Kevin R Coombes

List of Publications by Year
in descending order

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	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	27.8	10,282
2	An Epithelialâ€"Mesenchymal Transition Gene Signature Predicts Resistance to EGFR and PI3K Inhibitors and Identifies Axl as a Therapeutic Target for Overcoming EGFR Inhibitor Resistance. Clinical Cancer Research, 2013, 19, 279-290.	7.0	848
3	Co-occurring Genomic Alterations Define Major Subsets of <i>KRAS</i>-Mutant Lung Adenocarcinoma with Distinct Biology, Immune Profiles, and Therapeutic Vulnerabilities. Cancer Discovery, 2015, 5, 860-877.	9.4	696
4	Reproducibility of SELDI-TOF protein patterns in serum: comparing datasets from different experiments. Bioinformatics, 2004, 20, 777-785.	4.1	598
5	MicroRNA signatures associated with cytogenetics and prognosis in acute myeloid leukemia. Blood, 2008, 111, 3183-3189.	1.4	575
6	Proteomic Profiling Identifies Dysregulated Pathways in Small Cell Lung Cancer and Novel Therapeutic Targets Including PARP1. Cancer Discovery, 2012, 2, 798-811.	9.4	432
7	Effect of KRAS Oncogene Substitutions on Protein Behavior: Implications for Signaling and Clinical Outcome. Journal of the National Cancer Institute, 2012, 104, 228-239.	6.3	424
8	A Patient-Derived, Pan-Cancer EMT Signature Identifies Global Molecular Alterations and Immune Target Enrichment Following Epithelial-to-Mesenchymal Transition. Clinical Cancer Research, 2016, 22, 609-620.	7.0	388
9	Curcumin (diferuloylmethane) alters the expression profiles of microRNAs in human pancreatic cancer cells. Molecular Cancer Therapeutics, 2008, 7, 464-473.	4.1	377
10	Expression of Autotaxin and Lysophosphatidic Acid Receptors Increases Mammary Tumorigenesis, Invasion, and Metastases. Cancer Cell, 2009, 15, 539-550.	16.8	332
11	Signal in Noise: Evaluating Reported Reproducibility of Serum Proteomic Tests for Ovarian Cancer. Journal of the National Cancer Institute, 2005, 97, 307-309.	6.3	294
12	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. Proteomics, 2005, 5, 4107-4117.	2.2	293
13	Feature extraction and quantification for mass spectrometry in biomedical applications using the mean spectrum. Bioinformatics, 2005, 21, 1764-1775.	4.1	290
14	Deriving chemosensitivity from cell lines: Forensic bioinformatics and reproducible research in high-throughput biology. Annals of Applied Statistics, 2009, 3, .	1.1	251
15	Functional proteomic profiling of AML predicts response and survival. Blood, 2009, 113, 154-164.	1.4	235
16	Direct Tandem Mass Spectrometry Reveals Limitations in Protein Profiling Experiments for Plasma Biomarker Discovery. Journal of Proteome Research, 2005, 4, 972-981.	3.7	210
17	Quality Control and Peak Finding for Proteomics Data Collected from Nipple Aspirate Fluid by Surface-Enhanced Laser Desorption and Ionization. Clinical Chemistry, 2003, 49, 1615-1623.	3.2	203
18	A Technical Assessment of the Utility of Reverse Phase Protein Arrays for the Study of the Functional Proteome in Non-microdissected Human Breast Cancers. Clinical Proteomics, 2010, 6, 129-151.	2.1	203

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19	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
20	Non-parametric quantification of protein lysate arrays. Bioinformatics, 2007, 23, 1986-1994.	4.1	193
21	Prognostic impact and targeting of CRM1 in acute myeloid leukemia. Blood, 2013, 121, 4166-4174.	1.4	184
22	Cardiomyocyte PDGFR-Î² signaling is an essential component of the mouse cardiac response to load-induced stress. Journal of Clinical Investigation, 2010, 120, 472-484.	8.2	170
23	Human papillomavirus and the landscape of secondary genetic alterations in oral cancers. Genome Research, 2019, 29, 1-17.	5.5	166
