Steven A Eschrich

List of Publications by Year in descending order

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179 11,663 44
papers citations h-index

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188 188 all docs docs citations

188 times ranked 17920 citing authors

#	Article	IF	CITATIONS
1	Characterization of epigenomic alterations in HPV16+ head and neck squamous cell carcinomas. Cancer Epidemiology Biomarkers and Prevention, 2022, , cebp.EPI-21-0922-A.2021.	2.5	6
2	The Radiosensitivity Index Gene Signature Identifies Distinct Tumor Immune Microenvironment Characteristics Associated With Susceptibility to Radiation Therapy. International Journal of Radiation Oncology Biology Physics, 2022, 113, 635-647.	0.8	11
3	Volume doubling time and radiomic features predict tumor behavior of screen-detected lung cancers. Cancer Biomarkers, 2022, 33, 489-501.	1.7	4
4	Personalizing Radiotherapy Prescription Dose Using Genomic Markers of Radiosensitivity and Normal Tissue Toxicity in NSCLC. Journal of Thoracic Oncology, 2021, 16, 428-438.	1.1	32
5	Metabolic Changes Are Associated with Melphalan Resistance in Multiple Myeloma. Journal of Proteome Research, 2021, 20, 3134-3149.	3.7	11
6	Hypoxia-Related Radiomics and Immunotherapy Response: A Multicohort Study of Non-Small Cell Lung Cancer. JNCI Cancer Spectrum, 2021, 5, pkab048.	2.9	23
7	Enabling Precision Medicine in Cancer Care Through a Molecular Data Warehouse: The Moffitt Experience. JCO Clinical Cancer Informatics, 2021, 5, 561-569.	2.1	7
8	Effects of long-term norepinephrine treatment on normal immortalized ovarian and fallopian tube cells. Scientific Reports, 2021, 11, 14334.	3.3	1
9	Pan-cancer prediction of radiotherapy benefit using genomic-adjusted radiation dose (GARD): a cohort-based pooled analysis. Lancet Oncology, The, 2021, 22, 1221-1229.	10.7	76
10	Primary tumors from mucosal barrier organs drive unique eosinophil infiltration patterns and clinical associations. Oncolmmunology, 2021, 10, 1859732.	4.6	14
11	Tumor-immune ecosystem dynamics define an individual Radiation Immune Score to predict pan-cancer radiocurability. Neoplasia, 2021, 23, 1110-1122.	5.3	15
12	Managing a Large-Scale Multiomics Project: A Team Science Case Study in Proteogenomics. Methods in Molecular Biology, 2021, 2194, 187-221.	0.9	O
13	Genome-wide host methylation profiling of anal and cervical carcinoma. PLoS ONE, 2021, 16, e0260857.	2.5	9
14	GMSimpute: a generalized two-step Lasso approach to impute missing values in label-free mass spectrum analysis. Bioinformatics, 2020, 36, 257-263.	4.1	13
15	Using the Radiosensitivity Index (RSI) to Predict Pelvic Failure in Endometrial Cancer TreatedÂWithÂAdjuvant Radiation Therapy. International Journal of Radiation Oncology Biology Physics, 2020, 106, 496-502.	0.8	24
16	LC-HRMS of derivatized urinary estrogens and estrogen metabolites in postmenopausal women. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2020, 1154, 122288.	2.3	5
17	Utilizing the Genomic Immune Profile to Predict Progression in Melanoma. International Journal of Radiation Oncology Biology Physics, 2020, 108, E5-E6.	0.8	O
18	The Immune Cell Composition in Primary Lung Squamous Cell Carcinomas Influences Patterns of Recurrence and Survival. International Journal of Radiation Oncology Biology Physics, 2020, 108, e558-e559.	0.8	0

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19	Utilizing Immune Profiles to Predict Pelvic Failure in Endometrial Cancer. International Journal of Radiation Oncology Biology Physics, 2020, 108, S52-S53.	0.8	O
