer therapy based on the oracle of genetics. 2009, 16, 56-8 Clinical arrays of laboratory measures, or "clinarrays", built from an electronic health record enable disease subtyping by severity. 2007, 115-9 Alterations in human breast cancer adhesion-motility in response to changes in cell surface | 8 |
| 418 417 416 415 | Statistical issues and analyses of in vivo and in vitro genomic data in order to identify clinically relevant profiles. 2007, 3, 231-43 Genomancy: predicting tumour response to cancer therapy based on the oracle of genetics. 2009, 16, 56-8 Clinical arrays of laboratory measures, or "clinarrays", built from an electronic health record enable disease subtyping by severity. 2007, 115-9 Alterations in human breast cancer adhesion-motility in response to changes in cell surface glycoproteins displaying alpha-L-fucose moieties. 2008, 32, 797-807 Data perturbation independent diagnosis and validation of breast cancer subtypes using clustering | 4 8 27 |
| 418 417 416 415 414 | Statistical issues and analyses of in vivo and in vitro genomic data in order to identify clinically relevant profiles. 2007, 3, 231-43 Genomancy: predicting tumour response to cancer therapy based on the oracle of genetics. 2009, 16, 56-8 Clinical arrays of laboratory measures, or "clinarrays", built from an electronic health record enable disease subtyping by severity. 2007, 115-9 Alterations in human breast cancer adhesion-motility in response to changes in cell surface glycoproteins displaying alpha-L-fucose moieties. 2008, 32, 797-807 Data perturbation independent diagnosis and validation of breast cancer subtypes using clustering and patterns. 2007, 2, 243-74 Feature selection for predicting tumor metastases in microarray experiments using paired design. | 4 8 27 9 |

| 410 | State of the art of neoadjuvant chemotherapy in breast cancer: rationale, results and recent developments. 2005 , 3, Doc08 | 4 |
|---------------------------------|--|---|
| 409 | Multianalyte tests for the early detection of cancer: speedbumps and barriers. 2007, 2, 261-7 | |
| 408 | Trastuzumab in the management of early and advanced stage breast cancer. 2007, 1, 19-31 | 31 |
| 407 | Master regulators used as breast cancer metastasis classifier. 2009 , 504-15 | 41 |
| 406 | Technology as a force for improved diagnosis and treatment of breast disease. 2010 , 53, 268-77 | 18 |
| 405 | The Expression Patterns of ER, PR, HER2, CK5/6, EGFR, Ki-67 and AR by Immunohistochemical Analysis in Breast Cancer Cell Lines. 2010 , 4, 35-41 | 389 |
| 404 | Emerging tactical strategies for fighting the war on cancer based on the genetic landscape. 2011 , 3, 251-8 | 1 |
| 403 | Understanding tumor-stroma interplays for targeted therapies by armed mesenchymal stromal progenitors: the Mesenkillers. 2011 , 1, 787-805 | 22 |
| 402 | The role of survivin in diagnosis, prognosis and treatment of breast cancer. 2010 , 2, 100-10 | 47 |
| | | |
| 401 | Progress in myeloma stem cells. 2011 , 1, 135-45 | 15 |
| 400 | Progress in myeloma stem cells. 2011 , 1, 135-45 A Partitioning Based Adaptive Method for Robust Removal of Irrelevant Features from High-dimensional Biomedical Datasets. 2012 , 2012, 52-61 | 15 |
| | A Partitioning Based Adaptive Method for Robust Removal of Irrelevant Features from | |
| 400 | A Partitioning Based Adaptive Method for Robust Removal of Irrelevant Features from High-dimensional Biomedical Datasets. 2012, 2012, 52-61 A tale of mice and (wo)men: development of and insights from an "all human" animal model of breast cancer metastasis to bone. 2012, 123, 135-50; discussion 150-1 [Molecular classification of breast cancer in Morocco]. 2012, 13, 91 | 2 |
| 400 | A Partitioning Based Adaptive Method for Robust Removal of Irrelevant Features from High-dimensional Biomedical Datasets. 2012, 2012, 52-61 A tale of mice and (wo)men: development of and insights from an "all human" animal model of breast cancer metastasis to bone. 2012, 123, 135-50; discussion 150-1 | 3 |
| 400 399 398 | A Partitioning Based Adaptive Method for Robust Removal of Irrelevant Features from High-dimensional Biomedical Datasets. 2012, 2012, 52-61 A tale of mice and (wo)men: development of and insights from an "all human" animal model of breast cancer metastasis to bone. 2012, 123, 135-50; discussion 150-1 [Molecular classification of breast cancer in Morocco]. 2012, 13, 91 Correlation of tumor-infiltrating lymphocytes to histopathological features and molecular phenotypes in canine mammary carcinoma: A morphologic and immunohistochemical | 3 6 |
| 400 399 398 397 | A Partitioning Based Adaptive Method for Robust Removal of Irrelevant Features from High-dimensional Biomedical Datasets. 2012, 2012, 52-61 A tale of mice and (wo)men: development of and insights from an "all human" animal model of breast cancer metastasis to bone. 2012, 123, 135-50; discussion 150-1 [Molecular classification of breast cancer in Morocco]. 2012, 13, 91 Correlation of tumor-infiltrating lymphocytes to histopathological features and molecular phenotypes in canine mammary carcinoma: A morphologic and immunohistochemical morphometric study. 2013, 77, 142-9 | 2 3 6 5 |
| 400 399 398 397 396 | A Partitioning Based Adaptive Method for Robust Removal of Irrelevant Features from High-dimensional Biomedical Datasets. 2012, 2012, 52-61 A tale of mice and (wo)men: development of and insights from an "all human" animal model of breast cancer metastasis to bone. 2012, 123, 135-50; discussion 150-1 [Molecular classification of breast cancer in Morocco]. 2012, 13, 91 Correlation of tumor-infiltrating lymphocytes to histopathological features and molecular phenotypes in canine mammary carcinoma: A morphologic and immunohistochemical morphometric study. 2013, 77, 142-9 Classification of breast carcinomas according to gene expression profiles. 2013, 6, 14-7 Clinical implications for loss or diminution of expression of Raf-1 kinase inhibitory protein and its | 23657 |

(2020-2013)

| 392 | Modern Risk Assessment for Individualizing Treatment Concepts in Early-stage Breast Cancer. 2013 , 6, 165-73 | 3 |
|-----|---|-----|
| 391 | Differential expression of DNA repair genes in Hispanic women with breast cancer. 2013 , 1, 54 | 10 |
| 390 | T-ReCS: stable selection of dynamically formed groups of features with application to prediction of clinical outcomes. 2015 , 431-42 | 8 |
| 389 | Selective model averaging with bayesian rule learning for predictive biomedicine. 2014 , 2014, 17-22 | 2 |
| 388 | Bax inhibitor-1 is overexpressed in non-small cell lung cancer and promotes its progression and metastasis. 2015 , 8, 1411-8 | 11 |
| 387 | Application of Bayesian logistic regression to mining biomedical data. 2014 , 2014, 266-73 | 2 |
| 386 | Overexpression of NDC80 is correlated with prognosis of pancreatic cancer and regulates cell proliferation. 2015 , 5, 1730-40 | 18 |
| 385 | Breast cancer intrinsic subtype classification, clinical use and future trends. 2015 , 5, 2929-43 | 296 |
| 384 | Breed- and age-related differences in canine mammary tumors. 2016 , 80, 146-55 | 4 |
| 383 | Prognostic signatures of breast cancer: Perou's molecular subtypes and Schmidt's metagenes. 2012 , 11, 204-7 | 4 |
| 382 | RAS pathway biomarkers for breast cancer prognosis. 2016 , 40, 18-23 | 6 |
| 381 | Systematic Analysis of Free-Text Family History in Electronic Health Record. 2017 , 2017, 104-113 | 12 |
| 380 | Improving the efficiency of biomarker identification using biological knowledge. 2009 , 427-38 | 7 |
| 379 | Prognostic & predictive factors for planning adjuvant chemotherapy of early-stage breast cancer. 2017 , 146, 563-571 | 3 |
| 378 | Understanding Biomarkers in Early-Stage Invasive Breast Cancer: Tools From the ASCO Clinical Guideline. 2016 , 7, 666-671 | |
| 377 | Comparative study of gastric cancer and chronic gastritis via network analysis. 2018, 11, 343-351 | 11 |
| 376 | Egr-1 suppresses breast cancer cells proliferation by arresting cell cycle progression via down-regulating CyclinDs. 2017 , 10, 10212-10222 | 5 |
| 375 | Ribonuclease H2 Subunit A impacts invasiveness and chemoresistance resulting in poor survivability of breast cancer in ER dependent manner. 2020 , 12, 2281-2294 | 3 |