24	Serum proteomics profilingâ€"a young technology begins to mature. Nature Biotechnology, 2005, 23, 291-292.	17.5	162
25	A comprehensive approach to the analysis of matrix-assisted laser desorption/ionization-time of flight proteomics spectra from serum samples. Proteomics, 2003, 3, 1667-1672.	2.2	161
26	Prognostic Role of a Multigene Reverse Transcriptase-PCR Assay in Patients with Node-Negative Breast Cancer Not Receiving Adjuvant Systemic Therapy. Clinical Cancer Research, 2005, 11, 3315-3319.	7.0	160
27	The importance of experimental design in proteomic mass spectrometry experiments: Some cautionary tales. Briefings in Functional Genomics & Proteomics, 2005, 3, 322-331.	3.8	156
28	Robust Gene Expression Signature from Formalin-Fixed Paraffin-Embedded Samples Predicts Prognosis of Nonâ€"Small-Cell Lung Cancer Patients. Clinical Cancer Research, 2011, 17, 5705-5714.	7.0	150
29	The BATTLE-2 Study: A Biomarker-Integrated Targeted Therapy Study in Previously Treated Patients With Advanced Nonâ€"Small-Cell Lung Cancer. Journal of Clinical Oncology, 2016, 34, 3638-3647.	1.6	140
30	Microarrays: retracing steps. Nature Medicine, 2007, 13, 1276-1277.	30.7	134
31	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
32	miRNA expression profiles in head and neck squamous cell carcinoma and adjacent normal tissue. Head and Neck, 2009, 31, 642-654.	2.0	132
33	High expression of activation-induced cytidine deaminase (AID) and splice variants is a distinctive feature of poor-prognosis chronic lymphocytic leukemia. Blood, 2003, 101, 4903-4908.	1.4	130
34	Highly Phosphorylated FOXO3A Is an Adverse Prognostic Factor in Acute Myeloid Leukemia. Clinical Cancer Research, 2010, 16, 1865-1874.	7.0	130
35	Concomitant inhibition of DNA methyltransferase and BCL-2 protein function synergistically induce mitochondrial apoptosis in acute myelogenous leukemia cells. Annals of Hematology, 2012, 91, 1861-1870.	1.8	129
36	Plasma protein profiling for diagnosis of pancreatic cancer reveals the presence of host response proteins. Clinical Cancer Research, 2005, 11, 1110-8.	7.0	125

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37	Prognostic Biomarkers for Esophageal Adenocarcinoma Identified by Analysis of Tumor Transcriptome. PLoS ONE, 2010, 5, e15074.	2.5	122
38	HOX expression patterns identify a common signature for favorable AML. Leukemia, 2008, 22, 2041-2047.	7.2	120
39	MLL-Rearranged Acute Lymphoblastic Leukemias Activate BCL-2 through H3K79 Methylation and Are Sensitive to the BCL-2-Specific Antagonist ABT-199. Cell Reports, 2015, 13, 2715-2727.	6.4	118
40	Microarrays: handling the deluge of data and extracting reliable information. Trends in Biotechnology, 2001, 19, 463-468.	9.3	112
41	Applications of beta-mixture models in bioinformatics. Bioinformatics, 2005, 21, 2118-2122.	4.1	108
42	Erk Negative Feedback Control Enables Pre-B Cell Transformation and Represents a Therapeutic Target in Acute Lymphoblastic Leukemia. Cancer Cell, 2015, 28, 114-128.	16.8	107
43	The Bimodality Index: A criterion for Discovering and Ranking Bimodal Signatures from Cancer Gene Expression Profiling Data. Cancer Informatics, 2009, 7, CIN.S2846.	1.9	106
44	Identifying Differentially Expressed Genes in cDNA Microarray Experiments. Journal of Computational Biology, 2001, 8, 639-659.	1.6	103
45	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
46	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
47	Bayesian Analysis of Mass Spectrometry Proteomic Data Using Wavelet€Based Functional Mixed Models. Biometrics, 2008, 64, 479-489.	1.4	92
