

CITATION REPORT

List of articles citing

Classification of human lung carcinomas by mRNA expression profiling reveals distinct adenocarcinoma subclasses

DOI: 10.1073/pnas.191502998

Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 13790-5.

Source: <https://exaly.com/paper-pdf/32580474/citation-report.pdf>

Version: 2024-04-10

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
2142	The Geochemical Evolution of Anorthosite Residual Magmas in the Laramie Anorthosite Complex, Wyoming. 1996 , 37, 637-660		90
2141	Bilateral hippocampal atrophy: consequences to verbal memory following temporal lobectomy. 2001 , 57, 597-604		35
2140	Discordant protein and mRNA expression in lung adenocarcinomas. 2002 , 1, 304-13		719
2139	Integrated classification of lung tumors and cell lines by expression profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 12357-62	11.5	125
2138	Genome-wide coexpression dynamics: theory and application. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 16875-80	11.5	137
2137	Deciphering peripheral nerve myelination by using Schwann cell expression profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 8998-9003	11.5	108
2136	Changes in the proteome associated with the action of Bcr-Abl tyrosine kinase are not related to transcriptional regulation. 2002 , 1, 876-84		23
2135	Binary tree-structured vector quantization approach to clustering and visualizing microarray data. 2002 , 18 Suppl 1, S111-9		51
2134	An international database and integrated analysis tools for the study of cancer gene expression. 2002 , 2, 156-64		29
2133	Differential display in the time of microarrays. 2002 , 2, 209-16		10
2132	Linking gene expression data with patient survival times using partial least squares. 2002 , 18 Suppl 1, S120-7		83
2131	Transcriptional response of <i>Saccharomyces cerevisiae</i> to DNA-damaging agents does not identify the genes that protect against these agents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 8778-83	11.5	211
2130	TTF-1 expression in pulmonary adenocarcinomas. 2002 , 26, 767-73		307
2129	The molecular biology of lung cancer. 2002 , 8, 265-9		8
2128	Microarray analysis in prostate cancer research. 2002 , 12, 395-9		21
2127	Role of Thyroid Transcription Factor-1 in Pulmonary Adenocarcinoma. 2002 , 169-179		1
2126	Microarrays in pharmacogenomics--advances and future promise. 2002 , 3, 589-601		37

2125	Algorithms in Bioinformatics. 2002 ,	3
2124	Microarrays and molecular markers for tumor classification. 2002 , 3, comment2005	12
2123	Rules for making human tumor cells. 2002 , 347, 1593-603	750
2122	P-quasi complete linkage analysis for gene-expression data.	0
2121	Expression profiling of primary non-small cell lung cancer for target identification. 2002 , 21, 7749-63	130
2120	IV international conference on prevention and early detection of lung cancer, Reykjavik, Iceland, August 9-12, 2001. 2002 , 37, 325-44	11
2119	Molecular biology and early diagnosis in lung cancer. 2002 , 38, S5-8	11
2118	Using cancer genetics to guide the selection of anticancer drug targets. 2002 , 2, 366-73	39
2117	The value of microarray techniques for quantitative gene profiling in molecular diagnostics. 2002 , 8, 269-72	32
2116	Gene expression correlates of clinical prostate cancer behavior. 2002 , 1, 203-9	1829
2115	Understanding cancer through gene expression profiling. 2002 , 1246, 261-270	
2114	Microarrays as cancer keys: an array of possibilities. 2002 , 20, 3165-75	102
2113	Application of Microarrays to the Analysis of Gene Expression in Cancer. 2002 , 48, 1170-1177	116
2112	CEACAM1: a marker with a difference or more of the same?. 2002 , 20, 4273-5	16
2111	DNA microarrays in clinical oncology. 2002 , 20, 1932-41	283
2110	Optimal gene expression analysis by microarrays. 2002 , 2, 353-61	128
2109	News in brief. 2002 , 7, 93-97	
2108	Clinical relevance of molecular markers in lung cancer. 2002 , 11, 167-79	27

2107	Identification of differentially expressed genes in pulmonary adenocarcinoma by using cDNA array. 2002 , 21, 5804-13	158
2106	Genetic alterations of multiple tumor suppressors and oncogenes in the carcinogenesis and progression of lung cancer. 2002 , 21, 7421-34	175
2105	Innovative molecular and imaging approaches for the detection of lung cancer and its precursor lesions. 2002 , 21, 6949-59	51
2104	Novel candidate tumor marker genes for lung adenocarcinoma. 2002 , 21, 7598-604	78
2103	Decreased expression of 14-3-3sigma in neuroendocrine tumors is independent of origin and malignant potential. 2002 , 21, 8310-9	29
2102	Molecular portraits and the family tree of cancer. 2002 , 32 Suppl, 533-40	223
2101	Gene-expression profiles predict survival of patients with lung adenocarcinoma. 2002 , 8, 816-24	1597
2100	Modelling the molecular circuitry of cancer. 2002 , 2, 331-41	759
2099	Discussion on the meeting on Statistical modelling and analysis of genetic data 2002 , 64, 737-775	10
2098	Expression profiling with oligonucleotide arrays: technologies and applications for neurobiology. 2002 , 27, 1005-26	8
2097	Gene expression profiling of endocrine tumors using DNA microarrays: progress and promise. 2003 , 14, 107-16	11
2096	Relation Between Permutation-Test P Values and Classifier Error Estimates. 2003 , 52, 11-30	16
2095	Differential Gene Expression Analysis by DNA Microarray Technology and Its Application in Molecular Oncology. 2003 , 37, 486-494	8
2094	The future of cancer management: translating the genome, transcriptome, and proteome. 2003 , 10, 7-14	15
2093	Inhibition of FLT3 in MLL. Validation of a therapeutic target identified by gene expression based classification. 2003 , 3, 173-83	353
2092	Induction of small cell lung cancer by somatic inactivation of both Trp53 and Rb1 in a conditional mouse model. 2003 , 4, 181-9	429
2091	Epidemiology, cancer genetics and microarrays: making correct inferences, using appropriate designs. 2003 , 19, 690-5	40
2090	Trustworthiness and metrics in visualizing similarity of gene expression. 2003 , 4, 48	68

2089	Statistical significance for hierarchical clustering in genetic association and microarray expression studies. 2003 , 4, 62	20
2088	Prognostic implications of neuroendocrine differentiation and hormone production in patients with Stage I nonsmall cell lung carcinoma. 2003 , 97, 2487-97	76
2087	cDNA microarray analysis of gene expression in pathologic Stage IA nonsmall cell lung carcinomas. 2003 , 97, 2798-805	31
2086	Identification of TDE2 gene and its expression in non-small cell lung cancer. <i>International Journal of Cancer</i> , 2003 , 107, 238-43	7.5 21
2085	On the nature of genetic changes required for the development of esophageal cancer. 2003 , 36, 82-9	13
2084	Simultaneous classification and relevant feature identification in high-dimensional spaces: application to molecular profiling data. 2003 , 83, 729-743	50
2083	Surgery for early stage non-small cell lung cancer. 2003 , 21, 74-84	25
2082	Translational research in lung cancer. 2003 , 21, 205-19	13
2081	Differential expression of telomerase activity in neuroendocrine lung tumours: correlation with gene product immunophenotyping. 2003 , 201, 127-33	27
2080	WIF1, a component of the Wnt pathway, is down-regulated in prostate, breast, lung, and bladder cancer. 2003 , 201, 204-12	286
2079	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
2078	Advantages and limitations of microarray technology in human cancer. 2003 , 22, 6497-507	204
2077	MALAT-1, a novel noncoding RNA, and thymosin beta4 predict metastasis and survival in early-stage non-small cell lung cancer. 2003 , 22, 8031-41	1669
2076	DNA arrays in clinical oncology: promises and challenges. 2003 , 83, 305-16	32
2075	A molecular signature of metastasis in primary solid tumors. 2003 , 33, 49-54	1973
2074	Analysing differential gene expression in cancer. 2003 , 3, 869-76	109
2073	Issues and progress with protein kinase inhibitors for cancer treatment. 2003 , 2, 296-313	410
2072	Gene expression in lung adenocarcinomas of smokers and nonsmokers. 2003 , 29, 157-62	102

2071	Application of microarray technology in environmental and comparative physiology. 2003 , 65, 231-59	141
2070	Microarray analysis in the clinical management of cancer. 2003 , 17, 377-87	14
2069	The c-myc x E2F-1/p21 interactive gene expression index augments cytomorphologic diagnosis of lung cancer in fine-needle aspirate specimens. 2003 , 5, 176-83	12
2068	Molecular genetics of lung cancer. 2003 , 54, 73-87	250
2067	Classification of bladder cancer by microarray expression profiling: towards a general clinical use of microarrays in cancer diagnostics. 2003 , 3, 635-47	32
2066	The molecular basis of lung cancer: molecular abnormalities and therapeutic implications. 2003 , 4, 12	46
2065	Molecular fingerprinting in human lung cancer. 2003 , 5, 113-8	23
2064	Identification of a novel homeobox-containing gene, LAGY, which is downregulated in lung cancer. 2003 , 64, 450-8	36
2063	Non-small-cell lung cancer molecular signatures recapitulate lung developmental pathways. 2003 , 163, 1949-60	185
2062	Isolation of lung tumor specific peptides from a random peptide library: generation of diagnostic and cell-targeting reagents. 2003 , 202, 219-30	106
2061	Proteomic patterns of tumour subsets in non-small-cell lung cancer. 2003 , 362, 433-9	539
2060	Dissecting the genetic alterations involved in lung carcinogenesis. 2003 , 40, 111-21	30
2059	Molecular staging and pharmacogenomics. Clinical implications: from lab to patients and back. 2003 , 41 Suppl 1, S147-54	16
2058	E-27. Overview: Impact of microarray technology on lung cancer classification and biomarker development. 2003 , 41, S35-S36	
2057	Large-scale molecular and tissue microarray analysis of mesothelin expression in common human carcinomas. 2003 , 34, 605-9	132
2056	A mechanism of cyclin D1 action encoded in the patterns of gene expression in human cancer. 2003 , 114, 323-34	353
2055	Gene expression predictors of breast cancer outcomes. 2003 , 361, 1590-6	509
2054	Differentially expressed genes in gastric tumors identified by cDNA array. 2003 , 190, 199-211	22

2053	Pitfalls in the use of DNA microarray data for diagnostic and prognostic classification. 2003 , 95, 14-8	837
2052	Classification of cancers by expression profiling. 2003 , 13, 97-103	50
2051	Classifying human cancer by analysis of gene expression. 2003 , 9, 5-10	21
2050	Use of expression analysis to predict outcome after radical prostatectomy. 2003 , 170, S11-9; discussion S19-20	17
2049	Multiclass classification of microarray data with repeated measurements: application to cancer. 2003 , 4, R83	90
2048	Profiling of pathway-specific changes in gene expression following growth of human cancer cell lines transplanted into mice. 2003 , 4, R46	38
2047	Looking beyond morphology: cancer gene expression profiling using DNA microarrays. 2003 , 21, 937-49	38
2046	PATHOGENESIS OF RESPIRATORY DISEASES: NEW SOLUTIONS TO OLD PROBLEMS?. 2003 , 29, 3-92	
2045	Lung cancer. 9: Molecular biology of lung cancer: clinical implications. 2003 , 58, 892-900	86
2044	Pattern recognition in gene expression profiling using DNA array: a comparative study of different statistical methods applied to cancer classification. 2003 , 12, 823-36	38
2043	The Analysis of Gene Expression Data. 2003 ,	92
2042	Questions and answers on design of dual-label microarrays for identifying differentially expressed genes. 2003 , 95, 1362-9	65
2041	Protein profiles associated with survival in lung adenocarcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 13537-42	11.5 221
2040	Cluster Overlap Distribution Map: Visualization for Gene Expression Analysis Using Immersive Projection Technology. 2003 , 12, 96-109	3
2039	Developmental markers of B cells are superior to those of T cells for identification of stages with distinct gene expression profiles. 2003 , 74, 602-10	2
2038	Large-scale delineation of secreted protein biomarkers overexpressed in cancer tissue and serum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 3410-5	11.5 363
2037	Potts ferromagnets on coexpressed gene networks: identifying maximally stable partitions. 2003 , 90, 158102	13
2036	Gene Selection and Sample Classification Using a Genetic Algorithm and k-Nearest Neighbor Method. 2003 , 216-229	4

2035	Estimating dataset size requirements for classifying DNA microarray data. 2003 , 10, 119-42	191
2034	Airway stents provide symptomatic relief. 2003 , 58, 900-900	78
2033	The heparan sulfate proteoglycan GPC3 is a potential lung tumor suppressor. 2003 , 29, 694-701	86
2032	Prostate intraepithelial neoplasia induced by prostate restricted Akt activation: the MPAKT model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 7841-6	11.5 250
2031	Lung cancer. 6: The case for limited surgical resection in non-small cell lung cancer. 2003 , 58, 639-41	19
2030	Expression of CEACAM6 in resectable colorectal cancer: a factor of independent prognostic significance. 2003 , 21, 3638-46	126
2029	Profiling lung adenocarcinoma: insights from genes and more genes. 2003 , 2, 299-300	
2028	Functional genomics in lung cancer and biomarker detection. 2003 , 29, 153-6	12
2027	Gene expression in cancer: the application of microarrays. 2003 , 3, 185-200	35
2026	Improving classification of microarray data using prototype-based feature selection. 2003 , 5, 23-30	35
2025	Gene expression profiling of endocrine tumors by microarray analysis. 2003 , 10, 162-167	
2024	Classification of heterogeneous gene expression data. 2003 , 5, 69-78	11
2023	Classifying Microarray Data Using Support Vector Machines. 2003 , 166-185	23
2022	Protein Chip Technology in Proteomics Analysis. 235-254	
2021	Integration of Pharmacogenomics into Medical Practice. 135-161	2
2020	. 2003 ,	4
2019	. 2003 ,	24
2018	Global Genomic Analyses of Cardiovascular Disease: A Potential Map or Blind Alley?. 27-44	

2017	POE: Statistical Methods for Qualitative Analysis of Gene Expression. 2003 , 362-387	6
2016	Open Source Software for the Analysis of Microarray Data. 2003 , 34, S45-S51	172
2015	Expression imbalance map: a new visualization method for detection of mRNA expression imbalance regions. 2003 , 13, 31-46	25
2014	Statistical Challenges in Functional Genomics. 2003 , 18, 33	67
2013	Molecular Cancer Therapeutics: Will the Promise be Fulfilled?. 2004 , 7-40	2
2012	Comparison of Preprocessing Procedures for Oligo-nucleotide Micro-arrays by Parametric Bootstrap Simulation of Spike-in Experiments. 2004 , 43, 434-438	13
2011	. 2004 ,	348
2010	Blood level of phosphoglycerate kinase does not correlate with presence or extent of tumor. 2004 , 19, 170-2	
2009	S100 family members and trypsinogens are predictors of distant metastasis and survival in early-stage non-small cell lung cancer. 2004 , 64, 5564-9	154
2008	Fishing in the bloodstream: insights into the mechanisms of pulmonary hypertension?. 2004 , 170, 827-8	6
2007	Oxygen-dependent regulation of pulmonary circulation. 2004 , 381, 87-106	1
2006	A Serial Analysis of Gene Expression (SAGE) database analysis of chemosensitivity: comparing solid tumors with cell lines and comparing solid tumors from different tissue origins. 2004 , 64, 2805-16	96
2005	[Transcriptional activity of surfactant-apoproteins A1 and A2 in non small cell lung carcinomas and tumor-free lung tissues]. 2004 , 58, 395-9	7
2004	Multidimensional support vector machines for visualization of gene expression data. 2004 ,	5
2003	Gene microarray analysis of peripheral blood cells in pulmonary arterial hypertension. 2004 , 170, 911-9	131
2002	A Bayesian network classification methodology for gene expression data. 2004 , 11, 581-615	39
2001	Treating brain metastases: current approaches and future directions. 2004 , 4, 1015-22	5
2000	Large-scale meta-analysis of cancer microarray data identifies common transcriptional profiles of neoplastic transformation and progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 9309-14	11.5 790

1999	Identification of a transcriptional profile associated with in vitro invasion in non-small cell lung cancer cell lines. 2004 , 3, 624-31		12
1998	Effects of cigarette smoke on the human airway epithelial cell transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 10143-8	11.5	475
1997	A transgenic mouse model of metastatic carcinoma involving transdifferentiation of a gastric epithelial lineage progenitor to a neuroendocrine phenotype. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 4471-6	11.5	82
1996	Gene expression profiling of early- and late-relapse nonseminomatous germ cell tumor and primitive neuroectodermal tumor of the testis. 2004 , 10, 2368-78		45
1995	Tissue array-based predictions of pathobiology, prognosis, and response to treatment for renal cell carcinoma therapy. 2004 , 10, 6304S-9S		37
1994	TTF-1, Cytokeratin 7, 34 β 12, and CD56/NCAM Immunostaining in the Subclassification of Large Cell Carcinomas of the Lung. 2004 , 122, 884-893		85
1993	Activating mutations of the noonan syndrome-associated SHP2/PTPN11 gene in human solid tumors and adult acute myelogenous leukemia. 2004 , 64, 8816-20		404
1992	Down-regulation of the receptor for advanced glycation end-products (RAGE) supports non-small cell lung carcinoma. 2005 , 26, 293-301		114
1991	Functional genomics of lung disease. Second annual Pittsburgh International Lung Conference, October 2003. 2004 , 31, S1-81		10
1990	Lung cancers detected by screening with spiral computed tomography have a malignant phenotype when analyzed by cDNA microarray. 2004 , 10, 6023-8		59
1989	Assessing prognosis in non-small-cell lung cancer: avenues to a more complete picture?. 2004 , 22, 3209-11		4
1988	Identification of a gene expression signature associated with recurrent disease in squamous cell carcinoma of the head and neck. 2004 , 64, 55-63		331
1987	Conserved mechanisms across development and tumorigenesis revealed by a mouse development perspective of human cancers. 2004 , 18, 629-40		129
1986	Gene expression profiling in non-small cell lung cancer: from molecular mechanisms to clinical application. 2004 , 10, 3237-48		117
1985	Classification of human breast cancer using gene expression profiling as a component of the survival predictor algorithm. 2004 , 10, 2272-83		58
1984	Improving classification performance for heterogeneous cancer gene expression data. 2004 ,		1
1983	Integrated modeling of clinical and gene expression information for personalized prediction of disease outcomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 8431-6	11.5	174
1982	New targets for detection and treatment of small cell lung cancer. 2004 , 125, 154S		

1981	MergeMaid: R tools for merging and cross-study validation of gene expression data. 2004 , 3, Article29	17
1980	Global Gene Expression Analysis of Human Bronchial Epithelial Cells Treated with Tobacco Condensates. 2004 , 3, 1152-1166	28
1979	A cascading support vector machines system for gene expression data classification.	2
1978	Gene expression profiling identifies matriptase overexpression in malignant mesothelioma. 2004 , 125, 1843-52	84
1977	Cancer Bioinformatics: Addressing the Challenges of Integrated Postgenomic Cancer Research. 2004 , 22, 171-173	1
1976	A time series analysis of microarray data.	22
1975	A cross-study comparison of gene expression studies for the molecular classification of lung cancer. 2004 , 10, 2922-7	174
1974	Overexpression, amplification, and androgen regulation of TPD52 in prostate cancer. 2004 , 64, 3814-22	136
1973	Casein kinase II alpha subunit and C1-inhibitor are independent predictors of outcome in patients with squamous cell carcinoma of the lung. 2004 , 10, 5792-803	88
1972	Gene expression profiling of renal cell carcinoma. 2004 , 10, 6315S-21S	32
1971	JAGGED1 expression is associated with prostate cancer metastasis and recurrence. 2004 , 64, 6854-7	280
1970	Coexpression analysis of human genes across many microarray data sets. 2004 , 14, 1085-94	571
1969	Robust sparse hyperplane classifiers: application to uncertain molecular profiling data. 2004 , 11, 1073-89	24
1968	Applications of array technology: melanoma research and diagnosis. 2004 , 4, 549-57	8
1967	Gold nanoparticle probe-based gene expression analysis with unamplified total human RNA. 2004 , 32, e137	73
1966	Molecular signatures in biopsy specimens of lung cancer. 2004 , 170, 167-74	91
1965	Prognostic model of pulmonary adenocarcinoma by expression profiling of eight genes as determined by quantitative real-time reverse transcriptase polymerase chain reaction. 2004 , 22, 811-9	136
1964	Gene expression signature of fibroblast serum response predicts human cancer progression: similarities between tumors and wounds. 2004 , 2, E7	698

1963	Applications of microarrays to histopathology. 2004 , 44, 97-108	73
1962	Microarray reality checks in the context of a complex disease. 2004 , 22, 615-21	143
1961	The emerging roles of human tissue kallikreins in cancer. 2004 , 4, 876-90	523
1960	Gene expression profiling of colon cancer by DNA microarrays and correlation with histoclinical parameters. 2004 , 23, 1377-91	265
1959	High-resolution single-nucleotide polymorphism array and clustering analysis of loss of heterozygosity in human lung cancer cell lines. 2004 , 23, 2716-26	91
1958	Gene-expression profiling reveals distinct expression patterns for Classic versus Variant Merkel cell phenotypes and new classifier genes to distinguish Merkel cell from small-cell lung carcinoma. 2004 , 23, 2732-42	53
1957	Identification of genes whose expression is upregulated in lung adenocarcinoma cells in comparison with type II alveolar cells and bronchiolar epithelial cells in vivo. 2004 , 23, 3089-96	36
1956	Postgenomic global analysis of translational control induced by oncogenic signaling. 2004 , 23, 3248-64	81
1955	Maspin expression in normal lung and non-small-cell lung cancers: cellular property-associated expression under the control of promoter DNA methylation. 2004 , 23, 4041-9	48
1954	Deregulated expression of LRBA facilitates cancer cell growth. 2004 , 23, 4089-97	57
1953	Sil overexpression in lung cancer characterizes tumors with increased mitotic activity. 2004 , 23, 5371-7	44
1952	Gene expression-based, individualized outcome prediction for surgically treated lung cancer patients. 2004 , 23, 5360-70	120
1951	Modeling of lung cancer by an orthotopically growing H460SM variant cell line reveals novel candidate genes for systemic metastasis. 2004 , 23, 6316-24	29
1950	Suppression subtractive hybridization and expression profiling identifies a unique set of genes overexpressed in non-small-cell lung cancer. 2004 , 23, 7734-45	59
1949	Predicting biomarkers for ovarian cancer using gene-expression microarrays. 2004 , 90, 686-92	153
1948	S100A2 is strongly expressed in airway basal cells, preneoplastic bronchial lesions and primary non-small cell lung carcinomas. 2004 , 91, 1515-24	39
1947	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
1946	DNA microarrays and data analysis: an overview. 2004 , 136, 500-3	13

1945	Expression profiling of non-small cell lung carcinoma identifies metastatic genotypes based on lymph node tumor burden. 2004 , 127, 1332-41; discussion 1342	21
1944	Molecular classification of head and neck squamous cell carcinomas using patterns of gene expression. 2004 , 5, 489-500	516
1943	Molecular classification and molecular genetics of human lung cancers. 2004 , 31, 4-19	49
1942	Differentially expressed genes in nonsmall cell lung cancer: expression profiling of cancer-related genes in squamous cell lung cancer. 2004 , 149, 98-106	131
1941	Noise filtering and nonparametric analysis of microarray data underscores discriminating markers of oral, prostate, lung, ovarian and breast cancer. 2004 , 5, 185	21
1940	Joint analysis of two microarray gene-expression data sets to select lung adenocarcinoma marker genes. 2004 , 5, 81	178
1939	Pulmonary cytology: Current issues in research and practice. 2004 , 54, S506-S519	1
1938	Expression levels of protein kinase C-alpha in non-small-cell lung cancer. 2004 , 6, 184-9	36
1937	A primer on gene expression and microarrays for machine learning researchers. 2004 , 37, 293-303	24
1936	Multivariate selection of genetic markers in diagnostic classification. 2004 , 31, 155-67	7
1935	Application of sector protein microarrays to clinical samples. 2004 , 1, 91-99	4
1934	Pathology and molecular genetics of oligodendroglial tumors. 2004 , 82, 638-55	39
1933	Genchipdiagnostik. 2004 , 37, 203-209	
1932	Proteomic analysis distinguishes basaloid carcinoma as a distinct subtype of nonsmall cell lung carcinoma. 2004 , 4, 3394-400	57
1931	Micro Array Based Gene Expression Analysis using Parametric Multivariate Tests per Gene [A Generalized Application of Multiple Procedures with Data-driven Order of Hypotheses. 2004 , 46, 687-698	2
1930	Diagnostic strategies for unknown primary cancer. 2004 , 100, 1776-85	193
1929	Expression of syndecan-1 and expression of epidermal growth factor receptor are associated with survival in patients with nonsmall cell lung carcinoma. 2004 , 101, 1632-8	68
1928	On a resampling approach for tests on the number of clusters with mixture model-based clustering of tissue samples. 2004 , 90, 90-105	31

1927	Analyzing factorial designed microarray experiments. 2004 , 90, 19-43	17
1926	Clinical proteomics in lung diseases. 2004 , 200, 147-54	19
1925	State of the science: molecular classifications of breast cancer for clinical diagnostics. 2004 , 37, 572-8	13
1924	Statistical analysis of global gene expression data: some practical considerations. 2004 , 15, 52-7	24
1923	K-ranked covariance based missing values estimation for microarray data classification.	4
1922	A variant of SVM-RFE for gene selection in cancer classification with expression data.	10
1921	A graphical approach for quality control of oligonucleotide array data. 2004 , 14, 591-606	10
1920	Genome-scale analysis of lung cancer progression. 2004 , 4, 169-76	7
1919	American Society of Clinical Oncology treatment of unresectable non-small-cell lung cancer guideline: update 2003. 2004 , 22, 330-53	1154
1918	Mouse lung neuroendocrine carcinomas: distinct morphologies, same transcription factors. 2005 , 31, 37-55	12
1917	Multiclass Decision Forest--a novel pattern recognition method for multiclass classification in microarray data analysis. 2004 , 23, 685-94	33
1916	Gene expression profiles and molecular markers to predict recurrence of Dukes' B colon cancer. 2004 , 22, 1564-71	381
1915	Class discovery analysis of the lung cancer gene expression data. 2004 , 23, 715-21	6
1914	Identification and validation of commonly overexpressed genes in solid tumors by comparison of microarray data. 2004 , 6, 744-50	255
1913	Genomic profiles in stage I primary non small cell lung cancer using comparative genomic hybridization analysis of cDNA microarrays. 2004 , 6, 623-35	72
1912	Gene expression profiling identifies clinically relevant subtypes of prostate cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 811-6	11.5 1047
1911	Unraveling lung cancer biology by animal models and gene expression profiling. 2004 , 1, 25-30	
1910	The tumor protein D52 family: many pieces, many puzzles. 2004 , 325, 1115-21	73

1909	Outcome of patients with pulmonary carcinoid tumors receiving chemotherapy or chemoradiotherapy. 2004 , 44, 213-20	83
1908	Study design considerations in clinical outcome research of lung cancer using microarray analysis. 2004 , 46, 215-26	19
1907	Validating the prognostic value of marker genes derived from a non-small cell lung cancer microarray study. 2004 , 46, 197-204	39
1906	The biology of non-small-cell lung cancer: identifying new targets for rational therapy. 2004 , 46, 135-48	31
1905	Genome-wide screening for prognosis-predicting genes in early-stage non-small-cell lung cancer. 2004 , 45 Suppl 2, S145-50	26
1904	Can gene expression profiling predict survival for patients with squamous cell carcinoma of the lung?. 2004 , 3, 35	23
1903	Genetic alteration and gene expression modulation during cancer progression. 2004 , 3, 9	70
1902	Classification of proliferative pulmonary lesions of the mouse: recommendations of the mouse models of human cancers consortium. 2004 , 64, 2307-16	291
1901	Support vector machine and generalized regression neural network based classification fusion models for cancer diagnosis.	4
1900	Stability and heterogeneity of expression profiles in lung cancer specimens harvested following surgical resection. 2004 , 6, 761-7	40
1899	ONCOMINE: a cancer microarray database and integrated data-mining platform. 2004 , 6, 1-6	2548
1898	Identification of differentially expressed genes in human lung squamous cell carcinoma using suppression subtractive hybridization. 2004 , 212, 83-93	70
1897	Customizing chemotherapy for colon cancer: the potential of gene expression profiling. 2004 , 7, 209-18	14
1896	Distinct patterns of genetic alterations in adenocarcinoma and squamous cell carcinoma of the lung. 2004 , 40, 1082-94	62
1895	Biomarkers of ovarian tumours. 2004 , 40, 2604-12	68
1894	Gene expression microarray technologies in the development of new therapeutic agents. 2004 , 40, 2560-91	70
1893	Multi-platform, multi-site, microarray-based human tumor classification. 2004 , 164, 9-16	178
1892	Molecular classification of parathyroid neoplasia by gene expression profiling. 2004 , 165, 565-76	33

1891	The impact of transcriptome and proteome analyses on antibiotic drug discovery. 2004 , 7, 451-9	68
1890	Prognostic significance of thyroid transcription factor-1 expression in both early-stage conventional adenocarcinoma and bronchioloalveolar carcinoma of the lung. 2004 , 35, 3-7	72
1889	Identification of carboxypeptidase E and gamma-glutamyl hydrolase as biomarkers for pulmonary neuroendocrine tumors by cDNA microarray. 2004 , 35, 1196-209	62
1888	Prediction of lymph node metastasis by analysis of gene expression profiles in non-small cell lung cancer. 2004 , 122, 61-9	25
1887	Histopathologic classification of lung cancer: Relevance of cytokeratin and TTF-1 immunophenotyping. 2004 , 8, 259-67	81
1886	Gene expression studies in lung development and lung stem cell biology. 2004 , 64, 57-71	4
1885	Biomedical marker molecules for cancer [Current status and perspectives. 2004 , 3, 228-237	6
1884	Achaete-scute homolog-1 and Notch in lung neuroendocrine development and cancer. 2004 , 204, 159-69	98
1883	Two prognostically significant subtypes of high-grade lung neuroendocrine tumours independent of small-cell and large-cell neuroendocrine carcinomas identified by gene expression profiles. 2004 , 363, 775-81	210
1882	Screening for lung cancer: a review. 2004 , 10, 266-71	11
1881	Biomarkers in non-small cell lung cancer prevention. 2004 , 13, 425-36	26
1880	Gene expression patterns, prognostic and diagnostic markers, and lung cancer biology. 2004 , 125, 111S-5S	13
1879	Data mining as a tool for research and knowledge development in nursing. 2004 , 22, 123-31	30
1878	Genomic and proteomic approaches for studying human cancer: prospects for true patient-tailored therapy. 2004 , 1, 134-40	49
1877	Increased measurement accuracy for sequence-verified microarray probes. 2004 , 18, 308-15	67
1876	Genome-wide cDNA microarray screening to correlate gene expression profile with survival in patients with advanced lung cancer. 2004 , 11, 1041	2
1875	Gene expression profiling allows distinction between primary and metastatic squamous cell carcinomas in the lung. 2005 , 65, 3063-71	122
1874	Application of Survival and Meta-analysis to Gene Expression Data Combined from Two Studies. 2005 , 67-80	1