| 374 | Frequent Subgraph Mining of Functional Interaction Patterns Across Multiple Cancers. 2021 , 26, 261-272 | |
|-----|---|---|
| 373 | An immune-related signature that to improve prognosis prediction of breast cancer. 2021 , 11, 1267-1285 | 4 |
| 372 | Empirical Comparison of Continuous and Discrete-time Representations for Survival Prediction. 2021 , 146, 118-131 | |
| 371 | MELK expression in breast cancer is associated with infiltration of immune cell and pathological compete response (pCR) after neoadjuvant chemotherapy. 2021 , 11, 4421-4437 | 1 |
| 370 | A Text-Based Computational Framework for Patient-Specific Modeling for Classification of Cancers. | |
| 369 | Transcription factor NF- B , interleukin-1pand interleukin-8 expression and its association with tobacco smoking and severity in chronic obstructive pulmonary disease. 2022 , 26, 101453 | |
| 368 | A combinatory algorithm for identifying genes in childhood acute lymphoblastic leukemia. 2022 , 26, 101433 | |
| 367 | A novel filter based feature selection approach for microarray dataset. 2021 , | |
| 366 | Prognostic and Genomic Analysis of Proteasome 20S Subunit Alpha (PSMA) Family Members in Breast Cancer 2021 , 11, | 1 |
| 365 | Explore association of genes in PDL1/PD1 pathway to radiotherapy survival benefit based on interaction model strategy. 2021 , 16, 223 | 1 |
| 364 | Association of 17q22 Amplicon Via Cell-Free DNA With Platinum Chemotherapy Response in Metastatic Triple-Negative Breast Cancer. 2021 , 5, | 0 |
| 363 | Biomarker and multigene assay testing in ER positive, HER-2 negative breast carcinomas: An international guidelines-based approach. 2021 , 26, 300574 | 2 |
| 362 | Machine learning of genomic features in organotropic metastases stratifies progression risk of primary tumors. 2021 , 12, 6692 | 3 |
| 361 | MammaPrint and BluePrint comprehensively capture the cancer hallmarks in early-stage breast cancer patients. 2021 , | 1 |
| 360 | Germline breast cancer susceptibility genes, tumor characteristics, and survival. 2021, 13, 185 | 0 |
| 359 | Predictive Signatures for Lung Adenocarcinoma Prognostic Trajectory by Multiomics Data Integration and Ensemble Learning. 2021 , 9-23 | |
| 358 | Recurrencia y caracterŝticas clĥico patolĝicas en los grupos de riesgo establecidos por Oncotype Dx, original y TAILORx, en clicer de mama temprano. 2021 , 66, 263-272 | |
| 357 | Evaluation of the Effects of Nanomicellar Curcumin, Berberine, and Their Combination with 5-Fluorouracil on Breast Cancer Cells 2021 , 1328, 21-35 | O |

| 356 | A Hybrid Mutual Information-LASSO-Genetic Algorithm Selection Approach for Classifying Breast Cancer. 2022 , 547-560 | 1 |
|-----|--|---|
| 355 | Preclinical Evaluation of the HDAC Inhibitor Chidamide in Transformed Follicular Lymphoma 2021 , 11, 780118 | О |
| 354 | Precision Medicine: Technological Impact into Breast Cancer Diagnosis, Treatment and Decision Making 2021 , 11, | 1 |
| 353 | Multi-time scale transcriptomic analysis on the dynamic process of tamoxifen resistance development in breast cancer cell lines 2022 , 1 | |
| 352 | Predicting clinical outcomes of cancer patients with a p53 deficiency gene signature 2022, 12, 1317 | 0 |
| 351 | Robust multi-class feature selection via l2,0-norm regularization minimization. 2022 , 26, 57-73 | O |
| 350 | Breast Cancer Survival Prediction using Machine Learning and Gene Expression Profiles. | |
| 349 | ABI1-based expression signature predicts breast cancer metastasis and survival 2021, | О |
| 348 | An 11-Gene Signature Based on Treatment Responsiveness Predicts Radiation Therapy Survival Benefit Among Breast Cancer Patients 2021 , 11, 816053 | О |
| 347 | Bioinformatics Analysis of the Potentially Functional circRNA-miRNA-mRNA Network in Breast Cancer. | |
| 346 | Outcome of Patients With an Ultralow-Risk 70-Gene Signature in the MINDACT Trial 2022, JCO2102019 | 4 |
| 345 | SOX2-OT induced by PAI-1 promotes triple-negative breast cancer cells metastasis by sponging miR-942-5p and activating PI3K/Akt signaling 2022 , 79, 59 | 2 |
| 344 | X Curso internacional de avances en Oncologâ: investigaciñ y nuevos fîmacos. 2003 , 5, 98-110 | |
| 343 | Refining risk stratification in HR-positive/HER2-negative early breast cancer: how to select patients for treatment escalation?. 2022 , 1 | О |
| 342 | Aldehyde Dehydrogenase 2 Family Member (ALDH2) Is a Therapeutic Index for Oxaliplatin Response on Colorectal Cancer Therapy with Dysfunction p53 2022 , 2022, 1322788 | 1 |
| 341 | A framework to predict the applicability of Oncotype DX, MammaPrint, and E2F4 gene signatures for improving breast cancer prognostic prediction 2022 , 12, 2211 | |
| 340 | Transcriptome analysis method based on differential distribution evaluation 2022, | 0 |
| 339 | Differential gene expression and network analysis in head and neck squamous cell carcinoma 2022 , 1 | |