48	Survivin is highly expressed in CD34+38â˘̌ leukemic stem/progenitor cells and predicts poor clinical outcomes in AML. Blood, 2012, 120, 173-180.	1.4	90
49	Functional Characterization of CLPTM1L as a Lung Cancer Risk Candidate Gene in the 5p15.33 Locus. PLoS ONE, 2012, 7, e36116.	2.5	89
50	Validation of oligonucleotide microarray data using microfluidic low-density arrays: a new statistical method to normalize real-time RT-PCR data. BioTechniques, 2005, 38, 785-792.	1.8	89
51	Functional proteomics can define prognosis and predict pathologic complete response in patients with breast cancer. Clinical Proteomics, 2011, 8, 11.	2.1	85
52	Variable slope normalization of reverse phase protein arrays. Bioinformatics, 2009, 25, 1384-1389.	4.1	82
53	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. Blood, 2009, 113, 3168-3171.	1.4	82
54	Taxane-Platin-Resistant Lung Cancers Co-develop Hypersensitivity to JumonjiC Demethylase Inhibitors. Cell Reports, 2017, 19, 1669-1684.	6.4	82

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55	Synergistic Targeting of AML Stem/Progenitor Cells With IAP Antagonist Birinapant and Demethylating Agents. Journal of the National Cancer Institute, 2014, 106, djt440.	6.3	75
56	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
57	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
58	Transcriptomic Architecture of the Adjacent Airway Field Cancerization in Nonâ€"Small Cell Lung Cancer. Journal of the National Cancer Institute, 2014, 106, dju004.	6.3	72
59	Gene Expression Profile of Metastatic Human Pancreatic Cancer Cells Depends on the Organ Microenvironment. Cancer Research, 2007, 67, 139-148.	0.9	71
60	Low expression of PP2A regulatory subunit B55Î± 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
61	Run Batch Effects Potentially Compromise the Usefulness of Genomic Signatures for Ovarian Cancer. Journal of Clinical Oncology, 2008, 26, 1186-1187.	1.6	68
62	PrepMS: TOF MS data graphical preprocessing tool. Bioinformatics, 2007, 23, 264-265.	4.1	66
63	KEAP1-Dependent Synthetic Lethality Induced by AKT and TXNRD1 Inhibitors in Lung Cancer. Cancer Research, 2013, 73, 5532-5543.	0.9	66
64	Obtaining reliable information from minute amounts of RNA using cDNA microarrays. BMC Genomics, 2002, 3, 16.	2.8	64
65	VEGF/VEGFR-2 Upregulates EZH2 Expression in Lung Adenocarcinoma Cells and EZH2 Depletion Enhances the Response to Platinum-Based and VEGFR-2â€"Targeted Therapy. Clinical Cancer Research, 2014, 20, 3849-3861.	7.0	62
66	High-resolution serum proteomic patterns for ovarian cancer detection. Endocrine-Related Cancer, 2004, 11, 583-584.	3.1	58
67	Functional Proteomic Analysis of Advanced Serous Ovarian Cancer Using Reverse Phase Protein Array: TGF-Î² Pathway Signaling Indicates Response to Primary Chemotherapy. Clinical Cancer Research, 2010, 16, 2852-2860.	7.0	58
68	What Information Should Be Required to Support Clinical â€œOmicsâ€•Publications?. Clinical Chemistry, 2011, 57, 688-690.	3.2	58
69	Abnormal expression of FLI1 protein is an adverse prognostic factor in acute myeloid leukemia. Blood, 2011, 118, 5604-5612.	1.4	58
70	Proteomic Profiling Identifies Pathways Dysregulated in Non-small Cell Lung Cancer and an Inverse Association of AMPK and Adhesion Pathways with Recurrence. Journal of Thoracic Oncology, 2010, 5, 1894-1904.	1.1	57
71	Increased VEGFR-2 Gene Copy Is Associated with Chemoresistance and Shorter Survival in Patients with Nonâ€"Small-Cell Lung Carcinoma Who Receive Adjuvant Chemotherapy. Cancer Research, 2011, 71, 5512-5521.	0.9	55
72	Using reverse-phase protein arrays as pharmacodynamic assays for functional proteomics, biomarker discovery, and drug development in cancer. Seminars in Oncology, 2016, 43, 476-483.	2.2	55