1873	Differential Correlation Detects Complex Associations Between Gene Expression and Clinical Outcomes in Lung Adenocarcinomas. 2005 , 121-131	11
1872	Making Sense of Human Lung Carcinomas Gene Expression Data: Integration and Analysis of Two Affymetrix Platform Experiments. 2005 , 81-94	
1871	Introduction. 2005 , 1-8	
1870	Cancer: Clinical Challenges and Opportunities. 2005 , 9-20	
1869	Validation of intraoperative diagnoses using smear preparations from stereotactic brain biopsies: intraoperative versus final diagnosis--influence of clinical factors. 2005 , 56, 257-65; discussion 257-65	95
1868	EGFR mutation is specific for terminal respiratory unit type adenocarcinoma. 2005 , 29, 633-9	206
1867	Integration of Microarray Data for a Comparative Study of Classifiers and Identification of Marker Genes. 2005 , 147-162	
1866	Use of Micro Array Data via Model-based Classification in the Study and Prediction of Survival from Lung Cancer. 2005 , 163-173	4
1865	Prognóstico do cancro do pulmão: Novos factores biológicos e moleculares. 2005 , 11, S113-S122	
1864	A Combinatorial Approach to the Analysis of Differential Gene Expression Data. 2005 , 223-238	8
1863	Pooling Information Across Different Studies and Oligonucleotide Chip Types to Identify Prognostic Genes for Lung Cancer. 2005 , 51-66	14
1862	High Sensitivity Expression Profiling. 2005 , 229-250	1
1861	Exploring the structure of supervised data by Discriminant Isometric Mapping. 2005 , 38, 599-601	11
1860	Gene selection for classification of cancers using probabilistic model building genetic algorithm. 2005 , 82, 208-25	32
1859	Survival analysis of microarray expression data by transformation models. 2005 , 29, 91-4	6
1858	Genome-based identification of diagnostic molecular markers for human lung carcinomas by PLS-DA. 2005 , 29, 183-95	18
1857	Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 15545-50	11,5 24578
1856	Rare SP-A alleles and the SP-A1-6A(4) allele associate with risk for lung carcinoma. 2005 , 68, 128-36	24

1855	Throwing new light on lung cancer pathogenesis: updates on three recent topics. 2005 , 96, 63-8	19
1854	An oncogenic KRAS2 expression signature identified by cross-species gene-expression analysis. 2005 , 37, 48-55	361
1853	Sipa1 is a candidate for underlying the metastasis efficiency modifier locus Mtes1. 2005 , 37, 1055-62	142
1852	An array of problems. 2005 , 4, 362-3	57
1851	Focal adhesion kinase: in command and control of cell motility. 2005 , 6, 56-68	1884
1850	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
1849	Two subclasses of lung squamous cell carcinoma with different gene expression profiles and prognosis identified by hierarchical clustering and non-negative matrix factorization. 2005 , 24, 7105-13	80
1848	Colon cancer prognosis prediction by gene expression profiling. 2005 , 24, 6155-64	83
1847	Integrative genomic and proteomic analysis of prostate cancer reveals signatures of metastatic progression. 2005 , 8, 393-406	625
1846	GEMS: a system for automated cancer diagnosis and biomarker discovery from microarray gene expression data. 2005 , 74, 491-503	135
1845	Text-based analysis of genes, proteins, aging, and cancer. 2005 , 126, 193-208	4
1844	INK4a/ARF: a multifunctional tumor suppressor locus. 2005 , 576, 22-38	294
1843	The prospect of biologic staging of non-small-cell lung cancer. 2005 , 6, 217-24	5
1842	Integrative analysis of multiple gene expression profiles with quality-adjusted effect size models. 2005 , 6, 128	41
1841	stam--a Bioconductor compliant R package for structured analysis of microarray data. 2005 , 6, 211	2
1840	Comparison of normalization methods for CodeLink Bioarray data. 2005 , 6, 309	51
1839	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
1838	Role of cell-cycle regulators in lung cancer. 2005 , 205, 319-27	25

1837	Epithelial tight junction proteins as potential antibody targets for pancarcinoma therapy. 2005 , 54, 431-45	47
1836	Gene expression profiling of nonneoplastic mucosa may predict clinical outcome of colon cancer patients. 2005 , 48, 2238-48	25
1835	Mining the structural knowledge of high-dimensional medical data using isomap. 2005 , 43, 410-2	16
1834	Genomics of lung cancer may change diagnosis, prognosis and therapy. 2005 , 11, 5-10	15
1833	SPLUNC1 (PLUNC) is expressed in glandular tissues of the respiratory tract and in lung tumours with a glandular phenotype. 2005 , 205, 491-7	63
1832	Entropy and Survival-based Weights to Combine Affymetrix Array Types and Analyze Differential Expression and Survival. 2005 , 95-108	
1831	. 2005 ,	4
1830	DNA array-based gene profiling: from surgical specimen to the molecular portrait of cancer. 2005 , 241, 16-26	29
1829	Gene Expression Data and Survival Analysis. 2005 , 21-34	2
1828	Microarray Data Analysis of Survival Times of Patients with Lung Adenocarcinomas Using ADC and K-Medians Clustering. 2005 , 175-190	
1827	Small tumor size and limited smoking history predicts activated epidermal growth factor receptor in early-stage non-small cell lung cancer. 2005 , 128, 308-16	18
1826	Medical Diagnosis and Prognosis Based on the DNA Microarray Technology. 2005 , 209-236	
1825	Probabilistic Lung Cancer Models Conditioned on Gene Expression Microarray Data. 2005 , 133-146	
1824	Give lipids a START: the StAR-related lipid transfer (START) domain in mammals. 2005 , 118, 2791-801	289
1823	Microarray Data Analysis Using Neural Network Classifiers and Gene Selection Methods. 2005 , 207-222	4
1822	Construction of robust prognostic predictors by using projective adaptive resonance theory as a gene filtering method. 2005 , 21, 179-86	24
1821	Clinical pharmacogenomics and transcriptional profiling in early phase oncology clinical trials. 2005 , 5, 83-102	31
1820	Significance analysis of functional categories in gene expression studies: a structured permutation approach. 2005 , 21, 1943-9	266

1819	Personalized diagnostic and therapeutic strategies in oncology. 2005 , 2, 97-110	1
1818	Analysis of tumor-host interactions by gene expression profiling of lung adenocarcinoma xenografts identifies genes involved in tumor formation. 2005 , 3, 119-29	52
1817	Multidimensional support vector machines for visualization of gene expression data. 2005 , 21, 439-44	28
1816	Genomics and proteomics--the way forward. 2005 , 16 Suppl 2, ii30-44	19
1815	DIG--a system for gene annotation and functional discovery. 2005 , 21, 2957-9	1
1814	Molecular decomposition of complex clinical phenotypes using biologically structured analysis of microarray data. 2005 , 21, 1971-8	34
1813	Homozygous deletions and chromosome amplifications in human lung carcinomas revealed by single nucleotide polymorphism array analysis. 2005 , 65, 5561-70	285
1812	Overexpression of osteopontin is associated with more aggressive phenotypes in human non-small cell lung cancer. 2005 , 11, 4646-52	116
1811	Prediction of lymph node metastasis by analysis of gene expression profiles in primary lung adenocarcinomas. 2005 , 11, 4128-35	54
1810	A Bayesian regression approach to the inference of regulatory networks from gene expression data. 2005 , 21, 3131-7	80
1809	An overview of lung cancer genomics and proteomics. 2005 , 32, 169-76	132
1808	An efficient Monte Carlo approach to assessing statistical significance in genomic studies. 2005 , 21, 781-7	141
1807	Role of chemotherapy and the receptor tyrosine kinases KIT, PDGFRalpha, PDGFRbeta, and Met in large-cell neuroendocrine carcinoma of the lung. 2005 , 23, 8774-85	229
1806	Gene expression profiles predict early relapse in ovarian cancer after platinum-paclitaxel chemotherapy. 2005 , 11, 2149-55	129
1805	Gene expression profiling of human adrenocortical tumors using complementary deoxyribonucleic Acid microarrays identifies several candidate genes as markers of malignancy. 2005 , 90, 1819-29	204
1804	Chronic obstructive pulmonary disease as a prognostic factor in non-small cell lung cancer. 2005 , 28, 505-6; author reply 506	
1803	Simple and effective visual models for gene expression cancer diagnostics. 2005 ,	1
1802	Extraction of informative genes from microarray data. 2005 ,	18

1801	Lung adenocarcinoma global profiling identifies type II transforming growth factor-beta receptor as a repressor of invasiveness. 2005 , 172, 729-37		70
1800	Signaling networks in cutaneous melanoma metastasis identified by complementary DNA microarrays. 2005 , 141, 165-73		32
1799	K-means+ method for improving gene selection for classification of microarray data.		1
1798	Differential coexpression analysis using microarray data and its application to human cancer. 2005 , 21, 4348-55		201
1797	Overexpression of the aldo-keto reductase family protein AKR1B10 is highly correlated with smokers' non-small cell lung carcinomas. 2005 , 11, 1776-85		234
1796	Utility of high dimensional genomic composite biomarkers in therapeutic and/or diagnostic development.		1
1795	Toxicogenomics Applied to Hematotoxicology. 2005 , 583-608		1
1794	A comprehensive evaluation of multcategory classification methods for microarray gene expression cancer diagnosis. 2005 , 21, 631-43		607
1793	Individualised cancer therapeutics: dream or reality?. 2005 , 9, 1189-201		7
1792	Mutations in the epidermal growth factor receptor gene are linked to smoking-independent, lung adenocarcinoma. 2005 , 93, 355-63		141
1791	Phosphorylated FADD induces NF-kappaB, perturbs cell cycle, and is associated with poor outcome in lung adenocarcinomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 12507-12	11.5	111
1790	Identification of MMP-15 as an anti-apoptotic factor in cancer cells. 2005 , 280, 34123-32		56
1789	High-resolution genomic profiles of human lung cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 9625-30	11.5	326
1788	Prediction of radiation sensitivity using a gene expression classifier. 2005 , 65, 7169-76		155
1787	Evidence by molecular profiling for a placental origin of infantile hemangioma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 19097-102	11.5	149
1786	Efficient gene selection for classification of microarray data.		
1785	Cross-study validation and combined analysis of microarray data for cancer using vector cosine angle method. 2005 , 2005, 4810-3		
1784	Molecular pathology of non-small-cell lung cancer. 2005 , 72, 313-30		42

1783	Prognostic implications of cell cycle, apoptosis, and angiogenesis biomarkers in non-small cell lung cancer: a review. 2005 , 11, 3974-86	250
1782	Genetic classification of lung adenocarcinoma based on array-based comparative genomic hybridization analysis: its association with clinicopathologic features. 2005 , 11, 6177-85	93
1781	Identification of novel human CTL epitopes and their agonist epitopes of mesothelin. 2005 , 11, 6342-51	51
1780	Impact of molecular pathology on the clinical management of lung cancer. 2005 , 72, 229-32	4
1779	Reply to Spina et al. Molecular studies in lung cancer patients with chronic obstructive pulmonary diseases. 2005 , 28, 506-506	
1778	An integrated functional genomics and metabolomics approach for defining poor prognosis in human neuroendocrine cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 9901-6	11.5 96
1777	Use of gene expression profiling to direct in vivo molecular imaging of lung cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 14404-9	11.5 118
1776	Small, fuzzy and interpretable gene expression based classifiers. 2005 , 21, 1964-70	44
1775	Lack of telomerase activity in lung carcinoids is dependent on human telomerase reverse transcriptase transcription and alternative splicing and is associated with long telomeres. 2005 , 11, 2832-9	31
1774	Early diagnostic marker panel determination for microarray based clinical studies. 2005 , 4, Article9	5
1773	Lung cancer in women: emerging differences in epidemiology, biology, and therapy. 2005 , 128, 370-81	120
1772	Time-dependent RNA degradation affecting cDNA array quality in spontaneous canine tumours sampled using standard surgical procedures. 2005 , 16, 979	
1771	Overexpression of G protein-coupled receptors in cancer cells: Involvement in tumor progression. 2005 , 27, 1329	24
1770	Identification of metastasis-associated receptor tyrosine kinases in non-small cell lung cancer. 2005 , 65, 1778-82	111
1769	Enhanced microarray performance using low complexity representations of the transcriptome. 2005 , 33, e100	7
1768	Transformation of expression intensities across generations of Affymetrix microarrays using sequence matching and regression modeling. 2005 , 33, e157	7
1767	Prediction of cancer outcome with microarrays: a multiple random validation strategy. 2005 , 365, 488-92	815
1766	Role of nuclear receptors in lung tumourigenesis. 2005 , 41, 2561-8	29

1765	Redefinition of Affymetrix probe sets by sequence overlap with cDNA microarray probes reduces cross-platform inconsistencies in cancer-associated gene expression measurements. 2005 , 6, 107	99
1764	Human tissue kallikreins: from gene structure to function and clinical applications. 2005 , 39, 11-79	49
1763	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
1762	Pathology of the Future: Molecular Profiling for Targeted Therapy. 2005 , 23, 36-46	58
1761	Mouse models for human lung cancer. 2005 , 19, 643-64	228
1760	The octamer binding transcription factor Oct-1 is a stress sensor. 2005 , 65, 10750-8	93
1759	Discovery of gene expression patterns across multiple cancer types.	
1758	Inter-gene correlation on oligonucleotide arrays: how much does normalization matter?. 2005 , 5, 271-9	7
1757	Stacked regression ensemble for cancer class prediction.	3
1756	Molecular staging for survival prediction of colorectal cancer patients. 2005 , 23, 3526-35	285
1755	Genomic and proteomic profiling of lung cancers: lung cancer classification in the age of targeted therapy. 2005 , 23, 3219-26	78
1754	Functional expression and mutations of c-Met and its therapeutic inhibition with SU11274 and small interfering RNA in non-small cell lung cancer. 2005 , 65, 1479-88	470
1753	Partial least squares dimension reduction for microarray gene expression data with a censored response. 2005 , 193, 119-37	13
1752	Roles of fascin in human carcinoma motility and signaling: prospects for a novel biomarker?. 2005 , 37, 1787-804	224
1751	Human tissue kallikrein gene family: applications in cancer. 2005 , 224, 1-22	114
1750	Analysis of orthologous gene expression between human pulmonary adenocarcinoma and a carcinogen-induced murine model. 2005 , 167, 1763-75	243
1749	Interpreting expression profiles of cancers by genome-wide survey of breadth of expression in normal tissues. 2005 , 86, 127-41	218
1748	Discovering the mechanism of action of novel antibacterial agents through transcriptional profiling of conditional mutants. 2005 , 49, 749-59	84

1747	Discovering causes and cures for cancer from gene expression analysis. 2005 , 4, 548-63	11
1746	Comparative application of antibody and gene array for expression profiling in human squamous cell lung carcinoma. 2005 , 49, 145-54	100
1745	Prediction error estimation: a comparison of resampling methods. 2005 , 21, 3301-7	800
1744	The promise of gene signatures in cancer diagnosis and prognosis. 2005 ,	
1743	Simple decision rules for classifying human cancers from gene expression profiles. 2005 , 21, 3896-904	287
1742	Pathogenesis of lung cancer: 100 year report. 2005 , 33, 216-23	104
1741	Conserved transcription factor binding sites of cancer markers derived from primary lung adenocarcinoma microarrays. 2005 , 33, 409-21	25
1740	Biological and Medical Data Analysis. 2005 ,	3
1739	Searching for differentially expressed gene combinations. 2005 , 6, R88	46
1738	Tumor microenvironments, the immune system and cancer survival. 2005 , 6, 211	20
1737	A DNA microarray survey of gene expression in normal human tissues. 2005 , 6, R22	172
1736	Lung cancer preneoplasia. 2006 , 1, 331-48	150
1735	The retinoblastoma gene family in cell cycle regulation and suppression of tumorigenesis. 2006 , 42, 183-225	26
1734	Data Mining and Bioinformatics. 2006 ,	
1733	The wind of change in the therapy of lung cancer. 2006 , 6, 469-72	
1732	Improve survival prediction using principal components of gene expression data. 2006 , 4, 110-9	9
1731	Biomarkers in cancer screening, research and detection: present and future: a review. 2006 , 11, 385-405	93
1730	Ensemble attribute profile clustering: discovering and characterizing groups of genes with similar patterns of biological features. 2006 , 7, 147	6

1729	Lung cancer staging: proteomics. 2006 , 16, 339-43	1
1728	Diagnostic des CBP: Les « puces »ADN » en oncologie thoracique. 2006 , 23, 23-27	
1727	Lung cancer staging in the genomics era. 2006 , 16, 329-37	8
1726	A quantitative reverse transcriptase-polymerase chain reaction assay to identify metastatic carcinoma tissue of origin. 2006 , 8, 320-9	81
1725	Decreased kallikrein 11 messenger RNA expression in lung cancer. 2006 , 8, 45-8	11
1724	Improving the performance of SVM-RFE to select genes in microarray data. 2006 , 7 Suppl 2, S12	50
1723	A genomic strategy to refine prognosis in early-stage non-small-cell lung cancer. 2006 , 355, 570-80	512
1722	Missing Value Imputation Framework for Microarray Significant Gene Selection and Class Prediction. 2006 , 131-142	3
1721	Maspin nuclear localization is linked to favorable morphological features in pulmonary adenocarcinoma. 2006 , 51, 31-9	62
1720	Characterization of cell-type specific profiles in tissues and isolated cells from squamous cell carcinomas of the lung. 2006 , 53, 129-42	35
1719	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
1718	Comparative proteomics of pulmonary tumors with neuroendocrine differentiation. 2006 , 5, 643-50	19
1717	Tumor transcriptome reveals the predictive and prognostic impact of lysosomal protease inhibitors in non-small-cell lung cancer. 2006 , 24, 1729-44	50
1716	A Model-Free Greedy Gene Selection for Microarray Sample Class Prediction. 2006 ,	1
1715	Expression of two breast-specific molecules in the lung. 2006 , 8, 390-1; author reply 391-3	
1714	Pathway analysis using random forests classification and regression. 2006 , 22, 2028-36	182
1713	Molecular and genetic markers in thoracic surgery. 2006 , 82, 2335-6	
1712	Integrated genome-wide gene expression map and high-resolution analysis of aberrant chromosomal regions in squamous cell lung cancer. 2006 , 580, 2774-8	2

1711	SEL1L expression in non-small cell lung cancer. 2006 , 37, 505-12	12
1710	Functional screening for proapoptotic genes by reverse transfection cell array technology. 2006 , 87, 665-72	45
1709	. 2006 ,	25
1708	Microarray-based Expression Profiling: From Technological Basics to Diagnostic Perspectives. 728-754	
1707	Characterization of lung tumor subtypes through gene expression cluster validity assessment. 2006 , 40, 163-176	5
1706	An Empirical Study of Univariate and Genetic Algorithm-Based Feature Selection in Binary Classification with Microarray Data. 2006 , 2, 117693510600200	16
1705	Analysis of Differentially Expressed Genes in Neuroendocrine Carcinomas of the Lung. 2006 , 1, 780-786	10
1704	Analysis of Differentially Expressed Genes in Neuroendocrine Carcinomas of the Lung. 2006 , 1, 780-786	12
1703	Analysis of Microarray Gene Expression Data. 2006 , 1, 37-53	33
1702	Microarray Approaches to Gene Expression Analysis. 2006 , 121-148	1
1701	Prognostic Value of Fluorodeoxyglucose Positron Emission Tomography in Non-small Cell Lung Cancer: A Review. 2006 , 1, 152-159	24
1700	Microarray expression technology: from start to finish. 2006 , 7, 123-34	24
1699	Towards a lung adenocarcinoma proteome map: studies with SP-C/c-raf transgenic mice. 2006 , 6, 3127-37	24
1698	Worldwide trends in lung cancer pathology. 2006 , 11, 533-8	98
1697	A critical appraisal of prognostic and predictive factors for common lung cancers. 2006 , 48, 779-86	18
1696	Creation and implications of a phenome-genome network. 2006 , 24, 55-62	176
1695	Conservation of gene expression signatures between zebrafish and human liver tumors and tumor progression. 2006 , 24, 73-5	249
1694	A signature of chromosomal instability inferred from gene expression profiles predicts clinical outcome in multiple human cancers. 2006 , 38, 1043-8	782

1693	Common markers of proliferation. 2006 , 6, 99-106	402
1692	Functional facets of the pulmonary neuroendocrine system. 2006 , 86, 425-44	148
1691	Increasing expression of serine protease matriptase in ovarian tumors: tissue microarray analysis of immunostaining score with clinicopathological parameters. 2006 , 19, 447-52	32
1690	The insulinoma-associated 1: a novel promoter for targeted cancer gene therapy for small-cell lung cancer. 2006 , 13, 375-84	41
1689	Repression of the MSP/MST-1 gene contributes to the antiapoptotic gain of function of mutant p53. 2006 , 25, 359-69	50
1688	K-ras activation generates an inflammatory response in lung tumors. 2006 , 25, 2105-12	218
1687	Identification of tumor markers and differentiation markers for molecular diagnosis of lung adenocarcinoma. 2006 , 25, 4245-55	22
1686	Intrinsic focal adhesion kinase activity controls orthotopic breast carcinoma metastasis via the regulation of urokinase plasminogen activator expression in a syngeneic tumor model. 2006 , 25, 4429-40	84
1685	Interpretable gene expression classifier with an accurate and compact fuzzy rule base for microarray data analysis. 2006 , 85, 165-76	29
1684	Statistical analysis of gene regulatory networks reconstructed from gene expression data of lung cancer. 2006 , 370, 663-671	3
1683	Evaluation and comparison of gene clustering methods in microarray analysis. 2006 , 22, 2405-12	205
1682	Lung Cancer. 2006 , 552-628	1
1681	Proteomic and genomic technologies for biomarker discovery. 2006 , 2, 5-11	2
1680	Genes involved in neuroendocrine tumor biology. 2006 , 9, 165-78	2
1679	Current concepts in neuroendocrine cancer metabolism. 2006 , 9, 193-202	5
1678	Statistical Methods for Meta-Analysis of Microarray Data: A Comparative Study. 2006 , 8, 9-20	14
1677	Personalized medicine and development of targeted therapies: The upcoming challenge for diagnostic molecular pathology. A review. 2006 , 448, 744-55	75
1676	A clinical prognostic prediction of lymph node-negative breast cancer by gene expression profiles. 2006 , 132, 579-87	9

1675	High-density oligonucleotide microarrays and functional network analysis reveal extended lung carcinogenesis pathway maps and multiple interacting genes in NNK [4-(methylnitrosamino)-1-(3-pyridyle)-1-butanone] induced CD1 mouse lung tumor. 2007 , 133, 107-15	19
1674	Molecular classification of tumors with special reference to EGFR mutation in lung cancer. 2006 , 58, 17-23	6
1673	Genomic signatures in non-small-cell lung cancer: targeting the targeted therapies. 2006 , 8, 252-7	5
1672	Oral Abstracts. 2006 , 2, A1-A25	
1671	Randomized maps for assessing the reliability of patients clusters in DNA microarray data analyses. 2006 , 37, 85-109	26
1670	SAGE and related approaches for cancer target identification. 2006 , 11, 110-8	27
1669	Histologic grade is an independent prognostic factor for survival in non-small cell lung cancer: an analysis of 5018 hospital- and 712 population-based cases. 2006 , 131, 1014-20	110
1668	Differential diagnosis of solitary lung nodules with gene expression ratios. 2006 , 132, 621-7	8
1667	Tumor tissue identification based on gene expression data using DWT feature extraction and PNN classifier. 2006 , 69, 387-402	36
1666	Rapid chemokinetic movement and the invasive potential of lung cancer cells; a functional molecular study. 2006 , 6, 151	13
1665	Selection of suitable reference genes for accurate normalization of gene expression profile studies in non-small cell lung cancer. 2006 , 6, 200	71
1664	Profiling alternatively spliced mRNA isoforms for prostate cancer classification. 2006 , 7, 202	78
1663	A stable gene selection in microarray data analysis. 2006 , 7, 228	120
1662	Statistical modeling of biomedical corpora: mining the Caenorhabditis Genetic Center Bibliography for genes related to life span. 2006 , 7, 250	21
1661	Differential prioritization between relevance and redundancy in correlation-based feature selection techniques for multiclass gene expression data. 2006 , 7, 320	23
1660	The impact of sample imbalance on identifying differentially expressed genes. 2006 , 7 Suppl 4, S8	14
1659	Comparative analysis and integrative classification of NCI60 cell lines and primary tumors using gene expression profiling data. 2006 , 7, 166	41
1658	The molecular portraits of breast tumors are conserved across microarray platforms. 2006 , 7, 96	1016

1657	From differential display to DNA microarrays--a personal account. 2006 , 209, 653-8	7
1656	Gain of a region on 7p22.3, containing MAD1L1, is the most frequent event in small-cell lung cancer cell lines. 2006 , 45, 11-9	52
1655	Past, present and future of gene expression-tailored therapy for lung cancer. 2006 , 3, 165-175	3
1654	Identification of genes expressed differentially in an in vitro human lung carcinogenesis model. 2006 , 5, 665-73	8
1653	Molecular markers for discrimination of benign and malignant follicular thyroid tumors. 2006 , 27, 211-20	42
1652	Developing gene expression signatures of pathway deregulation in tumors. 2006 , 5, 2444-9	27
1651	Soluble mesothelin-related peptides in the diagnosis of malignant pleural mesothelioma. 2006 , 173, 1155-60	192
1650	Vascular biology: cellular and molecular profiling. 2006 , 26, 65-74	2
1649	HPtaa database-potential target genes for clinical diagnosis and immunotherapy of human carcinoma. 2006 , 34, D607-12	19
1648	The blood option: transcriptional profiling in clinical trials. 2006 , 7, 141-4	13
1647	Expression profiling defines a recurrence signature in lung squamous cell carcinoma. 2007 , 28, 760-6	84
1646	Independent component analysis-based penalized discriminant method for tumor classification using gene expression data. 2006 , 22, 1855-62	236
1645	A gene expression signature predicts survival of patients with stage I non-small cell lung cancer. 2006 , 3, e467	243
1644	Lung tumor diagnosis and subtype discovery by gene expression profiling. 2006 , 2006, 5868-71	1
1643	CASPAR: a hierarchical bayesian approach to predict survival times in cancer from gene expression data. 2006 , 22, 1495-502	35
1642	Stage II colon cancer prognosis prediction by tumor gene expression profiling. 2006 , 24, 4685-91	173
1641	Gene expression profiling reveals reproducible human lung adenocarcinoma subtypes in multiple independent patient cohorts. 2006 , 24, 5079-90	207
1640	Knockdown of contactin-1 expression suppresses invasion and metastasis of lung adenocarcinoma. 2006 , 66, 2553-61	57

1639	Gene expression signatures for predicting prognosis of squamous cell and adenocarcinomas of the lung. 2006 , 66, 7466-72		337
1638	Repression of prostaglandin dehydrogenase by epidermal growth factor and snail increases prostaglandin E2 and promotes cancer progression. 2006 , 66, 6649-56		94
1637	Constructing molecular classifiers for the accurate prognosis of lung adenocarcinoma. 2006 , 12, 3344-54		74
1636	Expression profile-defined classification of lung adenocarcinoma shows close relationship with underlying major genetic changes and clinicopathologic behaviors. 2006 , 24, 1679-88		257
1635	The role of human tissue kallikreins 7 and 8 in intracranial malignancies. 2006 , 387, 1607-12		24
1634	Expression of the human kallikrein genes 10 (KLK10) and 11 (KLK11) in cancerous and non-cancerous lung tissues. 2006 , 387, 783-8		22
1633	Pattern Recognition in Bioinformatics. 2006 ,		
1632	The future in diagnosis and staging of lung cancer. Molecular techniques. 2006 , 73, 575-80		9
1631	Application of oligonucleotide microarrays to assess the biological effects of neoadjuvant imatinib mesylate treatment for localized prostate cancer. 2006 , 12, 152-8		23
1630	Genomic approaches to lung cancer. 2006 , 12, 4384s-4391s		40
1629	Linkage between cellular communications, energy utilization, and proliferation in metastatic neuroendocrine cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 12505-10	11.5	28
1628	Towards a holistic, yet gene-centered analysis of gene expression profiles: a case study of human lung cancers. 2006 , 2006, 69141		40
1627	Microarray-Based Technology: Basic Principles, Advantages and Limitations. 2006 ,		1
1626	Epidermal growth factor receptor variant III mutations in lung tumorigenesis and sensitivity to tyrosine kinase inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 7817-22	11.5	229
1625	Thousands of samples are needed to generate a robust gene list for predicting outcome in cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 5923-8	11.5	528
1624	Gene expression profiling on lung cancer outcome prediction: present clinical value and future premise. 2006 , 15, 2063-8		31
1623	Topology-based cancer classification and related pathway mining using microarray data. 2006 , 34, 4069-80		32
1622	TUMOR CLASSIFICATION BASED ON INDEPENDENT COMPONENT ANALYSIS. 2006 , 20, 297-310		9

1621	Partial least squares: a versatile tool for the analysis of high-dimensional genomic data. 2007 , 8, 32-44	452
1620	Signal transducer and activator of transcription 3 is required for the oncogenic effects of non-small-cell lung cancer-associated mutations of the epidermal growth factor receptor. 2006 , 66, 3162-8	196
1619	Graph-based consensus clustering for class discovery from gene expression data. 2007 , 23, 2888-96	121
1618	Reproducibility of differential gene detection across multiple microarray studies. 2007 , 2007, 4231-4	5
1617	Utility of osteopontin and serum mesothelin in malignant pleural mesothelioma diagnosis and prognosis assessment. 2007 , 13, 2928-35	180
1616	Protein 4.1B suppresses prostate cancer progression and metastasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 12784-9	11.5 58
1615	Metagene projection for cross-platform, cross-species characterization of global transcriptional states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 5959-64	11.5 100
1614	Clinical validity of the lung cancer biomarkers identified by bioinformatics analysis of public expression data. 2007 , 67, 7431-8	76
1613	Increased expression and activity of nuclear cathepsin L in cancer cells suggests a novel mechanism of cell transformation. 2007 , 5, 899-907	103
1612	Histotype in Non-Small Cell Lung Cancer Therapy and Staging: The Emerging Role of an Old and Underrated Factor. 2007 , 3, 69-77	6
1611	Annotation-based distance measures for patient subgroup discovery in clinical microarray studies. 2007 , 23, 2256-64	11
1610	Incorporating prior knowledge of predictors into penalized classifiers with multiple penalty terms. 2007 , 23, 1775-82	52
1609	A 25-signal proteomic signature and outcome for patients with resected non-small-cell lung cancer. 2007 , 99, 858-67	63
1608	Integration of genome and chromatin structure with gene expression profiles to predict c-MYC recognition site binding and function. 2007 , 3, e63	26
1607	Network-based analysis of affected biological processes in type 2 diabetes models. 2007 , 3, e96	142
1606	Aberrant DNA methylation of OLIG1, a novel prognostic factor in non-small cell lung cancer. 2007 , 4, e108	36
1605	Critical role for Fas-associated death domain-like interleukin-1-converting enzyme-like inhibitory protein in anoikis resistance and distant tumor formation. 2007 , 99, 811-22	64
1604	Very sparse stable random projections for dimension reduction in \mathbb{R}^D . 2007 ,	4

1603	PADGE: analysis of heterogeneous patterns of differential gene expression. 2007 , 32, 154-9	17
1602	Identification of the retinoic acid-inducible Gprc5a as a new lung tumor suppressor gene. 2007 , 99, 1668-82	85
1601	Molecular pathogenesis of early-stage non-small cell lung cancer and a proposal for tissue banking to facilitate identification of new biomarkers. 2007 , 2, S128-35	17
1600	A platform for the selection of genes in DNA microarraydata using evolutionary algorithms. 2007 ,	3
1599	Expression profiling and lung cancer development. 2007 , 4, 127-32	27
1598	Gene expression profiling in pulmonary hypertension. 2007 , 4, 117-20	36
1597	Gene-expression profiling in lung cancer: still early days. 2007 , 8, 129-32	2
1596	Ambient Cardiac Expert: A Cardiac Patient Monitoring System using Genetic and Clinical Knowledge Fusion. 2007 ,	
1595	RefPlus: an R package extending the RMA Algorithm. 2007 , 23, 2493-4	35
1594	Ensemble clustering method based on the resampling similarity measure for gene expression data. 2007 , 16, 539-64	9
1593	A 10-gene classifier for distinguishing head and neck squamous cell carcinoma and lung squamous cell carcinoma. 2007 , 13, 2905-15	51
1592	MSVM-RFE: extensions of SVM-RFE for multiclass gene selection on DNA microarray data. 2007 , 23, 1106-14	174
1591	Differential expression and distribution of epithelial adhesion molecules in non-small cell lung cancer and normal bronchus. 2007 , 60, 608-14	47
1590	Three-gene prognostic classifier for early-stage non small-cell lung cancer. 2007 , 25, 5562-9	195
1589	Gene selection via the BAHSIC family of algorithms. 2007 , 23, i490-8	35
1588	Where next for lung cancer gene expression profiling?. 2007 , 30, 5-6	1
1587	Knock-in of oncogenic Kras does not transform mouse somatic cells but triggers a transcriptional response that classifies human cancers. 2007 , 67, 8468-76	28
1586	Use of a cytokine gene expression signature in lung adenocarcinoma and the surrounding tissue as a prognostic classifier. 2007 , 99, 1257-69	110

