

# Kevin R Coombes

## List of Publications by Year in descending order

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Version: 2024-02-01

193  
papers

25,134  
citations

17440

63  
h-index

7160

153  
g-index

206  
all docs

206  
docs citations

206  
times ranked

38282  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mercator: a pipeline for multi-method, unsupervised visualization and distance generation. <i>Bioinformatics</i> , 2021, 37, 2780-2781.	4.1	3
2	Pattern recognition in lymphoid malignancies using CytoGPS and Mercator. <i>BMC Bioinformatics</i> , 2021, 22, 100.	2.6	2
3	A novel model to label delirium in an intensive care unit from clinician actions. <i>BMC Medical Informatics and Decision Making</i> , 2021, 21, 97.	3.0	7
4	Simulation-derived best practices for clustering clinical data. <i>Journal of Biomedical Informatics</i> , 2021, 118, 103788.	4.3	10
5	RCytoGPS: an R package for reading and visualizing cytogenetics data. <i>Bioinformatics</i> , 2021, 37, 4589-4590.	4.1	3
6	Biostatistics and Bioinformatics in Clinical Trials. , 2020, , 284-295.e2.		1
7	Explaining Gene Expression Using Twenty-One MicroRNAs. <i>Journal of Computational Biology</i> , 2020, 27, 1157-1170.	1.6	5
8	CytoGPS: A large-scale karyotype analysis of CML data. <i>Cancer Genetics</i> , 2020, 248-249, 34-38.	0.4	2
9	Unsupervised machine learning and prognostic factors of survival in chronic lymphocytic leukemia. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2020, 27, 1019-1027.	4.4	18
10	LC-FACSeq is a method for detecting rare clones in leukemia. <i>JCI Insight</i> , 2020, 5, .	5.0	6
11	CytoGPS: a web-enabled karyotype analysis tool for cytogenetics. <i>Bioinformatics</i> , 2019, 35, 5365-5366.	4.1	8
12	Developmental subtypes assessed by DNA methylation-iPLEX forecast the natural history of chronic lymphocytic leukemia. <i>Blood</i> , 2019, 134, 688-698.	1.4	26
13	Time-to-progression after front-line fludarabine, cyclophosphamide, and rituximab chemoimmunotherapy for chronic lymphocytic leukaemia: a retrospective, multicohort study. <i>Lancet Oncology</i> , The, 2019, 20, 1576-1586.	10.7	26
14	Inferring clonal heterogeneity in cancer using SNP arrays and whole genome sequencing. <i>Bioinformatics</i> , 2019, 35, 2924-2931.	4.1	3
15	Human papillomavirus and the landscape of secondary genetic alterations in oral cancers. <i>Genome Research</i> , 2019, 29, 1-17.	5.5	166
16	Histone Modification Patterns Using RPPA-Based Profiling Predict Outcome in Acute Myeloid Leukemia Patients. <i>Proteomics</i> , 2018, 18, e1700379.	2.2	11
17	IntLIM: integration using linear models of metabolomics and gene expression data. <i>BMC Bioinformatics</i> , 2018, 19, 81.	2.6	34
18	Thirty biologically interpretable clusters of transcription factors distinguish cancer type. <i>BMC Genomics</i> , 2018, 19, 738.	2.8	6