| 338 | Theranostic Interpolation of Genomic Instability in Breast Cancer 2022, 23, | | O |
|-----|---|------|----|
| 337 | Development of Gene Expression-Based Random Forest Model for Predicting Neoadjuvant Chemotherapy Response in Triple-Negative Breast Cancer 2022 , 14, | | 1 |
| 336 | Needs and preferences of breast cancer survivors regarding outcome-based shared decision-making about personalised post-treatment surveillance 2022 , 1 | | 1 |
| 335 | TP53 knockout in MCF7 breast cancer cells induces sensitivity to fluoropyrimidine drugs | | |
| 334 | KRas-transformed epithelia cells invade and partially dedifferentiate by basal cell extrusion. 2021 , 12, 7180 | | 5 |
| 333 | Multi-omic machine learning predictor of breast cancer therapy response. <i>Nature</i> , 2021 , | 50.4 | 15 |
| 332 | A metastasis-on-a-chip approach to explore the sympathetic modulation of breast cancer bone metastasis 2022 , 13, 100219 | | Ο |
| 331 | Artificial Intelligence in Blood Transcriptomics. 2022 , 1109-1123 | | |
| 330 | Prognostic Values and Underlying Regulatory Network of Cohesin Subunits in Esophageal Carcinoma 2022 , 13, 1588-1602 | | O |
| 329 | Cost-Effectiveness Analysis from a Societal Perspective of Recurrence Index for Distant Recurrence (RecurIndex) in Women with Hormone Receptor-Positive and HER2-Negative Early-Stage Breast Cancer 2022 , 14, 761-773 | | |
| 328 | Identification of Immune Markers in Dilated Cardiomyopathies with Heart Failure by Integrated Weighted Gene Coexpression Network Analysis 2022 , 13, | | 0 |
| 327 | Early Changes in Quantitative Ultrasound Imaging Parameters during Neoadjuvant Chemotherapy to Predict Recurrence in Patients with Locally Advanced Breast Cancer 2022 , 14, | | O |
| 326 | A pan-cancer landscape of telomeric content shows that RAD21 and HGF alterations are associated with longer telomeres 2022 , 14, 25 | | 0 |
| 325 | Multiomics Topic Modeling for Breast Cancer Classification 2022 , 14, | | O |
| 324 | A Combined Feature Screening Approach of Random Forest and Filter-based Methods for Ultra-high Dimensional Data. 2022 , 17, | | 0 |
| 323 | The extended concurrent genes signature for disease-free survival in breast cancer 2022, | | O |
| 322 | The Role of the 21-Gene Recurrence Score Assay in Hormone Receptor-Positive, Node-Positive Breast Cancer: The Canadian Experience 2022 , 29, 2008-2020 | | 0 |
| 321 | Deciphering Tumour Heterogeneity: From Tissue to Liquid Biopsy 2022 , 14, | | 2 |

| 320 | Second-Generation JK-206 Targets the Oncogenic Signal Mediator RHOA in Gastric Cancer 2022 , 14, | О |
|-----|--|---|
| 319 | A text-based computational framework for patient -specific modeling for classification of cancers 2022 , 25, 103944 | 1 |
| 318 | NRG1/ERBB3/ERBB2 Axis Triggers Anchorage-Independent Growth of Basal-like/Triple-Negative Breast Cancer Cells 2022 , 14, | 1 |
| 317 | Clinically oriented prediction of patient response to targeted and immunotherapies from the tumor transcriptome. | Ο |
| 316 | Clinical and Molecular Characteristics of ER-Positive Ultralow Risk Breast Cancer Tumors Identified by the 70-Gene Signature 2022 , | 1 |
| 315 | Visualizing Cytokeratin-14 Levels in Basal-Like Breast Cancer via ImmunoSPECT Imaging 2022 , | Ο |
| 314 | NetRank Recovers Known Cancer Hallmark Genes as Universal Biomarker Signature for Cancer Outcome Prediction. 2022 , 2, | |
| 313 | ExhauFS: exhaustive search-based feature selection for classification and survival regression 2022 , 10, e13200 | 1 |
| 312 | Tumor cell intrinsic and extrinsic features predict prognosis in estrogen receptor positive breast cancer 2022 , 18, e1009495 | |
| 311 | Supporting shared decision making about personalised surveillance after breast cancer: the development of a patient decision aid integrating personalised recurrence risk calculations (Preprint). | |
| 310 | Optimized feature selection method using particle swarm intelligence with ensemble learning for cancer classification based on microarray datasets. 1 | 1 |
| 309 | PLUS: Predicting cancer metastasis potential based on positive and unlabeled learning 2022 , 18, e1009956 | 1 |
| 308 | Breast Cancer Subtype-Specific miRNAs: Networks, Impacts, and the Potential for Intervention 2022 , 10, | 1 |
| 307 | Transcriptome-wide association and prediction for carotenoids and tocochromanols in fresh sweet corn kernels 2022 , e20197 | Ο |
| 306 | The ability to classify patients based on gene-expression data varies by algorithm and performance metric 2022 , 18, e1009926 | 0 |
| 305 | Decision Theory versus Conventional Statistics for Personalized Therapy of Breast Cancer 2022 , 12, | Ο |
| 304 | Age-Independent Preoperative Chemosensitivity and 5-Year Outcome Determined by Combined 70- and 80-Gene Signature in a Prospective Trial in Early-Stage Breast Cancer 2022 , 1 | |
| 303 | NRF2 drives an oxidative stress response predictive of breast cancer 2022 , | Ο |

| 302 | A new feature selection method based on feature distinguishing ability and network influence 2022 , 128, 104048 | 4 |
|---------------------------------|---|-------------|
| 301 | Transcriptome profiling of curcumin-treated T47D human breast cancer cells by a system-based approach. 2022 , 27, 101556 | O |
| 300 | End-to-end computational approach to the design of RNA biosensors for detecting miRNA biomarkers of cervical cancer 2022 , 7, 802-814 | 0 |
| 299 | Outcome-guided sparse K-means for disease subtype discovery via integrating phenotypic data with high-dimensional transcriptomic data. 2022 , 71, 352-375 | |
| 298 | A probabilistic model for pathway-guided gene set selection. 2021 , | |
| 297 | geneExpressionFromGEO: An R Package to Facilitate Data Reading from Gene Expression Omnibus (GEO) 2022 , 2401, 187-194 | 1 |
| 296 | The incidence of discordant clinical and genomic risk in patients with invasive lobular or ductal carcinoma of the breast: a National Cancer Database Study 2021 , 7, 156 | 1 |
| 295 | Conjoint analysis of circulating tumor cells and solid tumors for exploring potential prognostic markers and constructing a robust novel predictive signature for breast cancer 2021 , 21, 708 | 2 |
| 294 | A robust drug representation learning model for eliminating cell specificity in gene expression profile and its application. 2021 , | _ |
| | | |
| 293 | Multi-omics Topic Modeling for Breast Cancer Classification. | |
| 293 292 | Multi-omics Topic Modeling for Breast Cancer Classification. High concordance of 70-gene recurrence risk signature and 80-gene molecular subtyping signature between core needle biopsy and surgical resection specimens in early-stage breast cancer 2021, | O |
| | High concordance of 70-gene recurrence risk signature and 80-gene molecular subtyping signature | 0 |
| 292 | High concordance of 70-gene recurrence risk signature and 80-gene molecular subtyping signature between core needle biopsy and surgical resection specimens in early-stage breast cancer 2021 , Radiomics in predicting recurrence for patients with locally advanced breast cancer using | |
| 292 | High concordance of 70-gene recurrence risk signature and 80-gene molecular subtyping signature between core needle biopsy and surgical resection specimens in early-stage breast cancer 2021, Radiomics in predicting recurrence for patients with locally advanced breast cancer using quantitative ultrasound 2021, 12, 2437-2448 Biomarker discovery studies for patient stratification using machine learning analysis of omics data: | 1 |
| 292 291 290 | High concordance of 70-gene recurrence risk signature and 80-gene molecular subtyping signature between core needle biopsy and surgical resection specimens in early-stage breast cancer 2021, Radiomics in predicting recurrence for patients with locally advanced breast cancer using quantitative ultrasound 2021, 12, 2437-2448 Biomarker discovery studies for patient stratification using machine learning analysis of omics data: a scoping review. 2021, 11, e053674 Predicting Breast Cancer Gene Expression Signature by Applying Deep Convolutional Neural | 1 4 |
| 292 291 290 289 | High concordance of 70-gene recurrence risk signature and 80-gene molecular subtyping signature between core needle biopsy and surgical resection specimens in early-stage breast cancer 2021, Radiomics in predicting recurrence for patients with locally advanced breast cancer using quantitative ultrasound 2021, 12, 2437-2448 Biomarker discovery studies for patient stratification using machine learning analysis of omics data: a scoping review. 2021, 11, e053674 Predicting Breast Cancer Gene Expression Signature by Applying Deep Convolutional Neural Networks From Unannotated Pathological Images 2021, 11, 769447 Adaptor SH3BGRL drives autophagy-mediated chemoresistance through promoting PIK3C3 | 1 4 0 |
| 292 291 290 289 288 | High concordance of 70-gene recurrence risk signature and 80-gene molecular subtyping signature between core needle biopsy and surgical resection specimens in early-stage breast cancer 2021, Radiomics in predicting recurrence for patients with locally advanced breast cancer using quantitative ultrasound 2021, 12, 2437-2448 Biomarker discovery studies for patient stratification using machine learning analysis of omics data: a scoping review. 2021, 11, e053674 Predicting Breast Cancer Gene Expression Signature by Applying Deep Convolutional Neural Networks From Unannotated Pathological Images 2021, 11, 769447 Adaptor SH3BGRL drives autophagy-mediated chemoresistance through promoting PIK3C3 translation and ATG12 stability in breast cancers. 2021, 1-19 | 1 4 0 |