1585	Gene expression signatures for tumor progression, tumor subtype, and tumor thickness in laser-microdissected melanoma tissues. 2007 , 13, 806-15	189
1584	Meta-analysis of gene expression data: a predictor-based approach. 2007 , 23, 1599-606	39
1583	CUL7 is a novel antiapoptotic oncogene. 2007 , 67, 9616-22	45
1582	Adenocarcinoma, a molecular perspective. 2007 , 18 Suppl 9, ix147-9	17
1581	Stage N2/IIIA Non Small Cell Lung Cancer: An Evidence-Based Review. 2007 , 3, 127-139	
1580	Gene expression of lung squamous cell carcinoma reflects mode of lymph node involvement. 2007 , 30, 21-5	16
1579	Decorrelation of the true and estimated classifier errors in high-dimensional settings. 2007 , 38473	33
1578	Autoantibody profiles reveal ubiquilin 1 as a humoral immune response target in lung adenocarcinoma. 2007 , 67, 3461-7	76
1577	Identification of an integrated SV40 T/t-antigen cancer signature in aggressive human breast, prostate, and lung carcinomas with poor prognosis. 2007 , 67, 8065-80	90
1576	Gene expression signature predicts recurrence in lung adenocarcinoma. 2007 , 13, 2946-54	95
1575	KIF14 messenger RNA expression is independently prognostic for outcome in lung cancer. 2007 , 13, 3229-34	78
1574	Visualization-based cancer microarray data classification analysis. 2007 , 23, 2147-54	51
1573	A non-genetic basis for cancer progression and metastasis: self-organizing attractors in cell regulatory networks. 2006 , 26, 27-54	120
1572	Classification of Patients. 957-991	2
1571	Hedgehog-independent overexpression of transforming growth factor- β in rhabdomyosarcoma of Patched1 mutant mice. 2007 ,	2
1570	Classifying Gene Expression Profiles with Evolutionary Computation. 21-40	
1569	Basic Helix-Loop-Helix Transcription Factor Profiling of Lung Tumors Shows Aberrant Expression of the Proneural Gene Atonal Homolog 1 (ATOH1, HATH1, MATH1) in Neuroendocrine Tumors. 2007 , 22, 114-123	9
1568	Classification Accuracy Based Microarray Missing Value Imputation. 2007 , 303-327	1

1567	Understanding systemic sclerosis through gene expression profiling. 2007 , 19, 561-7	4
1566	Immunophenotypic profiling of nonsmall cell lung cancer progression using the tissue microarray approach. 2007 , 15, 19-30	24
1565	Kallikrein 11 expressed in human breast cancer cells releases insulin-like growth factor through degradation of IGFBP-3. 2007 ,	2
1564	Gene expression and the concept of the phenotype. 2007 , 38, 238-54	24
1563	LRIG inhibitors of growth factor signalling - double-edged swords in human cancer?. 2007 , 43, 676-82	75
1562	Selective discussion and transparency in microarray research findings for cancer outcomes. 2007 , 43, 1999-2010	14
1561	S100A2-S100P expression profile and diagnosis of non-small cell lung carcinoma: impairment by advanced tumour stages and neoadjuvant chemotherapy. 2007 , 43, 1935-43	47
1560	Molecular profiling techniques and bioinformatics in cancer research. 2007 , 33, 255-65	15
1559	Integrative analysis and validation of robust gene signature in lung cancer. 2007 , 358, 710-5	2
1558	Human tissue kallikreins: the cancer biomarker family. 2007 , 249, 61-79	142
1557	A metastatic signature in entire lung adenocarcinomas irrespective of morphological heterogeneity. 2007 , 38, 702-9	47
1556	Transcriptional profiling of non-small cell lung cancer cells with activating EGFR somatic mutations. 2007 , 2, e1226	26
1555	Analysis of pathway activity in primary tumors and NCI60 cell lines using gene expression profiling data. 2007 , 5, 15-24	8
1554	A five-gene signature and clinical outcome in non-small-cell lung cancer. 2007 , 356, 11-20	754
1553	Osteopontin is linked to p65 and MMP-9 expression in pulmonary adenocarcinoma but not in malignant pleural mesothelioma. 2007 , 50, 720-6	19
1552	Characteristics of predictor sets found using differential prioritization. 2007 , 2, 7	2
1551	Threshold-free high-power methods for the ontological analysis of genome-wide gene-expression studies. 2007 , 8, R74	19
1550	Oligonucleotide Probes for RNA-Targeted Fluorescence In Situ Hybridization. 2007 , 79-115	34

1549	Molecular Pathology in Clinical Practice. 2007 ,	3
1548	Sparse Nonnegative Matrix Factorization for Classification of Gene Expression Data. 2007 ,	2
1547	A blocking strategy to improve gene selection for classification of gene expression data. 2007 , 4, 293-300	26
1546	Genomic signatures individualize therapeutic decisions in non-small-cell lung cancer. 2007 , 7, 837-44	6
1545	Molecular profiling of lung carcinoma: identifying clinically useful tumor markers for diagnosis and prognosis. 2007 , 7, 77-86	15
1544	Molecular analysis of deletions in human chromosome 3p21 and the role of resident cancer genes in disease. 2007 , 6, 19-39	56
1543	Cancer genomics: integrating form and function. 2007 , 28, 1387-92	14
1542	Prognostic modeling in early stage lung cancer: an evolving process from histopathology to genomics. 2007 , 17, 167-73, viii	10
1541	[DNA Chips in thoracic oncology: molecular diagnosis and the definition of new therapeutic targets, a revolution in progress]. 2007 , 24, 821-4	1
1540	Apport des ARNs et micro-ARNs dans la classification des carcinomes broncho-pulmonaires. 2007 , 27, 53-55	
1539	Distinguishing lung tumours from normal lung based on a small set of genes. 2007 , 55, 157-64	4
1538	Prognostic significance of RASSF1A promoter methylation on survival of non-small cell lung cancer patients treated with gemcitabine. 2007 , 56, 115-23	58
1537	Chromosomal aberrations and gene expression profiles in non-small cell lung cancer. 2007 , 56, 175-84	114
1536	Identification of genes differentially expressed in human primary lung squamous cell carcinoma. 2007 , 56, 307-17	67
1535	Abrogation of the interaction between osteopontin and alphavbeta3 integrin reduces tumor growth of human lung cancer cells in mice. 2007 , 57, 302-10	49
1534	Identification of key processes underlying cancer phenotypes using biologic pathway analysis. 2007 , 2, e425	96
1533	Common human cancer genes discovered by integrated gene-expression analysis. 2007 , 2, e1149	60
1532	Public Databases and Software for the Pathway Analysis of Cancer Genomes. 2007 , 3, 117693510700300	9

1531	Data Mining for Gene Networks Relevant to Poor Prognosis in Lung Cancer via Backward-Chaining Rule Induction. 2007 , 3, 117693510700300	1
1530	M06-04: Genomic signatures of prognosis in early stage non-small cell lung cancer. 2007 , 2, S168-S169	1
1529	Inactivation of LLC1 gene in nonsmall cell lung cancer. <i>International Journal of Cancer</i> , 2007 , 120, 2353-87.5	8
1528	Parathyroid hormone-related protein varies with sex and androgen status in nonsmall cell lung cancer. 2007 , 110, 1313-20	10
1527	Selecting a minimal number of relevant genes from microarray data to design accurate tissue classifiers. 2007 , 90, 78-86	24
1526	ESVM: evolutionary support vector machine for automatic feature selection and classification of microarray data. 2007 , 90, 516-28	70
1525	Genomics and proteomics: emerging technologies in clinical cancer research. 2007 , 61, 1-25	46
1524	Colorectal cancer therapeutics and the challenges of applied pharmacogenomics. 2007 , 31, 315-66	2
1523	Strategic plans to promote head and neck cancer translational research within the radiation therapy oncology group: a report from the translational research program. 2007 , 69, S67-78	12
1522	Comparative analysis of the gene co-regulatory network of normal and cancerous lung. 2007 , 384, 739-746	5
1521	Crystallization and preliminary crystallographic studies of human kallikrein 7, a serine protease of the multigene kallikrein family. 2007 , 63, 669-72	2
1520	Serum proteomics of lung adenocarcinomas induced by targeted overexpression of c-raf in alveolar epithelium identifies candidate biomarkers. 2007 , 7, 3980-91	28
1519	Airway epithelial gene expression in the diagnostic evaluation of smokers with suspect lung cancer. 2007 , 13, 361-6	416
1518	Proof concept for clinical justification of network mapping for personalized cancer therapeutics. 2007 , 14, 686-95	15
1517	Proteomics analysis in lung cancer: challenges and opportunities. 2007 , 12, 22-8	52
1516	Gene expression profiling of epidermal growth factor receptor/KRAS pathway activation in lung adenocarcinoma. 2007 , 98, 985-91	29
1515	Epidermal growth factor receptor mutations in lung cancers. 2007 , 57, 233-44	60
1514	Meta-analysis of several gene lists for distinct types of cancer: a simple way to reveal common prognostic markers. 2007 , 8, 118	23

1513	Selecting dissimilar genes for multi-class classification, an application in cancer subtyping. 2007 , 8, 206	32
1512	Large-scale integration of cancer microarray data identifies a robust common cancer signature. 2007 , 8, 275	72
1511	AffyMAPSDetector: a software tool to characterize Affymetrix GeneChip expression arrays with respect to SNPs. 2007 , 8, 276	13
1510	Inferring activity changes of transcription factors by binding association with sorted expression profiles. 2007 , 8, 452	60
1509	Selection of DDX5 as a novel internal control for Q-RT-PCR from microarray data using a block bootstrap re-sampling scheme. 2007 , 8, 140	241
1508	Evidence for systems-level molecular mechanisms of tumorigenesis. 2007 , 8, 185	28
1507	New data on robustness of gene expression signatures in leukemia: comparison of three distinct total RNA preparation procedures. 2007 , 8, 188	12
1506	Unravelling the hidden heterogeneities of diffuse large B-cell lymphoma based on coupled two-way clustering. 2007 , 8, 332	7
1505	Signalling via integrins: implications for cell survival and anticancer strategies. 2007 , 1775, 163-80	178
1504	Biotechnology. Gene expression and microchips: Problems of the quantitative analysis. 2007 , 77, 2071-2081	
1503	Thymosin beta-NB is the human isoform of rat thymosin beta15. 2007 , 1112, 286-96	15
1502	Differential prioritization in feature selection and classifier aggregation for multiclass microarray datasets. 2007 , 14, 329-366	17
1501	Prädiktive Biomarker. 2007 , 13, 56-66	0
1500	Neuro-endocrine tumours of the lung. A review of relevant pathological and molecular data. 2007 , 451 Suppl 1, S51-9	38
1499	Critical role for c-FLIP(L) on Fas resistance in colon carcinoma cell line HT-29. 2008 , 32, 329-36	6
1498	Genetic changes in small cell lung carcinoma. 2008 , 10, 189-97	27
1497	Kleinzelliges Lungenkarzinom. 2008 , 14, 762-773	1
1496	Pathohistologische und molekulargenetische Diagnostik beim CUP-Syndrom. 2008 , 14, 870-878	0

1495	RNA expression analysis from formalin fixed paraffin embedded tissues. 2008 , 130, 435-45	151
1494	Targeted disruption of the galectin-3 gene results in decreased susceptibility to NNK-induced lung tumorigenesis: an oligonucleotide microarray study. 2008 , 134, 777-88	28
1493	Identification of importin 8 (IPO8) as the most accurate reference gene for the clinicopathological analysis of lung specimens. 2008 , 9, 103	35
1492	Genome wide SNP comparative analysis between EGFR and KRAS mutated NSCLC and characterization of two models of oncogenic cooperation in non-small cell lung carcinoma. 2008 , 1, 25	28
1491	An expression meta-analysis of predicted microRNA targets identifies a diagnostic signature for lung cancer. 2008 , 1, 61	43
1490	Proteomics of lung physiopathology. 2008 , 8, 5053-73	12
1489	High-throughput proteomic analysis of formalin-fixed paraffin-embedded tissue microarrays using MALDI imaging mass spectrometry. 2008 , 8, 3715-24	252
1488	Expression signatures in lung cancer reveal a profile for EGFR-mutant tumours and identify selective PIK3CA overexpression by gene amplification. 2008 , 214, 347-56	77
1487	Expression profile of early lung adenocarcinoma: identification of MRP3 as a molecular marker for early progression. 2008 , 216, 75-82	22
1486	Gene expression profiling as a tool for basic analysis and clinical application of human cancer. 2008 , 47, 573-9	16
1485	Toward the individualization of lung cancer therapy. 2008 , 113, 1760-7	16
1484	Combination of 5-azacytidine and thalidomide for the treatment of myelodysplastic syndromes and acute myeloid leukemia. 2008 , 113, 1596-604	58
1483	Algorithmic Methods for the Analysis of Gene Expression Data. 115-145	
1482	Mammalian NDR protein kinases: from regulation to a role in centrosome duplication. 2008 , 1784, 3-15	51
1481	Feature selection using localized generalization error for supervised classification problems using RBFNN. 2008 , 41, 3706-3719	59
1480	Expression status of folate receptor alpha is significantly correlated with prognosis in non-small-cell lung cancers. 2008 , 15, 889-99	86
1479	Clinical significance of loss of Fhl1 expression in human gastric cancer. 2008 , 15, 2293-300	34
1478	Elevated thymosin beta15 expression is associated with progression and metastasis of non-small cell lung cancer. 2008 , 116, 484-90	7

1477	Glypican-3 is overexpressed in lung squamous cell carcinoma, but not in adenocarcinoma. 2008 , 21, 817-25	86
1476	A chimeric fusion of the hASH1 and EZH2 promoters mediates high and specific reporter and suicide gene expression and cytotoxicity in small cell lung cancer cells. 2008 , 15, 563-75	16
1475	Mutations in the LKB1 tumour suppressor are frequently detected in tumours from Caucasian but not Asian lung cancer patients. 2008 , 99, 245-52	130
1474	Gene expression-based survival prediction in lung adenocarcinoma: a multi-site, blinded validation study. 2008 , 14, 822-7	835
1473	Stability of gene contributions and identification of outliers in multivariate analysis of microarray data. 2008 , 9, 289	12
1472	New resampling method for evaluating stability of clusters. 2008 , 9, 42	9
1471	Discovery of dominant and dormant genes from expression data using a novel generalization of SNR for multi-class problems. 2008 , 9, 425	15
1470	Identifying differential correlation in gene/pathway combinations. 2008 , 9, 488	18
1469	Very Important Pool (VIP) genes--an application for microarray-based molecular signatures. 2008 , 9 Suppl 9, S9	5
1468	Cigarette smoke induces endoplasmic reticulum stress and the unfolded protein response in normal and malignant human lung cells. 2008 , 8, 229	131
1467	Identification of gene transcript signatures predictive for estrogen receptor and lymph node status using a stepwise forward selection artificial neural network modelling approach. 2008 , 43, 99-111	41
1466	On alpha-divergence based nonnegative matrix factorization for clustering cancer gene expression data. 2008 , 44, 1-5	11
1465	A simple two-gene prognostic model for adenocarcinoma of the lung. 2008 , 135, 627-34	15
1464	A support vector machine with integer parameters. 2008 , 72, 480-489	37
1463	Gene expression profiling of non-small-cell lung cancer. 2008 , 8, 167-78	26
1462	Tumor volume and tumor marker index based on CYFRA 21-1 and CEA are strong prognostic factors in operated early stage NSCLC. 2008 , 60, 408-15	30
1461	Quantitative reverse transcriptase real-time polymerase chain reaction (qRT-PCR) in translational oncology: lung cancer perspective. 2008 , 59, 147-54	21
1460	Gene expression profiling of non-small cell lung cancer. 2008 , 60, 313-24	50

1459	Molecular phenotyping of severe asthma using pattern recognition of bronchoalveolar lavage-derived cytokines. 2008 , 121, 30-37.e6	94
1458	Molecular profiling of non-small cell lung cancer: of what value in clinical practice?. 2008 , 17, 451-62	1
1457	Expression of kallikrein-related peptidases (KRP/hK5, 7, 6, 8) in subtypes of human lung carcinoma. 2008 , 8, 300-6	17
1456	Module map of stem cell genes guides creation of epithelial cancer stem cells. 2008 , 2, 333-44	542
1455	Lung cancer. 2008 , 359, 1367-80	1920
1454	CD200: a putative therapeutic target in cancer. 2008 , 366, 117-22	76
1453	Chemokine signaling via the CXCR2 receptor reinforces senescence. 2008 , 133, 1006-18	1161
1452	Clustering cancer gene expression data: a comparative study. 2008 , 9, 497	248
1451	Classification with reject option in gene expression data. 2008 , 24, 1889-95	42
1450	Carcinoma of unknown primary with a colon-cancer profile-changing paradigm and emerging definitions. 2008 , 9, 596-9	97
1449	Molecular genetics of lung cancer in people who have never smoked. 2008 , 9, 676-82	100
1448	Gene expression data classification using consensus independent component analysis. 2008 , 6, 74-82	33
1447	A transcriptional fingerprint of estrogen in human breast cancer predicts patient survival. 2008 , 10, 79-88	30
1446	Detection of heterogeneously expressed genes in cancer. 2008 ,	
1445	Hsp60 regulation of tumor cell apoptosis. 2008 , 283, 5188-94	199
1444	Data-driven Networking Reveals 5-Genes Signature for Early Detection of Lung Cancer. 2008 ,	1
1443	Embedded Gene Selection for Imbalanced Microarray Data Analysis. 2008 ,	2
1442	Information Visualization for DNA Microarray Data Analysis: A Critical Review. 2008 , 38, 42-54	6

1441	Expression of tissue and plasma kallikreins and kinin B1 and B2 receptors in lung cancer. 2008 , 389, 1225-33	45
1440	Whole genome exon arrays identify differential expression of alternatively spliced, cancer-related genes in lung cancer. 2008 , 36, 6535-47	86
1439	PathCluster: a framework for gene set-based hierarchical clustering. 2008 , 24, 1957-8	7
1438	Novel molecular subtypes of serous and endometrioid ovarian cancer linked to clinical outcome. 2008 , 14, 5198-208	1044
1437	Unbiased vs. biased approaches to the identification of cancer signatures: the case of lung cancer. 2008 , 7, 729-34	11
1436	Artificial Immune Recognition System for DNA Microarray Data Analysis. 2008 ,	2
1435	A multiparametric serum kallikrein panel for diagnosis of non-small cell lung carcinoma. 2008 , 14, 1355-62	49
1434	Gene Selection using the GMM-IG Framework based Integrative Analysis. 2008 ,	1
1433	The prognostic and predictive role of histology in advanced non-small cell lung cancer: a literature review. 2008 , 3, 1468-81	171
1432	Combining LPP with PCA for microarray data clustering. 2008 ,	1
1431	Controversies in the management of stage IIIA non-small-cell lung cancer. 2008 , 8, 1913-29	3
1430	EML4-ALK fusion gene and efficacy of an ALK kinase inhibitor in lung cancer. 2008 , 14, 4275-83	774
1429	COMBINING GENERALIZED NMF AND DISCRIMINATIVE MIXTURE MODELS FOR CLASSIFICATION OF GENE EXPRESSION DATA. 2008 , 22, 1587-1598	4
1428	Molecular profiling in the age of cancer genomics. 2008 , 8, 263-76	8
1427	Three-gene expression signature predicts survival in early-stage squamous cell carcinoma of the lung. 2008 , 14, 4794-9	83
1426	Genomic markers for malignant progression in pulmonary adenocarcinoma with bronchioloalveolar features. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 10155-60	11.5 59
1425	On the epistemological crisis in genomics. 2008 , 9, 69-79	21
1424	Microarray based diagnosis profits from better documentation of gene expression signatures. 2008 , 4, e22	20

1423	Principles of Molecular Oncology. 2008 ,	1
1422	Inferring pathway activity toward precise disease classification. 2008 , 4, e1000217	354
1421	An erythroid differentiation signature predicts response to lenalidomide in myelodysplastic syndrome. 2008 , 5, e35	132
1420	Gene expression studies demonstrate that the K-ras/Erk MAP kinase signal transduction pathway and other novel pathways contribute to the pathogenesis of cumene-induced lung tumors. 2008 , 36, 743-52	11
1419	Confirmation of gene expression-based prediction of survival in non-small cell lung cancer. 2008 , 14, 8213-20	82
1418	A multigene assay is prognostic of survival in patients with early-stage lung adenocarcinoma. 2008 , 14, 5565-70	69
1417	Quantitative RT-PCR analysis and immunohistochemical localization of the kallikrein-related peptidases 13 and 14 in lung. 2008 , 389, 781-6	17
1416	Key issues in conducting a meta-analysis of gene expression microarray datasets. 2008 , 5, e184	364
1415	Tumor cell dependence on Ran-GTP-directed mitosis. 2008 , 68, 1826-33	78
1414	TbetaRIII suppresses non-small cell lung cancer invasiveness and tumorigenicity. 2008 , 29, 528-35	90
1413	Tissue prostate-specific antigen facilitates refractory prostate tumor progression via enhancing ARA70-regulated androgen receptor transactivation. 2008 , 68, 7110-9	59
1412	The tumor suppressor semaphorin 3B triggers a prometastatic program mediated by interleukin 8 and the tumor microenvironment. 2008 , 205, 1155-71	79
1411	Non-overlapping and non-cell-type-specific gene expression signatures predict lung cancer survival. 2008 , 26, 877-83	82
1410	Prediction of recurrence-free survival in postoperative non-small cell lung cancer patients by using an integrated model of clinical information and gene expression. 2008 , 14, 7397-404	194
1409	Medikamentöse Therapie des kleinzelligen Bronchialkarzinoms (SCLC) - neue molekulare Therapieansätze. 2008 , 29, 81-90	
1408	[Drug therapy for small-cell lung cancer (SCLC)--new molecular strategies for therapy]. 2008 , 62, 23-30	1
1407	Sparse kernel methods for high-dimensional survival data. 2008 , 24, 1632-8	55
1406	Smoking-related genomic signatures in non-small cell lung cancer. 2008 , 178, 1164-72	33

1405	Clinical year in review I: Lung cancer, pleural disease, exercise testing and pulmonary rehabilitation, and sleep medicine. 2008 , 5, 739-44	4
1404	Comparative study on normalization procedures for cluster analysis of gene expression datasets. 2008 ,	20
1403	A Novel Mixture Classifier and its Application in Breast Cancer Prognosis. 2008 ,	
1402	Classification and Diagnostic Output Prediction of Cancer Using Gene Expression Profiling and Supervised Machine Learning Algorithms. 2008 , 41, 898-914	5
1401	Sparse p-norm Nonnegative Matrix Factorization for clustering gene expression data. 2008 , 2, 236-49	5
1400	Anatomie pathologique des cancers bronchopulmonaires. 2008 , 5, 1-22	
1399	Pathway targets to explore in the treatment of non-small cell lung cancer. 2008 , 3, 1342-52	8
1398	Lung adenocarcinoma: modification of the 2004 WHO mixed subtype to include the major histologic subtype suggests correlations between papillary and micropapillary adenocarcinoma subtypes, EGFR mutations and gene expression analysis. 2008 , 32, 810-27	315
1397	Stem cell biology in the lung and lung cancers: using pulmonary context and classic approaches. 2008 , 73, 479-90	10
1396	Combining multiple decisions: applications to bioinformatics. 2008 , 95, 012018	
1395	The GTPase Ran: regulation of cell life and potential roles in cell transformation. 2008 , 13, 4097-121	38
1394	Efficiency analysis of competing tests for finding differentially expressed genes in lung adenocarcinoma. 2008 , 6, 389-421	23
1393	Activation and Molecular Targets of Peroxisome Proliferator-Activated Receptor-gamma Ligands in Lung Cancer. 2008 , 2008, 156875	21
1392	References. 2009 , 217-236	
1391	. 2009 ,	8
1390	Likelihood estimation of conjugacy relationships in linear models with applications to high-throughput genomics. 2009 , 5, Article 18	
1389	Factors influencing the statistical power of complex data analysis protocols for molecular signature development from microarray data. 2009 , 4, e4922	16
1388	Expression signatures of metastatic capacity in a genetic mouse model of lung adenocarcinoma. 2009 , 4, e5401	60

1387	A systems biology-based gene expression classifier of glioblastoma predicts survival with solid tumors. 2009 , 4, e6274	17
1386	A predictive phosphorylation signature of lung cancer. 2009 , 4, e7994	12
1385	Gene expression profiles in peripheral blood mononuclear cells can distinguish patients with non-small cell lung cancer from patients with nonmalignant lung disease. 2009 , 69, 9202-10	125
1384	Disease Classification Based on the Activities of Interacting Molecular Modules with Condition-Responsive Correlation. 2009 ,	
1383	Tabu search and binary particle swarm optimization for feature selection using microarray data. 2009 , 16, 1689-703	46
1382	Bio-inspired machine learning in microarray gene selection and cancer classification. 2009 ,	1
1381	Meta-analysis of cancer gene-profiling data. 2010 , 576, 409-26	3
1380	Prediction of cancer outcome using DNA microarray technology: past, present and future. 2009 , 3, 157-65	11
1379	Prediction of clinical outcome in multiple lung cancer cohorts by integrative genomics: implications for chemotherapy selection. 2009 , 69, 1055-62	44
1378	High-throughput molecular analysis in lung cancer: insights into biology and potential clinical applications. 2009 , 34, 489-506	31
1377	The expression of three genes in primary non-small cell lung cancer is associated with metastatic spread to the brain. 2009 , 15, 1755-61	134
1376	Gene Expression Analysis Using Clustering. 2009 ,	5
1375	Prognostic gene signatures for non-small-cell lung cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 2824-8	11.5 159
1374	Blood-based transcriptomics: leukemias and beyond. 2009 , 9, 271-80	21
1373	Comparative transcriptome analyses revealed conserved biological and transcription factor target modules between the zebrafish and human tumors. 2009 , 6, 425-31	15
1372	Combined inhibition of the VEGFR and EGFR signaling pathways in the treatment of NSCLC. 2009 , 14, 399-411	76
1371	Identification of gene signatures and molecular markers for human lung cancer prognosis using an in vitro lung carcinogenesis system. 2009 , 2, 702-11	43
1370	Smoking-Related Gene Expression in Laser Capture-Microdissected Human Lung. 2009 , 15, 7562-7570	10

1369	Dimension reduction of microarray data in the presence of a censored survival response: a simulation study. 2009 , 8, Article 4	3
1368	A radiation-derived gene expression signature predicts clinical outcome for breast cancer patients. 2009 , 171, 141-54	8
1367	Characterizing the clinical relevance of an embryonic stem cell phenotype in lung adenocarcinoma. 2009 , 15, 7553-61	15
1366	MicroRNAs and lung cancer: new oncogenes and tumor suppressors, new prognostic factors and potential therapeutic targets. 2009 , 16, 1047-61	80
1365	HtrA serine proteases as potential therapeutic targets in cancer. 2009 , 9, 451-68	96
1364	Airway gene expression in chronic obstructive pulmonary disease. 2009 , 6, 697-700	23
1363	The involvement of the transcription factor Yin Yang 1 in cancer development and progression. 2009 , 8, 1367-72	111
1362	A Bayesian model for cross-study differential gene expression. 2009 , 104, 1295-1310	27
1361	How is gene-expression profiling going to challenge the future management of lung cancer?. 2009 , 5, 827-35	6
1360	Molecular biomarkers for quantitative and discrete COPD phenotypes. 2009 , 40, 359-67	84
1359	[Gene expression profiling in lung cancer. Experimental research and clinical application]. 2009 , 134, 519-21	3
1358	Genomics of lung cancer. 2009 , 6, 152-8	34
1357	Classification and sparse-signature extraction from gene-expression data. 2009 , 2009, P05001	4
1356	A method for constructing a confidence bound for the actual error rate of a prediction rule in high dimensions. 2009 , 10, 282-96	4
1355	Evaluating reproducibility of differential expression discoveries in microarray studies by considering correlated molecular changes. 2009 , 25, 1662-8	91
1354	Statistical methods for gene set co-expression analysis. 2009 , 25, 2780-6	107
1353	Sparse representation for classification of tumors using gene expression data. 2009 , 2009, 403689	53
1352	A genetic programming-based approach to the classification of multiclass microarray datasets. 2009 , 25, 331-7	57

1351	Is bagging effective in the classification of small-sample genomic and proteomic data?. 2009 , 158368	5
1350	An embryonic stem cell-like signature identifies poorly differentiated lung adenocarcinoma but not squamous cell carcinoma. 2009 , 15, 6386-90	50
1349	Ratio adjustment and calibration scheme for gene-wise normalization to enhance microarray inter-study prediction. 2009 , 25, 1655-61	17
1348	Cell proliferation and epidermal growth factor signaling in non-small cell lung adenocarcinoma cell lines are dependent on Rin1. 2009 , 284, 26331-9	27
1347	Relapse-related molecular signature in lung adenocarcinomas identifies patients with dismal prognosis. 2009 , 27, 2793-9	153
1346	An immune response enriched 72-gene prognostic profile for early-stage non-small-cell lung cancer. 2009 , 15, 284-90	123
1345	The SRY-HMG box gene, SOX4, is a target of gene amplification at chromosome 6p in lung cancer. 2009 , 18, 1343-52	91
1344	Meta-analysis of oncogenic protein kinase Ciota signaling in lung adenocarcinoma. 2009 , 15, 1527-33	34
1343	Prostate cancer-associated gene expression alterations determined from needle biopsies. 2009 , 15, 3135-42	12
1342	Identifying set-wise differential co-expression in gene expression microarray data. 2009 , 10, 109	58
1341	GAGE: generally applicable gene set enrichment for pathway analysis. 2009 , 10, 161	733
1340	Discovering collectively informative descriptors from high-throughput experiments. 2009 , 10, 431	4
1339	A new regularized least squares support vector regression for gene selection. 2009 , 10, 44	11
1338	A white-box approach to microarray probe response characterization: the BaFL pipeline. 2009 , 10, 449	4
1337	Computational analysis of gene expression space associated with metastatic cancer. 2009 , 10 Suppl 11, S6	1
1336	Identification of genes associated with multiple cancers via integrative analysis. 2009 , 10, 535	15
1335	A compact VEGF signature associated with distant metastases and poor outcomes. 2009 , 7, 9	132
1334	Gene expression profiling and non-small-cell lung cancer: where are we now?. 2009 , 10, 168-73	14

1333	Degree of differential prioritization: prediction for multiclass molecular classification. 2009 , 28, 45-51	
1332	Metabolic profiling identifies lung tumor responsiveness to erlotinib. 2009 , 87, 83-6	22
1331	The multifaceted roles of the receptor tyrosine kinase ROS in development and cancer. 2009 , 1795, 37-52	84
1330	Cancer gene discovery in mouse and man. 2009 , 1796, 140-61	8
1329	Interval based fuzzy systems for identification of important genes from microarray gene expression data: Application to carcinogenic development. 2009 , 42, 1022-8	8
1328	Emodin induces a reactive oxygen species-dependent and ATM-p53-Bax mediated cytotoxicity in lung cancer cells. 2009 , 623, 1-9	51
1327	Pathway level analysis by augmenting activities of transcription factor target genes. 2009 , 3, 534-42	
1326	Higher expression of chemokine receptor CXCR7 is linked to early and metastatic recurrence in pathological stage I nonsmall cell lung cancer. 2009 , 115, 2580-93	84
1325	Polymorphisms in innate immunity genes and lung cancer risk in Xuanwei, China. 2009 , 50, 285-90	15
1324	CCR1 knockdown suppresses human non-small cell lung cancer cell invasion. 2009 , 135, 695-701	16
1323	A sequential feature extraction approach for naïve bayes classification of microarray data. 2009 , 36, 9919-9923	42
1322	Mass-spectrometry-based metabolomics: limitations and recommendations for future progress with particular focus on nutrition research. 2009 , 5, 435-458	412
1321	Lung cancer biology: a genetic and genomic perspective. 2009 , 11, 263-9	13
1320	Pattern recognition methods in microarray based oncology study. 2009 , 4, 243-250	
1319	Genexpressionsprofile in der onkologischen Diagnostik. 2009 , 2, 44-52	
1318	[Small cell lung cancer: pathology and molecular pathology]. 2009 , 30, 131-40	4
1317	[Pathohistology and molecular genetic diagnostics in CUP syndrome]. 2009 , 30, 125-30	0
1316	A 2-DE MALDI-TOF study to identify disease regulated serum proteins in lung cancer of c-myc transgenic mice. 2009 , 9, 1044-56	27