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19	Trisomy 12 chronic lymphocytic leukemia expresses a unique set of activated and targetable pathways. <i>Haematologica</i> , 2018, 103, 2069-2078.	3.5	25
20	Thresher: determining the number of clusters while removing outliers. <i>BMC Bioinformatics</i> , 2018, 19, 9.	2.6	45
21	Decomposing the Apoptosis Pathway Into Biologically Interpretable Principal Components. <i>Cancer Informatics</i> , 2018, 17, 117693511877108.	1.9	20
22	Focal Adhesion Kinase as a Potential Target in AML and MDS. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 1133-1144.	4.1	30
23	Taxane-Platin-Resistant Lung Cancers Co-develop Hypersensitivity to JumonjiC Demethylase Inhibitors. <i>Cell Reports</i> , 2017, 19, 1669-1684.	6.4	82
24	Low expression of ASH2L protein correlates with a favorable outcome in acute myeloid leukemia. <i>Leukemia and Lymphoma</i> , 2017, 58, 1207-1218.	1.3	24
25	Cathepsin G is broadly expressed in acute myeloid leukemia and is an effective immunotherapeutic target. <i>Leukemia</i> , 2017, 31, 234-237.	7.2	30
26	Epidermal growth factor receptor is expressed and active in a subset of acute myeloid leukemia. <i>Journal of Hematology and Oncology</i> , 2016, 9, 64.	17.0	20
27	Preclinical Evaluation of the Novel BTK Inhibitor Acalabrutinib in Canine Models of B-Cell Non-Hodgkin Lymphoma. <i>PLoS ONE</i> , 2016, 11, e0159607.	2.5	49
28	The BATTLE-2 Study: A Biomarker-Integrated Targeted Therapy Study in Previously Treated Patients With Advanced Non-Small-Cell Lung Cancer. <i>Journal of Clinical Oncology</i> , 2016, 34, 3638-3647.	1.6	140
29	Using reverse-phase protein arrays as pharmacodynamic assays for functional proteomics, biomarker discovery, and drug development in cancer. <i>Seminars in Oncology</i> , 2016, 43, 476-483.	2.2	55
30	Selecting Reliable mRNA Expression Measurements across Platforms Improves Downstream Analysis. <i>Cancer Informatics</i> , 2016, 15, CIN.S38590.	1.9	2
31	A Patient-Derived, Pan-Cancer EMT Signature Identifies Global Molecular Alterations and Immune Target Enrichment Following Epithelial-to-Mesenchymal Transition. <i>Clinical Cancer Research</i> , 2016, 22, 609-620.	7.0	388
32	MLN0128, a novel mTOR kinase inhibitor, disrupts survival signaling and triggers apoptosis in AML and AML stem/progenitor cells. <i>Oncotarget</i> , 2016, 7, 55083-55097.	1.8	31
33	Aberrant Methylation and Decreased Expression of NRIP1 in IGHV-Unmutated CLL. <i>Blood</i> , 2016, 128, 1527-1527.	1.4	0
34	drexplorer: A tool to explore dose-response relationships and drug-drug interactions. <i>Bioinformatics</i> , 2015, 31, 1692-1694.	4.1	22
35	MLL-Rearranged Acute Lymphoblastic Leukemias Activate BCL-2 through H3K79 Methylation and Are Sensitive to the BCL-2-Specific Antagonist ABT-199. <i>Cell Reports</i> , 2015, 13, 2715-2727.	6.4	118
36	Phosphorylation of GSK3 $\beta$ correlates with activation of AKT and is prognostic for poor overall survival in acute myeloid leukemia patients. <i>BBA Clinical</i> , 2015, 4, 59-68.	4.1	37