(2020-2022)

| 284 | 'Breast Cancer Resistance Likelihood and Personalized Treatment Through Integrated Multiomics' 2022 , 9, 783494 | O |
|-----|---|---|
| 283 | Using Technology to Personalize Middle School Math Instruction: Evidence From a Blended Learning Program in Five Public Schools. 2022 , 7, | |
| 282 | Value of the 21-gene expression assay in predicting locoregional recurrence rates in estrogen receptor-positive breast cancer: a systematic review and network meta-analysis 2022 , | O |
| 281 | A comprehensive study of mRNA and long noncoding RNAs in Indian Breast cancer patients using transcriptomics approach. | |
| 280 | Ultrasonic Features and Molecular Subtype Predict Somatic Mutations in TP53 and PIK3CA Genes in Breast Cancer 2022 , | О |
| 279 | Weighted p-norm distance t kernel SVM classification algorithm based on improved polarization 2022 , 12, 6197 | 1 |
| 278 | HSVNN: an efficient medical data classification using dimensionality reduction combined with hybrid support vector neural network. 1 | O |
| 277 | CmP signaling network unveils novel biomarkers for triple negative breast cancer in African American women 2022 , | 3 |
| 276 | Treatment response and 5-year distant metastasis-free survival outcome in breast cancer patients after the use of MammaPrint and BluePrint to guide preoperative systemic treatment decisions 2022 , 167, 92-102 | O |
| 275 | Systems biology of cancer progression. 1-6 | |
| 274 | Data_Sheet_1.pdf. 2020 , | |
| 273 | Data_Sheet_1.PDF. 2019 , | |
| 272 | Table_1.xlsx. 2019 , | |
| 271 | Table_2.xlsx. 2019 , | |
| 270 | DataSheet_1.docx. 2019 , | |
| 269 | Image_1.tif. 2020 , | |
| 268 | Image_10.TIF. 2020 , | |
| 267 | Image_2.TIF. 2020 , | |



| 248 | Data_Sheet_1.pdf. 2019 , | |
|-----|---|---|
| 247 | Image_1.pdf. 2020 , | |
| 246 | Image_2.pdf. 2020 , | |
| 245 | Image_3.pdf. 2020 , | |
| 244 | Image_4.pdf. 2020 , | |
| 243 | Image_5.pdf. 2020, | |
| 242 | Image_6.pdf. 2020 , | |
| 241 | Image_7.pdf. 2020 , | |
| 240 | Table_1.pdf. 2020 , | |
| 239 | Incorporating Omics Data in Genomic Prediction 2022, 2467, 341-357 | O |
| 238 | KMT2C deficiency promotes small cell lung cancer metastasis through DNMT3A-mediated epigenetic reprogramming 2022 , | 2 |
| 237 | Insights into immune escape during tumor evolution and response to immunotherapy using a rat model of breast cancer 2022 , | 1 |
| 236 | Deep Mining from Omics Data 2022 , 2449, 349-386 | |
| 235 | Binary Bat Algorithm with Dynamic Bayesian Network for Feature Selection on Cancer Gene Expression Profiles. 2022 , 150-159 | |
| 234 | Precision diagnostics in cancer: Predict, prevent, and personalize. 2022, | |
| 233 | In Situ Analytical Tools to Resolve Stress Response Mechanisms of Foodborne Pathogens. 2022 , 575-607 | |
| 232 | Stitch Fix for Mapper and Topological Gains. 2022 , 265-294 | |
| 231 | Distinct Neoadjuvant Chemotherapy Response and 5-Year Outcome in Patients With Estrogen Receptor-Positive, Human Epidermal Growth Factor Receptor 2-Negative Breast Tumors That Reclassify as Basal-Type by the 80-Gene Signature 2022 , 6, e2100463 | 1 |

| 230 | Dynamic Risk Prediction via a Joint Frailty-Copula Model and IPD Meta-Analysis: Building Web Applications. 2022 , 24, 589 | 2 |
|-----|---|-----|
| 229 | Innovations in Genomics and Big Data Analytics for Personalized Medicine and Health Care: A Review 2022 , 23, | 4 |
| 228 | A narrative review of five multigenetic assays in breast cancer 2022 , 11, 897-907 | 1 |
| 227 | A boosting first-hitting-time model for survival analysis in high-dimensional settings 2022, | O |
| 226 | Sufficient principal component regression for pattern discovery in transcriptomic data. | |
| 225 | eRNAs Identify Immune Microenvironment Patterns and Provide a Novel Prognostic Tool in Acute Myeloid Leukemia 2022 , 9, 877117 | O |
| 224 | A Pairwise Imputation Strategy for Retaining Predictive Features When Combining Multiple Datasets. | |
| 223 | Bililm Teknolojileri letmenlerinin Blok TabanllKodlama Aralarfia likin 🛭 Yeterlik lianlarfifi Evrilmsel Sinir Afile Sfifiandfilmasfi | |
| 222 | GATA2-Mediated Transcriptional Activation of Notch3 Promotes Pancreatic Cancer Liver Metastasis 2022 , 45, 329-342 | |
| 221 | Association between tumor F-fluorodeoxyglucose metabolism and survival in women with estrogen receptor-positive, HER2-negative breast cancer 2022 , 12, 7858 | О |
| 220 | Gene expression signatures in early Breast Cancer: better together with clinicopathological features 2022 , 103708 | 0 |
| 219 | A Novel Five-Gene Signature Related to Clinical Outcome and Immune Microenvironment in Breast Cancer. 2022 , 13, | О |
| 218 | Genomic Analysis of a Spontaneous Model of Breast Cancer Metastasis to Bone Reveals a Role for the Extracellular Matrix. 2005 , 3, 1-13 | 159 |
| 217 | Distinct Gene Expression Profiles of Matched Primary and Metastatic Triple-Negative Breast Cancers. 2022 , 14, 2447 | |
| 216 | ANLN and UBE2T are prognostic biomarkers associated with immune regulation in breast cancer: a bioinformatics analysis 2022 , 22, 193 | 2 |
| 215 | Breast Cancer-Stromal Interactions: Adipose-derived stromal/stem cell Age and Cancer Subtype Mediated Remodeling 2022 , | О |
| 214 | Cluster analysis of transcriptomic datasets to identify endotypes of idiopathic pulmonary fibrosis 2022 , | 0 |
| 213 | Development of Novel Cancer Biomarkers for Diagnosis and Prognosis. 2022 , 277-343 | |