1315	Induction of the interleukin 6/ signal transducer and activator of transcription pathway in the lungs of mice sub-chronically exposed to mainstream tobacco smoke. 2009 , 2, 56	25
1314	A taxonomy of epithelial human cancer and their metastases. 2009 , 2, 69	15
1313	Systematic RNA interference reveals that oncogenic KRAS-driven cancers require TBK1. 2009 , 462, 108-12	1614
1312	Of the atypical PKCs, Par-4 and p62: recent understandings of the biology and pathology of a PB1-dominated complex. 2009 , 16, 1426-37	61
1311	On the sampling distribution of resubstitution and leave-one-out error estimators for linear classifiers. 2009 , 42, 2705-2723	31
1310	Multiclass cancer classification by support vector machines with class-wise optimized genes and probability estimates. 2009 , 259, 533-40	33
1309	Finding rule groups to classify high dimensional gene expression datasets. 2009 , 33, 108-13	7
1308	Linguistic recognition system for identification of some possible genes mediating the development of lung adenocarcinoma. 2009 , 10, 260-269	6
1307	Feature selection via Boolean independent component analysis. 2009 , 179, 3815-3831	8
1306	Cell Adhesion Molecules. 2009 , 19-28	
1305	Biomarker Discovery for Metastatic Disease. 2009 , 289-315	1
1304	A multiclass classification method based on decoding of binary classifiers. 2009 , 21, 2049-81	4
1303	Polymorphisms in the CASPASE genes and survival in patients with early-stage non-small-cell lung cancer. 2009 , 27, 5823-9	36
1302	Robust-linear-model normalization to reduce technical variability in functional protein microarrays. 2009 , 8, 5451-64	55
1301	The footprints of cancer development: Cancer biomarkers. 2009 , 35, 193-200	88
1300	A genome-wide RNAi screen identifies multiple synthetic lethal interactions with the Ras oncogene. 2009 , 137, 835-48	784
1299	MMSET is overexpressed in cancers: link with tumor aggressiveness. 2009 , 379, 840-5	63
1298	"Omics" data and levels of evidence for biomarker discovery. 2009 , 93, 13-6	66

1297	Expression levels of NF-Y target genes changed by CDKN1B correlate with clinical prognosis in multiple cancers. 2009 , 94, 219-27	16
1296	gammaH2AX: A potential DNA damage response biomarker for assessing toxicological risk of tobacco products. 2009 , 678, 43-52	31
1295	Global gene expression analysis reveals specific patterns of cell junctions in non-small cell lung cancer subtypes. 2009 , 63, 32-8	147
1294	Prediction of lymph node metastasis by gene expression profiling in patients with primary resected lung cancer. 2009 , 64, 86-91	15
1293	Core classification of lung cancer: correlating nuclear size and mitoses with ploidy and clinicopathological parameters. 2009 , 65, 312-8	53
1292	Impact and interactions between smoking and traditional prognostic factors in lung cancer progression. 2009 , 66, 386-92	31
1291	Alteration of transcriptional profile in human bronchial epithelial cells induced by cigarette smoke condensate. 2009 , 190, 23-31	13
1290	Immunotherapy in non-small-cell lung carcinoma: from inflammation to vaccination. 2009 , 10, 99-105	14
1289	Genomic prognostic models in early-stage lung cancer. 2009 , 10, 151-7	29
1288	Understanding prognostic gene expression signatures in lung cancer. 2009 , 10, 331-40	49
1287	Class discovery from gene expression data based on perturbation and cluster ensemble. 2009 , 8, 147-60	31
1286	A two-stage feature selection method for gene expression data. 2009 , 13, 127-37	22
1285	Pattern Recognition in Bioinformatics. 2009 ,	
1284	The human kallikrein gene family: new biomarkers for ovarian cancer. 2009 , 149, 165-87	22
1283	Basic Concepts of Molecular Pathology. 2009 ,	1
1282	Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics. 2009 ,	
1281	Comparison of linear discriminant analysis methods for the classification of cancer based on gene expression data. 2009 , 28, 149	24
1280	Lung cancer gene expression database analysis incorporating prior knowledge with support vector machine-based classification method. 2009 , 28, 103	24

1279	Tumor Classification via Sparse Representation Based on Metasample. 2009 ,	3
1278	A primary xenograft model of small-cell lung cancer reveals irreversible changes in gene expression imposed by culture in vitro. 2009 , 69, 3364-73	358
1277	Clinical Information Driven Ensemble Clustering for Inferring Robust Tumor Subtypes. 2009 ,	
1276	Prediction of cancer class with majority voting genetic programming classifier using gene expression data. 2009 , 6, 353-67	38
1275	Lasso based gene selection for linear classifiers. 2009 ,	1
1274	Integrating genomics and proteomics-oriented biomarkers to comprehend lung cancer. 2009 , 3, 167-80	3
1273	Application of a New Similarity Measure in Clustering Gene Expression Data. 2009 ,	
1272	K-means clustering versus validation measures: a data-distribution perspective. 2009 , 39, 318-31	130
1271	Upregulated INHBA expression may promote cell proliferation and is associated with poor survival in lung adenocarcinoma. 2009 , 11, 388-96	94
1270	Contemporary Computing. 2009 ,	2
1269	Identification of five candidate lung cancer biomarkers by proteomics analysis of conditioned media of four lung cancer cell lines. 2009 , 8, 2746-58	111
1268	Dimension reduction of microarray gene expression data: the accelerated failure time model. 2009 , 7, 939-54	4
1267	PCA consistency in high dimension, low sample size context. 2009 , 37,	141
1266	Finding large average submatrices in high dimensional data. 2009 , 3,	88
1265	Array of hope: expression profiling identifies disease biomarkers and mechanism. 2009 , 37, 855-62	23
1264	INHBA overexpression promotes cell proliferation and may be epigenetically regulated in esophageal adenocarcinoma. 2009 , 4, 455-62	40
1263	References. 2009 , 295-327	
1262	Investigating Multi-cancer Biomarkers and Their Cross-predictability in the Expression Profiles of Multiple Cancer Types. 2009 , 4, 57-79	16

1261	Investigation of reproducibility of differentially expressed genes in DNA microarrays through statistical simulation. 2009 , 3 Suppl 2, S4	7
1260	Current gene expression studies in esophageal carcinoma. 2009 , 10, 534-9	23
1259	PET scan 18F-fluorodeoxyglucose uptake and prognosis in patients with resected clinical stage IA non-small cell lung cancer. 2010 , 137, 1150-6	56
1258	Small-Sample Error Estimation for Bagged Classification Rules. 2010 , 2010,	1
1257	Application of Density Based Clustering to Microarray Data Analysis. 2010 , 56, 281-286	3
1256	Age- and sex-specific genomic profiles in non-small cell lung cancer. 2010 , 303, 535-43	42
1255	An adult tissue-specific stem cell molecular phenotype is activated in epithelial cancer stem cells and correlated to patient outcome. 2010 , 9, 321-7	16
1254	Predictors of outcomes after surgical treatment of synchronous primary lung cancers. 2010 , 5, 197-205	91
1253	The role of pemetrexed in advanced non small-cell lung cancer: special focus on pharmacology and mechanism of action. 2010 , 11, 37-47	39
1252	Features of potentially predictive biomarkers of chemotherapeutic efficacy in small cell lung cancer. 2010 , 5, 484-90	16
1251	Lung cancer genomic signatures. 2010 , 5, 1673-91	24
1250	Proteomic screening of completely resected tumors in relation to survival in patients with stage I non-small cell lung cancer. 2010 , 24, 637-45	10
1249	Dietary D-glucarate effects on the biomarkers of inflammation during early post-initiation stages of benzo[a]pyrene-induced lung tumorigenesis in A/J mice. 2011 , 2, 145-154	3
1248	Soluble mesothelin-related protein in pleural effusion from patients with malignant pleural mesothelioma. 2010 , 1, 313-317	11
1247	Pathologic diagnosis of advanced lung cancer based on small biopsies and cytology: a paradigm shift. 2010 , 5, 411-4	144
1246	Class prediction models of thrombocytosis using genetic biomarkers. 2010 , 115, 7-14	56
1245	Chronotherapy and the molecular clock: Clinical implications in oncology. 2010 , 62, 979-1001	118
1244	Profiling the cancer genome. 2010 , 11, 133-59	36

1243	Differential gene expression in acute lymphoblastic leukemia cells surviving allogeneic transplant. 2010 , 59, 1633-44	3
1242	Relationship of mRNA expressions of RanBP2 and topoisomerase II isoforms to cytotoxicity of amrubicin in human lung cancer cell lines. 2010 , 66, 237-43	10
1241	Identification of significant gene-sets differentially expressed in a specific disease by co-expressed functional gene modules generation. 2010 , 4, 204-209	1
1240	Non-prejudiced Detection and Characterization of Genetic Modifications. 2010 , 3, 120-128	10
1239	A validated gene expression profile for detecting clinical outcome in breast cancer using artificial neural networks. 2010 , 120, 83-93	47
1238	EGFR mutations and the terminal respiratory unit. 2010 , 29, 23-36	89
1237	Lung cancer progression and metastasis from the prognostic point of view. 2010 , 27, 389-97	22
1236	Pathology and pathogenesis of ovine pulmonary adenocarcinoma. 2010 , 142, 260-83	68
1235	Partitions selection strategy for set of clustering solutions. 2010 , 73, 2809-2819	8
1234	Development of a novel splice array platform and its application in the identification of alternative splice variants in lung cancer. 2010 , 11, 352	23
1233	Transcriptional regulation of the CRK/DUF26 group of receptor-like protein kinases by ozone and plant hormones in Arabidopsis. 2010 , 10, 95	175
1232	Gene expression profiles of lung adenocarcinoma linked to histopathological grading and survival but not to EGF-R status: a microarray study. 2010 , 10, 77	9
1231	IGF-I induced genes in stromal fibroblasts predict the clinical outcome of breast and lung cancer patients. 2010 , 8, 1	129
1230	Regulation patterns in signaling networks of cancer. 2010 , 4, 162	25
1229	A GMM-IG framework for selecting genes as expression panel biomarkers. 2010 , 48, 75-82	4
1228	Mixture classification model based on clinical markers for breast cancer prognosis. 2010 , 48, 129-37	27
1227	Management of carcinoid tumors. 2010 , 89, 998-1005	127
1226	The Aurora-A/TPX2 complex: a novel oncogenic holoenzyme?. 2010 , 1806, 230-9	45

1225	Comparative proteomic analysis of anti-benzo(a)pyrene-7,8-dihydrodiol-9,10-epoxide-transformed and normal human bronchial epithelial G0/G1 cells. 2010 , 186, 166-73	17
1224	Genes, proteins and complexes: the multifaceted nature of FHL family proteins in diverse tissues. 2010 , 14, 2702-20	70
1223	Gene expression profiling in head and neck squamous cell carcinoma: Clinical perspectives. 2010 , 32, 1712-9	25
1222	PTEN, RASSF1 and DAPK site-specific hypermethylation and outcome in surgically treated stage I and II nonsmall cell lung cancer patients. <i>International Journal of Cancer</i> , 2010 , 126, 1630-9	7.5 70
1221	ROS receptor tyrosine kinase: a new potential target for anticancer drugs. 2011 , 31, 794-818	37
1220	MicroRNA expression differentiates between primary lung tumors and metastases to the lung. 2010 , 206, 578-84	60
1219	Enhanced soft subspace clustering integrating within-cluster and between-cluster information. 2010 , 43, 767-781	142
1218	Predicting incomplete gene microarray data with the use of supervised learning algorithms. 2010 , 31, 2061-2069	12
1217	An evolutionary approach for gene selection and classification of microarray data based on SVM error-bound theories. 2010 , 100, 39-46	14
1216	Histopathologic and genetic alterations as predictors of response to treatment and survival in lung cancer: a review of published data. 2010 , 75, 94-109	32
1215	GAP: A graphical environment for matrix visualization and cluster analysis. 2010 , 54, 767-778	72
1214	Comparison of lung cancer cell lines representing four histopathological subtypes with gene expression profiling using quantitative real-time PCR. 2010 , 10, 2	39
1213	MUC1-associated proliferation signature predicts outcomes in lung adenocarcinoma patients. 2010 , 3, 16	49
1212	Molecular sampling of prostate cancer: a dilemma for predicting disease progression. 2010 , 3, 8	169
1211	Lung cancer stem cells: tools and targets to fight lung cancer. 2010 , 29, 4625-35	112
1210	Binding of pro-prion to filamin A: by design or an unfortunate blunder. 2010 , 29, 5329-45	13
1209	Identification of thymidylate synthase as a potential therapeutic target for lung cancer. 2010 , 103, 354-61	27
1208	Enzastaurin inhibits invasion and metastasis in lung cancer by diverse molecules. 2010 , 103, 802-11	17

1207	. 2010 ,	10
1206	SOX2 is an oncogene activated by recurrent 3q26.3 amplifications in human lung squamous cell carcinomas. 2010 , 5, e8960	241
1205	Gene expression-based classification of non-small cell lung carcinomas and survival prediction. 2010 , 5, e10312	543
1204	The use of P63 immunohistochemistry for the identification of squamous cell carcinoma of the lung. 2010 , 5, e12209	41
1203	A 12-gene genomic instability signature predicts clinical outcomes in multiple cancer types. 2010 , 25, 219-28	33
1202	Lipases and Related Molecules in Cancer. 2010 , 3, CGM.S2816	2
1201	On the Comparison of Classifiers for Microarray Data. 2010 , 5, 29-39	12
1200	CpG hypermethylation of human four-and-a-half LIM domains 1 contributes to migration and invasion activity of human bladder cancer. 2010 , 26, 241-7	16
1199	Identification of predictive markers of response to the MEK1/2 inhibitor selumetinib (AZD6244) in K-ras-mutated colorectal cancer. 2010 , 9, 3351-62	66
1198	Gene expression-based prognostic signatures in lung cancer: ready for clinical use?. 2010 , 102, 464-74	265
1197	Validation of a prognostic model to predict survival after non-small-cell lung cancer surgery. 2010 , 38, 615-9	10
1196	Raman microscopy in the diagnosis and prognosis of surgically resected nonsmall cell lung cancer. 2010 , 15, 026015	33
1195	[Molecular characteristics of lung cancer]. 2010 , 97, 1323-35	3
1194	Loss of p130 accelerates tumor development in a mouse model for human small-cell lung carcinoma. 2010 , 70, 3877-83	145
1193	DNA microarrays are predictive of cancer prognosis: a re-evaluation. 2010 , 16, 629-36	47
1192	Epigenetic inactivation of the potential tumor suppressor gene FOXF1 in breast cancer. 2010 , 70, 6047-58	63
1191	Expression of interleukin-1 receptor-associated kinase-1 in non-small cell lung carcinoma and preneoplastic lesions. 2010 , 16, 34-44	26
1190	Upregulation of SOX9 in lung adenocarcinoma and its involvement in the regulation of cell growth and tumorigenicity. 2010 , 16, 4363-73	98

1189	Exploring the within- and between-class correlation distributions for tumor classification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 6737-42	11.5	19
1188	Bayesian rule learning for biomedical data mining. 2010 , 26, 668-75		31
1187	Presence of a putative tumor-initiating progenitor cell population predicts poor prognosis in smokers with non-small cell lung cancer. 2010 , 70, 6639-48		46
1186	Transforming Growth Factor- β In Lung Cancer, Carcinogenesis, and Metastasis. 2010 , 633-671		1
1185	Gene profiling of clinical routine biopsies and prediction of survival in non-small cell lung cancer. 2010 , 181, 181-8		37
1184	A two-stage machine learning approach for pathway analysis. 2010 ,		2
1183	Diagnosis of uncertain primary tumors with the Pathwork tissue-of-origin test. 2010 , 10, 17-25		15
1182	New biomarkers for lung cancer. 2010 , 4, 201-24		9
1181	Role of Rad51 down-regulation and extracellular signal-regulated kinases 1 and 2 inactivation in emodin and mitomycin C-induced synergistic cytotoxicity in human non-small-cell lung cancer cells. 2010 , 77, 633-43		31
1180	Prognostic and predictive gene signature for adjuvant chemotherapy in resected non-small-cell lung cancer. 2010 , 28, 4417-24		350
1179	A multi-strategy approach to informative gene identification from gene expression data. 2010 , 8, 19-38		5
1178	Intestinal epithelial cells in vitro. 2010 , 19, 131-42		65
1177	Targeted cytosine deaminase-uracil phosphoribosyl transferase suicide gene therapy induces small cell lung cancer-specific cytotoxicity and tumor growth delay. 2010 , 16, 2308-19		23
1176	Reporting bias when using real data sets to analyze classification performance. 2010 , 26, 68-76		37
1175	Ensemble Rough Hypercuboid Approach for Classifying Cancers. 2010 , 22, 381-391		34
1174	Gene selection in microarray survival studies under possibly non-proportional hazards. 2010 , 26, 784-90		22
1173	Module-based prediction approach for robust inter-study predictions in microarray data. 2010 , 26, 2586-93		5
1172	Small-sample precision of ROC-related estimates. 2010 , 26, 822-30		195

1171	KRAB-zinc finger proteins and KAP1 can mediate long-range transcriptional repression through heterochromatin spreading. 2010 , 6, e1000869	228
1170	Key genes in lung cancer translational research: a meta-analysis. 2010 , 77, 53-63	11
1169	Gene expression profiles of non-small cell lung cancer: survival prediction and new biomarkers. 2010 , 79, 283-92	71
1168	Tissue banking of diagnostic lung cancer biopsies for extraction of high quality RNA. 2010 , 5, 956-63	21
1167	Multiclass microarray gene expression classification based on fusion of correlation features. 2010 ,	1
1166	Prognostic gene expression signature for squamous cell carcinoma of lung. 2010 , 16, 5038-47	26
1165	Development of Genomics-Based Gene Expression Signature Biomarkers in Oncology and Toxicology to Facilitate Drug Discovery and Translational Medicine. 2010 , 5, 109-117	4
1164	Prospects for molecular staging of non-small-cell lung cancer from genomic alterations. 2010 , 4, 499-508	5
1163	Editorial comment: Validation of a prognostic model to predict survival after non-small-cell lung cancer surgery. 2010 , 38, 619-20	
1162	Identification of full and partial class relevant genes. 2010 , 7, 263-77	29
1161	[Molecular diagnosis of unknown primary tumors]. 2010 , 30, 46-9	
1160	A Gprc5a tumor suppressor loss of expression signature is conserved, prevalent, and associated with survival in human lung adenocarcinomas. 2010 , 12, 499-505	28
1159	Interpreting Differential Coexpression of Gene Sets. 2010 , 131-150	
1158	A New Gene Expression Meta-Analysis Technique and its Application to Co-Analyze Three Independent Lung Cancer Datasets. 2010 , 253-277	
1157	Clustering: Unsupervised Learning in Large Biological Data. 2010 , 89-127	2
1156	Statistical methods for integrating multiple types of high-throughput data. 2010 , 620, 511-29	4
1155	Comparison of patient outcomes according to histology among pemetrexed-treated patients with stage IIIB/IV non-small-cell lung cancer in two phase II trials. 2010 , 11, 126-31	20
1154	A multiple-filter-multiple-wrapper approach to gene selection and microarray data classification. 2010 , 7, 108-17	102

1153	A simple yet effective data integration approach to tree-based microarray data classification. 2010 , 2010, 1503-6	1
1152	Sulf-2: an extracellular modulator of cell signaling and a cancer target candidate. 2010 , 14, 935-49	143
1151	Serum microRNA signatures identified in a genome-wide serum microRNA expression profiling predict survival of non-small-cell lung cancer. 2010 , 28, 1721-6	673
1150	Weighted Distance Weighted Discrimination and Its Asymptotic Properties. 2010 , 105, 401-414	62
1149	Tuberous sclerosis complex: linking cancer to metabolism. 2010 , 16, 329-35	27
1148	Differential diagnosis of hepatocellular carcinoma from metastatic tumors in the liver using microRNA expression. 2010 , 42, 1355-62	37
1147	Anti-cancer drug resistance: understanding the mechanisms through the use of integrative genomics and functional RNA interference. 2010 , 46, 2166-77	62
1146	Bioinformatic and Computational Analysis for Genomic Medicine. 2010 , 111-130	
1145	Co-activation of epidermal growth factor receptor and c-MET defines a distinct subset of lung adenocarcinomas. 2010 , 177, 2191-204	39
1144	DNA Microarrays and Genetic Testing. 2010 , 247-265	1
1143	The classification of lung carcinoma: time to change the morphology-based approach?. 2010 , 18, 161-72	19
1142	Cancer Gene Profiling. 2010 ,	1
1141	Clustering algorithms in biomedical research: a review. 2010 , 3, 120-54	198
1140	Genomics in the Diagnosis and Management of Lung Cancer. 2010 , 432-445	
1139	The Tumor Microenvironment. 2010 ,	4
1138	Ovarian Cancer. 2010 ,	1
1137	Multicategory cancer classification from gene expression data by multiclass NPPC ensemble. 2010 ,	11
1136	Sparse nonnegative matrix factorization with the elastic net. 2010 ,	2

1135	Discriminant analysis for fast multiclass data classification through regularized kernel function approximation. 2010 , 21, 1020-9	26
1134	Linear separability of gene expression data sets. 2010 , 7, 375-81	8
1133	Microarray Data Mining: A New Algorithm for Gene Selection Using Lorenz Curves & Gini Ratios. 2010 ,	1
1132	Oligonucleotide DNA microarray profiling of lung adenocarcinoma revealed significant downregulation and deletions of vasoactive intestinal peptide receptor 1. 2010 , 28, 487-94	9
1131	Metasample-based sparse representation for tumor classification. 2011 , 8, 1273-82	91
1130	Gene selection algorithm combining ReliefF and relative neighborhood rough set. 2011 ,	1
1129	Feature selection for multi-class problems by using pairwise-class and all-class techniques. 2011 , 40, 381-394	11
1128	Improving the Biological Relevance of Biclustering for Microarray Data in Using Ensemble Methods. 2011 ,	0
1127	A new gene subset selection approach based on linearly separating gene pairs. 2011 ,	1
1126	Bayesian networks classifiers for gene-expression data. 2011 ,	7
1125	. 2011 ,	1
1124	Integrating contextual miRNA and protein signatures for diagnostic and treatment decisions in cancer. 2011 , 11, 813-27	33
1123	Mixtures of common t-factor analyzers for clustering high-dimensional microarray data. 2011 , 27, 1269-76	57
1122	Nuclear factor I/B is an oncogene in small cell lung cancer. 2011 , 25, 1470-5	118
1121	Cyclophilin B expression is associated with in vitro radioresistance and clinical outcome after radiotherapy. 2011 , 13, 1122-31	17
1120	Subtyping of Leukemia with Gene Expression Analysis Using Compressive Sensing Method. 2011 ,	1
1119	Active immunotherapy for non-small-cell lung cancer: moving toward a reality. 2011 , 11, 1599-605	7
1118	Novel strategies for the treatment of small-cell lung carcinoma. 2011 , 8, 611-9	81

1117	Bronchoscopic microsampling is a useful complementary diagnostic tool for detecting lung cancer. 2011 , 72, 32-8	17
1116	Lung cancer in never smokers: change of a mindset in the molecular era. 2011 , 72, 9-15	65
1115	Personalized medicine: progress and promise. 2011 , 12, 217-44	183
1114	Statistics for Bioengineering Sciences. 2011 ,	34
1113	Densely interconnected transcriptional circuits control cell states in human hematopoiesis. 2011 , 144, 296-309	655
1112	An experimental comparison of gene selection by Lasso and Dantzig selector for cancer classification. <i>Computers in Biology and Medicine</i> , 2011 , 41, 1033-40	7 31
1111	The role of chalcones in suppression of NF- κ B-mediated inflammation and cancer. 2011 , 11, 295-309	237
1110	A comprehensive assessment of methods for de-novo reverse-engineering of genome-scale regulatory networks. 2011 , 97, 7-18	39
1109	Comparative study on dimension reduction techniques for cluster analysis of microarray data. 2011 ,	7
1108	Knowledge based cluster ensemble for cancer discovery from biomolecular data. 2011 , 10, 76-85	36
1107	Lung Cancer Metastasis. 369-381	2
1106	Lung tumors: an overview. 2011 ,	
1105	Survey of tyrosine kinase signaling reveals ROS kinase fusions in human cholangiocarcinoma. 2011 , 6, e15640	230
1104	Combining clinical, pathological, and demographic factors refines prognosis of lung cancer: a population-based study. 2011 , 6, e17493	14
1103	Identification of single- and multiple-class specific signature genes from gene expression profiles by group marker index. 2011 , 6, e24259	9
1102	CAFET algorithm reveals Wnt/PCP signature in lung squamous cell carcinoma. 2011 , 6, e25807	7
1101	Predicting disease phenotypes based on the molecular networks with condition-responsive correlation. 2011 , 5, 131-42	4
1100	Predicting response to chemotherapy with early-stage lung cancer. 2011 , 17, 49-56	10

1099	Embryonic morphogenetic field induces phenotypic reversion in cancer cells. Review article. 2011 , 12, 243-53	26
1098	What's new in non-small cell lung cancer for pathologists: the importance of accurate subtyping, EGFR mutations and ALK rearrangements. 2011 , 43, 103-15	46
1097	An adaptively weighted statistic for detecting differential gene expression when combining multiple transcriptomic studies. 2011 , 5,	77
1096	Development and validation of a quantitative real-time polymerase chain reaction classifier for lung cancer prognosis. 2011 , 6, 1481-7	26
1095	Genomic medicine in non-small cell lung cancer: paving the path to personalized care. 2011 , 16, 257-63	14
1094	Applying gene expression microarrays to pulmonary disease. 2011 , 16, 407-18	9
1093	An immunohistochemical analysis-based decision tree model for estimating the risk of lymphatic metastasis in pN0 squamous cell carcinomas of the lung. 2011 , 59, 882-91	6
1092	Osteopontin is up-regulated and associated with neutrophil and macrophage infiltration in glioblastoma. 2011 , 132, 39-48	63
1091	Statistical considerations for analysis of microarray experiments. 2011 , 4, 466-77	25
1090	Curcumin enhances the mitomycin C-induced cytotoxicity via downregulation of MKK1/2-ERK1/2-mediated Rad51 expression in non-small cell lung cancer cells. 2011 , 255, 327-38	32
1089	On the origin of cancer: can we ignore coherence?. 2011 , 106, 380-90	25
1088	AnyExpress: integrated toolkit for analysis of cross-platform gene expression data using a fast interval matching algorithm. 2011 , 12, 75	10
1087	Lung cancer: New biological insights and recent therapeutic advances. 2011 , 61, 91-112	329
1086	An efficient statistical feature selection approach for classification of gene expression data. 2011 , 44, 529-35	85
1085	Multi-objective design of hierarchical consensus functions for clustering ensembles via genetic programming. 2011 , 51, 794-809	16
1084	EEW-SC: Enhanced Entropy-Weighting Subspace Clustering for high dimensional gene expression data clustering analysis. 2011 , 11, 4798-4806	17
1083	Modulation of Rad51, ERCC1, and thymidine phosphorylase by emodin result in synergistic cytotoxic effect in combination with capecitabine. 2011 , 81, 680-90	25
1082	Investigating gene expression profile of non-small cell lung cancer. 2011 , 6, 608-615	1

1081	The role of LKB1 in lung cancer. 2011 , 10, 447-53	43
1080	Ternary Bradley-Terry model-based decoding for multi-class classification and its extensions. 2011 , 85, 249-272	5
1079	Neuro-logistic Models Based on Evolutionary Generalized Radial Basis Function for the Microarray Gene Expression Classification Problem. 2011 , 34, 117-131	10
1078	Molecular profiles and clinical outcome of stage UICC II colon cancer patients. 2011 , 26, 847-58	31
1077	Lung cancers unrelated to smoking: characterized by single oncogene addiction?. 2011 , 16, 294-305	22
1076	Large cell carcinoma of the lung is a vanishing entity?. 2011 , 4, 4-9	1
1075	A graph clustering algorithm based on a clustering coefficient for weighted graphs. 2011 , 17, 19-29	10
1074	Functional modules with disease discrimination abilities for various cancers. 2011 , 54, 189-93	3
1073	Loss of aquaporin-4 expression and putative function in non-small cell lung cancer. 2011 , 11, 161	29
1072	Possible role of death receptor-mediated apoptosis by the E3 ubiquitin ligases Siah2 and POSH. 2011 , 10, 57	24
1071	SULFs in human neoplasia: implication as progression and prognosis factors. 2011 , 9, 72	56
1070	A robust approach based on Weibull distribution for clustering gene expression data. 2011 , 6, 14	17
1069	Meta-analysis of multiple microarray datasets reveals a common gene signature of metastasis in solid tumors. 2011 , 4, 56	40
1068	ArrayInitiative - a tool that simplifies creating custom Affymetrix CDFs. 2011 , 12, 136	1
1067	Investigating the effect of paralogs on microarray gene-set analysis. 2011 , 12, 29	1
1066	Application of an efficient Bayesian discretization method to biomedical data. 2011 , 12, 309	27
1065	Consistent metagenes from cancer expression profiles yield agent specific predictors of chemotherapy response. 2011 , 12, 310	2
1064	Microarray-based cancer prediction using single genes. 2011 , 12, 391	37

1063	Finding consistent disease subnetworks across microarray datasets. 2011 , 12 Suppl 13, S15		25
1062	A robust tool for discriminative analysis and feature selection in paired samples impacts the identification of the genes essential for reprogramming lung tissue to adenocarcinoma. 2011 , 12 Suppl 3, S24		14
1061	Pulmonary response to surface-coated nanotitanium dioxide particles includes induction of acute phase response genes, inflammatory cascades, and changes in microRNAs: a toxicogenomic study. 2011 , 52, 425-39		129
1060	Robust penalized logistic regression with truncated loss functions. 2011 , 39, 300-323		19
1059	Gene expression profiling reveals novel biomarkers in nonsmall cell lung cancer. <i>International Journal of Cancer</i> , 2011 , 129, 355-64	7.5	172
1058	Robust approach for estimating probabilities in Naïve Bayes Classifier for gene expression data. 2011 , 38, 1293-1298		27
1057	Gene selection and prediction for cancer classification using support vector machines with a reject option. 2011 , 55, 1897-1908		22
1056	A sparse nearest mean classifier for high dimensional multi-class problems. 2011 , 32, 854-859		5
1055	Proteomic analysis of formalin-fixed, paraffin-embedded lung neuroendocrine tumor samples from hospital archives. 2011 , 74, 359-70		37
1054	A Gaussian Mixed Model for Learning Discrete Bayesian Networks. 2011 , 81, 220-230		5
1053	Neural gas based cluster ensemble algorithm and its application to cancer data. 2011 ,		4
1052	Neuroendocrine differentiation as an indicator of chemosensitivity and prognosis in nonsmall cell lung cancer. 2011 , 16, 311-20		22
1051	The molecular pathogenesis and management of bronchial carcinoids. 2011 , 15, 457-91		13
1050	Advances in proteomic strategies toward the early detection of lung cancer. 2011 , 8, 183-8		30
1049	Reinforced Multicategory Support Vector Machines. 2011 , 20, 901-919		37
1048	Robust gene expression signature from formalin-fixed paraffin-embedded samples predicts prognosis of non-small-cell lung cancer patients. 2011 , 17, 5705-14		121
1047	A new frontier in personalized cancer therapy: mapping molecular changes. 2011 , 7, 873-94		12
1046	A pathway for the control of anoikis sensitivity by E-cadherin and epithelial-to-mesenchymal transition. 2011 , 31, 4036-51		90