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37	Erk Negative Feedback Control Enables Pre-B Cell Transformation and Represents a Therapeutic Target in Acute Lymphoblastic Leukemia. <i>Cancer Cell</i> , 2015, 28, 114-128.	16.8	107
38	Co-occurring Genomic Alterations Define Major Subsets of <i>KRAS</i> -Mutant Lung Adenocarcinoma with Distinct Biology, Immune Profiles, and Therapeutic Vulnerabilities. <i>Cancer Discovery</i> , 2015, 5, 860-877.	9.4	696
39	Development of a robust classifier for quality control of reverse-phase protein arrays. <i>Bioinformatics</i> , 2015, 31, 912-918.	4.1	43
40	Loss of TRIM62 Expression Is an Independent Adverse Prognostic Factor in Acute Myeloid Leukemia. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2015, 15, 115-127.e15.	0.4	28
41	The Aberrantly Expressed Long Noncoding RNA, TRERNA1, Predicts for Aggressive Disease in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2015, 126, 2911-2911.	1.4	2
42	Enriched expression of PD-L1 and other immune targets after epithelial-mesenchymal transition (EMT) in squamous head and neck and lung cancers.. <i>Journal of Clinical Oncology</i> , 2015, 33, 6016-6016.	1.6	0
43	Focal Adhesion Kinase As a Potential Target in AML and MDS. <i>Blood</i> , 2015, 126, 3680-3680.	1.4	0
44	Genes suppressed by DNA methylation in non-small cell lung cancer reveal the epigenetics of epithelial-mesenchymal transition. <i>BMC Genomics</i> , 2014, 15, 1079.	2.8	45
45	Transcriptomic Architecture of the Adjacent Airway Field Cancerization in Non-Small Cell Lung Cancer. <i>Journal of the National Cancer Institute</i> , 2014, 106, dju004.	6.3	72
46	VEGF/VEGFR-2 Upregulates EZH2 Expression in Lung Adenocarcinoma Cells and EZH2 Depletion Enhances the Response to Platinum-Based and VEGFR-2-Targeted Therapy. <i>Clinical Cancer Research</i> , 2014, 20, 3849-3861.	7.0	62
47	Synergistic Targeting of AML Stem/Progenitor Cells With IAP Antagonist Birinapant and Demethylating Agents. <i>Journal of the National Cancer Institute</i> , 2014, 106, djt440.	6.3	75
48	The protein phosphatase 2A regulatory subunit B55 is a modulator of signaling and microRNA expression in acute myeloid leukemia cells. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 1969-1977.	4.1	32
49	Bayesian sparse graphical models for classification with application to protein expression data. <i>Annals of Applied Statistics</i> , 2014, 8, 1443-1468.	1.1	23
50	BATLLE-2: KRAS mutation and outcome in a biomarker-integrated study in previously treated patients (pts) with advanced non-small cell lung cancer (NSCLC).. <i>Journal of Clinical Oncology</i> , 2014, 32, 8042-8042.	1.6	2
51	Biostatistics and Bioinformatics in Clinical Trials. , 2014, , 282-293.e2.		0
52	Transglutaminase 2 expression in acute myeloid leukemia: Association with adhesion molecule expression and leukemic blast motility. <i>Proteomics</i> , 2013, 13, 2216-2224.	2.2	31
53	Genomic Variation by Whole-Genome SNP Mapping Arrays Predicts Time-to-Event Outcome in Patients with Chronic Lymphocytic Leukemia. <i>Journal of Molecular Diagnostics</i> , 2013, 15, 196-209.	2.8	24
54	Independent Validation of a Model Using Cell Line Chemosensitivity to Predict Response to Therapy. <i>Journal of the National Cancer Institute</i> , 2013, 105, 1284-1291.	6.3	18

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55	SIBER: systematic identification of bimodally expressed genes using RNAseq data. <i>Bioinformatics</i> , 2013, 29, 605-613.	4.1	26
56	An Epithelial-Mesenchymal Transition Gene Signature Predicts Resistance to EGFR and PI3K Inhibitors and Identifies Axl as a Therapeutic Target for Overcoming EGFR Inhibitor Resistance. <i>Clinical Cancer Research</i> , 2013, 19, 279-290.	7.0	848
57	KEAP1-Dependent Synthetic Lethality Induced by AKT and TXNRD1 Inhibitors in Lung Cancer. <i>Cancer Research</i> , 2013, 73, 5532-5543.	0.9	66
58	Characterizing the Molecular Spatial and Temporal Field of Injury in Early-Stage Smoker Non-Small Cell Lung Cancer Patients after Definitive Surgery by Expression Profiling. <i>Cancer Prevention Research</i> , 2013, 6, 8-17.	1.5	36
59	Prognostic impact and targeting of CRM1 in acute myeloid leukemia. <i>Blood</i> , 2013, 121, 4166-4174.	1.4	184
60	Proteomic Profiling Identifies Distinct Protein Patterns in Acute Myelogenous Leukemia CD34+CD38-Stem-Like Cells. <i>PLoS ONE</i> , 2013, 8, e78453.	2.5	48
61	Phosphorylation Of GSK3 $\beta$ Is Associated With Inferior Survival In Acute Myeloid Leukemia and Is An Indicator Of AKT Activation In AML Blasts and Bone Marrow Mesenchymal Stem Cells. <i>Blood</i> , 2013, 122, 2551-2551.	1.4	0
62	Effect of KRAS Oncogene Substitutions on Protein Behavior: Implications for Signaling and Clinical Outcome. <i>Journal of the National Cancer Institute</i> , 2012, 104, 228-239.	6.3	424
63	Proteomic Profiling Identifies Dysregulated Pathways in Small Cell Lung Cancer and Novel Therapeutic Targets Including PARP1. <i>Cancer Discovery</i> , 2012, 2, 798-811.	9.4	432
64	Latent feature decompositions for integrative analysis of diverse high-throughput genomic data. , 2012, , .		3
65	PKC $\zeta$ Regulates Translation Initiation through PKR and eIF2 $\gamma$ in Response to Retinoic Acid in Acute Myeloid Leukemia Cells. <i>Leukemia Research and Treatment</i> , 2012, 2012, 1-17.	2.0	8
66	Forensic Bioinformatics. , 2012, , 605-618.		0
67	integrIRTy: a method to identify genes altered in cancer by accounting for multiple mechanisms of regulation using item response theory. <i>Bioinformatics</i> , 2012, 28, 2861-2869.	4.1	7
68	Relax with CouchDB - Into the non-relational DBMS era of bioinformatics. <i>Genomics</i> , 2012, 100, 1-7.	2.9	32
69	Concomitant inhibition of DNA methyltransferase and BCL-2 protein function synergistically induce mitochondrial apoptosis in acute myelogenous leukemia cells. <i>Annals of Hematology</i> , 2012, 91, 1861-1870.	1.8	129
70	Melanoma antigen family A identified by the bimodality index defines a subset of triple negative breast cancers as candidates for immune response augmentation. <i>European Journal of Cancer</i> , 2012, 48, 12-23.	2.8	43
71	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , 2012, 490, 61-70.	27.8	10,282
72	Sources of variation in false discovery rate estimation include sample size, correlation, and inherent differences between groups. <i>BMC Bioinformatics</i> , 2012, 13, S1.	2.6	40

