

Parag Mallick

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

7,726
citations

331259

21
h-index

301761

39
g-index

44
all docs

44
docs citations

44
times ranked

14354
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome and genome evolution during HER2-amplified breast neoplasia. <i>Breast Cancer Research</i> , 2021, 23, 73.	2.2	2
2	Multicompartment modeling of protein shedding kinetics during vascularized tumor growth. <i>Scientific Reports</i> , 2020, 10, 16709.	1.6	4
3	ImmunoGlobe: enabling systems immunology with a manually curated intercellular immune interaction network. <i>BMC Bioinformatics</i> , 2020, 21, 346.	1.2	6
4	Improving Precursor Selectivity in Data-Independent Acquisition Using Overlapping Windows. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 669-684.	1.2	101
5	Loss of ER retention motif of AGR2 can impact mTORC signaling and promote cancer metastasis. <i>Oncogene</i> , 2019, 38, 3003-3018.	2.6	23
6	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	3.9	580
7	Global Transcriptome Analysis of RNA Abundance Regulation by ADAR in Lung Adenocarcinoma. <i>EBioMedicine</i> , 2018, 27, 167-175.	2.7	23
8	A blood biomarker for monitoring response to anti-EGFR therapy. <i>Cancer Biomarkers</i> , 2018, 22, 333-344.	0.8	3
9	Multi-lectin Affinity Chromatography and Quantitative Proteomic Analysis Reveal Differential Glycoform Levels between Prostate Cancer and Benign Prostatic Hyperplasia Sera. <i>Scientific Reports</i> , 2018, 8, 6509.	1.6	38
10	A Temporal Examination of Platelet Counts as a Predictor of Prognosis in Lung, Prostate, and Colon Cancer Patients. <i>Scientific Reports</i> , 2018, 8, 6564.	1.6	25
11	Proteogenomic Analysis of Surgically Resected Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2018, 13, 1519-1529.	0.5	17
12	A Bayesian Active Learning Experimental Design for Inferring Signaling Networks. <i>Journal of Computational Biology</i> , 2018, 25, 709-725.	0.8	1
13	Longitudinal Multiplexed Measurement of Quantitative Proteomic Signatures in Mouse Lymphoma Models Using Magneto-Nanosensors. <i>Theranostics</i> , 2018, 8, 1389-1398.	4.6	11
14	The Predictive Value of Inflammation-Related Peripheral Blood Measurements in Cancer Staging and Prognosis. <i>Frontiers in Oncology</i> , 2018, 8, 78.	1.3	73
15	A Robust Protocol for Protein Extraction and Digestion. <i>Methods in Molecular Biology</i> , 2017, 1550, 1-10.	0.4	4
16	Data Conversion with ProteoWizard msConvert. <i>Methods in Molecular Biology</i> , 2017, 1550, 339-368.	0.4	346
17	JUN-Mediated Downregulation of EGFR Signaling Is Associated with Resistance to Gefitinib in EGFR-mutant NSCLC Cell Lines. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 1645-1657.	1.9	18
18	Longitudinal Monitoring of Antibody Responses against Tumor Cells Using Magneto-nanosensors with a Nanoliter of Blood. <i>Nano Letters</i> , 2017, 17, 6644-6652.	4.5	13

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19	Platelet count as a predictor of metastasis and venous thromboembolism in patients with cancer. <i>Convergent Science Physical Oncology</i> , 2017, 3, 023001.	2.6	38
20	Assessing biological and technological variability in protein levels measured in pre-diagnostic plasma samples of women with breast cancer. <i>Biomarker Research</i> , 2017, 5, 30.	2.8	13
21	Protein biomarkers on tissue as imaged via MALDI mass spectrometry: A systematic approach to study the limits of detection. <i>Proteomics</i> , 2016, 16, 1660-1669.	1.3	12
22	Single cell dynamic phenotyping. <i>Scientific Reports</i> , 2016, 6, 34785.	1.6	16
23	A high-content image-based method for quantitatively studying context-dependent cell population dynamics. <i>Scientific Reports</i> , 2016, 6, 29752.	1.6	50
24	Epigenetic changes mediated by polycomb repressive complex 2 and E2a are associated with drug resistance in a mouse model of lymphoma. <i>Genome Medicine</i> , 2016, 8, 54.	3.6	12
25	Probabilistic Segmentation of Mass Spectrometry (MS) Images Helps Select Important Ions and Characterize Confidence in the Resulting Segments. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1761-1772.	2.5	54
26	The Impact of Microenvironmental Heterogeneity on the Evolution of Drug Resistance in Cancer Cells. <i>Cancer Informatics</i> , 2015, 14s4, CIN.S19338.	0.9	59
27	Building high-quality assay libraries for targeted analysis of SWATH MS data. <i>Nature Protocols</i> , 2015, 10, 426-441.	5.5	319
28	<i>Cardinal</i> : an R package for statistical analysis of mass spectrometry-based imaging experiments. <i>Bioinformatics</i> , 2015, 31, 2418-2420.	1.8	203
29	Neuronal Activity Promotes Glioma Growth through Neuroligin-3 Secretion. <i>Cell</i> , 2015, 161, 803-816.	13.5	550
30	Predictive Modeling of Drug Response in Non-Hodgkin's Lymphoma. <i>PLoS ONE</i> , 2015, 10, e0129433.	1.1	24
31	DD-03 * THE NATURALLY OCCURRING STEROID, WITHAFERIN A, IN SYNERGISTIC CONCERT WITH HER2/EGFR INHIBITORS ABROGATES PROLIFERATION OF HUMAN GLIOBLASTOMA CELL CULTURES AT NANOMOLAR CONCENTRATIONS. <i>Neuro-Oncology</i> , 2014, 16, v60-v60.	0.6	0
32	Anti-MET ImmunoPET for Non-Small Cell Lung Cancer Using Novel Fully Human Antibody Fragments. <i>Molecular Cancer Therapeutics</i> , 2014, 13, 2607-2617.	1.9	29
33	Anterior gradient 2 (AGR2): Blood-based biomarker elevated in metastatic prostate cancer associated with the neuroendocrine phenotype. <i>Prostate</i> , 2013, 73, 306-315.	1.2	60
34	A cross-platform toolkit for mass spectrometry and proteomics. <i>Nature Biotechnology</i> , 2012, 30, 918-920.	9.4	2,794
35	Evolutionary Modeling of Combination Treatment Strategies To Overcome Resistance to Tyrosine Kinase Inhibitors in Non-Small Cell Lung Cancer. <i>Molecular Pharmaceutics</i> , 2011, 8, 2069-2079.	2.3	55
36	Impact of Protein Stability, Cellular Localization, and Abundance on Proteomic Detection of Tumor-Derived Proteins in Plasma. <i>PLoS ONE</i> , 2011, 6, e23090.	1.1	15

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37	Proteomics: a pragmatic perspective. <i>Nature Biotechnology</i> , 2010, 28, 695-709.	9.4	374
38	Precursor-Ion Mass Re-Estimation Improves Peptide Identification on Hybrid Instruments. <i>Journal of Proteome Research</i> , 2008, 7, 4031-4039.	1.8	49
39	ProteoWizard: open source software for rapid proteomics tools development. <i>Bioinformatics</i> , 2008, 24, 2534-2536.	1.8	1,646
40	Analysis of the <i>Saccharomyces cerevisiae</i> proteome with PeptideAtlas. <i>Genome Biology</i> , 2006, 7, R106.	13.9	60