1045	Robust biclustering by sparse singular value decomposition incorporating stability selection. 2011 , 27, 2089-97	48
1044	A five-gene and corresponding protein signature for stage-I lung adenocarcinoma prognosis. 2011 , 17, 1490-501	55
1043	Deciphering squamous cell carcinoma using multidimensional genomic approaches. 2011 , 2011, 541405	7
1042	A comparison of methods for data-driven cancer outlier discovery, and an application scheme to semisupervised predictive biomarker discovery. 2011 , 10, 109-20	16
1041	Differential activity of NADPH-producing dehydrogenases renders rodents unsuitable models to study IDH1R132 mutation effects in human glioblastoma. 2011 , 59, 489-503	28
1040	Global gene expression profiling and validation in esophageal squamous cell carcinoma and its association with clinical phenotypes. 2011 , 17, 2955-66	177
1039	GPC5 gene and its related pathways in lung cancer. 2011 , 6, 2-5	27
1038	Medusa structure of the gene regulatory network: dominance of transcription factors in cancer subtype classification. 2011 , 236, 628-36	19
1037	Genomics and proteomics of pulmonary vascular disease. 2011 , 1, 467-83	5
1036	Immunotherapy as a strategy for the treatment of non-small-cell lung cancer. 2011 , 8, 43-54	42
1035	Aberrant signaling pathways in squamous cell lung carcinoma. 2011 , 10, 273-85	33
1034	Biological impact of missing-value imputation on downstream analyses of gene expression profiles. 2011 , 27, 78-86	42
1033	Lower confidence bounds for prediction accuracy in high dimensions via AROHIL Monte Carlo. 2011 , 27, 3129-34	
1032	A miRNA-regulatory network explains how dysregulated miRNAs perturb oncogenic processes across diverse cancers. 2012 , 22, 2302-14	128
1031	Twist1 suppresses senescence programs and thereby accelerates and maintains mutant Kras-induced lung tumorigenesis. 2012 , 8, e1002650	78
1030	Surgical implications of the new IASLC/ATS/ERS adenocarcinoma classification. 2012 , 39, 478-86	121
1029	IGDB.NSCLC: integrated genomic database of non-small cell lung cancer. 2012 , 40, D972-7	20
1028	In-depth proteomic analysis of nonsmall cell lung cancer to discover molecular targets and candidate biomarkers. 2012 , 11, 916-32	59

1027	Microarrays in Diagnostics and Biomarker Development. 2012 ,	3
1026	A framework for list representation, enabling list stabilization through incorporation of gene exchangeabilities. 2012 , 13, 129-41	4
1025	Cross-species functional analysis of cancer-associated fibroblasts identifies a critical role for CLCF1 and IL-6 in non-small cell lung cancer in vivo. 2012 , 72, 5744-56	75
1024	Research resource: Diagnostic and therapeutic potential of nuclear receptor expression in lung cancer. 2012 , 26, 1443-54	35
1023	Targeting of Noncanonical Wnt5a Signaling by AP-1 Blocker Dominant-Negative Jun When It Inhibits Skin Carcinogenesis. 2012 , 3, 37-50	20
1022	Diverse roles for the paxillin family of proteins in cancer. 2012 , 3, 362-70	55
1021	Tumor clustering based on hybrid cluster ensemble framework. 2012 ,	
1020	Independent and functional validation of a multi-tumour-type proliferation signature. 2012 , 107, 508-15	9
1019	Removal of uracil by uracil DNA glycosylase limits pemetrexed cytotoxicity: overriding the limit with methoxyamine to inhibit base excision repair. 2012 , 3, e252	56
1018	Global evaluation of Eph receptors and ephrins in lung adenocarcinomas identifies EphA4 as an inhibitor of cell migration and invasion. 2012 , 11, 2021-32	39
1017	Proteomic profiling identifies dysregulated pathways in small cell lung cancer and novel therapeutic targets including PARP1. 2012 , 2, 798-811	323
1016	Discriminative least squares regression for multiclass classification and feature selection. 2012 , 23, 1738-54	256
1015	Genome-scale analysis of DNA methylation in lung adenocarcinoma and integration with mRNA expression. 2012 , 22, 1197-211	361
1014	Feature selection based on bayes minimum error probability. 2012 ,	
1013	Targeting ROS1 with anaplastic lymphoma kinase inhibitors: a promising therapeutic strategy for a newly defined molecular subset of non-small-cell lung cancer. 2012 , 7, 1625-30	100
1012	Secreted protein, acidic and rich in cysteine-like 1 (SPARCL1) is down regulated in aggressive prostate cancers and is prognostic for poor clinical outcome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 14977-82	11.5 39
1011	Selective requirement for Mediator MED23 in Ras-active lung cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E2813-22	11.5 40
1010	Expression profiling-based subtyping identifies novel non-small cell lung cancer subgroups and implicates putative resistance to pemetrexed therapy. 2012 , 7, 105-14	33

1009	Anterior gradient 2 overexpression in lung adenocarcinoma. 2012 , 20, 31-6	24
1008	Changes in expression of human serine protease HtrA1, HtrA2 and HtrA3 genes in benign and malignant thyroid tumors. 2012 , 28, 1838-44	26
1007	To feature space and back: Identifying top-weighted features in polynomial Support Vector Machine models. 2012 , 16, 551-579	1
1006	Progressive lung cancer determined by expression profiling and transcriptional regulation. 2012 , 41, 242-52	5
1005	Inactivation of ribosomal protein L22 promotes transformation by induction of the stemness factor, Lin28B. 2012 , 120, 3764-73	109
1004	Adult lung stem cells and their contribution to lung tumourigenesis. 2012 , 2, 120094	38
1003	EnrichNet: network-based gene set enrichment analysis. 2012 , 28, i451-i457	204
1002	Biomarker identification and cancer classification based on microarray data using Laplace naive Bayes model with mean shrinkage. 2012 , 9, 1649-62	33
1001	Array-based pharmacogenomics of molecular-targeted therapies in oncology. 2012 , 12, 185-96	11
1000	AKT1 polymorphisms and survival of early stage non-small cell lung cancer. 2012 , 105, 167-74	35
999	Revisiting global gene expression analysis. 2012 , 151, 476-82	410
998	Early gene expression differences in inbred mouse strains with susceptibility to pulmonary adenomas. 2012 , 93, 455-61	5
997	Molecular markers for incidence, prognosis, and response to therapy. 2012 , 21, 161-75	6
996	Experimental analysis of feature selection stability for high-dimension and low-sample size gene expression classification task. 2012 ,	0
995	DICLENS: divisive clustering ensemble with automatic cluster number. 2012 , 9, 408-20	32
994	Proteins kinase Ce is required for non-small cell lung carcinoma growth and regulates the expression of apoptotic genes. 2012 , 31, 2593-600	31
993	Investigating topic models' capabilities in expression microarray data classification. 2012 , 9, 1831-6	20
992	A pathway-based approach to identify molecular biomarkers in cancer. 2012 , 19 Suppl 3, S620-4	

991	A method for design of data-tailored partitioning algorithms for optimizing the number of clusters in microarray analysis. 2012,	
990	Robust two-gene classifiers for cancer prediction. 2012, 99, 90-5	8
989	Challenges translating breast cancer gene signatures into the clinic. 2011, 9, 58-64	96
988	Prognostic PET 18F-FDG uptake imaging features are associated with major oncogenomic alterations in patients with resected non-small cell lung cancer. 2012, 72, 3725-34	91
987	From modules to medicine: How modular domains and their associated networks can enable personalized medicine. 2012, 586, 2580-5	13
986	Histology image analysis for carcinoma detection and grading. 2012, 107, 538-56	186
985	'maskBAD'--a package to detect and remove Affymetrix probes with binding affinity differences. 2012, 13, 56	5
984	Genomic signatures for predicting survival and adjuvant chemotherapy benefit in patients with non-small-cell lung cancer. 2012, 5, 30	31
983	Impact of collection and storage of lung tumor tissue on whole genome expression profiling. 2012, 14, 140-8	30
982	Insights into the achaete-scute homolog-1 gene (hASH1) in normal and neoplastic human lung. 2012, 75, 58-65	38
981	ASCL1-coexpression profiling but not single gene expression profiling defines lung adenocarcinomas of neuroendocrine nature with poor prognosis. 2012, 75, 119-25	32
980	Signaling pathway-based identification of extensive prognostic gene signatures for lung adenocarcinoma. 2012, 76, 98-105	18
979	EphB3 suppresses non-small-cell lung cancer metastasis via a PP2A/RACK1/Akt signalling complex. 2012, 3, 667	86
978	Distributed Computing and Artificial Intelligence. 2012,	
977	Molecular Pathology of Lung Cancer. 2012,	5
976	Molecular Basis for the Current Lung Cancer Classification. 2012, 75-85	
975	Stable feature selection and classification algorithms for multiclass microarray data. 2012, 7, 33	28
974	Exploiting the noise: improving biomarkers with ensembles of data analysis methodologies. 2012, 4, 84	14

973	Aberrant expression of proteins involved in signal transduction and DNA repair pathways in lung cancer and their association with clinical parameters. 2012 , 7, e31087	30
972	Divergent genomic and epigenomic landscapes of lung cancer subtypes underscore the selection of different oncogenic pathways during tumor development. 2012 , 7, e37775	50
971	Identification of novel deregulated RNA metabolism-related genes in non-small cell lung cancer. 2012 , 7, e42086	41
970	Gremlin is overexpressed in lung adenocarcinoma and increases cell growth and proliferation in normal lung cells. 2012 , 7, e42264	35
969	A novel five gene signature derived from stem-like side population cells predicts overall and recurrence-free survival in NSCLC. 2012 , 7, e43589	21
968	Development and validation of a prognostic gene-expression signature for lung adenocarcinoma. 2012 , 7, e44225	25
967	RAS Mutations and Oncogenesis: Not all RAS Mutations are Created Equally. 2011 , 2, 100	42
966	Molecular predictors of prognosis in lung cancer. 2012 , 19, 669-76	22
965	Coclustering a useful tool for chemometrics. 2012 , 26, 256-263	24
964	Relation between smoking history and gene expression profiles in lung adenocarcinomas. 2012 , 5, 22	31
963	Molecular subgroups of medulloblastoma: the current consensus. 2012 , 123, 465-72	1167
962	Pulmonary adenocarcinoma: a renewed entity in 2011. 2012 , 17, 50-65	56
961	Evolutionary Generalized Radial Basis Function neural networks for improving prediction accuracy in gene classification using feature selection. 2012 , 12, 1787-1800	51
960	Microarray gene expression classification with few genes: Criteria to combine attribute selection and classification methods. 2012 , 39, 7270-7280	32
959	Molecular and cellular biology of neuroendocrine lung tumors: evidence for separate biological entities. 2012 , 1826, 255-71	73
958	Gene expression profiling to dissect the complexity of cancer biology: pitfalls and promise. 2012 , 22, 250-60	24
957	Boundary behavior in High Dimension, Low Sample Size asymptotics of PCA. 2012 , 109, 190-203	28
956	Reduced rank stochastic regression with a sparse singular value decomposition. 2012 , 74, 203-221	61

955	RET finger protein expression is associated with prognosis in lung cancer with epidermal growth factor receptor mutations. 2012 , 62, 324-30	21
954	Biomarkers and transcriptome profiling of lung cancer. 2012 , 17, 620-6	18
953	Comparative evaluation of set-level techniques in predictive classification of gene expression samples. 2012 , 13 Suppl 10, S15	15
952	Finding biomarkers for non-small cell lung cancer diagnosis and prognosis. 2012 , 7, 14-23	3
951	Microarray meta-analysis defines global angiogenesis-related gene expression signatures in human carcinomas. 2013 , 52, 29-38	10
950	Computational purification of individual tumor gene expression profiles leads to significant improvements in prognostic prediction. 2013 , 5, 29	70
949	Molecular classification of non-small-cell lung cancer: diagnosis, individualized treatment, and prognosis. 2013 , 7, 157-71	24
948	Prostate Cancer. 2013 ,	5
947	Cancer Genomics. 2013 ,	4
946	Multiple Classifier Systems. 2013 ,	2
945	Non-negative matrix factorization by maximizing correntropy for cancer clustering. 2013 , 14, 107	75
944	Biclustering for the comprehensive search of correlated gene expression patterns using clustered seed expansion. 2013 , 14, 144	19
943	Assessment of reproducibility of cancer survival risk predictions across medical centers. 2013 , 13, 25	2
942	A novel method for finding non-small cell lung cancer diagnosis biomarkers. 2013 , 6 Suppl 1, S11	9
941	TSG: a new algorithm for binary and multi-class cancer classification and informative genes selection. 2013 , 6 Suppl 1, S3	26
940	Main histologic types of non-small-cell lung cancer differ in expression of prognosis-related genes. 2013 , 14, 666-673.e2	30
939	Gene signature critical to cancer phenotype as a paradigm for anticancer drug discovery. 2013 , 32, 3809-18	6
938	How many clusters: a validation index for arbitrary-shaped clusters. 2013 , 10, 401-14	19

937	Mesothelin and osteopontin as diagnostic and prognostic markers of malignant pleural mesothelioma in Egyptian patients undergoing pleurodesis. 2013 , 62, 115-120	2
936	Trends and Applications in Knowledge Discovery and Data Mining. 2013 ,	2
935	An ensemble of SVM classifiers based on gene pairs. <i>Computers in Biology and Medicine</i> , 2013 , 43, 729-37	38
934	Genetic alterations defining NSCLC subtypes and their therapeutic implications. 2013 , 82, 179-89	189
933	miRNA and mRNA cancer signatures determined by analysis of expression levels in large cohorts of patients. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 19160-5	57
932	ROS1 receptor tyrosine kinase, a druggable target, is frequently overexpressed in non-small cell lung carcinomas via genetic and epigenetic mechanisms. 2013 , 20, 200-8	38
931	Biomarkers in Oncology. 2013 ,	1
930	SciDB: A Database Management System for Applications with Complex Analytics. 2013 , 15, 54-62	103
929	Multiclass gene selection using Pareto-fronts. 2013 , 10, 87-97	18
928	High specific detection and near-infrared photothermal therapy of lung cancer cells with high SERS active aptamer-silver-gold shell-core nanostructures. 2013 , 138, 6501-10	56
927	Multiscale in situ analysis of the role of dyskerin in lung cancer cells. 2013 , 5, 402-13	11
926	An exploration of pathways involved in lung carcinoid progression using gene expression profiling. 2013 , 34, 2726-37	39
925	. 2013 ,	
924	A minimax probabilistic approach to feature transformation for multi-class data. 2013 , 13, 116-127	8
923	Kallikrein-related peptidase 4 (KLK4) mRNA predicts short-term relapse in colorectal adenocarcinoma patients. 2013 , 330, 106-12	28
922	Class-imbalanced classifiers for high-dimensional data. 2013 , 14, 13-26	169
921	Pluripotent stem cell protein Sox2 confers sensitivity to LSD1 inhibition in cancer cells. 2013 , 5, 445-57	90
920	An efficient and scalable family of algorithms for combining clusterings. 2013 , 26, 2525-2539	11

919	Prediction of lung cancer histological types by RT-qPCR gene expression in FFPE specimens. 2013 , 15, 485-97	11
918	A drug repositioning approach identifies tricyclic antidepressants as inhibitors of small cell lung cancer and other neuroendocrine tumors. 2013 , 3, 1364-77	272
917	Crizotinib. 2013 , 71-90	
916	Control of alveolar differentiation by the lineage transcription factors GATA6 and HOPX inhibits lung adenocarcinoma metastasis. 2013 , 23, 725-38	104
915	Prognostic factors in resected lung carcinomas. 2013 , 11, 137-49	6
914	Improving Logitboost with prior knowledge. 2013 , 14, 208-219	5
913	Identification of proteins expressed differently among surgically resected stage I lung adenocarcinomas. 2013 , 46, 369-77	12
912	Network-based approach identified cell cycle genes as predictor of overall survival in lung adenocarcinoma patients. 2013 , 80, 91-8	29
911	Lung Cancer. 2013 , 691-706	
910	POU domain transcription factor BRN2 is crucial for expression of ASCL1, ND1 and neuroendocrine marker molecules and cell growth in small cell lung cancer. 2013 , 63, 158-68	32
909	Heterogeneity of tumor-induced gene expression changes in the human metabolic network. 2013 , 31, 522-9	279
908	An Ant Colony Optimization Based Dimension Reduction Method for High-Dimensional Datasets. 2013 , 10, 231-241	43
907	Translational Bioinformatics for Genomic Medicine. 2013 , 272-286	4
906	ETS Fusion Genes in Prostate Cancer. 2013 , 139-183	4
905	Comparison of feature selection methods for cross-laboratory microarray analysis. 2013 , 10, 593-604	10
904	Pharmacogenomic biomarkers for personalized medicine. 2013 , 14, 969-80	13
903	Farletuzumab in lung cancer. 2013 , 80, 15-8	21
902	Multiple reaction monitoring of multiple low-abundance transcription factors in whole lung cancer cell lysates. 2013 , 12, 2582-96	13

901	Feature selection using dynamic weights for classification. 2013 , 37, 541-549	58
900	The reliability of estimated confidence intervals for classification error rates when only a single sample is available. 2013 , 46, 1067-1077	7
899	Nanotechnology for cancer screening and diagnosis. 2013 , 137-164	9
898	Dimensionality reduction for microarray data using local mean based discriminant analysis. 2013 , 35, 331-6	1
897	Multi-objective Optimization Using Pareto GA for Gene-Selection from Microarray Data for Disease Classification. 2013 ,	5
896	Hybrid fuzzy cluster ensemble framework for tumor clustering from biomolecular data. 2013 , 10, 657-70	44
895	Mining Causal Association Rules. 2013 ,	23
894	Biomarker discovery in non-small cell lung cancer: integrating gene expression profiling, meta-analysis, and tissue microarray validation. 2013 , 19, 194-204	219
893	. 2013 ,	
892	Transcriptomics. 2013 , 49-82	1
891	Biclustering with heterogeneous variance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 12253-8	11.5 17
890	Integrated cistromic and expression analysis of amplified NKX2-1 in lung adenocarcinoma identifies LMO3 as a functional transcriptional target. 2013 , 27, 197-210	47
889	Notch increases the shedding of HB-EGF by ADAM12 to potentiate invadopodia formation in hypoxia. 2013 , 201, 279-92	109
888	Uracil-DNA glycosylase expression determines human lung cancer cell sensitivity to pemetrexed. 2013 , 12, 2248-60	32
887	Recognition of multiple imbalanced cancer types based on DNA microarray data using ensemble classifiers. 2013 , 2013, 239628	22
886	The ribosomal protein Rpl22 controls ribosome composition by directly repressing expression of its own paralog, Rpl22l1. 2013 , 9, e1003708	58
885	Identification of interconnected markers for T-cell acute lymphoblastic leukemia. 2013 , 2013, 210253	5
884	Lung Cancer Gene Signatures and Clinical Perspectives. 2013 , 2, 318-39	12

883	Cullin7: a new gene involved in liver carcinogenesis related to metabolic syndrome. 2013 , 62, 911-9		33
882	Coordination of nutrient availability and utilization by MAX- and MLX-centered transcription networks. 2013 , 3, a014258		34
881	Identification of transcriptional subgroups in EGFR-mutated and EGFR/KRAS wild-type lung adenocarcinoma reveals gene signatures associated with patient outcome. 2013 , 19, 5116-26		17
880	LTSA Algorithm for Dimension Reduction of Microarray Data. 2013 , 645, 192-195		1
879	A molecular signature predictive of indolent prostate cancer. 2013 , 5, 202ra122		98
878	Differences and similarities in the transcriptional profile of peripheral whole blood in early and late-onset preeclampsia: insights into the molecular basis of the phenotype of preeclampsia. 2013 , 41, 485-504		27
877	The cross-validated AUC for MCP-logistic regression with high-dimensional data. 2013 , 22, 505-18		13
876	Combination of protein coding and noncoding gene expression as a robust prognostic classifier in stage I lung adenocarcinoma. 2013 , 73, 3821-32		43
875	CRL4A-FBXW5-mediated degradation of DLC1 Rho GTPase-activating protein tumor suppressor promotes non-small cell lung cancer cell growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 16868-73	11.5	45
874	Yin Yang gene expression ratio signature for lung cancer prognosis. 2013 , 8, e68742		11
873	Block clustering based on difference of convex functions (DC) programming and DC algorithms. 2013 , 25, 2776-807		8
872	Landscape of somatic allelic imbalances and copy number alterations in human lung carcinoma. <i>International Journal of Cancer</i> , 2013 , 132, 2020-31	7.5	27
871	Network-based Pathway Enrichment Analysis. 2013 , 218-221		8
870	Noise-Resistant Biclustor Recognition. 2013 ,		1
869	Anti-cancer Drug Development: Computational Strategies to Identify and Target Proteins Involved in Cancer Metabolism. 2013 , 19, 532-577		24
868	PRC2 overexpression and PRC2-target gene repression relating to poorer prognosis in small cell lung cancer. 2013 , 3, 1911		105
867	Potential Clinical Utility of Gene Expression Profiling in Identifying Tumors of Uncertain Origin. 2013 , 1, 35-46		
866	Intertumoral and intratumoral heterogeneity as a barrier for effective treatment of medulloblastoma. 2013 , 60 Suppl 1, 57-63		12

865 Update on recent prognostic markers in adenocarcinoma. **2013**, 2, 141-152

864 Listening to the brain: new techniques in intraoperative brain mapping. **2013**, 60 Suppl 1, 64-9 5

863 The role of epithelial-mesenchymal transition programming in invasion and metastasis: a clinical perspective. **2013**, 5, 187-95 102

862 Gene expression profiling and molecular pathway analysis for the identification of early-stage lung adenocarcinoma patients at risk for early recurrence. **2013**, 29, 1902-6 9

861 Platelet genetic biomarker quantification: comparison of fluorescent microspheres and PCR platforms. **2013**, 109, 337-46 3

860 Large cell carcinoma and adenosquamous carcinoma of the lung. 1114-1126

859 Biclustor and regulatory network analysis of differentially expressed genes in adenocarcinoma and squamous cell carcinoma. **2013**, 12, 1710-9 2

858 Metastatic Cancer. **2013**, 776-788 1

857 Alterations in gene expression of proprotein convertases in human lung cancer have a limited number of scenarios. **2013**, 8, e55752 22

856 Adenocarcinoma of the lung. 1043-1092 1

855 Evaluation of numbers of top ranked genes. **2013**, 8, 151-161

854 A fluorescence-coupled assay for gamma aminobutyric acid (GABA) reveals metabolic stress-induced modulation of GABA content in neuroendocrine cancer. **2014**, 9, e88667 20

853 A novel strategy for gene selection of microarray data based on gene-to-class sensitivity information. **2014**, 9, e97530 15

852 A kernel-based multivariate feature selection method for microarray data classification. **2014**, 9, e102541 32

851 Mining CK2 in cancer. **2014**, 9, e115609 98

850 Informative gene selection and direct classification of tumor based on Chi-square test of pairwise gene interactions. **2014**, 2014, 589290 7

849 Associations between clinical characteristics and oncogene expression in patients with non-small cell lung cancer. **2014**, 13, 8913-24 4

848 Expression of YY1 correlates with progression and metastasis in esophageal squamous cell carcinomas. **2014**, 7, 1753-9 13

847	Sox9 mediates Notch1-induced mesenchymal features in lung adenocarcinoma. 2014 , 5, 3636-50			58
846	A signature predicting poor prognosis in gastric and ovarian cancer represents a coordinated macrophage and stromal response. 2014 , 20, 2761-72			55
845	Expression Microarray Data Classification Using Counting Grids and Fisher Kernel. 2014 ,			1
844	Probabilistic non-negative matrix factorization: theory and application to microarray data analysis. 2014 , 12, 1450001			14
843	Uracil DNA glycosylase (UNG) loss enhances DNA double strand break formation in human cancer cells exposed to pemetrexed. 2014 , 5, e1045			25
842	Sparse representation for tumor classification based on feature extraction using latent low-rank representation. 2014 , 2014, 420856			7
841	A tumor classification model using least square regression. 2014 ,			1
840	Comparison of LLE and PCA Algorithms for Gene Expression Data Analysis. 2014 , 513-517, 378-381			
839	Hidden treasures in "ancient" microarrays: gene-expression portrays biology and potential resistance pathways of major lung cancer subtypes and normal tissue. <i>Frontiers in Oncology</i> , 2014 , 4, 251	5.3		8
838	A group-specific tuning parameter for hybrid of SVM and SCAD in identification of informative genes and pathways. 2014 , 10, 146-61			5
837	Prediction of Clinical Outcome for All Stages and Multiple Cell Types of Non-small Cell Lung Cancer in Five Countries Using Lung Cancer Prognostic Index. 2014 , 1, 156-66			7
836	Text mining and network analysis of molecular interaction in non-small cell lung cancer by using natural language processing. 2014 , 41, 8071-9			6
835	dCLIP: a computational approach for comparative CLIP-seq analyses. 2014 , 15, R11			41
834	K-nearest neighbors clustering algorithm. 2014 ,			
833	Analysis of tissue-specific differentially methylated genes with differential gene expression in non-small cell lung cancers. 2014 , 48, 694-700			2
832	TGF- β -inducible microRNA-183 silences tumor-associated natural killer cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 4203-8	11.5		136
831	Lung cancer histologic and immunohistochemical heterogeneity in the era of molecular therapies: analysis of 172 consecutive surgically resected, entirely sampled pulmonary carcinomas. 2014 , 38, 502-9			26
830	The Robustness of Pathway Analysis in Identifying Potential Drug Targets in Non-Small Cell Lung Carcinoma. 2014 , 3, 212-25			1

829	Empirical evaluation of consistency and accuracy of methods to detect differentially expressed genes based on microarray data. <i>Computers in Biology and Medicine</i> , 2014 , 46, 1-10	7	17
828	A novel class dependent feature selection method for cancer biomarker discovery. <i>Computers in Biology and Medicine</i> , 2014 , 47, 66-75	7	30
827	Epithelial-mesenchymal transition-associated secretory phenotype predicts survival in lung cancer patients. 2014 , 35, 1292-300		31
826	A network-assisted co-clustering algorithm to discover cancer subtypes based on gene expression. 2014 , 15, 37		55
825	Concordant integrative gene set enrichment analysis of multiple large-scale two-sample expression data sets. 2014 , 15 Suppl 1, S6		16
824	Proteomic profiles of human lung adeno and squamous cell carcinoma using super-SILAC and label-free quantification approaches. 2014 , 14, 795-803		24
823	Integrated genomic analysis illustrates the central role of JAK-STAT pathway activation in myeloproliferative neoplasm pathogenesis. 2014 , 123, e123-33		264
822	The 'omics' of adrenocortical tumours for personalized medicine. 2014 , 10, 215-28		38
821	A single-tube multiplexed assay for detecting ALK, ROS1, and RET fusions in lung cancer. 2014 , 16, 229-43		89
820	Genomics and Molecular Profiling of Lung Cancer. 2014 , 193-211		
819	Advances in Biotechnology. 2014 ,		5
818	Protein kinase C and cancer: what we know and what we do not. 2014 , 33, 5225-37		178
817	Probabilistic cluster structure ensemble. 2014 , 267, 16-34		22
816	Analysis of feature selection stability on high dimension and small sample data. 2014 , 71, 681-693		60
815	Gene expression profile of A549 cells from tissue of 4D model predicts poor prognosis in lung cancer patients. <i>International Journal of Cancer</i> , 2014 , 134, 789-98	7.5	25
814	Stabilization of cellular RNA in blood during storage at room temperature: a comparison of cell-free RNA BCT(fi) with K3EDTA tubes. 2014 , 18, 647-53		14
813	ASCL1 is a lineage oncogene providing therapeutic targets for high-grade neuroendocrine lung cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 14788-93	11.5	144
812	On integrating multi-experiment microarray data. 2014 , 372, 20130136		5

811	Altered β ,6-GlcNAc branched N-glycans impair TGF- β -mediated epithelial-to-mesenchymal transition through Smad signalling pathway in human lung cancer. 2014 , 18, 1975-91	29
810	Lung cancer classification using genetic algorithm to optimize prediction models. 2014 ,	8
809	The expression of four genes as a prognostic classifier for stage I lung adenocarcinoma in 12 independent cohorts. 2014 , 23, 2884-94	19
808	Feature selection for high-dimensional class-imbalanced data sets using Support Vector Machines. 2014 , 286, 228-246	171
807	KLK11 mRNA expression predicts poor disease-free and overall survival in colorectal adenocarcinoma patients. 2014 , 8, 671-85	23
806	A role for G-CSF and GM-CSF in nonmyeloid cancers. 2014 , 3, 737-46	70
805	Microarray data classification using the spectral-feature-based TLS ensemble algorithm. 2014 , 13, 289-99	3
804	Comprehensive molecular profiling of lung adenocarcinoma. 2014 , 511, 543-50	3310
803	Double Selection Based Semi-Supervised Clustering Ensemble for Tumor Clustering from Gene Expression Profiles. 2014 , 11, 727-40	45
802	Gene expression ratio test distinguishes normal lung from lung tumors in solid tissue and FNA biopsies. 2014 , 16, 267-72	7
801	Noise-free principal component analysis: An efficient dimension reduction technique for high dimensional molecular data. 2014 , 41, 7797-7804	8
800	Semi-supervised consensus clustering for gene expression data analysis. 2014 , 7, 7	21
799	Correlation between TS, MTHFR, and ERCC1 gene polymorphisms and the efficacy of platinum in combination with pemetrexed first-line chemotherapy in mesothelioma patients. 2014 , 15, 455-65	4
798	Multiclass feature selection algorithms base on R-SVM. 2014 ,	1
797	Using high-throughput transcriptomic data for prognosis: a critical overview and perspectives. 2014 , 74, 4612-21	38
796	A meta-analysis of lung cancer gene expression identifies PTK7 as a survival gene in lung adenocarcinoma. 2014 , 74, 2892-902	108
795	Risk classification of cancer survival using ANN with gene expression data from multiple laboratories. <i>Computers in Biology and Medicine</i> , 2014 , 48, 1-7	7 64
794	Combined therapeutic potential of nuclear receptors with receptor tyrosine kinase inhibitors in lung cancer. 2014 , 447, 490-5	9

793	Unlabeling data can improve classification accuracy. 2014 , 37, 15-23	5
792	Incorporation of gene exchangeabilities improves the reproducibility of gene set rankings. 2014 , 71, 588-598	
791	Overexpression of atypical protein kinase C in HeLa cells facilitates macropinocytosis via Src activation. 2014 , 26, 1235-42	7
790	Serum Proteomic Biomarkers. 2014 , 90-109	
789	The clonal evolution and therapeutic approaches of lung cancer. 2014 , 70, 63-71	5
788	A review of microarray datasets and applied feature selection methods. 2014 , 282, 111-135	352
787	Subspace clustering of high-dimensional data: a predictive approach. 2014 , 28, 736-772	40
786	Patterns of TPD52 overexpression in multiple human solid tumor types analyzed by quantitative PCR. 2014 , 44, 609-15	22
785	Prognostic and Predictive Biomarker Signatures. 2014 , 564-571	
784	Somatic Genome Alterations in Human Lung Cancers. 2014 , 67-89	1
783	Molecular Profiling. 2014 , 48-66	
782	The potential of genome-wide analyses to improve non-small-cell lung cancer care. 2014 , 3, 383-396	
781	Early-stage non-small-cell lung cancer: overview of adjuvant chemotherapy and promising advances. 2014 , 3, 85-99	
780	Molecular cancer classification using a meta-sample-based regularized robust coding method. 2014 , 15 Suppl 15, S2	4
779	A correlation based multilayer perceptron algorithm for cancer classification with gene-expression dataset. 2014 ,	5
778	Majority Voting of Semantic Genetic Programming for Microarray data. 2015 ,	
777	Transfer Entropy Weighting Soft Subspace Clustering. 2015 , 9, 413-425	0
776	Identifying CDKN3 Gene Expression as a Prognostic Biomarker in Lung Adenocarcinoma via Meta-analysis. 2015 , 14, 183-91	17