20	Genomic and Radiosensitivity Analyses of Patient-Matched Primary and Metastatic Tissues in Colon, Melanoma, Ovarian, and Lung Cancers. International Journal of Radiation Oncology Biology Physics, 2020, 108, S6.	0.8	0
21	Empirically-derived synthetic populations to mitigate small sample sizes. Journal of Biomedical Informatics, 2020, 105, 103408.	4.3	8
22	Peritumoral and intratumoral radiomic features predict survival outcomes among patients diagnosed in lung cancer screening. Scientific Reports, 2020, 10, 10528.	3.3	46
23	Metabolomics of primary cutaneous melanoma and matched adjacent extratumoral microenvironment. PLoS ONE, 2020, 15, e0240849.	2.5	14
24	Abstract C093: An interactive resource to probe ancestry in cancer cell lines. , 2020, , .		0
25	Abstract 3226: Facilitating personalized medicine with cloud-based storage and analytics. , 2020, , .		0
26	Abstract LB-359: Gene expression profile and tumor infiltrating lymphocytes in Hispanic women with breast cancer. , 2020 , , .		0
27	Abstract 5806: Hypoxia-related radiomics predict checkpoint blockade immunotherapy response of non-small cell lung cancer patients. , 2020, , .		1
28	Proteogenomic landscape of squamous cell lung cancer. Nature Communications, 2019, 10, 3578.	12.8	84
29	Utilizing the genomically adjusted radiation dose (GARD) to personalize adjuvant radiotherapy in triple negative breast cancer management. EBioMedicine, 2019, 47, 163-169.	6.1	38
30	Divergent Polypharmacology-Driven Cellular Activity of Structurally Similar Multi-Kinase Inhibitors through Cumulative Effects on Individual Targets. Cell Chemical Biology, 2019, 26, 1240-1252.e11.	5.2	15
31	EPB41L5 is Associated With the Metastatic Potential of Low-grade Pancreatic Neuroendocrine Tumors. Cancer Genomics and Proteomics, 2019, 16, 309-318.	2.0	4
32	Modeling Variability in Radiosensitivity and Tumor Immune Contexture to Personalize Radiotherapy. International Journal of Radiation Oncology Biology Physics, 2019, 105, S123-S124.	0.8	1
33	Proteometabolomics of Melphalan Resistance in Multiple Myeloma. Methods in Molecular Biology, 2019, 1996, 273-296.	0.9	6
34	An Interactive Resource to Probe Genetic Diversity and Estimated Ancestry in Cancer Cell Lines. Cancer Research, 2019, 79, 1263-1273.	0.9	43
35	Inhibition of the FAD containing ER oxidoreductin 1 (Ero1) protein by EN-460 as a strategy for treatment of multiple myeloma. Bioorganic and Medicinal Chemistry, 2019, 27, 1479-1488.	3.0	28
36	Transforming growth factor \hat{l}^2 -induced epithelial-to-mesenchymal signature predicts metastasis-free survival in non-small cell lung cancer. Oncotarget, 2019, 10, 810-824.	1.8	22

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37	Integrated Multi-Level Omics to Characterize Bortezomib Resistance in Multiple Myeloma. Blood, 2019, 134, 5534-5534.	1.4	O
38	Expression of CAS/CSE1L, the Cellular Apoptosis Susceptibility Protein, Correlates With Neoplastic Progression in Barrett's Esophagus. Applied Immunohistochemistry and Molecular Morphology, 2018, 26, 552-556.	1.2	7
39	Utilizing the Genomically Adjusted Radiation Dose (GARD) to Model Radiation Dose Personalization. International Journal of Radiation Oncology Biology Physics, 2018, 102, S136.	0.8	O
40	Radiosensitivity of Lung Metastases by Primary Histology and Implications for Stereotactic Body Radiation Therapy Using the Genomically Adjusted Radiation Dose. Journal of Thoracic Oncology, 2018, 13, 1121-1127.	1.1	59
41	Abstract 2708: Imputation-free analysis of high throughput TMT proteomics of $116\ \text{lung}$ squamous samples. , $2018,$, .		0
