

Michal Marczyk

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

48
papers

485
citations

12
h-index

20
g-index

55
ext. papers

679
ext. citations

4.2
avg, IF

3.8
L-index

#	Paper	IF	Citations
48	Gene set enrichment for reproducible science: comparison of CERNO and eight other algorithms. <i>Bioinformatics</i> , 2019 , 35, 5146-5154	7.2	45
47	Stage I non-small-cell lung cancer: long-term results of lobectomy versus sublobar resection from the Polish National Lung Cancer Registry. <i>European Journal of Cardio-thoracic Surgery</i> , 2017 , 52, 363-369 ³		43
46	Prognostic value of 5-microRNA based signature in T2-T3N0 colon cancer. <i>Clinical and Experimental Metastasis</i> , 2016 , 33, 765-773	4.7	41
45	Serum lipid profile discriminates patients with early lung cancer from healthy controls. <i>Lung Cancer</i> , 2017 , 112, 69-74	5.9	33
44	Adaptive filtering of microarray gene expression data based on Gaussian mixture decomposition. <i>BMC Bioinformatics</i> , 2013 , 14, 101	3.6	32
43	Ranking metrics in gene set enrichment analysis: do they matter?. <i>BMC Bioinformatics</i> , 2017 , 18, 256	3.6	31
42	Signal Partitioning Algorithm for Highly Efficient Gaussian Mixture Modeling in Mass Spectrometry. <i>PLoS ONE</i> , 2015 , 10, e0134256	3.7	28
41	Radiation-induced changes in serum lipidome of head and neck cancer patients. <i>International Journal of Molecular Sciences</i> , 2014 , 15, 6609-24	6.3	21
40	Serum mass profile signature as a biomarker of early lung cancer. <i>Lung Cancer</i> , 2016 , 99, 46-52	5.9	20
39	Germline variant burden in cancer genes correlates with age at diagnosis and somatic mutation burden. <i>Nature Communications</i> , 2020 , 11, 2438	17.4	17
38	Radiation-related changes in serum proteome profiles detected by mass spectrometry in blood of patients treated with radiotherapy due to larynx cancer. <i>Journal of Radiation Research</i> , 2011 , 52, 575-81	2.4	16
37	The impact of RNA extraction method on accurate RNA sequencing from formalin-fixed paraffin-embedded tissues. <i>BMC Cancer</i> , 2019 , 19, 1189	4.8	14
36	Influence of genetic background and oxidative stress response on risk of mandibular osteoradionecrosis after radiotherapy of head and neck cancer. <i>Head and Neck</i> , 2016 , 38, 387-93	4.2	12
35	Immunological Differences Between Immune-Rich Estrogen Receptor-Positive and Immune-Rich Triple-Negative Breast Cancers. <i>JCO Precision Oncology</i> , 2020 , 4,	3.6	11
34	BatchI: Batch effect Identification in high-throughput screening data using a dynamic programming algorithm. <i>Bioinformatics</i> , 2019 , 35, 1885-1892	7.2	10
33	Neoadjuvant durvalumab plus weekly nab-paclitaxel and dose-dense doxorubicin/cyclophosphamide in triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2021 , 7, 9	7.8	10
32	Defining Risk of Late Recurrence in Early-Stage Estrogen Receptor-Positive Breast Cancer: Clinical Versus Molecular Tools. <i>Journal of Clinical Oncology</i> , 2019 , 37, 1365-1369	2.2	9