775	Close relation of large cell carcinoma to adenocarcinoma by hierarchical cluster analysis: implications for histologic typing of lung cancer on biopsies. 2015 , 23, 550-7	3
774	Genetic alterations in glioblastoma multiforme. 323-344	
773	. 2015 ,	19
772	Clustering Methods Discussion. 2015 , 283-301	
771	Role of network biology and network medicine in early detection of cancer. 457-463	
770	Application of bioinformatics to analyze the expression of tissue-specific and housekeeping genes in cancer. 20-34	
769	LDOC1 silenced by cigarette exposure and involved in oral neoplastic transformation. 2015 , 6, 25188-201	11
768	SPARCoC: a new framework for molecular pattern discovery and cancer gene identification. 2015 , 10, e0117135	5
767	The Retinoblastoma Tumor Suppressor Transcriptionally Represses Pak1 in Osteoblasts. 2015 , 10, e0142406	2
766	The chemokine CXCL13 in lung cancers associated with environmental polycyclic aromatic hydrocarbons pollution. 2015 , 4,	35
765	Defective apical extrusion signaling contributes to aggressive tumor hallmarks. 2015 , 4, e04069	39
764	Siomycin A Induces Apoptosis in Human Lung Adenocarcinoma A549 Cells by Suppressing the Expression of FoxM1. 2015 , 10, 1934578X1501000	2
763	The Diagnosis and Treatment of Bronchopulmonary Carcinoid. 2015 , 112, 479-85	14
762	Development and validation of a gene expression tumour classifier for cancer of unknown primary. 2015 , 47, 7-12	26
761	ISOpureR: an R implementation of a computational purification algorithm of mixed tumour profiles. 2015 , 16, 156	21
760	Molecular portraits of epithelial, mesenchymal, and hybrid States in lung adenocarcinoma and their relevance to survival. 2015 , 75, 1789-800	128
759	Molecular fingerprints of environmental carcinogens in human cancer. 2015 , 33, 188-228	24
758	BMP2 response pattern in human lung fibroblasts predicts outcome in lung adenocarcinomas. 2015 , 8, 16	13

757	Probabilistic Graphical Models and Deep Belief Networks for Prognosis of Breast Cancer. 2015 ,	20
756	Multiple SVM-RFE for multi-class gene selection on DNA Microarray data. 2015 ,	6
755	Integrating RAS status into prognostic signatures for adenocarcinomas of the lung. 2015 , 21, 1477-86	11
754	Two stages weighted sampling strategy for detecting the relation between gene expression and disease. 2015 , 12, 207-23	1
753	A new evolutionary gene selection technique. 2015 ,	4
752	Facteurs pronostiques et cancers bronchopulmonaires. 2015 , 7, 322-330	1
751	Lung cancer classification tool using microarray data and support vector machines. 2015 ,	8
750	Effects of Slit3 silencing on the invasive ability of lung carcinoma A549 cells. 2015 , 34, 952-60	24
749	Diversity-driven generation of link-based cluster ensemble and application to data classification. 2015 , 42, 8259-8273	10
748	Integrative analysis of cancer imaging readouts by networks. 2015 , 9, 1-16	14
747	Prognostic significance of YY1 protein expression and mRNA levels by bioinformatics analysis in human cancers: a therapeutic target. 2015 , 150, 149-68	35
746	Model-Free Feature Screening for Ultrahigh Dimensional Discriminant Analysis. 2015 , 110, 630-641	112
745	Intrinsic cancer subtypes--next steps into personalized medicine. 2015 , 38, 3-16	20
744	Deviance residuals-based sparse PLS and sparse kernel PLS regression for censored data. 2015 , 31, 397-404	17
743	Semi-supervised adaptive-height snipping of the hierarchical clustering tree. 2015 , 16, 15	5
742	Computational cancer biology: education is a natural key to many locks. 2015 , 15, 7	6
741	Identification and validation of gene module associated with lung cancer through coexpression network analysis. 2015 , 563, 56-62	28
740	PF-06463922 is a potent and selective next-generation ROS1/ALK inhibitor capable of blocking crizotinib-resistant ROS1 mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 3493-8	11.5 169

739	Origins, genetic landscape, and emerging therapies of small cell lung cancer. 2015 , 29, 1447-62	133
738	Pathway activity transformation for multi-class classification of lung cancer datasets. 2015 , 165, 81-89	20
737	Gene expression profiling offers insights into the role of innate immune signaling in SSc. 2015 , 37, 501-9	21
736	A common gene signature across multiple studies relate biomarkers and functional regulation in tolerance to renal allograft. 2015 , 87, 984-95	65
735	In-depth proteomic analysis of six types of exudative pleural effusions for nonsmall cell lung cancer biomarker discovery. 2015 , 14, 917-32	28
734	Kernel Penalized K-means: A feature selection method based on Kernel K-means. 2015 , 322, 150-160	26
733	Statistical completion of a partially identified graph with applications for the estimation of gene regulatory networks. 2015 , 16, 670-85	11
732	Identification of TPD54 as a candidate marker of oral epithelial carcinogenesis. 2015 , 27, 770-774	3
731	Prioritizing therapeutics for lung cancer: an integrative meta-analysis of cancer gene signatures and chemogenomic data. 2015 , 11, e1004068	27
730	Commercially available prognostic molecular models in early-stage lung cancer: a review of the Pervenio Lung RS and Myriad myPlan Lung Cancer tests. 2015 , 15, 589-96	15
729	A fast gene selection method for multi-cancer classification using multiple support vector data description. 2015 , 53, 381-9	34
728	Csk-homologous kinase (Chk/Matk): a molecular policeman suppressing cancer formation and progression. 2015 , 10, 195-202	0
727	Chromosomal instability as a prognostic marker in cervical cancer. 2015 , 15, 361	12
726	Cancer biomarker detection: recent achievements and challenges. 2015 , 44, 2963-97	633
725	The comparative pathology of genetically engineered mouse models for neuroendocrine carcinomas of the lung. 2015 , 10, 553-64	71
724	Identification of stage-specific biomarkers in lung adenocarcinoma based on RNA-seq data. 2015 , 36, 6391-9	12
723	Robust meta-analysis of gene expression using the elastic net. 2015 , 43, e79	76
722	Cancer classification using collaborative representation classifier based on non-convex lp-norm and novel decision rule. 2015 ,	2

721	Statistical thermodynamics of transcription profiles in normal development and tumorigenesis in cohorts of patients. 2015 , 44, 709-26	8
720	Poly(A)-specific ribonuclease and Nocturnin in squamous cell lung cancer: prognostic value and impact on gene expression. 2015 , 14, 187	18
719	CXCL7-induced macrophage infiltration in lung tumor is independent of CXCR2 expression: CXCL7-induced macrophage chemotaxis in LLC tumors. 2015 , 75, 330-7	16
718	Low expression of ITIH5 in adenocarcinoma of the lung is associated with unfavorable patients' outcome. 2015 , 10, 903-12	23
717	. 2015 , 27, 3176-3189	61
716	Similarity-Based Pattern Recognition. 2015 ,	4
715	Membership-margin based feature selection for mixed type and high-dimensional data: Theory and applications. 2015 , 322, 174-196	11
714	Cancer adjuvant chemotherapy strategic classification by artificial neural network with gene expression data: An example for non-small cell lung cancer. 2015 , 56, 1-7	19
713	Lipid phosphate phosphatases and their roles in mammalian physiology and pathology. 2015 , 56, 2048-60	87
712	Nuclear Localization of DNAJB6 Is Associated With Survival of Patients With Esophageal Cancer and Reduces AKT Signaling and Proliferation of Cancer Cells. 2015 , 149, 1825-1836.e5	32
711	Spectral Clustering of High-Dimensional Data via k-Nearest Neighbor Based Sparse Representation Coefficients. 2015 , 363-374	1
710	Integrating Tumor and Stromal Gene Expression Signatures With Clinical Indices for Survival Stratification of Early-Stage Non-Small Cell Lung Cancer. 2015 , 107,	43
709	A systematic analysis reveals heterogeneous changes in the endocytic activities of cancer cells. 2015 , 75, 4640-50	30
708	Gene expression profiling of pulmonary neuroendocrine neoplasms: A comprehensive overview. 2015 , 4, 148-160	3
707	An Arf-Egr-C/EBP β pathway linked to ras-induced senescence and cancer. 2015 , 35, 866-83	27
706	Linear discriminant analysis for the small sample size problem: an overview. 2015 , 6, 443-454	76
705	Elevated levels of preoperative circulating CD44+ lymphocytes and neutrophils predict poor survival for non-small cell lung cancer patients. 2015 , 439, 172-7	7
704	Adaptive Fuzzy Consensus Clustering Framework for Clustering Analysis of Cancer Data. 2015 , 12, 887-901	39

703	Prediction of individual response to anticancer therapy: historical and future perspectives. 2015 , 72, 729-57	33
702	Comparison of gene expression patterns across 12 tumor types identifies a cancer supercluster characterized by TP53 mutations and cell cycle defects. 2015 , 34, 2732-40	39
701	Application of MATLAB in -Omics and Systems Biology. 2016 ,	
700	Analyzing TCGA Lung Cancer Genomic and Expression Data Using SVM With Embedded Parameter Tuning. 2016 , 343-356	
699	Profile of farletuzumab and its potential in the treatment of solid tumors. 2016 , 9, 1181-8	15
698	Upregulation of long intergenic noncoding RNA 00673 promotes tumor proliferation via LSD1 interaction and repression of NCALD in non-small-cell lung cancer. 2016 , 7, 25558-75	55
697	Gene Selection Methods for Microarray Data. 2016 , 45-78	2
696	Cartography of Pathway Signal Perturbations Identifies Distinct Molecular Pathomechanisms in Malignant and Chronic Lung Diseases. 2016 , 7, 79	5
695	Exploratory Study to Identify Radiomics Classifiers for Lung Cancer Histology. <i>Frontiers in Oncology</i> , 2016 , 6, 71	5:3 211
694	Cloning and Transcriptional Activity of the Mouse Omi/HtrA2 Gene Promoter. 2016 , 17,	5
693	Identifying Cancer Subtypes from miRNA-TF-mRNA Regulatory Networks and Expression Data. 2016 , 11, e0152792	36
692	Receiver operating characteristic analysis under tree orderings of disease classes. 2016 , 35, 1907-26	5
691	Biomarker development in the precision medicine era: lung cancer as a case study. 2016 , 16, 525-37	288
690	A p-norm singular value decomposition method for robust tumor clustering. 2016 ,	
689	Novel biomarkers that assist in accurate discrimination of squamous cell carcinoma from adenocarcinoma of the lung. 2016 , 16, 760	30
688	Three-Dimensional Gene Map of Cancer Cell Types: Structural Entropy Minimisation Principle for Defining Tumour Subtypes. 2016 , 6, 20412	7
687	Gene selection for cancer classification with the help of bees. 2016 , 9 Suppl 2, 47	14
686	Traveling on discrete embeddings of gene expression. 2016 , 70, 1-11	1

685	A multi-objective heuristic algorithm for gene expression microarray data classification. 2016 , 59, 13-19	38
684	Simplifying pattern recognition problems via a scatter search algorithm. 2016 , 17, 315-321	5
683	[Typical and Atypical Carcinoids of the Lung: a Surgical Treatment Strategy]. 2016 , 141, 105-20	
682	Significance analysis of high-dimensional, low-sample size partially labeled data. 2016 , 176, 78-94	2
681	Leaf spectral clusters as potential optical leaf functional types within California ecosystems. 2016 , 184, 229-246	13
680	Iterative ensemble feature selection for multiclass classification of imbalanced microarray data. 2016 , 23, 13	20
679	A Structured Sparse Plus Structured Low-Rank Framework for Subspace Clustering and Completion. 2016 , 64, 6557-6570	42
678	miR-1298 Inhibits Mutant KRAS-Driven Tumor Growth by Repressing FAK and LAMB3. 2016 , 76, 5777-5787	39
677	Cytohistology of papillary carcinoid and emerging concept of pulmonary neuroendocrine neoplasms. 2016 , 44, 52-60	1
676	Hessian regularization based symmetric nonnegative matrix factorization for clustering gene expression and microbiome data. 2016 , 111, 80-84	17
675	Identification of informative genes and pathways using an improved penalized support vector machine with a weighting scheme. <i>Computers in Biology and Medicine</i> , 2016 , 77, 102-15	7 15
674	Sparse Multinomial Logistic Regression via Approximate Message Passing. 2016 , 64, 5485-5498	7
673	Using the two-population genetic algorithm with distance-based k-nearest neighbour voting classifier for high-dimensional data. 2016 , 14, 315	5
672	Lung cancer incidence in never smokers: Genetic and gender basis. 2016 , 4, 198-207	6
671	Ion channels expression and function are strongly modified in solid tumors and vascular malformations. 2016 , 14, 285	31
670	T cell factor-4 functions as a co-activator to promote NF- κ B-dependent MMP-15 expression in lung carcinoma cells. 2016 , 6, 24025	13
669	ASAClu: Selecting Diverse and Relevant Clusters. 2016 ,	
668	Sampling based hybrid algorithms for imbalanced data classification. 2016 , 13, 77-86	8

667	Tetracyclines increase lipid phosphate phosphatase expression on plasma membranes and turnover of plasma lysophosphatidate. 2016 , 57, 597-606	22
666	A novel feature extraction approach based on ensemble feature selection and modified discriminant independent component analysis for microarray data classification. 2016 , 36, 521-529	36
665	Impact of intracellular ion channels on cancer development and progression. 2016 , 45, 685-707	34
664	The role of ribosomal proteins in the regulation of cell proliferation, tumorigenesis, and genomic integrity. 2016 , 59, 656-72	69
663	Informative gene selection and the direct classification of tumors based on relative simplicity. 2016 , 17, 44	14
662	Genetics of Lung Disease. 2016 , 32-43.e3	
661	Interleukin-33 enhances programmed oncosis of ST2L-positive low-metastatic cells in the tumour microenvironment of lung cancer. 2016 , 7, e2057	30
660	Molecular basis of antibody binding to mucin glycopeptides in lung cancer. 2016 , 48, 587-94	9
659	A spontaneous metastasis model reveals the significance of claudin-9 overexpression in lung cancer metastasis. 2016 , 33, 263-75	11
658	Characteristic Gene Selection Based on Robust Graph Regularized Non-Negative Matrix Factorization. 2016 , 13, 1059-1067	19
657	Classification of gene expression data: A hubness-aware semi-supervised approach. 2016 , 127, 105-13	15
656	Bayesian Hierarchical Mixture Models. 2016 , 91-103	1
655	Next-Generation Sequencing of Pulmonary Large Cell Neuroendocrine Carcinoma Reveals Small Cell Carcinoma-like and Non-Small Cell Carcinoma-like Subsets. 2016 , 22, 3618-29	242
654	A survey on soft subspace clustering. 2016 , 348, 84-106	71
653	Windowing improvements towards more comprehensible models. 2016 , 92, 9-22	2
652	Diagnosis of Brain Metastases from Lung Cancer Using a Modified Electromagnetism like Mechanism Algorithm. 2016 , 40, 35	7
651	A Granular Self-Organizing Map for Clustering and Gene Selection in Microarray Data. 2016 , 27, 1890-906	22
650	Supervised, Unsupervised, and Semi-Supervised Feature Selection: A Review on Gene Selection. 2016 , 13, 971-989	256

649	A novel sparse coding algorithm for classification of tumors based on gene expression data. 2016 , 54, 869-76	14
648	Weighted doubly regularized support vector machine and its application to microarray classification with noise. 2016 , 173, 595-605	17
647	Heat-shock factor 2 is a suppressor of prostate cancer invasion. 2016 , 35, 1770-84	38
646	Biology of Lung Cancer. 2016 , 912-926.e6	0
645	A Scoring Scheme for Online Feature Selection: Simulating Model Performance Without Retraining. 2017 , 28, 405-414	4
644	Fast clustering using adaptive density peak detection. 2017 , 26, 2800-2811	43
643	A Gene Selection Method for Microarray Data Based on Binary PSO Encoding Gene-to-Class Sensitivity Information. 2017 , 14, 85-96	42
642	Feature Selection Based on Structured Sparsity: A Comprehensive Study. 2017 , 28, 1490-1507	180
641	Statistical significance for hierarchical clustering. 2017 , 73, 811-821	62
640	Non-convex regularized self-representation for unsupervised feature selection. 2017 , 60, 22-29	27
639	LSD1/KDM1 isoform LSD1+8a contributes to neural differentiation in small cell lung cancer. 2017 , 9, 86-94	5
638	Myc suppresses tumor invasion and cell migration by inhibiting JNK signaling. 2017 , 36, 3159-3167	27
637	Non-Small-cell Lung Cancer Patients With Adenocarcinoma Morphology Have a Better Outcome Compared With Patients Diagnosed With Non-Small-cell Lung Cancer Favor Adenocarcinoma. 2017 , 18, 316-323.e1	5
636	An integrative approach unveils FOSL1 as an oncogene vulnerability in KRAS-driven lung and pancreatic cancer. 2017 , 8, 14294	73
635	Fast and Scalable Feature Selection for Gene Expression Data Using Hilbert-Schmidt Independence Criterion. 2017 , 14, 167-181	24
634	Inverse correlation between the metastasis suppressor RKIP and the metastasis inducer YY1: Contrasting roles in the regulation of chemo/immuno-resistance in cancer. 2017 , 30, 28-38	28
633	Systematic analysis of the achaete-scute complex-like gene signature in clinical cancer patients. 2017 , 6, 7-18	15
632	Molecular Biology, Genomics, Proteomics, and Mouse Models of Human Cancer. 2017 , 1-31	

631	Cancer Genomics and Evolution. 2017 , 1-27	0
630	Clustering by fast search and merge of local density peaks for gene expression microarray data. 2017 , 7, 45602	34
629	Maxdenominator Reweighted Sparse Representation for Tumor Classification. 2017 , 7, 46030	7
628	Oncogenic function of TUSC3 in non-small cell lung cancer is associated with Hedgehog signalling pathway. 2017 , 1863, 1749-1760	16
627	Recent advances in feature selection and its applications. 2017 , 53, 551-577	126
626	Gene Expression Profiling of Large Cell Lung Cancer Links Transcriptional Phenotypes to the New Histological WHO 2015 Classification. 2017 , 12, 1257-1267	34
625	Statistical Contributions to Bioinformatics: Design, Modeling, Structure Learning, and Integration. 2017 , 17, 245-289	9
624	Identification of transcription factors that may reprogram lung adenocarcinoma. 2017 , 83, 52-57	15
623	Combinatorial Mixtures of Multiparameter Distributions: An Application to Bivariate Data. 2017 , 13,	
622	Structured Sparse Subspace Clustering: A Joint Affinity Learning and Subspace Clustering Framework. 2017 , 26, 2988-3001	112
621	Identification of early-stage lung adenocarcinoma prognostic signatures based on statistical modeling. 2017 , 18, 117-123	3
620	Large cell neuroendocrine carcinoma of the lung: chemotherapy regimen depends on how "large" your diagnostic criteria are. 2017 , 50,	1
619	Integrated Classifier: A Tool for Microarray Analysis. 2017 , 30-43	
618	A binary-constrained Geometric Semantic Genetic Programming for feature selection purposes. 2017 , 100, 59-66	10
617	SMYD5 Controls Heterochromatin and Chromosome Integrity during Embryonic Stem Cell Differentiation. 2017 , 77, 6729-6745	14
616	A novel approach for data integration and disease subtyping. 2017 , 27, 2025-2039	78
615	Surfactant Protein B Suppresses Lung Cancer Progression by Inhibiting Secretory Phospholipase A2 Activity and Arachidonic Acid Production. 2017 , 42, 1684-1700	13
614	Identifying the miRNA signature associated with survival time in patients with lung adenocarcinoma using miRNA expression profiles. 2017 , 7, 7507	46

613	Classification of multi-class microarray datasets using a minimizing class-overlapping based ECOC algorithm. 2017 ,	2
612	Identification of relevant subtypes via preweighted sparse clustering. 2017 , 116, 139-154	5
611	Thy-1 Cancer-associated Fibroblasts Adversely Impact Lung Cancer Prognosis. 2017 , 7, 6478	21
610	An efficient concordant integrative analysis of multiple large-scale two-sample expression data sets. 2017 , 33, 3852-3860	4
609	Voltage-gated calcium channels: Novel targets for cancer therapy. 2017 , 14, 2059-2074	70
608	Robust and Efficient Biomolecular Clustering of Tumor Based on $\{p\}$ -Norm Singular Value Decomposition. 2017 , 16, 341-348	5
607	Building Diversified Multiple Trees for classification in high dimensional noisy biomedical data. 2017 , 5, 5	1
606	Granular Fuzzy Possibilistic C-Means Clustering approach to DNA microarray problem. 2017 , 133, 53-65	14
605	Development and Validation of an Individualized Immune Prognostic Signature in Early-Stage Nonsquamous Non-Small Cell Lung Cancer. 2017 , 3, 1529-1537	255
604	Development of Kras mutant lung adenocarcinoma in mice with knockout of the airway lineage-specific gene Gprc5a. <i>International Journal of Cancer</i> , 2017 , 141, 1589-1599	7-5 13
603	Downregulation of PKC δ /Pard3/Pard6b is responsible for lung adenocarcinoma cell EMT and invasion. 2017 , 38, 49-59	15
602	The Beta Subunit of Hemoglobin (HBB2/HBB) Suppresses Neuroblastoma Growth and Metastasis. 2017 , 77, 14-26	17
601	Exploiting the ensemble paradigm for stable feature selection: A case study on high-dimensional genomic data. 2017 , 35, 132-147	68
600	Genetic Modifiers of Progression-Free Survival in Never-Smoking Lung Adenocarcinoma Patients Treated with First-Line Tyrosine Kinase Inhibitors. 2017 , 195, 663-673	16
599	Knockdown of Immature Colon Carcinoma Transcript 1 Inhibits Proliferation and Promotes Apoptosis of Non-Small Cell Lung Cancer Cells. 2017 , 16, 559-569	3
598	Methods to increase reproducibility in differential gene expression via meta-analysis. 2017 , 45, e1	75
597	A comprehensive genomic pan-cancer classification using The Cancer Genome Atlas gene expression data. 2017 , 18, 508	79
596	Clinical verification of plasma messenger RNA as novel noninvasive biomarker identified through bioinformatics analysis for lung cancer. 2017 , 8, 43978-43989	18

595	Pathway Enrichment Analysis with Networks. 2017 , 8,	11
594	Gene Feature Extraction Based on Nonnegative Dual Graph Regularized Latent Low-Rank Representation. 2017 , 2017, 1096028	1
593	Long intergenic noncoding RNA 00673 promotes non-small-cell lung cancer metastasis by binding with EZH2 and causing epigenetic silencing of HOXA5. 2017 , 8, 32696-32705	35
592	Reduced expression of IQGAP2 and higher expression of IQGAP3 correlates with poor prognosis in cancers. 2017 , 12, e0186977	29
591	Network analysis of DEGs and verification experiments reveal the notable roles of PTTG1 and MMP9 in lung cancer. 2018 , 15, 257-263	8
590	Investigation of the role of tumor necrosis factor-like weak inducer of apoptosis in non-small cell lung cancer. 2018 , 39, 573-581	2
589	The transcription levels and prognostic values of seven proteasome alpha subunits in human cancers. 2017 , 8, 4501-4519	17
588	Integrative Analysis of Gene Networks and Their Application to Lung Adenocarcinoma Studies. 2017 , 16, 1176935117690778	1
587	Identification of novel gene expression signature in lung adenocarcinoma by using next-generation sequencing data and bioinformatics analysis. 2017 , 8, 104831-104854	40
586	Dealing with high-dimensional class-imbalanced datasets: Embedded feature selection for SVM classification. 2018 , 67, 94-105	93
585	Cell of origin markers identify different prognostic subgroups of lung adenocarcinoma. 2018 , 75, 167-178	9
584	Sonic hedgehog signaling pathway promotes INSM1 transcription factor in neuroendocrine lung cancer. 2018 , 46, 83-91	15
583	Continuum directions for supervised dimension reduction. 2018 , 125, 27-43	3
582	Concomitance of EGFR mutations and ALK rearrangement in patients with Lung Cancer. 2018 , 11, 196-204	1
581	Kallikrein-related peptidases in lung diseases. 2018 , 399, 959-971	15
580	Sparse Fisher's linear discriminant analysis for partially labeled data. 2018 , 11, 17-31	4
579	The Molecular Biology of NET: Current Status and Evaluation of Biomarkers for Prediction and Prognosis. 2018 , 51-75	
578	Neuroendocrine Tumors in Real Life. 2018 ,	1

577	Monoglyceride lipase gene knockout in mice leads to increased incidence of lung adenocarcinoma. 2018 , 9, 36	11
576	Proliferation genes in lung development associated with the prognosis of lung adenocarcinoma but not squamous cell carcinoma. 2018 , 109, 308-316	7
575	Integrative genomic profiling of large-cell neuroendocrine carcinomas reveals distinct subtypes of high-grade neuroendocrine lung tumors. 2018 , 9, 1048	152
574	On the number of principal components in high dimensions. 2018 , 105, 389-402	5
573	Local-Nearest-Neighbors-Based Feature Weighting for Gene Selection. 2018 , 15, 1538-1548	9
572	Revealing community structures by ensemble clustering using group diffusion. 2018 , 42, 24-36	10
571	A discriminative multi-class feature selection method via weighted l2,1-norm and Extended Elastic Net. 2018 , 275, 1140-1149	7
570	New fast feature selection methods based on multiple support vector data description. 2018 , 48, 1776-1790	4
569	Microenvironment and Lung Cancer. 2018 , 121-128.e4	0
568	Clinical Presentation and Prognostic Factors in Lung Cancer. 2018 , 186-198.e6	
567	Pulmonary large cell neuroendocrine carcinoma with adenocarcinoma-like features: napsin A expression and genomic alterations. 2018 , 31, 111-121	38
566	Venetoclax Is Effective in Small-Cell Lung Cancers with High BCL-2 Expression. 2018 , 24, 360-369	46
565	Transcriptional E2F1/2/5/8 as potential targets and transcriptional E2F3/6/7 as new biomarkers for the prognosis of human lung carcinoma. 2018 , 10, 973-987	49
564	Bidirectional compressive sensing for classification of gene expression data. 2018 , 33, e5120	
563	Transcriptional deregulation underlying the pathogenesis of small cell lung cancer. 2018 , 7, 4-20	12
562	A liquid biopsy for bronchopulmonary/lung carcinoid diagnosis. 2018 , 9, 7182-7196	16
561	Constrained Sparse Subspace Clustering with Side-Information. 2018 ,	3
560	Differentially expressed microRNAs in lung adenocarcinoma invert effects of copy number aberrations of prognostic genes. 2018 , 9, 9137-9155	6

559	Summary of Biological Information Based on Intelligence Analysis. 2018,	
558	Inferring Genome-Wide Interaction Networks Using the Phi-Mixing Coefficient, and Applications to Lung and Breast Cancer (Invited Paper). 2018, 4, 123-139	3
557	CDK5 Functions as a Tumor Promoter in Human Lung Cancer. 2018, 9, 3950-3961	16
556	Expression of TARBP1 protein in human non-small-cell lung cancer and its prognostic significance. 2018, 15, 7182-7190	3
555	Network analysis of differentially expressed smoking-associated mRNAs, lncRNAs and miRNAs reveals key regulators in smoking-associated lung cancer. 2018, 16, 4991-5002	7
554	Random ensemble oblique decision stumps for classifying gene expression data. 2018,	4
553	Overview of Technological Advances and Predictive Assays. 2018, 664-679	
552	Special Types of Lung Cancer. 2018, 131-146	
551	Effect of machine learning methods on predicting NSCLC overall survival time based on Radiomics analysis. 2018, 13, 197	27
550	Upregulation of HOXA11 during the progression of lung adenocarcinoma detected via multiple approaches. 2018, 42, 2650-2664	21
549	Significance test of clustering under high dimensional setting with applications to cancer data. 2018, 88, 3349-3378	0
548	An Integrative Analysis of Transcriptome and Epigenome Features of ASCL1-Positive Lung Adenocarcinomas. 2018, 13, 1676-1691	13
547	Molecular signatures in IASLC/ATS/ERS classified growth patterns of lung adenocarcinoma. 2018, 13, e0206132	4
546	SBC: A New Strategy for Multiclass Lung Cancer Classification Based on Tumour Structural Information and Microarray Data. 2018,	5
545	A two-stage gene selection method for biomarker discovery from microarray data for cancer classification. 2018, 183, 47-58	34
544	AHNAK Loss in Mice Promotes Type II Pneumocyte Hyperplasia and Lung Tumor Development. 2018, 16, 1287-1298	13
543	Unified Simultaneous Clustering and Feature Selection for Unlabeled and Labeled Data. 2018, 29, 6083-6098	10
542	Feature genes selection using Fisher transformation method. 2018, 34, 4291-4300	2

541	Identification of candidate biomarkers and pathways associated with SCLC by bioinformatics analysis. 2018 , 18, 1538-1550	14
540	Signature Gene Identification of Cancer Occurrence and Pattern Recognition. 2018 , 25, 907-916	6
539	Bioinformatic analysis of prognostic value of ZW10 interacting protein in lung cancer. 2018 , 11, 1683-1695	15
538	Overexpression of Zwint predicts poor prognosis and promotes the proliferation of hepatocellular carcinoma by regulating cell-cycle-related proteins. 2018 , 11, 689-702	45
537	Multiclass Classification and Feature Selection Based on Least Squares Regression with Large Margin. 2018 , 30, 2781-2804	6
536	Evaluation of the HOXA11 level in patients with lung squamous cancer and insights into potential molecular pathways via bioinformatics analysis. 2018 , 16, 109	13
535	Discriminative embedded unsupervised feature selection. 2018 , 112, 219-225	13
534	Identification of an early diagnostic biomarker of lung adenocarcinoma based on co-expression similarity and construction of a diagnostic model. 2018 , 16, 205	6
533	Downregulation of NDR1 contributes to metastasis of prostate cancer cells via activating epithelial-mesenchymal transition. 2018 , 7, 3200	5
532	Cancer Characteristic Gene Selection via Sample Learning Based on Deep Sparse Filtering. 2018 , 8, 8270	8
531	The ERBB network facilitates KRAS-driven lung tumorigenesis. 2018 , 10,	53
530	Efficient Feature Selection via $\ell_{2,0}$ -norm Constrained Sparse Regression. 2019 , 31, 880-893	29
529	Feature Extraction Based on Support Vector Data Description. 2019 , 49, 643-659	2
528	Contribution of annexin A1 to anticancer immunosurveillance. 2019 , 8, e1647760	10
527	Meta-analysis of gene expression alterations and clinical significance of the HECT domain-containing ubiquitin ligase HUWE1 in cancer. 2019 , 18, 2292-2303	6
526	CT-NNBI: Method to Impute Gene Expression Data using DCT Based Sparsity and Nuclear Norm Constraint with Split Bregman Iteration. 2019 ,	2
525	Distinct signatures of lung cancer types: aberrant mucin O-glycosylation and compromised immune response. 2019 , 19, 824	16
524	Predicting chromosome 1p/19q codeletion by RNA expression profile: a comparison of current prediction models. 2019 , 11, 974-985	2