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73	Serial dilution curve: a new method for analysis of reverse phase protein array data. Bioinformatics, 2009, 25, 650-654.	4.1	53
74	Array CGH analysis of chronic lymphocytic leukemia reveals frequent cryptic monoallelic and biallelic deletions of chromosome 22q11 that include the PRAME gene. Leukemia Research, 2009, 33, 1276-1281.	0.8	52
75	Zonal Heterogeneity for Gene Expression in Human Pancreatic Carcinoma. Cancer Research, 2007, 67, 7597-7604.	0.9	51
76	Pre-Processing Mass Spectrometry Data. , 2007, , 79-102.		50
77	Clinical evaluation of chemotherapy response predictors developed from breast cancer cell lines. Breast Cancer Research and Treatment, 2010, 121, 301-309.	2.5	50
78	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
79	Preclinical Evaluation of the Novel BTK Inhibitor Acalabrutinib in Canine Models of B-Cell Non-Hodgkin Lymphoma. PLoS ONE, 2016, 11, e0159607.	2.5	49
80	Proteomic Profiling Identifies Distinct Protein Patterns in Acute Myelogenous Leukemia CD34+CD38- Stem-Like Cells. PLoS ONE, 2013, 8, e78453.	2.5	48
81	Genes suppressed by DNA methylation in non-small cell lung cancer reveal the epigenetics of epithelialâ€"mesenchymal transition. BMC Genomics, 2014, 15, 1079.	2.8	45
82	Thresher: determining the number of clusters while removing outliers. BMC Bioinformatics, 2018, 19, 9.	2.6	45
83	Comparison of the Predictive Accuracy of DNA Array-Based Multigene Classifiers across cDNA Arrays and Affymetrix GeneChips. Journal of Molecular Diagnostics, 2005, 7, 357-367.	2.8	44
84	Melanoma antigen family A identified by the bimodality index defines a subset of triple negative breast cancers as candidates for immune response augmentation. European Journal of Cancer, 2012, 48, 12-23.	2.8	43
85	Development of a robust classifier for quality control of reverse-phase protein arrays. Bioinformatics, 2015, 31, 912-918.	4.1	43
86	Understanding the Characteristics of Mass Spectrometry Data through the use of Simulation. Cancer Informatics, 2005, 1, 117693510500100.	1.9	42
87	Identifying and Quantifying Sources of Variation in Microarray Data Using High-Density cDNA Membrane Arrays. Journal of Computational Biology, 2002, 9, 655-669.	1.6	41
88	Analysis of Mass Spectrometry Profiles of the Serum Proteome. Clinical Chemistry, 2005, 51, 1-2.	3.2	41
89	Role of Peroxisome Proliferator-Activated Receptor-Î³ and Its Coactivator DRIP205 in Cellular Responses to CDDO (RTA-401) in Acute Myelogenous Leukemia. Cancer Research, 2010, 70, 4949-4960.	0.9	40
90	Sources of variation in false discovery rate estimation include sample size, correlation, and inherent differences between groups. BMC Bioinformatics, 2012, 13, S1.	2.6	40

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91	Upregulation of c-MYC in WT1-mutant tumors: assessment of WT1 putative transcriptional targets using cDNA microarray expression profiling of genetically defined Wilms' tumors. Oncogene, 2003, 22, 3821-3826.	5.9	38
92	A comparative analysis of data generated using two different target preparation methods for hybridization to high-density oligonucleotide microarrays. BMC Genomics, 2004, 5, 2.	2.8	38
93	Phosphorylation of GSK3Î±/Î² correlates with activation of AKT and is prognostic for poor overall survival in acute myeloid leukemia patients. BBA Clinical, 2015, 4, 59-68.	4.1	37
94	Hurwitz families and arithmetic Galois groups. Duke Mathematical Journal, 1985, 52, 821.	1.5	36
95	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
96	Characterizing the Molecular Spatial and Temporal Field of Injury in Early-Stage Smoker Nonâ€"Small Cell Lung Cancer Patients after Definitive Surgery by Expression Profiling. Cancer Prevention Research, 2013, 6, 8-17.	1.5	36