42	Proteometabolomics of Melphalan Resistance in Multiple Myeloma. Blood, 2018, 132, 5619-5619.	1.4	0
43	Relative protein quantification and accessible biology in lung tumor proteomes from four LCâ€MS/MS discovery platforms. Proteomics, 2017, 17, 1600300.	2.2	15
44	Regional Radiation Therapy Impacts Outcome for Node-Positive Cutaneous Melanoma. Journal of the National Comprehensive Cancer Network: JNCCN, 2017, 15, 473-482.	4.9	25
45	The radiosensitivity of brain metastases based upon primary histology utilizing a multigene index of tumor radiosensitivity. Neuro-Oncology, 2017, 19, 1145-1146.	1.2	20
46	A genome-based model for adjusting radiotherapy dose (GARD): a retrospective, cohort-based study. Lancet Oncology, The, 2017, 18, 202-211.	10.7	377
47	Tumour radiosensitivity is associated with immune activation in solid tumours. European Journal of Cancer, 2017, 84, 304-314.	2.8	44
48	Characteristics and Validation Techniques for PCA-Based Gene-Expression Signatures. International Journal of Genomics, 2017, 2017, 1-13.	1.6	19
49	Evaluating somatic tumor mutation detection without matched normal samples. Human Genomics, 2017, 11, 22.	2.9	42
50	Integrating Biological Covariates into Gene Expression-Based Predictors of Radiation Sensitivity. International Journal of Genomics, 2017, 2017, 1-9.	1.6	6
51	Use of the Total Cancer Care System to Enrich Screening for CD30-Positive Solid Tumors for Patient Enrollment Into a Brentuximab Vedotin Clinical Trial: A Pilot Study to Evaluate Feasibility. JMIR Research Protocols, 2017, 6, e45.	1.0	6
52	Methylomic classifiers of anal cancer outcomes: An NRG Oncology / RTOG 98-11 tissue study Journal of Clinical Oncology, 2017, 35, 588-588.	1.6	0
53	Abstract 206: Proteogenomic classifications and outcome in squamous cell carcinoma of the lung. , 2017, , .		0
54	Abstract 221: Integrated functional proteomics of MET/VEGFR inhibitors reveals complex mechanism of action of foretinib in NSCLC., 2017,,.		0

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55	Abstract 1565: OnPLS-based integrative proteogenomics analysis of lung squamous cell cancer. , 2017, , .		O
56	Abstract 205: Underlying mechanisms of genome-proteome discordance in squamous cell lung cancer. , 2017, , .		0
57	Activity-Based Proteomics Reveals Heterogeneous Kinome and ATP-Binding Proteome Responses to MEK Inhibition in KRAS Mutant Lung Cancer. Proteomes, 2016, 4, 16.	3.5	5
58	ZEB1 Mediates Acquired Resistance to the Epidermal Growth Factor Receptor-Tyrosine Kinase Inhibitors in Non-Small Cell Lung Cancer. PLoS ONE, 2016, 11, e0147344.	2.5	81
59	Association Between Computed Tomographic Features and Kirsten Rat Sarcoma Viral Oncogene Mutations in Patients With Stage I Lung Adenocarcinoma and Their Prognostic Value. Clinical Lung Cancer, 2016, 17, 271-278.	2.6	17
60	Radiosensitivity Differences Between Liver Metastases Based on Primary Histology Suggest Implications for Clinical Outcomes After Stereotactic Body Radiation Therapy. International Journal of Radiation Oncology Biology Physics, 2016, 95, 1399-1404.	0.8	127
61	Differences in the Radiosensitivity Index (RSI) Between Lung Metastases Based Upon Primary Histology. International Journal of Radiation Oncology Biology Physics, 2016, 96, S68.	0.8	1
62	APOSTL: An Interactive Galaxy Pipeline for Reproducible Analysis of Affinity Proteomics Data. Journal of Proteome Research, 2016, 15, 4747-4754.	3.7	16
63	Knockdown of CSE1L Gene in Colorectal Cancer Reduces Tumorigenesis inÂVitro. American Journal of Pathology, 2016, 186, 2761-2768.	3.8	24
