

# Michal Marczyk

## List of Publications by Year in descending order

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Version: 2024-02-01

51  
papers

834  
citations

516561

16  
h-index

552653

26  
g-index

55  
all docs

55  
docs citations

55  
times ranked

1614  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene set enrichment for reproducible science: comparison of CERNO and eight other algorithms. <i>Bioinformatics</i> , 2019, 35, 5146-5154.	1.8	83
2	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.	0.6	65
3	Serum lipid profile discriminates patients with early lung cancer from healthy controls. <i>Lung Cancer</i> , 2017, 112, 69-74.	0.9	57
4	Prognostic value of 5-microRNA based signature in T2-T3N0 colon cancer. <i>Clinical and Experimental Metastasis</i> , 2016, 33, 765-773.	1.7	52
5	Germline variant burden in cancer genes correlates with age at diagnosis and somatic mutation burden. <i>Nature Communications</i> , 2020, 11, 2438.	5.8	52
6	Ranking metrics in gene set enrichment analysis: do they matter?. <i>BMC Bioinformatics</i> , 2017, 18, 256.	1.2	51
7	Adaptive filtering of microarray gene expression data based on Gaussian mixture decomposition. <i>BMC Bioinformatics</i> , 2013, 14, 101.	1.2	41
8	Neoadjuvant durvalumab plus weekly nab-paclitaxel and dose-dense doxorubicin/cyclophosphamide in triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2021, 7, 9.	2.3	35
9	Signal Partitioning Algorithm for Highly Efficient Gaussian Mixture Modeling in Mass Spectrometry. <i>PLoS ONE</i> , 2015, 10, e0134256.	1.1	31
10	The impact of RNA extraction method on accurate RNA sequencing from formalin-fixed paraffin-embedded tissues. <i>BMC Cancer</i> , 2019, 19, 1189.	1.1	30
11	Radiation-Induced Changes in Serum Lipidome of Head and Neck Cancer Patients. <i>International Journal of Molecular Sciences</i> , 2014, 15, 6609-6624.	1.8	29
12	Serum mass profile signature as a biomarker of early lung cancer. <i>Lung Cancer</i> , 2016, 99, 46-52.	0.9	25
13	Immunological Differences Between Immune-Rich Estrogen Receptor-Positive and Immune-Rich Triple-Negative Breast Cancers. <i>JCO Precision Oncology</i> , 2020, 4, 767-779.	1.5	23
14	Batch: Batch effect Identification in high-throughput screening data using a dynamic programming algorithm. <i>Bioinformatics</i> , 2019, 35, 1885-1892.	1.8	20
15	Treatment scheduling effects on the evolution of drug resistance in heterogeneous cancer cell populations. <i>Npj Breast Cancer</i> , 2021, 7, 60.	2.3	19
16	Molecular Profiling for Predictors of Radiosensitivity in Patients with Breast or Head-and-Neck Cancer. <i>Cancers</i> , 2020, 12, 753.	1.7	18
17	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.	0.8	17
18	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, 575-581.	0.8	16

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19	Predictive Markers of Response to Neoadjuvant Durvalumab with Nab-Paclitaxel and Dose-Dense Doxorubicin/Cyclophosphamide in Basal-Like Triple-Negative Breast Cancer. <i>Clinical Cancer Research</i> , 2022, 28, 2587-2597.	3.2	16
20	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, 387-393.	0.9	14
21	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.	1.4	12
22	Multi-Omics Investigation of Innate Navitoclax Resistance in Triple-Negative Breast Cancer Cells. <i>Cancers</i> , 2020, 12, 2551.	1.7	12
23	Diverse immune response of DNA damage repair-deficient tumors. <i>Cell Reports Medicine</i> , 2021, 2, 100276.	3.3	12
24	Sources of High Variance between Probe Signals in Affymetrix Short Oligonucleotide Microarrays. <i>Sensors</i> , 2014, 14, 532-548.	2.1	10
25	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, 555-563.	0.3	10
26	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, 711-719.	1.0	9
27	GaMRed – adaptive filtering of high-throughput biological data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	1.9	9
28	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.	0.8	8
29	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.	0.1	6
30	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.	1.1	6
31	Mixture Modeling of 2-D Gel Electrophoresis Spots Enhances the Performance of Spot Detection. <i>IEEE Transactions on Nanobioscience</i> , 2017, 16, 91-99.	2.2	5
32	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.	1.5	5
33	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.	1.1	4
34	Comprehensive Analysis of Metabolic Isozyme Targets in Cancer. <i>Cancer Research</i> , 2022, 82, 1698-1711.	0.4	4
35	Quantifying Spatial Heterogeneity of Tumor-Infiltrating Lymphocytes to Predict Survival of Individual Cancer Patients. <i>Journal of Personalized Medicine</i> , 2022, 12, 1113.	1.1	4
36	Modeling of Imaging Mass Spectrometry Data and Testing by Permutation for Biomarkers Discovery in Tissues. <i>Procedia Computer Science</i> , 2015, 51, 693-702.	1.2	3

#	ARTICLE	IF	CITATIONS
37	Analysis of the Applicability of microRNAs in Peripheral Blood Leukocytes as Biomarkers of Sensitivity and Exposure to Fractionated Radiotherapy towards Breast Cancer. International Journal of Molecular Sciences, 2021, 22, 8705.	1.8	3
38	Reproducibility of Finding Enriched Gene Sets in Biological Data Analysis. Advances in Intelligent Systems and Computing, 2017, , 146-154.	0.5	3
39	Affymetrix Chip Definition Files Construction Based on Custom Probe Set Annotation Database. Studies in Computational Intelligence, 2011, , 135-144.	0.7	3
40	Cancer Relevance of Human Genes. Journal of the National Cancer Institute, 2022, 114, 988-995.	3.0	2
41	Improving peak detection by Gaussian mixture modeling of mass spectral signal. , 2017, , .		1
42	Immunological differences between immune-rich estrogen receptor-positive and -negative breast cancers. Annals of Oncology, 2019, 30, v60-v61.	0.6	1
43	Sensitivity, Specificity and Prioritization of Gene Set Analysis When Applying Different Ranking Metrics. Advances in Intelligent Systems and Computing, 2016, , 61-69.	0.5	1
44	Efficient Algorithm for Microarray Probes Re-annotation. Lecture Notes in Computer Science, 2011, , 281-289.	1.0	1
45	Improved Detection of 2D Gel Electrophoresis Spots by Using Gaussian Mixture Model. Lecture Notes in Computer Science, 2016, , 284-294.	1.0	1
46	Abstract P5-17-01: Targeting Acetyl-CoA carboxylase in pre-clinical breast cancer models. Cancer Research, 2022, 82, P5-17-01-P5-17-01.	0.4	1
47	Finding Significantly Enriched Cells in Single-Cell RNA Sequencing by Single-Sample Approaches. Lecture Notes in Computer Science, 2022, , 33-44.	1.0	1
48	An Efficient Algorithm for Microarray Probes Re-annotation. Lecture Notes in Computer Science, 2014, , 201-218.	1.0	0
49	Least Squares Estimators of Peptide Species Concentrations Based on Gaussian Mixture Decompositions of Protein Mass Spectra. Springer Proceedings in Mathematics and Statistics, 2015, , 425-432.	0.1	0
50	Mixture Model Based Efficient Method for Magnetic Resonance Spectra Quantification. Lecture Notes in Computer Science, 2015, , 406-417.	1.0	0
51	Processing 2D Gel Electrophoresis Images for Efficient Gaussian Mixture Modeling. Advances in Intelligent Systems and Computing, 2017, , 35-42.	0.5	0