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73	Functional Characterization of CLPTM1L as a Lung Cancer Risk Candidate Gene in the 5p15.33 Locus. PLoS ONE, 2012, 7, e36116.	2.5	89
74	Survivin is highly expressed in CD34+38 <sup>+</sup> leukemic stem/progenitor cells and predicts poor clinical outcomes in AML. Blood, 2012, 120, 173-180.	1.4	90
75	Perifosine plus docetaxel in patients with platinum and taxane resistant or refractory high-grade epithelial ovarian cancer. Gynecologic Oncology, 2012, 126, 47-53.	1.4	74
76	What Information Should Be Required to Support Clinical "Omics" Publications?. Clinical Chemistry, 2011, 57, 688-690.	3.2	58
77	Transformation of Human Mesenchymal Cells and Skin Fibroblasts into Hematopoietic Cells. PLoS ONE, 2011, 6, e21250.	2.5	32
78	A Two-Gene Signature, SKI and SLAMF1, Predicts Time-to-Treatment in Previously Untreated Patients with Chronic Lymphocytic Leukemia. PLoS ONE, 2011, 6, e28277.	2.5	20
79	Expression of ARC (apoptosis repressor with caspase recruitment domain), an antiapoptotic protein, is strongly prognostic in AML. Blood, 2011, 117, 780-787.	1.4	50
80	LDOC1 mRNA is differentially expressed in chronic lymphocytic leukemia and predicts overall survival in untreated patients. Blood, 2011, 117, 4076-4084.	1.4	28
81	Abnormal expression of FLI1 protein is an adverse prognostic factor in acute myeloid leukemia. Blood, 2011, 118, 5604-5612.	1.4	58
82	Proteomic biomarkers apolipoprotein A1, truncated transthyretin and connective tissue activating protein III enhance the sensitivity of CA125 for detecting early stage epithelial ovarian cancer. Gynecologic Oncology, 2011, 122, 548-553.	1.4	73
83	Functional proteomics can define prognosis and predict pathologic complete response in patients with breast cancer. Clinical Proteomics, 2011, 8, 11.	2.1	85
84	Robust Gene Expression Signature from Formalin-Fixed Paraffin-Embedded Samples Predicts Prognosis of Non-Small-Cell Lung Cancer Patients. Clinical Cancer Research, 2011, 17, 5705-5714.	7.0	150
85	Reproducibility of SELDI Spectra across Time and Laboratories. Cancer Informatics, 2011, 10, CIN.S6438.	1.9	14
86	Increased VEGFR-2 Gene Copy Is Associated with Chemoresistance and Shorter Survival in Patients with Non-Small-Cell Lung Carcinoma Who Receive Adjuvant Chemotherapy. Cancer Research, 2011, 71, 5512-5521.	0.9	55
87	Low expression of PP2A regulatory subunit B55 <sup>+</sup> is associated with T308 phosphorylation of AKT and shorter complete remission duration in acute myeloid leukemia patients. Leukemia, 2011, 25, 1711-1717.	7.2	71
88	Use of Reverse Phase Protein Microarrays to Study Protein Expression in Leukemia: Technical and Methodological Lessons Learned. Methods in Molecular Biology, 2011, 785, 141-155.	0.9	26
89	Recurrent expression signatures of cytokines and chemokines are present and are independently prognostic in acute myelogenous leukemia and myelodysplasia. Blood, 2010, 116, 4251-4261.	1.4	134
90	microRNA fingerprinting of CLL patients with chromosome 17p deletion identify a miR-21 score that stratifies early survival. Blood, 2010, 116, 945-952.	1.4	200