64	Phosphoproteomics Reveals MAPK Inhibitors Enhance MET- and EGFR-Driven AKT Signaling in <i>KRAS</i> -Mutant Lung Cancer. Molecular Cancer Research, 2016, 14, 1019-1029.	3.4	53
65	Sull45 Expression of CAS/CSElL, the Cellular Apoptosis Susceptibility Protein, Correlates With Neoplastic Progression in Barrett's Esophagus. Gastroenterology, 2016, 150, S482-S483.	1.3	1
66	Differential association of STK11 and TP53 with KRAS mutation-associated gene expression, proliferation and immune surveillance in lung adenocarcinoma. Oncogene, 2016, 35, 3209-3216.	5.9	260
67	Differences in Patient Outcomes of Prevalence, Interval, and Screen-Detected Lung Cancers in the CT Arm of the National Lung Screening Trial. PLoS ONE, 2016, 11, e0159880.	2.5	46
68	Early2 factor (E2F) deregulation is a prognostic and predictive biomarker in lung adenocarcinoma. Oncotarget, 2016, 7, 82254-82265.	1.8	6
69	Radiosensitivity differences between liver metastases based on primary histology suggest implications for clinical outcomes following SBRT Journal of Clinical Oncology, 2016, 34, 239-239.	1.6	2
70	Genomically adjusted radiation dose to predict for survival with adjuvant radiation in resectable pancreatic cancer Journal of Clinical Oncology, 2016, 34, 240-240.	1.6	0
71	Abstract LB-140: Scaling discovery proteomics to large lung cancer cohorts using data independent acquisition. , $2016, , .$		0
72	Tolerance Associated Gene Expression following Allogeneic Hematopoietic Cell Transplantation. PLoS ONE, 2015, 10, e0117001.	2.5	9

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73	Quantitative Computed Tomographic Descriptors Associate Tumor Shape Complexity and Intratumor Heterogeneity with Prognosis in Lung Adenocarcinoma. PLoS ONE, 2015, 10, e0118261.	2.5	207
74	Differences Between Colon Cancer Primaries and Metastases Using a Molecular Assay for Tumor Radiation Sensitivity Suggest Implications for Potential Oligometastatic SBRT Patient Selection. International Journal of Radiation Oncology Biology Physics, 2015, 92, 837-842.	0.8	82
75	Semiquantitative Computed Tomography Characteristics for Lung Adenocarcinoma and Their Association With Lung Cancer Survival. Clinical Lung Cancer, 2015, 16, e141-e163.	2.6	43
76	Radiosensitivity index predicts for survival with adjuvant radiation in resectable pancreatic cancer. Radiotherapy and Oncology, 2015, 117, 159-164.	0.6	75
77	Integration of a Radiosensitivity Molecular Signature Into the Assessment of Local Recurrence Risk in Breast Cancer. International Journal of Radiation Oncology Biology Physics, 2015, 93, 631-638.	0.8	102
78	Differences Between Breast Cancer Primaries and Metastases Utilizing a Molecular Assay for Tumor Radiosensitivity Suggest Implications for Radiation Dose Selection. International Journal of Radiation Oncology Biology Physics, 2015, 93, S138-S139.	0.8	0
79	Differences between colon cancer primaries and metastases utilizing a molecular assay for tumor radiosensitivity and implications for potential oligometastatic SBRT patient selection Journal of Clinical Oncology, 2015, 33, 569-569.	1.6	1
80	A Pilot Proteogenomic Study with Data Integration Identifies MCT1 and GLUT1 as Prognostic Markers in Lung Adenocarcinoma. PLoS ONE, 2015, 10, e0142162.	2.5	31
81	The radiosensitivity index predicts for overall survival in glioblastoma. Oncotarget, 2015, 6, 34414-34422.	1.8	100
82	Radiosensensitivity index prognostic for survival with adjuvant radiation in resectable pancreatic cancer Journal of Clinical Oncology, 2015, 33, 398-398.	1.6	0
83	Abstract 3752: Integrating proteomics and metabolomics characterizes active pathways and potential drug targets in small cell lung cancer. , 2015, , .		1