| 212 | Emerging Concepts in Managing Malignancy in Kidney Transplant Patients. 2022 , 42, 63-75 | О |
|-----|--|---|
| 211 | Neuregulin 4 Boosts the Efficacy of Anti-ERBB2 Neutralizing Antibodies. 2022 , 12, | O |
| 210 | Clinicopathological characteristics and prognosis of microinvasive breast cancer: A population-based analysis. | |
| 209 | The regulatory landscape of retinoblastoma: a pathway analysis perspective. 2022 , 9, | O |
| 208 | Machine learning enables accurate prediction of breast cancer five-year survival using somatic genomic variants. | |
| 207 | Advancing microfluidic diagnostic chips for clinical use. | 1 |
| 206 | The Ramp Atlas: facilitating tissue and cell-specific ramp sequence analyses through an intuitive web interface. 2022 , 4, | 1 |
| 205 | XIST loss impairs mammary stem cell differentiation and increases tumorigenicity through Mediator hyperactivation. 2022 , | 1 |
| 204 | A Novel Method for Feature Selection Based on Molecular Interactive Effect Network. 2022 , 114873 | |
| 203 | Hypoxia Selectively Increases a SMAD3 Signaling Axis to Promote Cancer Cell Invasion. 2022 , 14, 2751 | 1 |
| 202 | Making Biomarkers Relevant to Healthcare Innovation and Precision Medicine. 2022, 10, 1107 | 1 |
| 201 | 5thomiR-183-5p +2 elicits tumor suppressor activity in a negative feedback loop with E2F1. 2022 , 41, | |
| 200 | Translational Epidemiology in Cancer Research: The Less Travelled Path. 2022, 349-366 | |
| 199 | A Comprehensive Survey of Recent Hybrid Feature Selection Methods in Cancer Microarray Gene Expression Data. 2022 , 1-1 | 1 |
| 198 | CFTR reduces the proliferation of lung adenocarcinoma and is a strong predictor of survival in both smokers and non-smokers. | О |
| 197 | Classification of triple negative breast cancer by epithelial mesenchymal transition and the tumor immune microenvironment. 2022 , 12, | О |
| 196 | NTN4 as a prognostic marker and a hallmark for immune infiltration in breast cancer. 2022, 12, | 1 |
| 195 | NR2F1, a Tumor Dormancy Marker, Is Expressed Predominantly in Cancer-Associated Fibroblasts and Is Associated with Suppressed Breast Cancer Cell Proliferation. 2022 , 14, 2962 | 1 |

| 194 | Stem Cell Theory of Cancer: Origin of Metastasis and Sub-clonality. 2022, | |
|-----|--|----|
| 193 | MicroRNA-126 expression in the peripheral white blood cells of patients with breast and ovarian cancer is a potential biomarker for the early prediction of cancer risk in the carriers of methylated BRCA1. 2022 , 24, | |
| 192 | L0-Regularized Learning for High-Dimensional Additive Hazards Regression. | О |
| 191 | Targeting Breast Cancer-Derived Stem Cells by Dietary Phytochemicals: A Strategy for Cancer Prevention and Treatment. 2022 , 14, 2864 | 0 |
| 190 | Breast cancer in the era of precision medicine. | O |
| 189 | Circular RNA circ-ABCB10 Promotes Proliferation and Inhibits Apoptosis of Laryngeal Carcinoma by Inhibiting KLF6. 2022 , 2022, 1-8 | |
| 188 | Extended endocrine therapy in breast cancer: A basket of length-constraint feature selection metaheuristics to balance Type I against Type II errors. 2022 , 131, 104112 | |
| 187 | Tailoring the Omission of Radiotherapy for Early-Stage Breast Cancer Based on Tumor Biology. 2022 , 32, 198-206 | 1 |
| 186 | Perinucleolar Compartment Prevalence Has an Independent Prognostic Value for Breast Cancer. 2005 , 65, 246-253 | 19 |
| 185 | Distinct gene expression patterns in a tamoxifen-sensitive human mammary carcinoma xenograft and its tamoxifen-resistant subline MaCa 3366/TAM. 2005 , 4, 151-170 | 17 |
| 184 | Tissue-Based Biomarkers of Tumor-Vascular Interactions. 2022 , 17-30 | |
| 183 | A Comparative Study of Model Selection for High Dimensional Data. 2022 , 342-350 | |
| 182 | The evolution of gene expression profiling in breast cancer 🖪 narrative review. 2022, | |
| 181 | Gene Expression Signatures of the Tumor Microenvironment: Relation to Tumor Phenotypes and Progress in Breast Cancer. 2022 , 401-424 | |
| 180 | Tumor Microenvironment Heterogeneity-Based Score System Predicts Clinical Prognosis and Response to Immune Checkpoint Blockade in Multiple Colorectal Cancer Cohorts. 9, | |
| 179 | Role of germline variants in the metastasis of breast carcinomas. 2022 , 13, 843-862 | |
| 178 | Multimodal Prediction of Breast Cancer Recurrence Assays and Risk of Recurrence. | 0 |
| 177 | The 21-Gene Recurrence Score in Clinically High-Risk Lobular and Ductal Breast Cancer: A National Cancer Database Study. | 1 |

| 176 | Role of immunohistochemical markers in breast carcinoma and other breast pathologies: A review with a note on recent update. 2022 , 9, 23-29 | |
|-----|---|----|
| 175 | Degraded RNA from human anterior cruciate ligaments yields valid gene expression profiles. | |
| 174 | The risk of relapse in breast cancer patients is associated with MMP-9 gene polymorphism: a prospective study in a sample of the Iranian population. 1-12 | |
| 173 | A Novel Prognostic Nomogram for Predicting Survival of Hormone Receptor-Positive and HER2 Negative Advanced Breast Cancer Among the Han-Population. 12, | Ο |
| 172 | Design of Marker Panels for Prediction of Neoadjuvant Chemotherapy Response of Triple-Negative Breast Tumors Based on the Results of Genome-Wide DNA Methylation Screening. 2022 , 58, 835-843 | |
| 171 | Deep survival forests for extremely high censored data. | |
| 170 | Predicting continuous values of prognostic markers in breast cancer from microarray gene expression profiles. 2004 , 3, 161-168 | 6 |
| 169 | Signatures of Environmental Exposures Using Peripheral Leukocyte Gene Expression: Tobacco Smoke. 2004 , 13, 445-453 | 24 |
| 168 | Gene Expression in Kidney Cancer Is Associated with Cytogenetic Abnormalities, Metastasis Formation, and Patient Survival. 2005 , 11, 646-655 | 15 |
| 167 | A Predictor Based on the Somatic Genomic Changes of the BRCA1/BRCA2 Breast Cancer Tumors Identifies the Non-BRCA1/BRCA2 Tumors with BRCA1 Promoter Hypermethylation. 2005 , 11, 1146-1153 | 19 |
| 166 | Protein Expression Profiling Identifies Subclasses of Breast Cancer and Predicts Prognosis. 2005 , 65, 767-779 | 37 |
| 165 | Transcriptional Profiles in Peripheral Blood Mononuclear Cells Prognostic of Clinical Outcomes in Patients with Advanced Renal Cell Carcinoma. 2005 , 11, 1181-1189 | 22 |
| 164 | Toward the Last Cohort. 2004 , 13, 895-897 | 6 |
| 163 | Mammographic Density and Estrogen Receptor Status of Breast Cancer. 2004 , 13, 2090-2095 | 23 |
| 162 | Twenty-Year Benefit From Adjuvant Goserelin and Tamoxifen in Premenopausal Patients With Breast Cancer in a Controlled Randomized Clinical Trial. | 1 |
| 161 | A Review of Artificial Intelligence and Robotics in Transformed Health Ecosystems. 9, | |
| 160 | Multi-Omics Binary Integration via Lasso Ensembles (MOBILE) for identification of context-specific networks and new regulatory mechanisms. | 0 |
| 159 | Prognosis of NonBmall Cell Lung Cancer Patients by Detecting Circulating Cancer Cells in the Peripheral Blood with Multiple Marker Genes. 2005 , 11, 173-179 | 27 |