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91	Proteomic Profiling Identifies Pathways Dysregulated in Non-small Cell Lung Cancer and an Inverse Association of AMPK and Adhesion Pathways with Recurrence. <i>Journal of Thoracic Oncology</i> , 2010, 5, 1894-1904.	1.1	57
92	A Technical Assessment of the Utility of Reverse Phase Protein Arrays for the Study of the Functional Proteome in Non-microdissected Human Breast Cancers. <i>Clinical Proteomics</i> , 2010, 6, 129-151.	2.1	203
93	Clinical evaluation of chemotherapy response predictors developed from breast cancer cell lines. <i>Breast Cancer Research and Treatment</i> , 2010, 121, 301-309.	2.5	50
94	Host lung gene expression patterns predict infectious etiology in a mouse model of pneumonia. <i>Respiratory Research</i> , 2010, 11, 101.	3.6	10
95	Blasted Cell Line Names. <i>Cancer Informatics</i> , 2010, 9, CIN.S5613.	1.9	0
96	Functional Proteomic Analysis of Advanced Serous Ovarian Cancer Using Reverse Phase Protein Array: TGF- $\beta$ 2 Pathway Signaling Indicates Response to Primary Chemotherapy. <i>Clinical Cancer Research</i> , 2010, 16, 2852-2860.	7.0	58
97	Highly Phosphorylated FOXO3A Is an Adverse Prognostic Factor in Acute Myeloid Leukemia. <i>Clinical Cancer Research</i> , 2010, 16, 1865-1874.	7.0	130
98	Role of Peroxisome Proliferator-Activated Receptor- $\beta$ 3 and Its Coactivator DRIP205 in Cellular Responses to CDDO (RTA-401) in Acute Myelogenous Leukemia. <i>Cancer Research</i> , 2010, 70, 4949-4960.	0.9	40
99	Immunohistochemical detection of ZAP70 in chronic lymphocytic leukemia predicts immunoglobulin heavy chain gene mutation status and time to progression. <i>Modern Pathology</i> , 2010, 23, 1518-1523.	5.5	19
100	Statistical Contributions to Proteomic Research. <i>Methods in Molecular Biology</i> , 2010, 641, 143-166.	0.9	17
101	Cardiomyocyte PDGFR- $\beta$ 2 signaling is an essential component of the mouse cardiac response to load-induced stress. <i>Journal of Clinical Investigation</i> , 2010, 120, 472-484.	8.2	170
102	Prognostic Biomarkers for Esophageal Adenocarcinoma Identified by Analysis of Tumor Transcriptome. <i>PLoS ONE</i> , 2010, 5, e15074.	2.5	122
103	The Bimodality Index: A criterion for Discovering and Ranking Bimodal Signatures from Cancer Gene Expression Profiling Data. <i>Cancer Informatics</i> , 2009, 7, CIN.S2846.	1.9	106
104	Serial dilution curve: a new method for analysis of reverse phase protein array data. <i>Bioinformatics</i> , 2009, 25, 650-654.	4.1	53
105	Variable slope normalization of reverse phase protein arrays. <i>Bioinformatics</i> , 2009, 25, 1384-1389.	4.1	82
106	Expression of Autotaxin and Lysophosphatidic Acid Receptors Increases Mammary Tumorigenesis, Invasion, and Metastases. <i>Cancer Cell</i> , 2009, 15, 539-550.	16.8	332
107	miRNA expression profiles in head and neck squamous cell carcinoma and adjacent normal tissue. <i>Head and Neck</i> , 2009, 31, 642-654.	2.0	132
108	Array CGH analysis of chronic lymphocytic leukemia reveals frequent cryptic monoallelic and biallelic deletions of chromosome 22q11 that include the PRAME gene. <i>Leukemia Research</i> , 2009, 33, 1276-1281.	0.8	52