84	Abstract 1817: Quantitative proteomics identifies unique signaling phenotypes in NSCLC., 2015,,.		0
85	Expanding Epigenomics to Archived FFPE Tissues: An Evaluation of DNA Repair Methodologies. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2622-2631.	2.5	23
86	Quantification of peptides from immunoglobulin constant and variable regions by LCâ€MRM MS for assessment of multiple myeloma patients. Proteomics - Clinical Applications, 2014, 8, 783-795.	1.6	33
87	Epigenomic Characterization of Locally Advanced Anal Cancer. Diseases of the Colon and Rectum, 2014, 57, 941-957.	1.3	14
88	Test–Retest Reproducibility Analysis of Lung CT Image Features. Journal of Digital Imaging, 2014, 27, 805-823.	2.9	216
89	A Molecular Signature of Radiosensitivity (RSI) is an RT-specific Biomarker in Prostate Cancer. International Journal of Radiation Oncology Biology Physics, 2014, 90, S157.	0.8	11
90	Radiosensensitivity Index Shows Promise for Predicting Outcomes With Adjuvant Radiation in Resected Pancreatic Cancer Patients. International Journal of Radiation Oncology Biology Physics, 2014, 90, S174.	0.8	5

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91	Differences Between Colon Cancer Primaries and Metastases Utilizing a Molecular Assay for Tumor Radiosensitivity Suggest Implications for Potential Oligometastatic SBRT Patient Selection. International Journal of Radiation Oncology Biology Physics, 2014, 90, S20.	0.8	1
92	Abstract 3250: Survival of patients with incident lung cancer following screening by computed tomography in the National Lung Screening Trial. , 2014, , .		1
93	Abstract 914: Development of a prognostic and predictive E2F signature in formalin-fixed, paraffin-embedded early-stage non-small cell lung cancer samples. , 2014, , .		0
94	Abstract 1614: Kinases in lung squamous cell carcinoma and inhibitor matching using quantitative activity-based protein profiling. , 2014, , .		0
95	Abstract 4159: Characterization of three recurring STK11/LKB1 mutants in lung adenocarcinoma. , 2014, , .		0
96	Abstract A31: Activity-based protein profiling reveals adaptive response to pharmacological MEK inhibition in KRAS mutant non-small cell lung cancer. , 2014, , .		0
97	Computational methods and opportunities for phosphorylation network medicine. Translational Cancer Research, 2014, 3, 266-278.	1.0	8
98	Iterative rank-order normalization of gene expression microarray data. BMC Bioinformatics, 2013, 14, 153.	2.6	103
99	Development and application of a novel metric to assess effectiveness of biomedical data. BMJ Open, 2013, 3, e003220.	1.9	1
100	Perturbation of the mutated EGFR interactome identifies vulnerabilities and resistance mechanisms. Molecular Systems Biology, 2013, 9, 705.	7.2	42
101	Dissection of TBK1 signaling via phosphoproteomics in lung cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12414-12419.	7.1	88
102	Personalized medicine for radiation therapy. Personalized Medicine, 2013, 10, 107-110.	1.5	0
103	42. Epigenomic profiling of anal cancer: does size matter? An RTOG 98-11 specimen study. Sexual Health, 2013, 10, 590.	0.9	0
104	Abstract A61: Characterization of KRAS-driven survival signaling networks via phosphoproteomics in lung cancer , $2013, \dots$		0
105	Validation of a Radiosensitivity Molecular Signature in Breast Cancer. Clinical Cancer Research, 2012, 18, 5134-5143.	7.0	174
106	The Metabolomic Signature of Malignant Glioma Reflects Accelerated Anabolic Metabolism. Cancer Research, 2012, 72, 5878-5888.	0.9	147