| 158 | Analyzing biomarker discovery: Estimating the reproducibility of biomarker sets. 2022 , 17, e0252697 | |
|-----|---|----|
| 157 | Clinical Utility of Genomic Assay in Node-Positive Early-Stage Breast Cancer. 2022 , 29, 5139-5149 | |
| 156 | Firmas gĥicas en el cficer de mama. 2022 , 35, S67-S86 | |
| 155 | Machine learning models based on immunological genes to predict the response to neoadjuvant therapy in breast cancer patients. 13, | O |
| 154 | A tumor microenvironment-related risk model for predicting the prognosis and tumor immunity of breast cancer patients. 13, | О |
| 153 | Bayesian nonnegative matrix factorization in an incremental manner for data representation. | |
| 152 | A Review of the Nucleic Acid-Based Lateral Flow Assay for Detection of Breast Cancer from Circulating Biomarkers at a Point-of-Care in Low Income Countries. 2022 , 12, 1973 | 2 |
| 151 | Novel estrogen-responsive genes (ERGs) for the evaluation of estrogenic activity. 2022 , 17, e0273164 | О |
| 150 | Prediction of Breast Cancer Distant Metastasis by Artificial Intelligence Methods from an Epidemiological Perspective. 2022 , 23, 210-215 | О |
| 149 | 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 | |
| 148 | Accurate determination of CRISPR-mediated gene fitness in transplantable tumours. 2022, 13, | |
| 147 | Phage antibodies against heat shock proteins as tools for in vitro cancer diagnosis. 2022 , 11, 100211 | |
| 146 | The current staging and classification systems of breast cancer and their pitfalls: Is it possible to integrate the complexity of this neoplasm into a unified staging system?. 2022 , 178, 103781 | 1 |
| 145 | Tailoring neoadjuvant treatment of HR-positive/HER2-negative breast cancers: Which role for gene expression assays?. 2022 , 110, 102454 | 1 |
| 144 | Interlaboratory Comparability Study of Cancer Gene Expression Analysis Using Oligonucleotide Microarrays. 2005 , 11, 565-572 | 25 |
| 143 | Deep View of HCC Gene Expression Signatures and Their Comparison with Other Cancers. 2022 , 14, 4322 | O |
| 142 | Genomic Classification of HER2-Positive Patients With 80-Gene and 70-Gene Signatures Identifies Diversity in Clinical Outcomes With HER2-Targeted Neoadjuvant Therapy. 2022 , | 1 |
| 141 | Ten-year follow-up of the observational RASTER study, prospective evaluation of the 70-gene signature in ER-positive, HER2-negative, node-negative, early breast cancer. 2022 , 175, 169-179 | O |

| 140 | Deep survival forests with feature screening. 2023 , 79, 104195 | 0 |
|-----|---|---|
| 139 | Biomarkers, Prognosis, and Prediction Factors. 2023 , 49-70 | О |
| 138 | Explainable machine learning of the breast cancer staging for designing smart biomarker sensors. 2022 , 3, 100202 | 3 |
| 137 | Proposal of SVM Utility Kernel for Breast Cancer Survival Estimation. 2022 , 1-12 | o |
| 136 | Using classification and K-means methods to predict breast cancer recurrence in gene expression data. 2022 , 12, 122 | 0 |
| 135 | The Clinical Research and Latest Application of Genomic Assays in Early-Stage Breast Cancer. 2022 , 21, 153303382211174 | O |
| 134 | Supporting shared decision making about surveillance after breast cancer with personalised recurrence risk calculations: the development of a patient decision aid using the IPDAS development process in combination with a mixed-methods design (Preprint). | o |
| 133 | Computational Studies in Breast Cancer. 2022 , 434-456 | O |
| 132 | Development and testing of a polygenic risk score for breast cancer aggressiveness. | O |
| 131 | TIGER: A Web Portal of Tumor Immunotherapy Gene Expression Resource. 2022, | 1 |
| 130 | Transcriptomic Harmonization as the Way for Suppressing Cross-Platform Bias and Batch Effect. 2022 , 10, 2318 | 0 |
| 129 | Hybrid Feature Selection of Breast Cancer Gene Expression Microarray Data Based on Metaheuristic Methods: A Comprehensive Review. 2022 , 14, 1955 | 1 |
| 128 | TGFB2-AS1 inhibits triple-negative breast cancer progression via interaction with SMARCA4 and regulating its targets TGFB2 and SOX2. 2022 , 119, | 1 |
| 127 | Particle Swarm Optimization Artificial Intelligence technique for gene signature discovery in transcriptomic cohorts. 2022 , | o |
| 126 | Cost and Clinical Benefits Associated with Oncotype DXII Test in Patients with Early-Stage HR+/HER2- Node-Negative Breast Cancer in the Netherlands. 2022 , 2022, 1-12 | 0 |
| 125 | MTRRE-Net: A deep learning model for detection of breast cancer from histopathological images. 2022 , 106155 | 1 |
| 124 | Improving prediction of response to neoadjuvant treatment in patients with breast cancer by combining liquid biopsies with multiparametric MRI: protocol of the LIMA study has multicentre prospective observational cohort study. 2022 , 12, e061334 | 0 |
| 123 | A vicious circle in breast cancer: The interplay between inflammation, reactive oxygen species, and microRNAs. 12, | O |

| 122 | Collagen fiber features and COL1A1: are they associated with elastic parameters in breast lesions, and can COL1A1 predict axillary lymph node metastasis?. 2022 , 22, | О |
|-----|--|---|
| 121 | Molecular Classification of Breast Cancer. 2022 , | O |
| 120 | Effect of heat stress on DNA damage: a systematic literature review. | 0 |
| 119 | Big data in basic and translational cancer research. | 3 |
| 118 | Self-organizing map with granular competitive learning: Application to microarray clustering. 2022 , 16, 505-521 | 0 |
| 117 | Spectrophotometric Detection of the BRCA1 Gene via Exponential Isothermal Amplification and Hybridization Chain Reaction of Surface-Bound Probes. 2022 , 38, 12050-12057 | O |
| 116 | Gene reduction and machine learning algorithms for cancer classification based on microarray gene expression data: A comprehensive review. 2022 , 118946 | 1 |
| 115 | Single Nucleotide Variants in KIF14 Gene May Have Prognostic Value in Breast Cancer. | O |
| 114 | Construction of novel lncRNA-miRNA-mRNA ceRNA networks associated with prognosis of hepatitis C virus related hepatocellular carcinoma. 2022 , 8, e10832 | 0 |
| 113 | A graph based preordonnances theoretic supervised feature selection in high dimensional data. 2022 , 257, 109899 | O |
| 112 | MiR-135a-5p suppresses breast cancer cell proliferation, migration, and invasion by regulating BAG3. 2022 , 77, 100115 | 0 |
| 111 | Wildtype heterogeneity contributes to clonal variability in genome edited cells. 2022 , 12, | 1 |
| 110 | Extended adjuvant endocrine treatment for premenopausal women: A Delphi approach to guide clinical practice. 12, | О |
| 109 | Transcriptomic profiling of Indian breast cancer patients revealed subtype-specific mRNA and lncRNA signatures. 13, | O |
| 108 | Bioinformatics and Experimental Analyses Reveal Immune-Related LncRNAthRNA Pair AC011483.1-CCR7 as a Biomarker and Therapeutic Target for Ischemic Cardiomyopathy. 2022 , 23, 11994 | 0 |
| 107 | Prognostic and Predictive Significance of Stromal Tumor-Infiltrating Lymphocytes (sTILs) in ER-Positive/HER2Negative Postmenopausal Breast Cancer Patients. 2022 , 14, 4844 | O |
| 106 | Molecular Biology, Genetics, and Translational Models of Human Cancer. 1-34 | О |
| 105 | Cancer Genomics and Evolution. 1-30 | O |

