

# CITATION REPORT

List of articles citing

**Prognostic gene signatures for patient stratification in breast cancer: accuracy, stability and interpretability of gene selection approaches using prior knowledge on protein-protein interactions**

**DOI: 10.1186/1471-2105-13-69**  
**BMC Bioinformatics, 2012, 13, 69.**

**Source:** <https://exaly.com/paper-pdf/53695802/citation-report.pdf>

**Version:** 2024-04-25

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
42	Cancer bioinformatics: a new approach to systems clinical medicine. <i>BMC Bioinformatics</i> , <b>2012</b> , 13, 71	3.6	42
41	Biomarker gene signature discovery integrating network knowledge. <i>Biology</i> , <b>2012</b> , 1, 5-17	4.9	22
40	Network and data integration for biomarker signature discovery via network smoothed T-statistics. <i>PLoS ONE</i> , <b>2013</b> , 8, e73074	3.7	45
39	Current composite-feature classification methods do not outperform simple single-genes classifiers in breast cancer prognosis. <i>Frontiers in Genetics</i> , <b>2013</b> , 4, 289	4.5	30
38	RRHGE: a novel approach to classify the estrogen receptor based breast cancer subtypes. <i>Scientific World Journal, The</i> , <b>2014</b> , 2014, 362141	2.2	3
37	Computational prognostic indicators for breast cancer. <i>Cancer Management and Research</i> , <b>2014</b> , 6, 301-326	1.3	7
36	Robust clinical outcome prediction based on Bayesian analysis of transcriptional profiles and prior causal networks. <i>Bioinformatics</i> , <b>2014</b> , 30, i69-77	7.2	14
35	Tamoxifen integromics and personalized medicine: dynamic modular transformations underpinning response to tamoxifen in breast cancer treatment. <i>OMICS A Journal of Integrative Biology</i> , <b>2014</b> , 18, 15-33	3.8	18
34	netClass: an R-package for network based, integrative biomarker signature discovery. <i>Bioinformatics</i> , <b>2014</b> , 30, 1325-6	7.2	18
33	Including network knowledge into Cox regression models for biomarker signature discovery. <i>Biometrical Journal</i> , <b>2014</b> , 56, 287-306	1.5	9
32	Reverse phase protein array based tumor profiling identifies a biomarker signature for risk classification of hormone receptor-positive breast cancer. <i>Translational Proteomics</i> , <b>2014</b> , 2, 52-59		16
31	Network-constrained group lasso for high-dimensional multinomial classification with application to cancer subtype prediction. <i>Cancer Informatics</i> , <b>2014</b> , 13, 25-33	2.4	9
30	Network-based biomarkers enhance classical approaches to prognostic gene expression signatures. <i>BMC Systems Biology</i> , <b>2014</b> , 8 Suppl 4, S5	3.5	17
29	Data Requirements for Model-Based Cancer Prognosis Prediction. <i>Cancer Informatics</i> , <b>2015</b> , 14, 123-38	2.4	1
28	FERAL: network-based classifier with application to breast cancer outcome prediction. <i>Bioinformatics</i> , <b>2015</b> , 31, i311-9	7.2	30
27	Gene expression profiling for targeted cancer treatment. <i>Expert Opinion on Drug Discovery</i> , <b>2015</b> , 10, 91-9	6.2	16
26	A Stromal Immune Module Correlated with the Response to Neoadjuvant Chemotherapy, Prognosis and Lymphocyte Infiltration in HER2-Positive Breast Carcinoma Is Inversely Correlated with Hormonal Pathways. <i>PLoS ONE</i> , <b>2016</b> , 11, e0167397	3.7	4

25	Differential distribution improves gene selection stability and has competitive classification performance for patient survival. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e119	20.1	10
24	Biological network-driven gene selection identifies a stromal immune module as a key determinant of triple-negative breast carcinoma prognosis. <i>Oncotmunology</i> , <b>2016</b> , 5, e1061176	7.2	19
23	De novo pathway-based biomarker identification. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e151	20.1	36
22	New insight for pharmacogenomics studies from the transcriptional analysis of two large-scale cancer cell line panels. <i>Scientific Reports</i> , <b>2017</b> , 7, 15126	4.9	5
21	Robust phenotype prediction from gene expression data using differential shrinkage of co-regulated genes. <i>Scientific Reports</i> , <b>2018</b> , 8, 1237	4.9	16
20	From hype to reality: data science enabling personalized medicine. <i>BMC Medicine</i> , <b>2018</b> , 16, 150	11.4	139
19	Circulating microRNA-301 as a promising diagnostic biomarker of hepatitis C virus-related hepatocellular carcinoma. <i>Molecular Biology Reports</i> , <b>2019</b> , 46, 5759-5765	2.8	5
18	Large-Scale Automatic Feature Selection for Biomarker Discovery in High-Dimensional OMICs Data. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 452	4.5	27
17	Incorporating Pathway Information into Feature Selection towards Better Performed Gene Signatures. <i>BioMed Research International</i> , <b>2019</b> , 2019, 2497509	3	5
16	PIMKL: Pathway-Induced Multiple Kernel Learning. <i>Npj Systems Biology and Applications</i> , <b>2019</b> , 5, 8	5	11
15	EMT network-based feature selection improves prognosis prediction in lung adenocarcinoma. <i>PLoS ONE</i> , <b>2019</b> , 14, e0204186	3.7	4
14	Significant random signatures reveals new biomarker for breast cancer. <i>BMC Medical Genomics</i> , <b>2019</b> , 12, 160	3.7	1
13	A Pipeline for Integrated Theory and Data-Driven Modeling of Biomedical Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2021</b> , 18, 811-822	3	1
12	Roles of tetraspanins during trophoblast development: bioinformatics and new perspectives. <i>Cell and Tissue Research</i> , <b>2021</b> , 386, 157-171	4.2	
11	Informed Attentive Predictors: A Generalisable Architecture for Prior Knowledge-Based Assisted Diagnosis of Cancers. <i>Sensors</i> , <b>2021</b> , 21,	3.8	
10	Data-Driven Metabolic Pathway Compositions Enhance Cancer Survival Prediction. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1005125	5	6
9	Pareto Optimization Identifies Diverse Set of Phosphorylation Signatures Predicting Response to Treatment with Dasatinib. <i>PLoS ONE</i> , <b>2015</b> , 10, e0128542	3.7	3
8	EMT network-based feature selection improves prognosis prediction in lung adenocarcinoma.		

7 Big Data, Real-World Data, and Machine Learning. **2019**, 167-195

6 Gene set analysis with graph embedded kernel association test.. *Bioinformatics*, **2021**,

7.2

5 Data\_Sheet\_1.docx. **2019**,

4 Data\_Sheet\_2.xlsx. **2019**,

3 PriPath: identifying dysregulated pathways from differential gene expression via grouping, scoring, and modeling with an embedded feature selection approach. **2023**, 24,

1

2 Circular RNA Expression Signatures Provide Promising Diagnostic and Therapeutic Biomarkers for Chronic Lymphocytic Leukemia. **2023**, 15, 1554

0

1 Identification of a gene expression signature associated with breast cancer survival and risk that improves clinical genomic platforms. **2023**, 3,

0