107	ITERATIVE FEATURE PERTURBATION AS A GENE SELECTOR FOR MICROARRAY DATA. International Journal of Pattern Recognition and Artificial Intelligence, 2012, 26, 1260003.	1.2	26
108	Phosphoproteomics Identifies Driver Tyrosine Kinases in Sarcoma Cell Lines and Tumors. Cancer Research, 2012, 72, 2501-2511.	0.9	107

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109	12-Chemokine Gene Signature Identifies Lymph Node-like Structures in Melanoma: Potential for Patient Selection for Immunotherapy?. Scientific Reports, 2012, 2, 765.	3.3	307
110	Radiomics: the process and the challenges. Magnetic Resonance Imaging, 2012, 30, 1234-1248.	1.8	1,675
111	A Smad4-modulated Wnt target gene expression profile identifies high-risk colorectal cancer patients. Journal of the American College of Surgeons, 2012, 215, S30-S31.	0.5	0
112	Targeting CSE1L in colorectal cancer. Journal of the American College of Surgeons, 2012, 215, S127.	0.5	0
113	Smad4-Mediated Signaling Inhibits Intestinal Neoplasia by Inhibiting Expression of \hat{l}^2 -Catenin. Gastroenterology, 2012, 142, 562-571.e2.	1.3	156
114	Informatics methods to enable sharing of quantitative imaging research data. Magnetic Resonance Imaging, 2012, 30, 1249-1256.	1.8	17
115	DNA Methylation Profiling across the Spectrum of HPV-Associated Anal Squamous Neoplasia. PLoS ONE, 2012, 7, e50533.	2.5	19
116	Abstract IA2: Network models in oncogene-addicted lung cancer. Clinical Cancer Research, 2012, 18, IA2-IA2.	7.0	0
117	Abstract 678: Validation of a radiosensitivity molecular signature in breast cancer. , 2012, , .		1
118	Abstract 3395: $TGF\hat{l}^2$ response signature in non-small cell lung carcinoma. , 2012, , .		0
119	Mass Spectrometry Mapping of Epidermal Growth Factor Receptor Phosphorylation Related to Oncogenic Mutations and Tyrosine Kinase Inhibitor Sensitivity. Journal of Proteome Research, 2011, 10, 305-319.	3.7	56
120	Claudin-1 Up-regulates the Repressor ZEB-1 to Inhibit E-Cadherin Expression in Colon Cancer Cells. Gastroenterology, 2011, 141, 2140-2153.	1.3	143
121	Necdin, a Negative Growth Regulator, Is a Novel STAT3 Target Gene Down-Regulated in Human Cancer. PLoS ONE, 2011, 6, e24923.	2.5	16
122	Claudin-2 expression increases tumorigenicity of colon cancer cells: role of epidermal growth factor receptor activation. Oncogene, 2011, 30, 3234-3247.	5.9	133
123	Evolutionary computation with noise perturbation and cluster analysis to discover biomarker sets. Procedia Computer Science, 2011, 6, 153-158.	2.0	2
124	Partial Least Squares (PLS) Applied to Medical Bioinformatics. Procedia Computer Science, 2011, 6, 273-278.	2.0	26
125	A database of reaction monitoring mass spectrometry assays for elucidating therapeutic response in cancer. Proteomics - Clinical Applications, 2011, 5, 383-396.	1.6	48
126	Procedure for stability analysis of gene selection from cross-site gene expression data., 2011,,.		0

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127	BAD Phosphorylation Determines Ovarian Cancer Chemosensitivity and Patient Survival. Clinical Cancer Research, 2011, 17, 6356-6366.	7.0	97
128	Monitoring a Nuclear Factor-l̂ºB Signature of Drug Resistance in Multiple Myeloma. Molecular and Cellular Proteomics, 2011, 10, M110.005520.	3.8	30
129	Abstract 5111: Integrative phospho-proteomic and genomic analyses identify AXL as a potential biomarker and therapeutic target for NRAS-mutated melanoma. , $2011, , .$		7
130	BVES regulates EMT in human corneal and colon cancer cells and is silenced via promoter methylation in human colorectal carcinoma. Journal of Clinical Investigation, 2011, 121, 4056-4069.	8.2	60