| 104 | PKC-mediated phosphorylation and activation of the MEK/ERK pathway as a mechanism of acquired trastuzumab resistance in HER2-positive breast cancer. 13, | О |
|-----|---|---|
| 103 | Prediction of Cancer Treatment using Advancements in Machine Learning. 2022, 18, | O |
| 102 | Genomic Profiling and Liquid Biopsies for Breast Cancer. 2022, | О |
| 101 | Tackling the translational challenges of multi-omics research in the realm of European personalised medicine: A workshop report. 9, | O |
| 100 | A Robust Personalized Classification Method for Breast Cancer Metastasis Prediction. 2022 , 14, 5327 | О |
| 99 | Systems Biology and Genomics. 1-11 | O |
| 98 | The Gene Expression Landscape of Prostate Cancer BM Reveals Close Interaction with the Bone Microenvironment. 2022 , 23, 13029 | 0 |
| 97 | A hybrid feature selection approach for Microarray datasets using graph theoretic-based method. 2022 , 615, 449-474 | O |
| 96 | Anterior Gradient 2 is a Significant Prognostic Biomarker in Bone Metastasis of Breast Cancer. 28, | О |
| 95 | Label consistency-based deep semisupervised NMF for tumor recognition. 2023 , 117, 105511 | O |
| 94 | Plectin as a putative novel biomarker for breast cancer: an in silico study. 2022, 11, | О |
| 93 | Non-Invasive and Real-Time Monitoring of the Breast Cancer Metastasis Degree Via Metabolomics. 2022 , 14, 5589 | O |
| 92 | KGA: integrating KPCA and GAN for microbial data augmentation. | О |
| 91 | Five-gene Signature for the Prediction of Response to Immune Checkpoint Inhibitors in Patients with Gastric and Urothelial Carcinomas. 2022 , 154233 | O |
| 90 | Signatures of Breast Cancer Progression in the Blood: What Could Be Learned from Circulating Tumor Cell Transcriptomes. 2022 , 14, 5668 | 1 |
| 89 | Breast Cancer Pathology in the Era of Genomics. 2023 , 37, 33-50 | Ο |
| 88 | Genomics and Disease Progression in IgA Nephritis. 2013 , 42, 674-680 | 0 |
| 87 | Random Survival Forests Incorporated by the Nadaraya-Watson Regression. 2022 , 21, 851-880 | Ο |

| 86 | Imputation Strategies for Clustering Mixed-Type Data with Missing Values. | O |
|----|--|---|
| 85 | The Potential Role of MUC16 (CA125) Biomarker in Lung Cancer: A Magic Biomarker but with Adversity. 2022 , 12, 2985 | O |
| 84 | Analysis of Proposed and Traditional Boosting Algorithm with Standalone Classification Methods for Classifying Gene Expresssion Microarray Data Using a Reject Option. 2022 , 36, | О |
| 83 | An Approach for Systems-Level Understanding of Prostate Cancer from High-Throughput Data Integration to Pathway Modeling and Simulation. 2022 , 11, 4121 | O |
| 82 | Clinically oriented prediction of patient response to targeted and immunotherapies from the tumor transcriptome. 2022 , | О |
| 81 | Artificial intelligence in breast cancer diagnostics. 2022 , 3, 100851 | 0 |
| 80 | DNA methylation patterns define subtypes of differentiated follicular cell-derived thyroid neoplasms: an unsupervised machine learning approach. | О |
| 79 | Locally finite distance clustering with discriminative information. 2022, | O |
| 78 | Combined 70- and 80-gene signatures identify tumors with genomically luminal biology responsive to neoadjuvant endocrine therapy and are prognostic of 5-year outcome in early-stage breast cancer. 2022 , 45, 101885 | О |
| 77 | A novel 9-gene signature for the prediction of postoperative recurrence in stage II/III colorectal cancer. 13, | 0 |
| 76 | Cancer Prognosis and Diagnosis Methods Based on Ensemble Learning. | 0 |
| 75 | Prognosis according to the timing of recurrence in breast cancer. 2023 , 104, 1 | 0 |
| 74 | Polygenic risk score for prediction of radiotherapy efficacy and radiosensitivity in patients with non-metastatic breast cancer. 2023 , | O |
| 73 | Construction of a lncRNA-mediated ceRNA network and a genomic-clinicopathologic nomogram to predict survival for breast cancer patients. 2023 , 36, 83-96 | O |
| 72 | A signature of immune-related genes correlating with clinical prognosis and immune microenvironment in sepsis. 2023 , 24, | О |
| 71 | Screening and identification of potential key biomarkers for glucocorticoid-induced osteonecrosis of the femoral head. 2023 , 18, | 1 |
| 70 | Memetic micro-genetic algorithms for cancer data classification. 2023 , 17, 200173 | 2 |
| 69 | Self-supervised learning-based Multi-Scale feature Fusion Network for survival analysis from whole slide images. 2023 , 153, 106482 | 0 |

| 68 | Feature selection combined with top-down and bottom-up strategies for survival analysis: A case of prognostic prediction in glioblastoma. 2023 , 153, 106486 | O |
|----|--|---|
| 67 | Heterogeneity of cGMP signalling in tumour cells and the tumour microenvironment: Challenges and chances for cancer pharmacology and therapeutics. 2023 , 242, 108337 | Ο |
| 66 | Comparing of feature selection algorithms. 2022, | O |
| 65 | The Prognostic and Predictive Value of Genomic Assays in Guiding Adjuvant Breast Radiation Therapy. 2023 , 11, 98 | O |
| 64 | A pairwise strategy for imputing predictive features when combining multiple datasets. 2023, 39, | О |
| 63 | The investigation of levels of endothelial cell-specific molecule, progranuline, clusterin, and human epididymis protein 4 in the differential diagnosis of malignant pleural effusions. 2022 , 101, e32471 | O |
| 62 | Molecular Diagnostics. 2019 , 226-248 | O |
| 61 | A Two-Step Feature Selection Radiomic Approach to Predict Molecular Outcomes in Breast Cancer. 2023 , 23, 1552 | O |
| 60 | The genomic regulation of metastatic dormancy. | O |
| 59 | Matrix metalloproteinases as therapeutic targets in breast cancer. 12, | 0 |
| 58 | The emerging role of MCPH1/BRIT1 in carcinogenesis. 13, | O |
| 57 | Degraded RNA from Human Anterior Cruciate Ligaments Yields Valid Gene Expression Profiles. 2023 , 24, 1895 | 0 |
| 56 | Gene Expression Profiles in Cancers and Their Therapeutic Implications. 2023, 29, 9-14 | O |
| 55 | Construction and characterization of a cuproptosis- and immune checkpoint-based LncRNAs signature for breast cancer risk stratification. | O |
| 54 | Assessment of stained direct cytology smears of breast cancer for whole transcriptome and targeted messenger RNA sequencing. | 0 |
| 53 | Automated Molecular Subtyping of Breast Carcinoma using Deep Learning Techniques. 2023, 1-1 | O |
| 52 | A Comprehensive Investigation of Genomic Variants in Prostate Cancer Reveals 30 Putative Regulatory Variants. 2023 , 24, 2472 | О |
| 51 | Associations of a Breast Cancer Polygenic Risk Score With Tumor Characteristics and Survival. | Ο |