523	An efficient framework for unsupervised feature selection. 2019 , 366, 194-207	9
522	TFAP2C increases cell proliferation by downregulating GADD45B and PMAIP1 in non-small cell lung cancer cells. 2019 , 52, 35	18
521	A Review of Microarray Datasets: Where to Find Them and Specific Characteristics. 2019 , 1986, 65-85	7
520	Expression of CENPE and its Prognostic Role in Non-small Cell Lung Cancer. 2019 , 14, 497-502	12
519	On the Role of Clustering and Visualization Techniques in Gene Microarray Data. 2019 , 12, 123	4
518	A memetic algorithm using emperor penguin and social engineering optimization for medical data classification. 2019 , 85, 105773	34
517	N-acetylgalactosamine-6-sulfatase (GALNS), Similar to Glycodelin, Is a Potential General Biomarker for Multiple Malignancies. 2019 , 39, 6317-6324	2
516	Overexpression of CENPF correlates with poor prognosis and tumor bone metastasis in breast cancer. 2019 , 19, 264	54
515	An Improved SVM-RFE Based on $\Phi\Phi$ -Statistic and mPDC for Gene Selection in Cancer Classification. <i>IEEE Access</i> , 2019 , 7, 147617-147628	3.5 3
514	A Probabilistic Derivation of LASSO and L12-Norm Feature Selections. 2019 , 33, 4586-4593	9
513	Screening and Identification of Potential Prognostic Biomarkers in Adrenocortical Carcinoma. 2019 , 10, 821	13
512	Uridine-cytidine kinase 2 (UCK2): A potential diagnostic and prognostic biomarker for lung cancer. 2019 , 110, 2734-2747	15
511	DYRK1A inhibition suppresses STAT3/EGFR/Met signalling and sensitizes EGFR wild-type NSCLC cells to AZD9291. 2019 , 23, 7427-7437	18
510	CFHR1 is a potentially downregulated gene in lung adenocarcinoma. 2019 , 20, 3642-3648	4
509	Biocatalysis. 2019 ,	5
508	MGKA: A genetic algorithm-based clustering technique for genomic data. 2019 ,	3
507	Novel hybrid DCNNBVM model for classifying RNA-sequencing gene expression data** This paper is an extended version of 11th Asian Conference on Intelligent Information and Database Systems (ACIIDS 2018) Paper (Huynh, Nguyen, & Do, 2018a). In this paper, in addition to ACIIDS 2018 paper, we have been built DCNNBVM model RNA-Seq gene expression data classification. This model	6
506	Identification of candidate genes associated with the pathogenesis of small cell lung cancer via integrated bioinformatics analysis. 2019 , 18, 3723-3733	18

505	Epigenetic identification of ADCY4 as a biomarker for breast cancer: an integrated analysis of adenylate cyclases. 2019 , 11, 1561-1579	10
504	Loss of thymidine kinase 1 inhibits lung cancer growth and metastatic attributes by reducing GDF15 expression. 2019 , 15, e1008439	17
503	Analysis of high-dimensional genomic data employing a novel bio-inspired algorithm. 2019 , 77, 520-532	26
502	A survey of neural network-based cancer prediction models from microarray data. 2019 , 97, 204-214	37
501	A novel gene selection algorithm for cancer classification using microarray datasets. 2019 , 12, 10	35
500	Sliced inverse regression for integrative multi-omics data analysis. 2019 , 18,	1
499	Discriminative Dimension Reduction via Maximin Separation Probability Analysis. 2021 , 51, 4100-4111	1
498	Identification of key modules and hub genes for small-cell lung carcinoma and large-cell neuroendocrine lung carcinoma by weighted gene co-expression network analysis of clinical tissue-proteomes. 2019 , 14, e0217105	16
497	Model-based clustering of censored data via mixtures of factor analyzers. 2019 , 140, 104-121	11
496	Elevated integrin β expression is involved in the occurrence and development of lung adenocarcinoma, and predicts a poor prognosis: a study based on immunohistochemical analysis and bioinformatics. 2019 , 145, 1681-1693	12
495	Vitis vinifera gene expression differential analysis assessing microarrays data pre-processing dynamism by RNA-Seq approach. 2019 , 10, 1-14	
494	Dimensionality Reduction in Gene Expression Data Sets. <i>IEEE Access</i> , 2019 , 7, 61136-61144	3.5 10
493	A hybrid gene selection method based on gene scoring strategy and improved particle swarm optimization. 2019 , 20, 289	4
492	Identification of CD4+ T cell biomarkers for predicting the response of patients with relapsing-remitting multiple sclerosis to natalizumab treatment. 2019 , 20, 678-684	22
491	Gene Expression Profiling of Lung Atypical Carcinoids and Large Cell Neuroendocrine Carcinomas Identifies Three Transcriptomic Subtypes with Specific Genomic Alterations. 2019 , 14, 1651-1661	44
490	Metabolic reprogramming and Notch activity distinguish between non-small cell lung cancer subtypes. 2019 , 121, 51-64	23
489	Insulinoma-Associated-1: From Neuroendocrine Tumor Marker to Cancer Therapeutics. 2019 , 17, 1597-1604	16
488	A hybrid framework for optimal feature subset selection. 2019 , 36, 2247-2259	19

487	Analysis of high-dimensional biomedical data using an evolutionary multi-objective emperor penguin optimizer. 2019 , 48, 262-273	32
486	Identification of a Clinically Relevant Signature for Early Progression in KRAS-Driven Lung Adenocarcinoma. 2019 , 11,	4
485	Potentially functional genetic variants in the TNF/TNFR signaling pathway genes predict survival of patients with non-small cell lung cancer in the PLCO cancer screening trial. 2019 , 58, 1094-1104	6
484	TV-DCT: Method to Impute Gene Expression Data Using DCT Based Sparsity and Total Variation Denoising. 2019 ,	2
483	Gene Expression Classification of Lung Adenocarcinoma into Molecular Subtypes. 2020 , 17, 1187-1197	13
482	Pulmonary Adenocarcinoma Pathology and Molecular Testing. 2019 , 13-33	1
481	Pyrroline-5-Carboxylate Reductase 1 Accelerates the Migration and Invasion of Nonsmall Cell Lung Cancer. 2019 , 34, 380-387	10
480	Multimomics Analysis Reveals that GLS and GLS2 Differentially Modulate the Clinical Outcomes of Cancer. 2019 , 8,	37
479	Modified Firefly Algorithm With Chaos Theory for Feature Selection. 2019 , 10, 1-20	7
478	Screening of important lncRNAs associated with the prognosis of lung adenocarcinoma, based on integrated bioinformatics analysis. 2019 , 19, 4067-4080	5
477	NDR2 kinase contributes to cell invasion and cytokinesis defects induced by the inactivation of RASSF1A tumor-suppressor gene in lung cancer cells. 2019 , 38, 158	13
476	Extended adaptive Lasso for multi-class and multi-label feature selection. 2019 , 173, 28-36	22
475	A hybrid gene selection algorithm based on interaction information for microarray-based cancer classification. 2019 , 14, e0212333	12
474	Structured orthogonal matching pursuit for feature selection. 2019 , 349, 164-172	4
473	Adaptive improved binary PSO-based learnable Bayesian classifier for dimensionality reduced microarray data. 2019 , 11, 265	1
472	Particle Swarm Optimized Hybrid Kernel-Based Multiclass Support Vector Machine for Microarray Cancer Data Analysis. 2019 , 2019, 4085725	8
471	Osteopontin Mediates Cetuximab Resistance via the MAPK Pathway in NSCLC Cells. 2019 , 12, 10177-10185	2
470	RBFA: Radial Basis Function Autoencoders. 2019 ,	2

- 469 Importance of Feature Weighing in Cervical Cancer Subtypes Identification. **2019**,
- 468 Deep gene selection method to select genes from microarray datasets for cancer classification. **2019**, 20, 608 6
- 467 Weighted k-nearest neighbors feature selection for high-dimensional multi-class data. **2019**,
- 466 IRF1 Negatively Regulates Oncogenic KPNA2 Expression Under Growth Stimulation and Hypoxia in Lung Cancer Cells. **2019**, 12, 11475-11486 6
- 465 New Gene Selection Method Using Gene Expression Programing Approach on Microarray Data Sets. **2019**, 17-31 3
- 464 Encoding sparse and competitive structures among tasks in multi-task learning. **2019**, 88, 689-701 3
- 463 Prevalence of ROS1 fusion in Chinese patients with non-small cell lung cancer. **2019**, 10, 47-53 17
- 462 Expression and prognosis analyses of forkhead box A (FOXA) family in human lung cancer. **2019**, 685, 202-210 16
- 461 Novel STAT3 Inhibitor LDOC1 Targets Phospho-JAK2 for Degradation by Interacting with LNX1 and Regulates the Aggressiveness of Lung Cancer. **2019**, 11, 12
- 460 Mixtures of Gaussian copula factor analyzers for clustering high dimensional data. **2019**, 48, 480-492 2
- 459 Adaptive Semi-Supervised Classifier Ensemble for High Dimensional Data Classification. **2019**, 49, 366-379 31
- 458 Multiobjective Semisupervised Classifier Ensemble. **2019**, 49, 2280-2293 14
- 457 Biomarker Identification for Cancer Disease Using Biclustering Approach: An Empirical Study. **2018**, 7
- 456 Feature selection based on correlation deflation. **2019**, 31, 6383-6392 3
- 455 C-mix: A high-dimensional mixture model for censored durations, with applications to genetic data. **2019**, 28, 1523-1539 5
- 454 Learning a Structural and Functional Representation for Gene Expressions: To Systematically Dissect Complex Cancer Phenotypes. **2019**, 16, 1729-1742 1
- 453 Automatic detection of lung cancer from biomedical data set using discrete AdaBoost optimized ensemble learning generalized neural networks. **2020**, 32, 777-790 44
- 452 Performance of gene expression-based single sample predictors for assessment of clinicopathological subgroups and molecular subtypes in cancers: a case comparison study in non-small cell lung cancer. **2020**, 21, 729-740 8

451	Multi-Source Causal Feature Selection. 2020 , 42, 2240-2256	24
450	Category-Adaptive Variable Screening for Ultra-High Dimensional Heterogeneous Categorical Data. 2020 , 115, 747-760	12
449	Population-guided large margin classifier for high-dimension low-sample-size problems. 2020 , 97, 107030	4
448	Suboptimal Comparison of Partitions. 2020 , 37, 435-461	1
447	A new optimal gene selection approach for cancer classification using enhanced Jaya-based forest optimization algorithm. 2020 , 32, 8599-8616	12
446	The Role of Cell Growth-Related Gene Copy Number Variation in Autoimmune Thyroid Disease. 2020 , 195, 409-416	4
445	Biclustering via sparse clustering. 2020 , 76, 348-358	2
444	A study on metaheuristics approaches for gene selection in microarray data: algorithms, applications and open challenges. 2020 , 13, 309-329	9
443	Inhibition of glutaminase to reverse fibrosis in iatrogenic laryngotracheal stenosis. 2020 , 130, E773-E781	5
442	Integrating tumor hypoxic stress in novel and more adaptable strategies for cancer immunotherapy. 2020 , 65, 140-154	30
441	Facile Strategy To Enhance Specificity and Sensitivity of Molecular Beacons by an Aptamer-Functionalized Delivery Vector. 2020 , 92, 2088-2096	16
440	Plakophilin 1 enhances MYC translation, promoting squamous cell lung cancer. 2020 , 39, 5479-5493	9
439	A Hierarchical Clustering algorithm based on Silhouette Index for cancer subtype discovery from genomic data. 2020 , 32, 11459-11476	8
438	Fuzzy entropy clustering by searching local border points for the analysis of gene expression data. 2020 , 190, 105309	5
437	Structured Optimal Graph-Based Clustering With Flexible Embedding. 2020 , 31, 3801-3813	2
436	Geometric consistency of principal component scores for high-dimensional mixture models and its application. 2020 , 47, 899-921	1
435	SGL-SVM: A novel method for tumor classification via support vector machine with sparse group Lasso. 2020 , 486, 110098	29
434	Multi-scale supervised clustering-based feature selection for tumor classification and identification of biomarkers and targets on genomic data. 2020 , 21, 650	11

433	Unsupervised feature selection based on adaptive similarity learning and subspace clustering. 2020 , 95, 103855		4
432	Lipid Phosphate Phosphatases and Cancer. 2020 , 10,		13
431	Transformation Based Tri-Level Feature Selection Approach Using Wavelets and Swarm Computing for Prostate Cancer Classification. <i>IEEE Access</i> , 2020 , 8, 127462-127476	3.5	8
430	The design of variable-length coding matrix for improving error correcting output codes. 2020 , 534, 192-217		4
429	Type-specific classification of bronchogenic carcinomas using bi-layer mutated particle swarm optimisation. 2020 , 13, 360		
428	Binary Political Optimizer for Feature Selection Using Gene Expression Data. 2020 , 2020, 8896570		4
427	A study of data pre-processing techniques for imbalanced biomedical data classification. 2020 , 16, 290		1
426	Methylation Patterns and Chromatin Accessibility in Neuroendocrine Lung Cancer. 2020 , 12,		3
425	Novel evidence for retinoic acid-induced G (Rig-G) as a tumor suppressor by activating p53 signaling pathway in lung cancer. 2020 , 34, 11900-11912		3
424	Role of Adipose Tissue-Derived Autotaxin, Lysophosphatidate Signaling, and Inflammation in the Progression and Treatment of Breast Cancer. 2020 , 21,		14
423	Involvement of the NF- κ B signaling pathway in proliferation and invasion inhibited by Zwint-1 deficiency in Pancreatic Cancer Cells. 2020 , 11, 5601-5611		5
422	Improvements in the Large p, Small n Classification Issue. 2020 , 1, 1		3
421	Protein-altering germline mutations implicate novel genes related to lung cancer development. 2020 , 11, 2220		6
420	Highly Expressed FOXF1 Inhibit Non-Small-Cell Lung Cancer Growth via Inducing Tumor Suppressor and G1-Phase Cell-Cycle Arrest. 2020 , 21,		2
419	Identification of Novel Candidate Biomarkers for Oral Squamous Cell Carcinoma Based on Whole Gene Expression Profiling. 2020 , 26, 2315-2325		5
418	EZH2 has a non-catalytic and PRC2-independent role in stabilizing DDB2 to promote nucleotide excision repair. 2020 , 39, 4798-4813		14
417	Comprehensive analysis of the expression and prognosis for TFAP2 in human lung carcinoma. 2020 , 42, 779-789		2
416	Analysis of Expression and Its Clinical Significance of the Secreted Phosphoprotein 1 in Lung Adenocarcinoma. 2020 , 11, 547		12

415	Ensemble feature selection in high dimension, low sample size datasets: Parallel and serial combination approaches. 2020 , 203, 106097	17
414	The Deubiquitinase USP4 Stabilizes Twist1 Protein to Promote Lung Cancer Cell Stemness. 2020 , 12,	9
413	Lung cancer histology-driven strategic therapeutic approaches. 2020 , 4, 29-29	2
412	Data maximum dispersion classifier in projection space for high-dimension low-sample-size problems. 2020 , 193, 105420	2
411	Feature selection inspired by human intelligence for improving classification accuracy of cancer types. 2020 ,	7
410	The top 100 cited articles in lung cancer - a bibliometric analysis. 2020 , 24, 17-28	3
409	Identification of Sca-1Abcg1 bronchioalveolar epithelial cells as the origin of lung adenocarcinoma in Gprc5a-knockout mouse model through the interaction between lung progenitor AT2 and Lgr5 cells. 2020 , 39, 3754-3773	3
408	Unified methods for feature selection in large-scale genomic studies with censored survival outcomes. 2020 , 36, 3409-3417	2
407	Chaotic emperor penguin optimised extreme learning machine for microarray cancer classification. 2020 , 14, 85-95	11
406	Cellular processes involved in lung cancer cells exposed to direct current electric field. 2020 , 10, 5289	0
405	Analyses of expressions and prognostic values of Polo-like kinases in non-small cell lung cancer. 2020 , 146, 2447-2460	4
404	EHMT2 Inhibition Induces Cell Death in Human Non-Small Cell Lung Cancer by Altering the Cholesterol Biosynthesis Pathway. 2020 , 21,	5
403	. <i>IEEE Access</i> , 2020 , 8, 40138-40150	3.5 4
402	Learning From High-Dimensional Biomedical Datasets: The Issue of Class Imbalance. <i>IEEE Access</i> , 2020 , 8, 13527-13540	3.5 14
401	Autotaxin and Breast Cancer: Towards Overcoming Treatment Barriers and Sequelae. 2020 , 12,	15
400	Tumor-suppressive proteases revisited: Role in inhibiting tumor progression and metastasis. 2020 , 391-416	
399	Common and distinct features of potentially predictive biomarkers in small cell lung carcinoma and large cell neuroendocrine carcinoma of the lung by systematic and integrated analysis. 2020 , 8, e1126	2
398	Supervised Dimension Reduction for Large-Scale "Omics" Data With Censored Survival Outcomes Under Possible Non-Proportional Hazards. 2021 , 18, 2032-2044	2

397	Simplified molecular classification of lung adenocarcinomas based on EGFR, KRAS, and TP53 mutations. 2020 , 20, 83	7
396	Nanotechnology for cancer screening and diagnosis: from innovations to clinical applications. 2020 , 261-289	2
395	An Approach to Supervised Learning: Dynamic Multi-Hyperplane Partitioning. <i>IEEE Access</i> , 2020 , 8, 22048-22071	9.5
394	Non-Coding RNAs in Lung Tumor Initiation and Progression. 2020 , 21,	12
393	The STK38-XPO1 axis, a new actor in physiology and cancer. 2021 , 78, 1943-1955	1
392	A gene expression-based single sample predictor of lung adenocarcinoma molecular subtype and prognosis. <i>International Journal of Cancer</i> , 2021 , 148, 238-251	7.5 3
391	Hybridization of Moth flame optimization algorithm and quantum computing for gene selection in microarray data. 2021 , 12, 2731-2750	13
390	Gene selection and classification of microarray data method based on mutual information and moth flame algorithm.. 2021 , 166, 114012	14
389	Ceramide synthases: insights into the expression and prognosis of lung cancer. 2021 , 47, 37-53	2
388	Role of tight junctions in the epithelial-to-mesenchymal transition of cancer cells. 2021 , 1863, 183503	15
387	SARA: A memetic algorithm for high-dimensional biomedical data. 2021 , 101, 107009	11
386	. 2021 , 33, 2847-2862	3
385	mRelief: A Reward Penalty Based Feature Subset Selection Considering Data Overlapping Problem. 2021 , 278-292	1
384	The Mad2-Binding Protein p31 as a Potential Target for Human Cancer Therapy. 2021 , 21, 401-415	0
383	Autotaxin is an important component of the tumor microenvironment and a major modulator of therapy responses for breast cancer. 2021 , 47-63	
382	Gene expression and prognosis of x-ray repair cross-complementing family members in non-small cell lung cancer. 2021 , 12, 6210-6228	0
381	Comprehensive Analysis of Expression and Prognostic Value of GATAs in Lung Cancer. 2021 , 12, 3862-3876	1
380	The fastest L1,00 prox in the west. 2021 , PP,	1

379	The histologic phenotype of lung cancers may be driven by transcriptomic features rather than genomic characteristics.		
378	Immunoexpression of TTF1 and p63 Differentiates Lung Adenocarcinomas in Sputum Samples. 2021 , 38, 151-157		0
377	Deep Neural Networks Regularization Using a Combination of Sparsity Inducing Feature Selection Methods. 2021 , 53, 701-720		
376	Joint Lp-Norm and L-Norm Constrained Graph Laplacian PCA for Robust Tumor Sample Clustering and Gene Network Module Discovery. 2021 , 12, 621317		1
375	A Review on Lung Cancer Diagnosis Using Data Mining Algorithms. 2021 , 17, 16-26		0
374	Dynamic roles of inflammasomes in inflammatory tumor microenvironment. 2021 , 5, 18		14
373	Loss of Smad4 promotes aggressive lung cancer metastasis by de-repression of PAK3 via miRNA regulation.		
372	Prognostic and clinicopathological value of BUB1B expression in patients with lung adenocarcinoma: a meta-analysis. 2021 , 21, 795-803		7
371	Radiomics-Based Features for Prediction of Histological Subtypes in Central Lung Cancer. <i>Frontiers in Oncology</i> , 2021 , 11, 658887	5:3	4
370	Expression, Prognosis and Gene Regulation Network of NFAT Transcription Factors in Non-Small Cell Lung Cancer. 2021 , 27, 529240		
369	Application of the Interaction between Tissue Immunohistochemistry Staining and Clinicopathological Factors for Evaluating the Risk of Oral Cancer Progression by Hierarchical Clustering Analysis: A Case-Control Study in a Taiwanese Population. 2021 , 11,		1
368	Abnormal Expression and Prognostic Significance of Bone Morphogenetic Proteins and Their Receptors in Lung Adenocarcinoma. 2021 , 2021, 6663990		0
367	Improving the Subtype Classification of Non-small Cell Lung Cancer by Elastic Deformation Based Machine Learning. 2021 , 34, 605-617		0
366	A systematic dissection of the epigenomic heterogeneity of lung adenocarcinoma reveals two different subclasses with distinct prognosis and core regulatory networks. 2021 , 22, 156		5
365	RPCA-induced self-representation for subspace clustering. 2021 , 437, 249-260		1
364	The Unsupervised Feature Selection Algorithms Based on Standard Deviation and Cosine Similarity for Genomic Data Analysis. 2021 , 12, 684100		3
363	A recursive feature retention method for semi-supervised feature selection. 2021 , 12, 2639-2657		1
362	Identification and assessment of PLK1/2/3/4 in lung adenocarcinoma and lung squamous cell carcinoma: Evidence from methylation profile. 2021 , 25, 6652-6663		2

361	Diagnostic and Prognostic Significance of Keap1 mRNA Expression for Lung Cancer Based on Microarray and Clinical Information from Oncomine Database. 2021 , 41, 597-609		
360	Ensemble clustering using extended fuzzy k-means for cancer data analysis. 2021 , 172, 114622		8
359	Relationship between Lung Carcinogenesis and Chronic Inflammation in Rodents. 2021 , 13,		2
358	Aggressive early-stage lung adenocarcinoma is characterized by epithelial cell plasticity with acquirement of stem-like traits and immune evasion phenotype. 2021 , 40, 4980-4991		1
357	SOX9 has distinct roles in the formation and progression of different non-small cell lung cancer histotypes. 2021 , 255, 16-29		0
356	Expression and Gene Regulation Network of Adenosine Receptor A2B in Lung Adenocarcinoma: A Potential Diagnostic and Prognostic Biomarker. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 663011	5.6	2
355	Identification of Predictive Biomarkers for Lymph Node Involvement in Obese Women With Endometrial Cancer. <i>Frontiers in Oncology</i> , 2021 , 11, 695404	5.3	1
354	A circular RNAs dataset landscape reveals potential signatures for the detection and prognosis of early-stage lung adenocarcinoma. 2021 , 21, 781		3
353	Amine oxidase, copper containing 3 exerts anti-mesenchymal transformation and enhances CD4 T-cell recruitment to prolong survival in lung cancer. 2021 , 46,		0
352	Decoding Clinical Biomarker Space of COVID-19: Exploring Matrix Factorization-based Feature Selection Methods. 2021 ,		5
351	Prognostic value of baculoviral IAP repeat containing 5 expression as a new biomarker in lung adenocarcinoma: a meta-analysis. 2021 , 21, 973-981		1
350	Gene Expression-Assisted Cancer Prediction Techniques. 2021 , 2021, 4242646		13
349	Loss of Smad4 promotes aggressive lung cancer metastasis by de-repression of PAK3 via miRNA regulation. 2021 , 12, 4853		5
348	Gene expression profiling after LINC00472 overexpression in an NSCLC cell line1. 2021 , 32, 175-188		1
347	Unsupervised feature selection via multi-step markov probability relationship. 2021 , 453, 241-253		0
346	High CTSL2 expression predicts poor prognosis in patients with lung adenocarcinoma. 2021 , 13, 22315-22331		
345	Stochastic Mutual Information Gradient Estimation for Dimensionality Reduction Networks. 2021 , 570, 298-305		5
344	Gene Expression Profiling as a Potential Tool for Precision Oncology in Non-Small Cell Lung Cancer. 2021 , 13,		1

343	An ensemble feature selection algorithm based on PageRank centrality and fuzzy logic. 2021 , 107538	4
342	Clustering by principal component analysis with Gaussian kernel in high-dimension, low-sample-size settings. 2021 , 185, 104779	4
341	Comprehensive analysis of the transcriptional expressions and prognostic value of S100A family in pancreatic ductal adenocarcinoma. 2021 , 21, 1039	1
340	Derandomizing Knockoffs. 1-11	3
339	Carboxypeptidase E mRNA: Overexpression predicts recurrence and death in lung adenocarcinoma cancer patients. 2021 ,	1
338	Adaptive graph-based generalized regression model for unsupervised feature selection. 2021 , 227, 107156	1
337	Development and Validation of a Prognostic Autophagy-Related Gene Pair Index Related to Tumor-Infiltrating Lymphocytes in Early-Stage Lung Adenocarcinoma. 2021 , 9, 719011	0
336	Efficient high-dimension feature selection based on enhanced equilibrium optimizer. 2022 , 187, 115882	0
335	Feature Selection Based on a Sparse Neural-Network Layer With Normalizing Constraints. 2021 , PP,	
334	Statistics for Bioinformatics. 2021 , 21-50	
333	Pattern Recognition Algorithms for Multi-Omics Data Analysis. 2021 , 141-158	1
332	Relevance, Redundancy and Differential Prioritization in Feature Selection for Multiclass Gene Expression Data. 2005 , 367-378	5
331	Collateral Missing Value Estimation: Robust Missing Value Estimation for Consequent Microarray Data Processing. 2005 , 274-283	5
330	Simultaneous Relevant Feature Identification and Classification in High-Dimensional Spaces. 2002 , 1-9	4
329	Genetic Programming for Classifying Cancer Data and Controlling Humanoid Robots. 2007 , 41-59	1
328	Common Non-Small-Cell Carcinomas and Their Variants. 2008 , 216-307	4
327	Rotation of random forests for genomic and proteomic classification problems. 2011 , 696, 211-21	10
326	Improving the accuracy of gene expression profile classification with Lorenz curves and Gini ratios. 2011 , 696, 83-90	3

325	Adenocarcinoma. 2012 , 119-162		1
324	Functional Genomics for Identifying Surrogate Endpoint Biomarkers in Breast Cancer Chemoprevention. 2005 , 115-122		2
323	Molecular Basis of Lung Carcinogenesis. 2017 , 447-496		1
322	cDNA Microarrays. 2008 , 269-289		1
321	Gene Selection for Microarray Data Classification Using Hybrid Meta-Heuristics. <i>Lecture Notes in Networks and Systems</i> , 2019 , 119-132	0.5	2
320	Clinical Significance of Enzymes in Disease and Diagnosis. 2019 , 213-231		2
319	Non-convex Regularized Self-representation for Unsupervised Feature Selection. 2015 , 55-65		2
318	Robust Initialization for Learning Latent Dirichlet Allocation. 2015 , 117-132		2
317	A Coupling Support Vector Machines with the Feature Learning of Deep Convolutional Neural Networks for Classifying Microarray Gene Expression Data. 2018 , 233-243		7
316	Transcriptional Gene Regulatory Network Reconstruction Through Cross Platform Gene Network Fusion. 2007 , 274-285		1
315	A Framework for Multi-class Learning in Micro-array Data Analysis. 2009 , 275-284		1
314	FCM for Gene Expression Bioinformatics Data. 2009 , 521-532		2
313	A Modified Two-Stage SVM-RFE Model for Cancer Classification Using Microarray Data. 2011 , 668-675		4
312	The Uniform Effect of K-means Clustering. 2012 , 17-35		3
311	Pathway-Based Multi-class Classification of Lung Cancer. 2012 , 697-702		3
310	Stable L2-Regularized Ensemble Feature Weighting. 2013 , 167-178		2
309	A Hybrid of SVM and SCAD with Group-Specific Tuning Parameters in Identification of Informative Genes and Biological Pathways. 2013 , 258-269		1
308	Applications of transcriptional profiling in antibiotics discovery and development. 2007 , 64, 21, 23-47		3

307	DNA Microarray. 2014 , 71-104	4
306	Genomic Pathology of Lung Cancer. 2013 , 1-46	1
305	Cancer of the Lung: Non-Small Cell Lung Cancer and Small Cell Lung Cancer. 2008 , 1307-1366	4
304	Dedifferentiation of neuroendocrine carcinoma of the uterine cervix in hypoxia. 2020 , 524, 398-404	3
303	CHAPTER 1:Introduction: Biomarkers in Translational and Personalized Medicine. 2013 , 3-39	1
302	Comprehensive analysis of inhibitor of differentiation/DNA-binding gene family in lung cancer using bioinformatics methods. 2020 , 40,	5
301	E12-01: NCI Director's challenge gene profiling of lung adenocarcinomas: impact on histologic classification. 2007 , 2, S254-S256	1
300	Prognostic Value of Fluorodeoxyglucose Positron Emission Tomography in Non-small Cell Lung Cancer: A Review. 2006 , 1, 152-159	30
299	Clinical impact of high-throughput gene expression studies in lung cancer. 2009 , 4, 109-18	21
298	The ERBB network facilitates KRAS-driven lung tumorigenesis.	0
297	Revisiting Feature Selection with Data Complexity.	3
296	Common and contrasting genomic profiles among the major human lung cancer subtypes. 2005 , 70, 11-24	18
295	A Feature Weighting-Assisted Approach for Cancer Subtypes Identification from Paired Expression profiles. 2020 , PP,	1
294	Detecting Meaningful Clusters from High-dimensional Data: A Strongly Consistent Sparse Center-based Clustering Approach. 2020 , PP,	8
293	High expression of CXCL14 is a biomarker of lung adenocarcinoma with micropapillary pattern. 2020 , 111, 2588-2597	7
292	Identification of 5-Gene Signature Improves Lung Adenocarcinoma Prognostic Stratification Based on Differential Expression Invasion Genes of Molecular Subtypes. 2020 , 2020, 8832739	12
291	Profiling cancer testis antigens in non-small-cell lung cancer. 2016 , 1, e86837	65
290	Microarray analysis identifies a death-from-cancer signature predicting therapy failure in patients with multiple types of cancer. 2005 , 115, 1503-21	697

289	Stem cell-ness: a "magic marker" for cancer. 2005 , 115, 1463-7	27
288	The retinoblastoma tumor suppressor modifies the therapeutic response of breast cancer. 2007 , 117, 218-28	152
287	New molecularly targeted therapies for lung cancer. 2007 , 117, 2740-50	154
286	Survival prediction of stage I lung adenocarcinomas by expression of 10 genes. 2007 , 117, 3436-44	94
285	Patients with lung cancer and paraneoplastic Hu syndrome harbor HuD-specific type 2 CD8+ T cells. 2009 , 119, 2042-51	73
284	Predicting drug susceptibility of non-small cell lung cancers based on genetic lesions. 2009 , 119, 1727-40	205
283	Six1 expands the mouse mammary epithelial stem/progenitor cell pool and induces mammary tumors that undergo epithelial-mesenchymal transition. 2009 , 119, 2663-77	138
282	Wilms tumor 1 (WT1) regulates KRAS-driven oncogenesis and senescence in mouse and human models. 2010 , 120, 3940-52	102
281	ERK3 signals through SRC-3 coactivator to promote human lung cancer cell invasion. 2012 , 122, 1869-80	78
280	Targeting the FOXO1/KLF6 axis regulates EGFR signaling and treatment response. 2012 , 122, 2637-51	65
279	ZEB1 drives prometastatic actin cytoskeletal remodeling by downregulating miR-34a expression. 2012 , 122, 3170-83	119
278	ZEB1 sensitizes lung adenocarcinoma to metastasis suppression by PI3K antagonism. 2014 , 124, 2696-708	90
277	Lysyl hydroxylase 2 induces a collagen cross-link switch in tumor stroma. 2015 , 125, 1147-62	102
276	A statistical framework for testing functional categories in microarray data. 2008 , 2,	42
275	Reconstruction of a high-dimensional low-rank matrix. 2016 , 10,	2
274	Semi-supervised methods to predict patient survival from gene expression data. 2004 , 2, E108	457
273	Predicting survival within the lung cancer histopathological hierarchy using a multi-scale genomic model of development. 2006 , 3, e232	63
272	Extracellular sulfatases, elements of the Wnt signaling pathway, positively regulate growth and tumorigenicity of human pancreatic cancer cells. 2007 , 2, e392	144