131	Abstract 1919: Baseline characteristics of colorectal cancer patients enrolled in the colorectal cancer outcomes, prognosis and epidemiology cohort (The COPE) study., 2011,,.		0
132	Abstract 1679: Increased expression of hCAS/CSE1L in colorectal cancer: Correlation with tumor progression. , 2011, , .		0
133	Abstract 1627: Proteome-wide analysis of echinoderm microtubule associated protein like 4 – anaplastic lymphoma kinase (EML4-ALK) network in lung cancer. , 2011, , .		0
134	Discovery and Validation of a Novel Set of Putative Progression Markers in Well-Differentiated Primary Pancreatic Endocrine Carcinomas. Pancreas, 2010, 39, 277-278.	1.1	1
135	Gene Expression Profiling of Colorectal Mucinous Adenocarcinomas. Diseases of the Colon and Rectum, 2010, 53, 936-943.	1.3	40
136	Methods for investigation of targeted kinase inhibitor therapy using chemical proteomics and phosphorylation profiling. Biochemical Pharmacology, 2010, 80, 739-747.	4.4	15
137	HDAC inhibitors regulate claudin-1 expression in colon cancer cells through modulation of mRNA stability. Oncogene, 2010, 29, 305-312.	5.9	83
138	A chemical and phosphoproteomic characterization of dasatinib action in lung cancer. Nature Chemical Biology, 2010, 6, 291-299.	8.0	254
139	Characterizing Tyrosine Phosphorylation Signaling in Lung Cancer Using SH2 Profiling. PLoS ONE, 2010, 5, e13470.	2.5	33
140	Experimentally Derived Metastasis Gene Expression Profile Predicts Recurrence and Death in Patients With Colon Cancer. Gastroenterology, 2010, 138, 958-968.	1.3	576
141	Filtering for improved gene selection on microarray data. , 2010, , .		2
142	Biomarkers to Discern Transplantation Tolerance after Allogeneic Hematopoietic Cell Transplantation. Biology of Blood and Marrow Transplantation, 2010, 16, 729-738.	2.0	7
143	Quantification of \hat{l}^2 -Catenin Signaling Components in Colon Cancer Cell Lines, Tissue Sections, and Microdissected Tumor Cells using Reaction Monitoring Mass Spectrometry. Journal of Proteome Research, 2010, 9, 4215-4227.	3.7	45
144	Abstract 2961: Expression of ZEB1, an E-cadherin repressor correlates with poor patient survival in colon cancer and mediates claudin-1 dependent repression of E-cadherin., 2010,,.		0

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145	Abstract 3076: BVES, a novel adhesion molecule, acts as tumor modifier through modulation of tight-junction-associated signaling. , 2010 , , .		O
146	Abstract 4636: Increased expression of CSE1L/hCAS in colorectal cancer: Correlation with tumor progression. , 2010 , , .		0
147	Metastasis-Associated Gene Expression Changes Predict Poor Outcomes in Patients with Dukes Stage B and C Colorectal Cancer. Clinical Cancer Research, 2009, 15, 7642-7651.	7.0	395
148	A Gene Expression Model of Intrinsic Tumor Radiosensitivity: Prediction of Response and Prognosis After Chemoradiation. International Journal of Radiation Oncology Biology Physics, 2009, 75, 489-496.	0.8	283
149	Systems Biology Modeling of the Radiation Sensitivity Network: A Biomarker Discovery Platform. International Journal of Radiation Oncology Biology Physics, 2009, 75, 497-505.	0.8	228
150	Gene Expression Profiles as Predictors of Poor Outcomes in Stage II Colorectal Cancer: A Systematic Review and Meta-analysis. Clinical Colorectal Cancer, 2009, 8, 207-214.	2.3	27
151	Removal of Hybridization and Scanning Noise From Microarrays. IEEE Transactions on Nanobioscience, 2009, 8, 210-218.	3.3	7
152	The gene expression profiles of primary and metastatic melanoma yields a transition point of tumor progression and metastasis. BMC Medical Genomics, 2008, 1, 13.	1.5	425