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109	Deriving chemosensitivity from cell lines: Forensic bioinformatics and reproducible research in high-throughput biology. <i>Annals of Applied Statistics</i> , 2009, 3, .	1.1	251
110	Functional proteomic profiling of AML predicts response and survival. <i>Blood</i> , 2009, 113, 154-164.	1.4	235
111	Relevance of the immunoglobulin VH somatic mutation status in patients with chronic lymphocytic leukemia treated with fludarabine, cyclophosphamide, and rituximab (FCR) or related chemoimmunotherapy regimens. <i>Blood</i> , 2009, 113, 3168-3171.	1.4	82
112	Bayesian Analysis of Mass Spectrometry Proteomic Data Using Wavelet-Based Functional Mixed Models. <i>Biometrics</i> , 2008, 64, 479-489.	1.4	92
113	HOX expression patterns identify a common signature for favorable AML. <i>Leukemia</i> , 2008, 22, 2041-2047.	7.2	120
114	RPPAML/RIMS: A metadata format and an information management system for reverse phase protein arrays. <i>BMC Bioinformatics</i> , 2008, 9, 555.	2.6	13
115	Curcumin (diferuloylmethane) alters the expression profiles of microRNAs in human pancreatic cancer cells. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 464-473.	4.1	377
116	Run Batch Effects Potentially Compromise the Usefulness of Genomic Signatures for Ovarian Cancer. <i>Journal of Clinical Oncology</i> , 2008, 26, 1186-1187.	1.6	68
117	A Semantic Web Management Model for Integrative Biomedical Informatics. <i>PLoS ONE</i> , 2008, 3, e2946.	2.5	26
118	Real-Time Gene Expression: Statistical Challenges in Design and Inference. <i>Journal of Computational Biology</i> , 2008, 15, 611-623.	1.6	3
119	MicroRNA signatures associated with cytogenetics and prognosis in acute myeloid leukemia. <i>Blood</i> , 2008, 111, 3183-3189.	1.4	575
120	Ovarian Cancer: Linking Genomics to New Target Discovery and Molecular Markers – The Way Ahead. <i>Advances in Experimental Medicine and Biology</i> , 2008, 617, 23-40.	1.6	13
121	Proteomic Profiling of 150 Proteins in 511 Acute Myelogenous Leukemia (AML) Patient Samples Using Reverse Phase Proteins Arrays (RPPA) Reveals Recurrent Proteins Expression Signatures with Prognostic Implications. <i>Blood</i> , 2008, 112, 759-759.	1.4	5
122	Exploratory Analysis of the Copy Number Alterations in Glioblastoma Multiforme. <i>PLoS ONE</i> , 2008, 3, e4076.	2.5	34
123	Gene Expression Profile of Metastatic Human Pancreatic Cancer Cells Depends on the Organ Microenvironment. <i>Cancer Research</i> , 2007, 67, 139-148.	0.9	71
124	Enrichment analysis in high-throughput genomics – accounting for dependency in the NULL. <i>Briefings in Bioinformatics</i> , 2007, 8, 71-77.	6.5	16
125	Non-parametric quantification of protein lysate arrays. <i>Bioinformatics</i> , 2007, 23, 1986-1994.	4.1	193
126	Zonal Heterogeneity for Gene Expression in Human Pancreatic Carcinoma. <i>Cancer Research</i> , 2007, 67, 7597-7604.	0.9	51