271	Sex determining region Y-Box 2 (SOX2) is a potential cell-lineage gene highly expressed in the pathogenesis of squamous cell carcinomas of the lung. 2010 , 5, e9112	110
270	Comparative Membranome expression analysis in primary tumors and derived cell lines. 2010 , 5, e11742	14
269	Hybrid models identified a 12-gene signature for lung cancer prognosis and chemoresponse prediction. 2010 , 5, e12222	43
268	Differential expression of CHL1 gene during development of major human cancers. 2011 , 6, e15612	70
267	Differential pathogenesis of lung adenocarcinoma subtypes involving sequence mutations, copy number, chromosomal instability, and methylation. 2012 , 7, e36530	158
266	Novel genes and pathways modulated by syndecan-1: implications for the proliferation and cell-cycle regulation of malignant mesothelioma cells. 2012 , 7, e48091	35
265	Multi-scale clustering by building a robust and self correcting ultrametric topology on data points. 2013 , 8, e56259	20
264	EZH2-Mediated H3K27me3 Is Involved in Epigenetic Repression of Deleted in Liver Cancer 1 in Human Cancers. 2013 , 8, e68226	41
263	Impact of delay to cryopreservation on RNA integrity and genome-wide expression profiles in resected tumor samples. 2013 , 8, e79826	18
262	Online survival analysis software to assess the prognostic value of biomarkers using transcriptomic data in non-small-cell lung cancer. 2013 , 8, e82241	1161
261	biDCG: a new method for discovering global features of DNA microarray data via an iterative re-clustering procedure. 2014 , 9, e102445	4
260	Gene expression profiling in human lung development: an abundant resource for lung adenocarcinoma prognosis. 2014 , 9, e105639	17
259	Meta-Analysis of Public Microarray Datasets Reveals Voltage-Gated Calcium Gene Signatures in Clinical Cancer Patients. 2015 , 10, e0125766	58
258	EAMA: Empirically adjusted meta-analysis for large-scale simultaneous hypothesis testing in genomic experiments. 2017 , 12, e0187287	2
257	Identification of potential target genes and crucial pathways in small cell lung cancer based on bioinformatic strategy and human samples. 2020 , 15, e0242194	2
256	The prognostic value of whole blood SOX2, NANOG and OCT4 mRNA expression in advanced small-cell lung cancer. 2016 , 50, 188-96	21
255	Computerized techniques pave the way for drug-drug interaction prediction and interpretation. 2016 , 6, 71-8	16
254	Modulating redox homeostasis and cellular reprogramming through inhibited methylenetetrahydrofolate dehydrogenase 2 enzymatic activities in lung cancer. 2020 , 12, 17930-17947	2

253	Consensus of gene expression phenotypes and prognostic risk predictors in primary lung adenocarcinoma. 2016 , 7, 52957-52973	9
252	Decreased expression of FOXF2 as new predictor of poor prognosis in stage I non-small cell lung cancer. 2016 , 7, 55601-55610	16
251	Targeted depletion of PIK3R2 induces regression of lung squamous cell carcinoma. 2016 , 7, 85063-85078	11
250	Amyloid precursor like protein-1 promotes JNK-mediated cell migration in Drosophila. 2017 , 8, 49725-49734	1
249	Generating a robust prediction model for stage I lung adenocarcinoma recurrence after surgical resection. 2017 , 8, 79712-79721	3
248	subfamily suppression in lung cancer pathogenesis: a high-potential marker for early detection. 2017 , 8, 68230-68241	8
247	Molecular profiling identifies prognostic markers of stage IA lung adenocarcinoma. 2017 , 8, 74846-74855	6
246	Decoding c-Myc networks of cell cycle and apoptosis regulated genes in a transgenic mouse model of papillary lung adenocarcinomas. 2015 , 6, 31569-92	22
245	Growth-stimulatory activity of TIMP-2 is mediated through c-Src activation followed by activation of FAK, PI3-kinase/AKT, and ERK1/2 independent of MMP inhibition in lung adenocarcinoma cells. 2015 , 6, 42905-22	13
244	Unique roles of Akt1 and Akt2 in IGF-IR mediated lung tumorigenesis. 2016 , 7, 3297-316	22
243	Adoptive immunotherapy using T lymphocytes redirected to glypican-3 for the treatment of lung squamous cell carcinoma. 2016 , 7, 2496-507	27
242	DANGER is involved in high glucose-induced radioresistance through inhibiting DAPK-mediated anoikis in non-small cell lung cancer. 2016 , 7, 7193-206	19
241	Distinct lymphocyte antigens 6 (Ly6) family members Ly6D, Ly6E, Ly6K and Ly6H drive tumorigenesis and clinical outcome. 2016 , 7, 11165-93	53
240	Effective growth-suppressive activity of maternal embryonic leucine-zipper kinase (MELK) inhibitor against small cell lung cancer. 2016 , 7, 13621-33	36
239	Down-regulation of LAPTM5 in human cancer cells. 2016 , 7, 28320-8	12
238	Integrative transcriptome analysis identifies deregulated microRNA-transcription factor networks in lung adenocarcinoma. 2016 , 7, 28920-34	41
237	Gene identification for risk of relapse in stage I lung adenocarcinoma patients: a combined methodology of gene expression profiling and computational gene network analysis. 2016 , 7, 30561-74	31
236	Four and a half LIM domains protein 1 can be as a double-edged sword in cancer progression. 2020 , 17, 270-281	5

235	A Combination of Shuffled Frog-Leaping Algorithm and Genetic Algorithm for Gene Selection. 2008 , 12, 218-226	7
234	Categorization & Recognition of Lung Tumor Using Machine Learning Representations. 2019 , 15, 405-413	3
233	Identification of Marker Genes for Cancer Based on Microarrays Using a Computational Biology Approach. 2014 , 9, 140-146	4
232	Lung Cancer Classification and Gene Selection by Combining Affinity Propagation Clustering and Sparse Group Lasso. 2020 , 15, 703-712	5
231	[Neuroendocrine differentiation as a survival prognostic factor in advanced non-small cell lung cancer]. 2007 , 64, 525-9	5
230	A ground truth based comparative study on clustering of gene expression data. 2008 , 13, 3839-49	5
229	[Expression of KIF23 and Its Prognostic Role in Non-small Cell Lung Cancer: ?Analysis Based on the Data-mining of Oncomine]. 2017 , 20, 822-826	5
228	Evaluation of the TRPM protein family as potential biomarkers for various types of human cancer using public database analyses. 2020 , 20, 770-785	2
227	Diagnostic and prognostic value of the BEX family in lung adenocarcinoma. 2019 , 18, 5523-5533	3
226	Clinical and prognostic significance of in lung cancer. 2020 , 19, 3899-3906	5
225	Atonal bHLH transcription factor 1 is an important factor for maintaining the balance of cell proliferation and differentiation in tumorigenesis. 2020 , 20, 2595-2605	3
224	Identification of lung adenocarcinoma biomarkers based on bioinformatic analysis and human samples. 2020 , 43, 1437-1450	9
223	Use of Proteomics Analysis for Molecular Precision Approaches in Cancer Therapy. 2008 , 3, DTI.S649	1
222	Metasample-Based Robust Sparse Representation for Tumor Classification. 2013 , 05, 78-83	11
221	Identification of a 12-Gene Signature for Lung Cancer Prognosis through Machine Learning. 2011 , 02, 148-156	6
220	A systems biological approach to identify key transcription factors and their genomic neighborhoods in human sarcomas. 2011 , 30, 27-40	5
219	Mixed adenocarcinomas of the lung: place in new proposals in classification, mandatory for target therapy. 2010 , 134, 55-65	25
218	Diagnosis of metastatic neoplasms: molecular approaches for identification of tissue of origin. 2010 , 134, 216-24	67

217	Comprehensive analysis of the expression of the metastasis-associated gene 1 in human neoplastic tissue. 2006 , 130, 989-96	27
216	Commonly encountered difficulties in pathologic staging of lung cancer. 2007 , 131, 1016-26	24
215	An improved hybrid of SVM and SCAD for pathway analysis. 2011 , 7, 169-75	2
214	Bioinformatics analysis reveals connection of squamous cell carcinoma and adenocarcinoma of the lung. 2012 , 13, 1477-82	6
213	Evaluation of Machine Learning Algorithm Utilization for Lung Cancer Classification Based on Gene Expression Levels. 2016 , 17, 835-8	37
212	A Sparse-Modeling Based Approach for Class Specific Feature Selection. 2019 , 5, e237	7
211	A tropomyosin receptor kinase family protein, NTRK2 is a potential predictive biomarker for lung adenocarcinoma. 2019 , 7, e7125	8
210	Expression and prognostic analyses of , and in human non-small cell lung cancer. 2019 , 7, e8299	17
209	FGL2 is positively correlated with enhanced antitumor responses mediated by T cells in lung adenocarcinoma. 2020 , 8, e8654	5
208	Transcription levels and prognostic significance of the NFI family members in human cancers. 2020 , 8, e8816	9
207	Discovering Geometry in Data Arrays. 2021 , 23, 42-51	
206	DNA-methylation patterns imply a common cellular origin of virus- and UV-associated Merkel cell carcinoma. 2021 ,	1
205	Target discovery and validation. 2004 , 19-46	
204	Molecular and Cell Biology of Lung Carcinoma. 2004 , 3-27	
203	Genetische Grundlagen der Kanzerogenese. 2004 , 75-145	1
202	Solving Clinical Problems in Nutrition Research with Microarrays. 2004 , 205-235	
201	Molecular Mechanisms of Asbestos- and Silica-Induced Lung Cancer. 2004 ,	
200	Clustering and Metaclustering with Nonnegative Matrix Decompositions. 2005 , 10-22	3

- 199 Lung Cancer. **2005**, 319-340
- 198 DNA Microarrays and Computational Analysis of DNA Microarray Data in Cancer Research. **2005**, 243-262
- 197 Impact of Sample Handling and Preparation on Gene Signatures as Exemplified for Transcriptome Analysis of Peripheral Blood. **2005**, 15-30
- 196 OVA Scheme vs. Single Machine Approach in Feature Selection for Microarray Datasets. **2006**, 10-23 1
- 195 Identification of Phenotype-Defining Gene Signatures Using the Gene-Pair Matrix Based Clustering. **2006**, 106-119
- 194 Investigating the Class-Specific Relevance of Predictor Sets Obtained from DDP-Based Feature Selection Technique. **2006**, 60-70
- 193 Protein Expression Profiling for Identification of Molecular Mechanism in Human NSCLC by Mass Spectrometry. **2006**, 46, 231-236 1
- 192 Semantic Web Reasoning for Analyzing Gene Expression Profiles. **2006**, 78-89
- 191 Cancer Classification by Kernel Principal Component Self-regression. **2006**, 719-728 1
- 190 Morphologic and Molecular Classification of Human Cancer. **2006**, 10-20 0
- 189 Microarray Studies (Beyond Histology). **2007**, 313-318
- 188 Molecular Classification of Lung Adenocarcinoma by Genetic Alteration Profiling. **2007**, 47, 905-908
- 187 Molecular Pathology of the Lung Cancer -Molecular Classification of Lung Cancer Based on Expression Profile-. **2007**, 47, 909-913
- 186 Gene Expression Arrays for Pathway Analysis in Cancer Research. **2008**, 135-152
- 185 Selecting the Right Targets for Cancer Therapy. **2008**, 1-26
- 184 BIOLOGY AND EPIDEMIOLOGY OF LUNG CANCER. **2008**, 708-728 0
- 183 Microarray Analysis for Detection of Metastasis and Evaluation of Prognosis in Lung Cancers. **2008**, 48, 247-253
- 182 A Study on the Importance of Differential Prioritization in Feature Selection Using Toy Datasets. **2008**, 311-322

- 181 Fundamentals of Cancer Genomics and Proteomics. **2008**, 1925-1932
- 180 Whole-Genome Analysis of Cancer. **2009**, 1-30
- 179 The impact of gene expression microarrays in the evaluation of lung carcinoma subtypes and DNA copy number. **2008**, 132, 1562-5 3
- 178 Consensus Clustering Using Spectral Theory. **2009**, 461-468
- 177 Genomics of Lung Cancer. **2009**, 856-868
- 176 Extracellular Matrix-Mediated Drug Resistance. **2009**, 115-135 1
- 175 Microarray Studies (Beyond Histology). **2009**, 145-150
- 174 DNA Computing Hardware Design and Application to Multiclass Cancer Data. **2009**, 1072-1079 1
- 173 Bioinformatic and Computational Analysis for Genomic Medicine. **2009**, 206-225
- 172 F-score with Pareto Front Analysis for Multiclass Gene Selection. **2009**, 56-67 2
- 171 Molecular Biomarker for Lung Cancer. **2009**, 99-105
- 170 Multiclass Microarray Gene Expression Analysis Based on Mutual Dependency Models. **2009**, 46-55
- 169 Descriptive and Systematic Comparison of Clustering Methods in Microarray Data Analysis. **2009**, 22, 89-106
- 168 Introduction and Overview of Technological Advances and Predictive Assays. **2010**, 623-640
- 167 Biology of NonSmall Cell Lung Cancer. **2010**, 1080-1097 1
- 166 Molecular Pathology of Lung Cancer. **2010**, 1-25 1
- 165 Computational and Statistical Methodologies for Data Mining in Bioinformatics. **2010**, 337-350
- 164 The Use of Genetic Science in Thoracic Disease. **2010**, 669-681

¹⁶³ Mendelian Genetics, Disease Modifying or Associated Genes, and Epigenetics of Lung Disease. **2010**, 38-52

¹⁶² Tumor Microenvironment. **2010**, 27-69

1

¹⁶¹ Genomic Applications to Study Pulmonary Hypertension. **2011**, 581-590

¹⁶⁰ Inference for Censored Data and Survival Analysis. **2011**, 701-731

¹⁵⁹ Translational Research in Lung Cancer. **2011**, 793-808

¹⁵⁸ Comparative Evaluation of Set-Level Techniques in Microarray Classification. **2011**, 274-285

1

¹⁵⁷ High-Throughput Genomic and Proteomic Technologies in the Post-genomic Era. **2011**, 1463-1477

¹⁵⁶ Knowledge-Driven, Data-Assisted Integrative Pathway Analytics. **2011**, 225-247

¹⁵⁵ New Gene Subset Selection Approaches Based on Linear Separating Genes and Gene-Pairs. **2011**, 50-62

¹⁵⁴ Diagnostic, Prognostic, and Therapeutic Value of Gene Signatures in Non-Small Cell Lung Cancer. **2012**, 81-94

¹⁵³ A Hybrid of SVM and SCAD with Group-Specific Tuning Parameter for Pathway-Based Microarray Analysis. **2012**, 387-394

¹⁵² A Novel Analytical Method for Structural Characteristics of Gene Networks and its Application. **2012**, 02, 92-101

¹⁵¹ Analysis of Array Data and Clinical Validation of Array-Based Assays. **2012**, 171-210

¹⁵⁰ Markers in Lung Cancer. **2013**, 163-187

1

¹⁴⁹ Statistical Methods in Bioinformatics. **2013**, 101-149

¹⁴⁸ Dimensionality Reduction for Microarray Data Using Local Mean Based Discriminant Analysis. **2013**, 267-276

o

¹⁴⁷ Cell Cycle Control and Growth Factor Systems in Metastasis. **2013**, 57-78

¹⁴⁶ Pathology, Biomarkers, and Molecular Diagnostics. **2014**, 226-252.e6

145 Revised Classification for Adenocarcinoma. **2012**, 71-74

144 The ROS1 Receptor Family. **2015**, 641-684

143 The high expressed serum soluble neural cell adhesion molecule, a high risk factor indicating hepatic encephalopathy in hepatocellular carcinoma patients. **2015**, 16, 3131-5 2

142 Gene Expression Analysis: Current Methods. **2016**, 107-136 O

141 Hybrid Ensemble Learning Methods for Classification of Microarray Data. **2016**, 17-36

140 Semi-supervised Naive Hubness Bayesian k-Nearest Neighbor for Gene Expression Data. **2016**, 101-110

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

138 The Influence of the Global Gene Expression Shift on Downstream Analyses. **2016**, 11, e0153903 1

137 Granular Neighborhood Function for Self-organizing Map: Clustering and Gene Selection. **2017**, 135-162

136 CancerDiscover: A configurable pipeline for cancer prediction and biomarker identification using machine learning framework.

135 Metaheuristic-Based Hybrid Feature Selection Models. **2018**, 1-22

134 Matrix Entropy Driven Maximum Margin Feature Learning. **2018**, 375-387

133 Sex-biased long non-coding RNAs negatively correlated with sex-opposite protein coding gene co-expression networks in Diversity Outbred mouse liver.

132 Challenges in Developing Prediction Models for Multi-modal High-Throughput Biomedical Data. **2019**, 1056-1069

131 Different molecular signatures in lung cancer types from integrative bioinformatic analyses of RNASeq data.

130 Simplified Molecular Classification of Lung Adenocarcinomas Based on EGFR, KRAS, and TP53 Mutations.

129 G-Protein Coupled Receptors in Cancer and Targeting Strategies. **2019**, 171-196

128 [Carcinoma with unknown primary site: Morphological diagnosis]. **2019**, 81, 51-58

- 127 Supervised dimension reduction for large-scale Omics Data with censored survival outcomes under possible non-proportional hazards.
- 126 Fast Backward Iterative Laplacian Score for Unsupervised Feature Selection. **2020**, 409-420 0
- 125 Unified Methods for Feature Selection in Large-Scale Genomic Studies with Censored Survival Outcomes.
- 124 Novel Biomarkers Aim at Detecting Metastatic Sentinel Lymph Nodes in Breast Cancer. **2020**, 24, 183-91 1
- 123 A Survey of Modern Gene Expression Based Techniques for Cancer Detection and Diagnosis. **2021**, 35-50 1
- 122 A Survey of Metrics Measuring Difference for Rooted Phylogenetic Trees. **2020**, 15, 697-702 2
- 121 A Brief Overview on Intelligent Computing-Based Biological Data and Image Analysis. **2020**, 65-89
- 120 Genetic Diagnosis of Cancer by Evolutionary Fuzzy-Rough based Neural-Network Ensemble. **2020**, 645-662 1
- 119 Systematic Analysis of Spleen Tyrosine Kinase Expression and its Clinical Outcomes in Various Cancers. **2020**, 8, 95-104
- 118 Hybrid Ensemble Learning Methods for Classification of Microarray Data. **2020**, 707-725
- 117 Forward Iterative Feature Selection Based on Laplacian Score. **2020**, 381-392 0
- 116 HSD17B6 downregulation predicts poor prognosis and drives tumor progression via activating Akt signaling pathway in lung adenocarcinoma. **2021**, 7, 341 1
- 115 SMAD-6, -7 and -9 are potential molecular biomarkers for the prognosis in human lung cancer. **2020**, 20, 2633-2644 4
- 114 Knowledge-Driven, Data-Assisted Integrative Pathway Analytics. 173-194
- 113 Higher Dimensional Approach for Classification of Lung Cancer Microarray Data. **2005**, 191-205
- 112 A gene expression analysis system for medical diagnosis. **2006**, 459-466
- 111 Pathologic and Molecular Techniques Used in the Diagnosis and Treatment Planning of Sarcomas. **2006**, 13-34
- 110 Molecular Biology of Lung Cancer. **2006**, 67-80

109	Genomics. 2006 , 166-174	
108	Finding Minimal Sets of Informative Genes in Microarray Data. 2007 , 227-236	
107	Analysis of Array Data and Clinical Validation of Array-Based Assays. 2012 , 171-210	0
106	The role of SOX9 in non-small cell lung cancer progression is histopathology-selective.	
105	Deregulation of lysophosphatidic acid metabolism in oral cancer promotes cell migration via the up-regulation of COX-2. 2020 , 8, e10328	2
104	Integrative clustering methods for high-dimensional molecular data. 2014 , 3, 202-216	20
103	HITON: a novel Markov Blanket algorithm for optimal variable selection. 2003 , 21-5	44
102	Renal cell carcinoma and the use of sorafenib. 2006 , 2, 87-98	11
101	Finding disease-related genomic experiments within an international repository: first steps in translational bioinformatics. 2006 , 106-10	32
100	Data mining for gene networks relevant to poor prognosis in lung cancer via backward-chaining rule induction. 2007 , 3, 93-114	4
99	Public databases and software for the pathway analysis of cancer genomes. 2007 , 3, 379-97	6
98	Carcinoma of unknown primary origin. 2007 , 1, 229-35	18
97	An empirical study of univariate and genetic algorithm-based feature selection in binary classification with microarray data. 2007 , 2, 313-27	11
96	A Partitioning Based Adaptive Method for Robust Removal of Irrelevant Features from High-dimensional Biomedical Datasets. 2012 , 2012, 52-61	2
95	Manic fringe inhibits tumor growth by suppressing Notch3 degradation in lung cancer. 2013 , 3, 490-9	11
94	Expression of peroxiredoxin 1 and 4 promotes human lung cancer malignancy. 2014 , 4, 445-60	29
93	Highlight report: Validation of prognostic genes in lung cancer. 2014 , 13, 457-60	3
92	Silencing of advanced glycosylation and glycosylation and product-specific receptor (RAGE) inhibits the metastasis and growth of non-small cell lung cancer. 2017 , 9, 2760-2774	7

- 91 Expression of Human Kallikreins 4, 8, 10, 11 and 13 in Pleomorphic Adenomas and Mucoepidermoid Carcinomas. **2016**, 11, 334-344
- 90 The Functional Properties of Preserved Eggs: From Anti-cancer and Anti-inflammatory Aspects. **2018**, 38, 615-628 2
- 89 Prognostic and Clinicopathological Value of ZWINT Expression Levels in Patients with Lung Adenocarcinoma: A Systematic Review and Meta-analysis. **2021**, 76, e3222
- 88 A Method of Dimensionality Reduction of Analog Circuit Fault Feature. **2022**, 839-848
- 87 Paxillin Promotes Breast Tumor Collective Cell Invasion through Maintenance of Adherens Junction Integrity. **2021**, mbcE21090432 1
- 86 Mutations and clinical significance of calcium voltage-gated channel subunit alpha 1E (CACNA1E) in non-small cell lung cancer.. **2022**, 102, 102527 0
- 85 Revisiting Feature Selection with Data Complexity. **2020**, 1
- 84 Robust multi-class feature selection via l2,0-norm regularization minimization. **2022**, 26, 57-73 0
- 83 Systemic analysis the expression, prognostic, and immune infiltrates significance of MS4A family in lung cancer. **2022**, 15, 134-146
- 82 Treatment of kidney clear cell carcinoma, lung adenocarcinoma and glioblastoma cell lines with hydrogels made of DNA nanostars.. **2022**, 1
- 81 Relations Between Entropy and Accuracy Trends in Complex Artificial Neural Networks. **2022**, 452-460
- 80 FBXW7-mediated ERK3 degradation regulates the proliferation of lung cancer cells.. **2022**, 0
- 79 Analysis of the effect of NEKs on the prognosis of patients with non-small-cell lung carcinoma based on bioinformatics.. **2022**, 12, 1705 0
- 78 Robust meta-analysis for large-scale genomic experiments based on an empirical approach.. **2022**, 22, 43
- 77 Small cell lung cancer; recent advances of its biology and therapeutic perspective.. **2021**, 0
- 76 Empirical Analysis of the Effect of Resampling on Supervised Learning Algorithms in Predicting the Types of Lung Cancer on Multiclass Imbalanced Microarray Gene Expression Data. **2022**, 15-27
- 75 Analysis of prognostic and therapeutic values of drug resistance-related genes in the lung cancer microenvironment.. **2022**, 11, 339-357
- 74 The High Expression of Minichromosome Maintenance Complex Component 5 Is an Adverse Prognostic Factor in Lung Adenocarcinoma.. **2022**, 2022, 4338793 0

73	SNRPD1/E/F/G Serve as Potential Prognostic Biomarkers in Lung Adenocarcinoma.. 2022 , 13, 813285		1
72	High-dimensional correlation matrix estimation for general continuous data with Bagging technique. 1		1
71	Different thresholding methods on Nearest Shrunken Centroid algorithm. 1-17		
70	Decoding clinical biomarker space of COVID-19: Exploring matrix factorization-based feature selection methods.. <i>Computers in Biology and Medicine</i> , 2022 , 146, 105426	7	5
69	Impact of Epithelial Cell Shedding on Intestinal Homeostasis.. 2022 , 23,		1
68	YBX1 Enhances Metastasis and Stemness by Transcriptionally Regulating MUC1 in Lung Adenocarcinoma.. <i>Frontiers in Oncology</i> , 2021 , 11, 702491	53	0
67	Protumor Effects of Histone H3-H4 Chaperone Antisilencing Feature 1B Gene on Lung Adenocarcinoma: In Silico and Analyses.. 2021 , 2021, 5005459		1
66	Enhancing the generalization of feature construction using genetic programming for imbalanced data with augmented non-overlap degree. 2021 ,		
65	The histologic phenotype of lung cancers is associated with transcriptomic features rather than genomic characteristics. 2021 , 12, 7081		1
64	A novel ensemble feature selection method through Type I fuzzy. 2022 ,		
63	H3K4 demethylase KDM5B regulates cancer cell identity and epigenetic plasticity.. 2022 ,		0
62	Systems biology of cancer progression. 1-6		
61	Deregulated signaling networks in lung cancer. 421-442		
60	Cancer pharmacogenomics: challenges, promises, and its application to cancer drug discovery. 499-517		
59	Table_1.DOCX. 2020 ,		
58	Table_2.DOCX. 2020 ,		
57	Image_1.tif. 2019 ,		
56	Image_2.tif. 2019 ,		

55	Image_3.tif. 2019 ,		
54	Image_4.tif. 2019 ,		
53	Image_5.tif. 2019 ,		
52	Comprehensive Landscape of STEAP Family Members Expression in Human Cancers: Unraveling the Potential Usefulness in Clinical Practice Using Integrated Bioinformatics Analysis. 2022 , 7, 64	2	
51	Human Tissue Kallikreins: Physiologic Roles and Applications in Cancer. 2004 , 2, 257-280		241
50	Frequent HIN-1 Promoter Methylation and Lack of Expression in Multiple Human Tumor Types. 2004 , 2, 489-494		33
49	SDDSMOTE:Synthetic Minority Oversampling Technique based on Sample Density Distribution for Enhanced Classification on Imbalanced Microarray Data. 2022 ,		
48	Rethinking Embedded Unsupervised Feature Selection: A Simple Joint Approach. 2022 , 1-1		0
47	Comprehensive analysis of the prognostic value and immune implications of the TTK gene in lung adenocarcinoma: a meta-analysis and bioinformatics analysis. <i>Animal Cells and Systems</i> , 1-11	2.3	
46	G-CSF / GM-CSF -induced hematopoietic dysregulation in the progression of solid tumors. <i>FEBS Open Bio</i> ,	2.7	1
45	An Integrated Study of User Acceptance and Resistance on Voice Commerce. <i>International Journal of Innovation and Technology Management</i> ,	1.1	
44	Synergy Mechanisms of Rhizoma Paradis Saponins on Non-small Cell Lung Cancer: Segmented Solid Phase Extraction, Bioactivity Screening, and Network Pharmacology. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2022 , 22,	2.2	
43	A Comprehensive Survey of Recent Hybrid Feature Selection Methods in Cancer Microarray Gene Expression Data. <i>IEEE Access</i> , 2022 , 1-1	3.5	1
42	Stem Cell Theory of Cancer: Origin of Metastasis and Sub-clonality. <i>Seminars in Diagnostic Pathology</i> , 2022 ,	4.3	
41	SGAClust: Semi-supervised Graph Attraction Clustering of gene expression data. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2022 , 11,	1.6	
40	Incorporating Measurement Error in Astronomical Object Classification. <i>Astronomical Journal</i> , 2022 , 164, 6	4.9	1
39	Genome-wide methylation profiling reveals differentially methylated genes in blood DNA of small-cell lung cancer patients. <i>Precision Clinical Medicine</i> ,	6.7	
38	Optimal Gene Selection and Classification of Microarray Data Using Fuzzy Min-Max Neural Network with LASSO. <i>Lecture Notes in Networks and Systems</i> , 2022 , 777-784	0.5	0

37	Systematic analysis of expression profiles of HMGB family members for prognostic application in non-small cell lung cancer. <i>Frontiers in Molecular Biosciences</i> , 9,	5.6	o
36	An ensemble framework for microarray data classification based on feature subspace partitioning. <i>Computers in Biology and Medicine</i> , 2022 , 105820	7	1
35	Neuronal survival factor VGF promotes chemoresistance and predicts poor prognosis in lung cancers with neuroendocrine feature. <i>International Journal of Cancer</i> ,	7.5	
34	Validation and analysis of expression, prognosis and immune infiltration of WNT gene family in non-small cell lung cancer. <i>Frontiers in Oncology</i> , 12,	5.3	o
33	Interlaboratory Comparability Study of Cancer Gene Expression Analysis Using Oligonucleotide Microarrays. 2005 , 11, 565-572		25
32	Translational Research in Lung Cancer. 2022 ,		o
31	Recursive integration of synergised graph representations of multi-omics data for cancer subtypes identification. 2022 , 12,		o
30	Immune depletion of the methylated phenotype of colon cancer is closely related to resistance to immune checkpoint inhibitors. 13,		o
29	Comprehensive bioinformatics analysis on exportins in lung adenocarcinoma and lung squamous cell carcinoma.		o
28	A graph based preordonnances theoretic supervised feature selection in high dimensional data. 2022 , 257, 109899		o
27	Prognostic and Immunological Role of STK38 across Cancers: Friend or Foe?. 2022 , 23, 11590		1
26	Molecular Biology, Genetics, and Translational Models of Human Cancer. 1-34		o
25	Cancer Genomics and Evolution. 1-30		o
24	NDR1 activates CD47 transcription by increasing protein stability and nuclear location of ASCL1 to enhance cancer stem cell properties and evasion of phagocytosis in small cell lung cancer. 2022 , 39,		o
23	Association of the Timeless Gene with Prognosis and Clinical Characteristics of Human Lung Cancer. 2022 , 12, 2681		o
22	Circadian rhythm-related factors of PER and CRY family genes function as novel therapeutic targets and prognostic biomarkers in lung adenocarcinoma.		o
21	LINC02126 is a potential diagnostic, prognostic and immunotherapeutic target for lung adenocarcinoma. 2022 , 22,		o
20	SAMHD1 deacetylation by SIRT1 promotes DNA end resection by facilitating DNA binding at double-strand breaks. 2022 , 13,		o

19	The Future of Clinical Cancer Management: One Tumor, One Chip. 2003 , 69, 41-44	4
18	A generic model-free feature screening procedure for ultra-high dimensional data with categorical response. 2023 , 229, 107269	0
17	Cancer Segmentation by Entropic Analysis of Ordered Gene Expression Profiles. 2022 , 24, 1744	0
16	SMOTE-LASSO-DeepNet Framework for Cancer Subtyping from Gene Expression Data. 2022 ,	0
15	ST3GAL5 -catalyzed gangliosides inhibit TGF- β -induced epithelial-mesenchymal transition via TBI degradation.	1
14	A high-dimensional feature selection method based on modified Gray Wolf Optimization. 2023 , 110031	0
13	Memetic micro-genetic algorithms for cancer data classification. 2023 , 17, 200173	2
12	Penetrating Exploration of Prognostic Correlations of the FKBP Gene Family with Lung Adenocarcinoma. 2023 , 13, 49	0
11	Gene Expression Profiles in Cancers and Their Therapeutic Implications. 2023 , 29, 9-14	0
10	A review and comparative study of cancer detection using machine learning: SBERT and SimCSE application. 2023 , 24,	0
9	Learning from high dimensional data based on weighted feature importance in decision tree ensembles.	0
8	A unified view of feature selection based on Hilbert-Schmidt independence criterion. 2023 , 236, 104807	0
7	A New Evolutionary Ensemble Learning of Multimodal Feature Selection from Microarray Data.	0
6	The Hurdle of Precision Medicine in Cancer Immunotherapy: Personalization Now or Then?. 2023 , 1-32	0
5	Multimodal feature selection from microarray data based on Dempster-Shafer evidence fusion.	0
4	The Role of Mammalian STK38 in DNA Damage Response and Targeting for Radio-Sensitization. 2023 , 15, 2054	0
3	Anchoring Filament Protein Ladinin-1 is an Immunosuppressive Microenvironment and Cold Tumor Correlated Prognosticator in Lung Adenocarcinoma.	0
2	Nanotechnology-empowered lung cancer therapy: From EMT role in cancer metastasis to application of nanoengineered structures for modulating growth and metastasis. 2023 , 115942	0

- 1 Iterative constraint score based on hypothesis margin for semi-supervised feature selection. **2023**, 110577 ○