31	Radiation-induced changes in levels of selected proteins in peripheral blood serum of breast cancer patients as a potential triage biodosimeter for large-scale radiological emergencies. <i>Health Physics</i> , 2014 , 107, 555-63	2.3	9
30	Sources of high variance between probe signals in Affymetrix short oligonucleotide microarrays. <i>Sensors</i> , 2013 , 14, 532-48	3.8	9
29	Association between plasma proteome profiles analysed by mass spectrometry, a lymphocyte-based DNA-break repair assay and radiotherapy-induced acute mucosal reaction in head and neck cancer patients. <i>International Journal of Radiation Biology</i> , 2011 , 87, 711-9	2.9	9
28	Comparison of peptide cancer signatures identified by mass spectrometry in serum of patients with head and neck, lung and colorectal cancers: association with tumor progression. <i>International Journal of Oncology</i> , 2012 , 40, 148-56	4.4	9
27	Molecular Profiling for Predictors of Radiosensitivity in Patients with Breast or Head-and-Neck Cancer. <i>Cancers</i> , 2020 , 12,	6.6	9
26	Multi-Omics Investigation of Innate Navitoclax Resistance in Triple-Negative Breast Cancer Cells. <i>Cancers</i> , 2020 , 12,	6.6	7
25	Initializing the EM Algorithm for Univariate Gaussian, Multi-Component, Heteroscedastic Mixture Models by Dynamic Programming Partitions. <i>International Journal of Computational Methods</i> , 2018 , 15, 1850012	1.1	5
24	Treatment scheduling effects on the evolution of drug resistance in heterogeneous cancer cell populations. <i>Npj Breast Cancer</i> , 2021 , 7, 60	7.8	4
23	GaMRed-Adaptive Filtering of High-Throughput Biological Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 149-157	3	4
22	Mixture Modeling of 2-D Gel Electrophoresis Spots Enhances the Performance of Spot Detection. <i>IEEE Transactions on Nanobioscience</i> , 2017 , 16, 91-99	3.4	3
21	Technical Validity of a Customized Assay of Sensitivity to Endocrine Therapy Using Sections from Fixed Breast Cancer Tissue. <i>Clinical Chemistry</i> , 2020 , 66, 934-945	5.5	3
20	Affymetrix Chip Definition Files Construction Based on Custom Probe Set Annotation Database. <i>Studies in Computational Intelligence</i> , 2011 , 135-144	0.8	3
19	Diverse immune response of DNA damage repair-deficient tumors. <i>Cell Reports Medicine</i> , 2021 , 2, 1002768	6.8	3
18	Lung cancer survival and comorbidities in lung cancer screening participants of the Gdańsk screening cohort. <i>European Journal of Public Health</i> , 2019 , 29, 1114-1117	2.1	2
17	Modeling of Imaging Mass Spectrometry Data and Testing by Permutation for Biomarkers Discovery in Tissues. <i>Procedia Computer Science</i> , 2015 , 51, 693-702	1.6	2
16	Comparison of Algorithms for Profile-Based Alignment of Low Resolution MALDI-ToF Spectra. <i>Advances in Intelligent Systems and Computing</i> , 2014 , 193-201	0.4	2
15	Improving peak detection by Gaussian mixture modeling of mass spectral signal 2017 ,		1
14	Sensitivity, Specificity and Prioritization of Gene Set Analysis When Applying Different Ranking Metrics. <i>Advances in Intelligent Systems and Computing</i> , 2016 , 61-69	0.4	1

13	Reproducibility of Finding Enriched Gene Sets in Biological Data Analysis. <i>Advances in Intelligent Systems and Computing</i> , 2017 , 146-154	0.4	1
12	Efficient Algorithm for Microarray Probes Re-annotation. <i>Lecture Notes in Computer Science</i> , 2011 , 281-289		1
11	Improved Detection of 2D Gel Electrophoresis Spots by Using Gaussian Mixture Model. <i>Lecture Notes in Computer Science</i> , 2016 , 284-294	0.9	1
10	Targeted RNAseq assay incorporating unique molecular identifiers for improved quantification of gene expression signatures and transcribed mutation fraction in fixed tumor samples. <i>BMC Cancer</i> , 2021 , 21, 114	4.8	1
9	Analysis of the Applicability of microRNAs in Peripheral Blood Leukocytes as Biomarkers of Sensitivity and Exposure to Fractionated Radiotherapy towards Breast Cancer. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
8	Importance of SNP Dependency Correction and Association Integration for Gene Set Analysis in Genome-Wide Association Studies.. <i>Frontiers in Genetics</i> , 2021 , 12, 767358	4.5	1
7	Least Squares Estimators of Peptide Species Concentrations Based on Gaussian Mixture Decompositions of Protein Mass Spectra. <i>Springer Proceedings in Mathematics and Statistics</i> , 2015 , 425-432	0.2	
6	Mixture Model Based Efficient Method for Magnetic Resonance Spectra Quantification. <i>Lecture Notes in Computer Science</i> , 2015 , 406-417	0.9	
5	Processing 2D Gel Electrophoresis Images for Efficient Gaussian Mixture Modeling. <i>Advances in Intelligent Systems and Computing</i> , 2017 , 35-42	0.4	
4	An Efficient Algorithm for Microarray Probes Re-annotation. <i>Lecture Notes in Computer Science</i> , 2014 , 201-218	0.9	
3	Abstract P5-17-01: Targeting Acetyl-CoA carboxylase in pre-clinical breast cancer models. <i>Cancer Research</i> , 2022 , 82, P5-17-01-P5-17-01	10.1	
2	Investigating Sources of Zeros in 10 ⁵ Single-Cell RNAseq Data. <i>Lecture Notes in Computer Science</i> , 2022 , 71-80	0.9	
1	Finding Significantly Enriched Cells in Single-Cell RNA Sequencing by Single-Sample Approaches. <i>Lecture Notes in Computer Science</i> , 2022 , 33-44	0.9	