| 50 | Breast Cancer Disease Exploitation to Recure a Healthy Lifestyle. 2022, 2617-2635 | O |
|----|--|---|
| 49 | Establishment and validation of a multigene model to predict the risk of relapse in hormone receptor-positive early-stage Chinese breast cancer patients. 2023 , 136, 184-193 | O |
| 48 | Molecular Subtypes of Breast Cancer and CDk Dysregulation. 2023, 133-148 | O |
| 47 | Opportunities and Challenges for the Development of MRCK Kinases Inhibitors as Potential Cancer Chemotherapeutics. 2023 , 12, 534 | O |
| 46 | Mechanistic modeling of metastatic relapse in early breast cancer to investigate the biological impact of prognostic biomarkers. 2023 , 231, 107401 | О |
| 45 | Deciphering breast cancer: from biology to the clinic. 2023 , 186, 1708-1728 | O |
| 44 | Integration of clinical features and deep learning on pathology for the prediction of breast cancer recurrence assays and risk of recurrence. 2023 , 9, | О |
| 43 | Aiding Cancer Buweet Tooth ERole of Hexokinases in Metabolic Reprogramming. 2023, 13, 946 | O |
| 42 | Molecular principles of tissue invasion and metastasis. 2023 , 324, C971-C991 | O |
| 41 | Both fine-grained and coarse-grained spatial patterns of neural activity measured by functional MRI show preferential encoding of pain in the human brain. 2023 , 272, 120049 | O |
| 40 | The effect of attendance in the Dutch breast cancer screening program on breast tumor characteristics among migrant women. 2023 , 69, 290-298 | O |
| 39 | Meta-analysis of engineered nanoparticles dynamic aggregation in freshwater-like systems using machine learning techniques. 2023 , 337, 117739 | O |
| 38 | Searching for DNA methylation in patients triple-negative breast cancer: a liquid biopsy approach. 2023 , 23, 41-51 | O |
| 37 | Chromatin profile-based identification of a novel ER-positive breast cancer subgroup with reduced ER-responsive element accessibility. 2023 , 128, 1208-1222 | O |
| 36 | Pan-cancer molecular subtypes of metastasis reveal distinct and evolving transcriptional programs. 2023 , 4, 100932 | 1 |
| 35 | Molecular profiling in contemporary breast cancer management. | O |
| 34 | Evaluation and comparison of different breast cancer prognosis scores based on gene expression data. 2023 , 25, | 0 |
| 33 | A New Evolutionary Ensemble Learning of Multimodal Feature Selection from Microarray Data. | O |

| 32 | Hybrid Filter and Genetic Algorithm-Based Feature Selection for Improving Cancer Classification in High-Dimensional Microarray Data. 2023 , 11, 562 | 1 |
|----|--|---|
| 31 | Premenopausal women with breast cancer in the early postpartum period show molecular profiles of invasion and are associated with poor prognosis. | O |
| 30 | Lessons from other fields of medicine, Part 1: Breast cancer. 2023 , 101-118 | О |
| 29 | Clinically relevant gene signatures provide independent prognostic information in older breast cancer patients. | O |
| 28 | Association of Neighborhood-Level Household Income With 21-Gene Recurrence Score and Survival Among Patients With Estrogen Receptor Positive Breast Cancer. 2023 , 6, e230179 | О |
| 27 | Exploration of prognostic genes and risk signature in breast cancer patients based on RNA binding proteins associated with ferroptosis. 14, | O |
| 26 | Cancer Diagnostics. 2023 , 459-481 | 0 |
| 25 | Circulating tumor DNA reveals complex biological features with clinical relevance in metastatic breast cancer. 2023 , 14, | Ο |
| 24 | Molecular Profiling in Early ER + Breast Cancer to Aid Systemic Therapy Decisions. 2023 , 25, 491-500 | 0 |
| 23 | Genetic Considerations in the Locoregional Management of Breast Cancer: a Review of Current Evidence. 2023 , 15, 48-57 | O |
| 22 | Sensitivity Analysis for Survival Prognostic Prediction with Gene Selection: A Copula Method for Dependent Censoring. 2023 , 11, 797 | О |
| 21 | Leveraging transcriptomics for precision diagnosis: Lessons learned from cancer and sepsis. 14, | O |
| 20 | Improving the robustness and stability of a machine learning model for breast cancer prognosis through the use of multi-modal classifiers. 2023 , 13, | О |
| 19 | Biology of Cancer-Testis Antigens and Their Therapeutic Implications in Cancer. 2023 , 12, 926 | O |
| 18 | Systemic therapy for hormone receptor-positive/human epidermal growth factor receptor 2-negative early stage and metastatic breast cancer. | 0 |
| 17 | Disease progression based feature screening for ultrahigh-dimensional survival-associated biomarkers. | O |
| 16 | Special Studies. 2013 , 279-304 | О |
| 15 | Loss of TTC17 promotes breast cancer metastasis through RAP1/CDC42 signaling and sensitizes it to rapamycin and paclitaxel. 2023 , 13, | O |

| 14 | Multimodal feature selection from microarray data based on DempsterBhafer evidence fusion. | O |
|----|--|---|
| 13 | Molecular breast cancer subtype identification using photoacoustic spectral analysis and machine learning at the biomacromolecular level. 2023 , 30, 100483 | O |
| 12 | The Response of Triple-Negative Breast Cancer to Neoadjuvant Chemotherapy and the Epithelial Mesenchymal Transition. 2023 , 24, 6422 | O |
| 11 | Evaluating the Necessity for Routine Sentinel Lymph Node Biopsy in Postmenopausal Patients Being Treated for Clinically Node Negative Breast Cancer the Era of RxPONDER. 2023 , | O |
| 10 | RRM2 and CDC6 are novel effectors of XBP1-mediated endocrine resistance and predictive markers of tamoxifen sensitivity. 2023 , 23, | О |
| 9 | Majority voting based on different feature ranking techniques from gene expression. 2023 , 1-15 | O |
| 8 | A New hybrid Feature selection-Classification model to Improve Cancer Sample Classification Accuracy in Microarray Gene Expression Data. 2023 , | О |
| 7 | Applying a GAN-based classifier to improve transcriptome-based prognostication in breast cancer. 2023 , 19, e1011035 | O |
| 6 | Radiomic tumor phenotypes augment molecular profiling in predicting recurrence free survival after breast neoadjuvant chemotherapy. 2023 , 3, | O |
| 5 | A novel gene signature to predict response to neoadjuvant chemotherapy and endocrine treatment in estrogen receptor-positive breast cancer patients. | O |
| 4 | Bioengineering and Bioinformatic Approaches to Study Extracellular Matrix Remodeling and CancerMacrophage Crosstalk in the Breast Tumor Microenvironment. 2023 , 201-229 | О |
| 3 | Development and validation of a nomogram for predicting axillary lymph node metastasis in breast cancer. 2023 , | O |
| 2 | The Role of TGF-B in Radiation Response. 2023 , 24, 7614 | 0 |
| 1 | Single cell trajectory analysis reveals a CD9 positive state to contribute to exit from stem cell-like and embryonic diapause states and transit to drug resistant states. | O |