97	IntLIM: integration using linear models of metabolomics and gene expression data. BMC Bioinformatics, 2018, 19, 81.	2.6	34
98	Exploratory Analysis of the Copy Number Alterations in Glioblastoma Multiforme. PLoS ONE, 2008, 3, e4076.	2.5	34
99	Transformation of Human Mesenchymal Cells and Skin Fibroblasts into Hematopoietic Cells. PLoS ONE, 2011, 6, e21250.	2.5	32
100	Relax with CouchDB â€" Into the non-relational DBMS era of bioinformatics. Genomics, 2012, 100, 1-7.	2.9	32
101	The protein phosphatase 2A regulatory subunit B55Î± is a modulator of signaling and microRNA expression in acute myeloid leukemia cells. Biochimica Et Biophysica Acta - Molecular Cell Research, 2014, 1843, 1969-1977.	4.1	32
102	Stem cell-ness: a "magic marker" for cancer. Journal of Clinical Investigation, 2005, 115, 1463-1467.	8.2	32
103	Transglutaminase 2 expression in acute myeloid leukemia: Association with adhesion molecule expression and leukemic blast motility. Proteomics, 2013, 13, 2216-2224.	2.2	31
104	MLN0128, a novel mTOR kinase inhibitor, disrupts survival signaling and triggers apoptosis in AML and AML stem/ progenitor cells. Oncotarget, 2016, 7, 55083-55097.	1.8	31
105	Understanding the characteristics of mass spectrometry data through the use of simulation. Cancer Informatics, 2005, 1, 41-52.	1.9	31
106	Association between ductal fluid proteomic expression profiles and the presence of lymph node metastases in women with breast cancer. Surgery, 2004, 136, 1061-1069.	1.9	30
107	Focal Adhesion Kinase as a Potential Target in AML and MDS. Molecular Cancer Therapeutics, 2017, 16, 1133-1144.	4.1	30
108	Cathepsin G is broadly expressed in acute myeloid leukemia and is an effective immunotherapeutic target. Leukemia, 2017, 31, 234-237.	7.2	30

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109	Molecular analysis of anoikis resistance in oral cavity squamous cell carcinoma. Oral Oncology, 2007, 43, 440-454.	1.5	28
110	LDOC1 mRNA is differentially expressed in chronic lymphocytic leukemia and predicts overall survival in untreated patients. Blood, 2011, 117, 4076-4084.	1.4	28
111	Loss of TRIM62 Expression Is an Independent Adverse Prognostic Factor in Acute MyeloidÂLeukemia. Clinical Lymphoma, Myeloma and Leukemia, 2015, 15, 115-127.e15.	0.4	28
112	Analysis of dose-response effects on gene expression data with comparison of two microarray platforms. Bioinformatics, 2005, 21, 3524-3529.	4.1	26
113	A Semantic Web Management Model for Integrative Biomedical Informatics. PLoS ONE, 2008, 3, e2946.	2.5	26
114	SIBER: systematic identification of bimodally expressed genes using RNAseq data. Bioinformatics, 2013, 29, 605-613.	4.1	26
115	Developmental subtypes assessed by DNA methylation-iPLEX forecast the natural history of chronic lymphocytic leukemia. Blood, 2019, 134, 688-698.	1.4	26
116	Time-to-progression after front-line fludarabine, cyclophosphamide, and rituximab chemoimmunotherapy for chronic lymphocytic leukaemia: a retrospective, multicohort study. Lancet Oncology, The, 2019, 20, 1576-1586.	10.7	26
117	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
118	Application of protein lysate microarrays to molecular marker verification and quantification. Proteome Science, 2005, 3, 9.	1.7	25
119	Trisomy 12 chronic lymphocytic leukemia expresses a unique set of activated and targetable pathways. Haematologica, 2018, 103, 2069-2078.	3.5	25
120	Genomic Variation by Whole-Genome SNP Mapping Arrays Predicts Time-to-Event Outcome in Patients with Chronic Lymphocytic Leukemia. Journal of Molecular Diagnostics, 2013, 15, 196-209.	2.8	24