153	Downâ€regulation of Baxâ€interacting factorâ€1 in colorectal adenocarcinoma. Cancer, 2008, 113, 2665-2670.	4.1	80
154	Insig2 is associated with colon tumorigenesis and inhibits Baxâ€mediated apoptosis. International Journal of Cancer, 2008, 123, 273-282.	5.1	15
155	Gene expression–based survival prediction in lung adenocarcinoma: a multi-site, blinded validation study. Nature Medicine, 2008, 14, 822-827.	30.7	1,015
156	A Predictive Risk Probability Approach for Microarray Data with Survival as an Endpoint. Journal of Biopharmaceutical Statistics, 2008, 18, 841-852.	0.8	1
157	Toward a measure of classification complexity in gene expression signatures. , 2008, 2008, 5704-7.		3
158	IPEP: an <i>in silico</i> tool to examine proteolytic peptides for mass spectrometry. Bioinformatics, 2008, 24, 2801-2802.	4.1	11
159	Towards a framework for analysis of biophotonic images of mouse models of cancer. , 2008, 2008, 3079-82.		2
160	Feature selection for microarray data by AUC analysis. Conference Proceedings IEEE International Conference on Systems, Man, and Cybernetics, 2008, , .	0.0	6
161	Tissue-specific RMA models to incrementally normalize Affymetrix GeneChip data., 2008, 2008, 2419-22.		3
162	Libaffy: software for processing Affymetrix(R) GeneChip(R) data. Bioinformatics, 2007, 23, 1562-1564.	4.1	11

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163	Transcriptional recapitulation and subversion of embryonic colon development by mouse colon tumor models and human colon cancer. Genome Biology, 2007, 8, R131.	8.8	299
164	Multivariate Feature Selection using Random Subspace Classifiers for Gene Expression Data., 2007,,.		3
165	Green tea catechins suppress the DNA synthesis marker MCM7 in the TRAMP model of prostate cancer. Molecular Oncology, 2007, 1, 196-204.	4.6	22
166	An Exact Test for Detecting Inconsistency in Readers Interpretation Over Time in Screening Mammograms. Biometrical Journal, 2007, 49, 672-681.	1.0	1
167	Elucidation of a protein signature discriminating six common types of adenocarcinoma. International Journal of Cancer, 2007, 120, 769-775.	5.1	36
168	Noise-Based Feature Perturbation as a Selection Method for Microarray Data., 2007,, 237-247.		7
169	Persistent Activation of Stat3 Signaling Induces Survivin Gene Expression and Confers Resistance to Apoptosis in Human Breast Cancer Cells. Clinical Cancer Research, 2006, 12, 11-19.	7.0	491
170	Slicing: A Distributed Learning Approach. , 2006, , 55-97.		0
171	Molecular fingerprint of green tea in TRAMP model of prostate neoplasia. Journal of the American College of Surgeons, 2005, 201, S39-S40.	0.5	0
172	Prediction of Radiation Sensitivity Using a Gene Expression Classifier. Cancer Research, 2005, 65, 7169-7176.	0.9	197
173	Molecular Staging for Survival Prediction of Colorectal Cancer Patients. Journal of Clinical Oncology, 2005, 23, 3526-3535.	1.6	313
174	A Comparison of Ensemble Creation Techniques. Lecture Notes in Computer Science, 2004, , 223-232.	1.3	34
175	DNA microarrays and data analysis: an overview. Surgery, 2004, 136, 500-503.	1.9	13
176	Multi-Platform, Multi-Site, Microarray-Based Human Tumor Classification. American Journal of Pathology, 2004, 164, 9-16.	3.8	207
177	Fast accurate fuzzy clustering through data reduction. IEEE Transactions on Fuzzy Systems, 2003, 11, 262-270.	9.8	180
178	Is Error-Based Pruning Redeemable?. International Journal on Artificial Intelligence Tools, 2003, 12, 249-264.	1.0	6
179	Harnessing Tumor Immune Ecosystem Dynamics to Personalize Radiation Therapy. SSRN Electronic Journal, 0, , .	0.4	2