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127	Pre-Processing Mass Spectrometry Data. , 2007, , 79-102.		50
128	PrepMS: TOF MS data graphical preprocessing tool. Bioinformatics, 2007, 23, 264-265.	4.1	66
129	Identification and Validation of Biomarkers of IgVH Mutation Status in Chronic Lymphocytic Leukemia Using Microfluidics Quantitative Real-Time Polymerase Chain Reaction Technology. Journal of Molecular Diagnostics, 2007, 9, 546-555.	2.8	23
130	Microarrays: retracing steps. Nature Medicine, 2007, 13, 1276-1277.	30.7	134
131	Molecular analysis of anoikis resistance in oral cavity squamous cell carcinoma. Oral Oncology, 2007, 43, 440-454.	1.5	28
132	Merging microarray data, robust feature selection, and predicting prognosis in prostate cancer. Cancer Informatics, 2007, 2, 87-97.	1.9	14
133	An Introduction to High-Throughput Bioinformatics Data. , 2006, , 1-39.		4
134	RefSeq Refinements of UniGene-Based Gene Matching Improve the Correlation of Expression Measurements Between Two Microarray Platforms. Applied Bioinformatics, 2006, 5, 89-98.	1.6	8
135	Tissue-Specific Function of Lymph Node Fibroblastic Reticulum Cells. Pathobiology, 2006, 73, 71-81.	3.8	23
136	Studentizing Microarray Data. , 2006, , 49-59.		0
137	Merging Microarray Data, Robust Feature Selection, and Predicting Prognosis in Prostate Cancer. Cancer Informatics, 2006, 2, 117693510600200.	1.9	13
138	Statistical Considerations in the Assessment of cDNA Microarray Data Obtained Using Amplification. , 2006, , 21-36.		3
139	Molecular signatures associated with clinical outcome in patients with high-risk head-and-neck squamous cell carcinoma treated by surgery and radiation. International Journal of Radiation Oncology Biology Physics, 2006, 64, 670-677.	0.8	36
140	Gene sequence signatures revealed by mining the UniGene affiliation network. Bioinformatics, 2006, 22, 385-391.	4.1	5
141	Chemoprevention of Skin Carcinogenesis by Phenylretinamides: Retinoid Receptor-Independent Tumor Suppression. Clinical Cancer Research, 2006, 12, 969-979.	7.0	19
142	Identification of Cell Cycle Regulatory Genes as Principal Targets of p53-mediated Transcriptional Repression. Journal of Biological Chemistry, 2006, 281, 25134-25142.	3.4	102
143	Serum proteomics profiling—a young technology begins to mature. Nature Biotechnology, 2005, 23, 291-292.	17.5	162
144	Significant differences in nipple aspirate fluid protein expression between healthy women and those with breast cancer demonstrated by time-of-flight mass spectrometry. Breast Cancer Research and Treatment, 2005, 89, 149-157.	2.5	98

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145	Improved peak detection and quantification of mass spectrometry data acquired from surface-enhanced laser desorption and ionization by denoising spectra with the undecimated discrete wavelet transform. <i>Proteomics</i> , 2005, 5, 4107-4117.	2.2	293
146	Bias, Randomization, and Ovarian Proteomic Data: A Reply to "Producers and Consumers". <i>Cancer Informatics</i> , 2005, 1, 117693510500100.	1.9	20
147	Understanding the Characteristics of Mass Spectrometry Data through the use of Simulation. <i>Cancer Informatics</i> , 2005, 1, 117693510500100.	1.9	42
148	Analysis of Mass Spectrometry Profiles of the Serum Proteome - Reply. <i>Clinical Chemistry</i> , 2005, 51, 1309-1309.	3.2	1
149	Analysis of dose-response effects on gene expression data with comparison of two microarray platforms. <i>Bioinformatics</i> , 2005, 21, 3524-3529.	4.1	26
150	Prognostic Role of a Multigene Reverse Transcriptase-PCR Assay in Patients with Node-Negative Breast Cancer Not Receiving Adjuvant Systemic Therapy. <i>Clinical Cancer Research</i> , 2005, 11, 3315-3319.	7.0	160
151	The importance of experimental design in proteomic mass spectrometry experiments: Some cautionary tales. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2005, 3, 322-331.	3.8	156
152	Applications of beta-mixture models in bioinformatics. <i>Bioinformatics</i> , 2005, 21, 2118-2122.	4.1	108
153	Feature extraction and quantification for mass spectrometry in biomedical applications using the mean spectrum. <i>Bioinformatics</i> , 2005, 21, 1764-1775.	4.1	290
154	Analysis of Mass Spectrometry Profiles of the Serum Proteome. <i>Clinical Chemistry</i> , 2005, 51, 1-2.	3.2	41
155	Serum amyloid A as a tumor marker in sera of nude mice with orthotopic human pancreatic cancer and in plasma of patients with pancreatic cancer. <i>International Journal of Oncology</i> , 2005, 27, 1361.	3.3	18
156	Biological Validation of Differentially Expressed Genes in Chronic Lymphocytic Leukemia Identified by Applying Multiple Statistical Methods to Oligonucleotide Microarrays. <i>Journal of Molecular Diagnostics</i> , 2005, 7, 337-345.	2.8	15
157	Comparison of the Predictive Accuracy of DNA Array-Based Multigene Classifiers across cDNA Arrays and Affymetrix GeneChips. <i>Journal of Molecular Diagnostics</i> , 2005, 7, 357-367.	2.8	44
158	Inter-Gene Correlation on Oligonucleotide Arrays. <i>Molecular Diagnosis and Therapy</i> , 2005, 5, 271-279.	3.3	8
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