121	Low expression of ASH2L protein correlates with a favorable outcome in acute myeloid leukemia. Leukemia and Lymphoma, 2017, 58, 1207-1218.	1.3	24
122	Tissue-Specific Function of Lymph Node Fibroblastic Reticulum Cells. Pathobiology, 2006, 73, 71-81.	3.8	23
123	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
124	Bayesian sparse graphical models for classification with application to protein expression data. Annals of Applied Statistics, 2014, 8, 1443-1468.	1.1	23
125	drexplorer: A tool to explore doseâ€"response relationships and drugâ€"drug interactions. Bioinformatics, 2015, 31, 1692-1694.	4.1	22
126	Bias, Randomization, and Ovarian Proteomic Data: A Reply to â€œProducers and Consumersâ€. Cancer Informatics, 2005, 1, 117693510500100.	1.9	20

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127	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
128	Epidermal growth factor receptor is expressed and active in a subset of acute myeloid leukemia. Journal of Hematology and Oncology, 2016, 9, 64.	17.0	20
129	Decomposing the Apoptosis Pathway Into Biologically Interpretable Principal Components. Cancer Informatics, 2018, 17, 117693511877108.	1.9	20
130	Chemoprevention of Skin Carcinogenesis by Phenylretinamides: Retinoid Receptor–Independent Tumor Suppression. Clinical Cancer Research, 2006, 12, 969-979.	7.0	19
131	Immunohistochemical detection of ZAP70 in chronic lymphocytic leukemia predicts immunoglobulin heavy chain gene mutation status and time to progression. Modern Pathology, 2010, 23, 1518-1523.	5.5	19
132	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. International Journal of Oncology, 2005, 27, 1361.	3.3	18
133	Independent Validation of a Model Using Cell Line Chemosensitivity to Predict Response to Therapy. Journal of the National Cancer Institute, 2013, 105, 1284-1291.	6.3	18
134	Unsupervised machine learning and prognostic factors of survival in chronic lymphocytic leukemia. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 1019-1027.	4.4	18
135	Attack priming and aggressive arousal in female Syrian golden hamsters,Mesocricetus auratus. Animal Behaviour, 1995, 49, 931-947.	1.9	17
136	Statistical Contributions to Proteomic Research. Methods in Molecular Biology, 2010, 641, 143-166.	0.9	17
137	Every rational surface is separably split. Commentarii Mathematici Helvetici, 1988, 63, 305-311.	0.7	16
138	Enrichment analysis in high-throughput genomics—accounting for dependency in the NULL. Briefings in Bioinformatics, 2007, 8, 71-77.	6.5	16
139	On Heterogeneous Spaces. Journal of the London Mathematical Society, 1989, s2-40, 385-397.	1.0	15
140	Biological Validation of Differentially Expressed Genes in Chronic Lymphocytic Leukemia Identified by Applying Multiple Statistical Methods to Oligonucleotide Microarrays. Journal of Molecular Diagnostics, 2005, 7, 337-345.	2.8	15
141	Reproducibility of SELDI Spectra across Time and Laboratories. Cancer Informatics, 2011, 10, CIN.S6438.	1.9	14
142	Merging microarray data, robust feature selection, and predicting prognosis in prostate cancer. Cancer Informatics, 2007, 2, 87-97.	1.9	14
143	A comprehensive assessment of p53-responsive genes following adenoviral-p53 gene transfer in Bcl-2-expressing prostate cancer cells. Oncogene, 2004, 23, 1712-1723.	5.9	13
144	Merging Microarray Data, Robust Feature Selection, and Predicting Prognosis in Prostate Cancer. Cancer Informatics, 2006, 2, 117693510600200.	1.9	13

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145	RPPAML/RIMS: A metadata format and an information management system for reverse phase protein arrays. BMC Bioinformatics, 2008, 9, 555.	2.6	13
146	Ovarian Cancer: Linking Genomics to New Target Discovery and Molecular Markers â€" The Way Ahead. Advances in Experimental Medicine and Biology, 2008, 617, 23-40.	1.6	13
147	Bias, randomization, and ovarian proteomic data: a reply to "producers and consumers". Cancer Informatics, 2005, 1, 9-14.	1.9	12
148	Histone Modification Patterns Using RPPAâ€Based Profiling Predict Outcome in Acute Myeloid Leukemia Patients. Proteomics, 2018, 18, e1700379.	2.2	11
149	Establishment and Characterization by Gene Expression Profiling of a New Diffuse Large B-Cell Lymphoma Cell Line, EJ-1, Carrying t(14;18) and t(8;14) Translocations. Laboratory Investigation, 2003, 83, 913-916.	3.7	10
150	Host lung gene expression patterns predict infectious etiology in a mouse model of pneumonia. Respiratory Research, 2010, 11, 101.	3.6	10
151	Simulation-derived best practices for clustering clinical data. Journal of Biomedical Informatics, 2021, 118, 103788.	4.3	10
152	Zero cycles on del Pezzo surfaces over local fields. Journal of Algebra, 1985, 97, 438-460.	0.7	8
153	Inter-Gene Correlation on Oligonucleotide Arrays. Molecular Diagnosis and Therapy, 2005, 5, 271-279.	3.3	8
154	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
155	PKCÎ´ Regulates Translation Initiation through PKR and eIF2Î± in Response to Retinoic Acid in Acute Myeloid Leukemia Cells. Leukemia Research and Treatment, 2012, 2012, 1-17.	2.0	8
156	CytoGPS: a web-enabled karyotype analysis tool for cytogenetics. Bioinformatics, 2019, 35, 5365-5366.	4.1	8
157	integIRTy: a method to identify genes altered in cancer by accounting for multiple mechanisms of regulation using item response theory. Bioinformatics, 2012, 28, 2861-2869.	4.1	7
158	A novel model to label delirium in an intensive care unit from clinician actions. BMC Medical Informatics and Decision Making, 2021, 21, 97.	3.0	7
159	Thirty biologically interpretable clusters of transcription factors distinguish cancer type. BMC Genomics, 2018, 19, 738.	2.8	6
160	LC-FACSeq is a method for detecting rare clones in leukemia. JCI Insight, 2020, 5, .	5.0	6
161	The arithmetic of zero cycles on surfaces with geometric genus and irregularity zero. Mathematische Annalen, 1991, 291, 429-452.	1.4	5
162	Gene sequence signatures revealed by mining the UniGene affiliation network. Bioinformatics, 2006, 22, 385-391.	4.1	5

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163	Explaining Gene Expression Using Twenty-One MicroRNAs. Journal of Computational Biology, 2020, 27, 1157-1170.	1.6	5
164	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. Blood, 2008, 112, 759-759.	1.4	5
165	An Introduction to High-Throughput Bioinformatics Data. , 2006, , 1-39.		4
166	Motifs,L-functions, and theK-cohomology of rational surfaces over finite fields. Mathematische Annalen, 1987, 276, 255-267.	1.4	4
167	Statistical Considerations in the Assessment of cDNA Microarray Data Obtained Using Amplification. , 2006, , 21-36.		3
168	Real-Time Gene Expression: Statistical Challenges in Design and Inference. Journal of Computational Biology, 2008, 15, 611-623.	1.6	3
169	Latent feature decompositions for integrative analysis of diverse high-throughput genomic data. , 2012, , .		3
170	Inferring clonal heterogeneity in cancer using SNP arrays and whole genome sequencing. Bioinformatics, 2019, 35, 2924-2931.	4.1	3
171	Mercator: a pipeline for multi-method, unsupervised visualization and distance generation. Bioinformatics, 2021, 37, 2780-2781.	4.1	3
172	Umpire 2.0: Simulating realistic, mixed-type, clinical data for machine learning. F1000Research, 0, 9, 1186.	1.6	3
173	RCytoGPS: an R package for reading and visualizing cytogenetics data. Bioinformatics, 2021, 37, 4589-4590.	4.1	3
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