

Maksim I Sorokin

List of Publications by Year in descending order

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69
papers

1,686
citations

331670

21
h-index

330143

37
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71
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71
docs citations

71
times ranked

1659
citing authors

#	ARTICLE	IF	CITATIONS
1	A Review of Recent Studies on the Effects of SARS-CoV-2 Infection and SARS-CoV-2 Vaccines on Male Reproductive Health. <i>Medical Science Monitor</i> , 2022, 28, e935879.	1.1	12
2	Better Agreement of Human Transcriptomic and Proteomic Cancer Expression Data at the Molecular Pathway Activation Level. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2611.	4.1	4
3	Transcriptomic Portraits and Molecular Pathway Activation Features of Adult Spinal Intramedullary Astrocytomas. <i>Frontiers in Oncology</i> , 2022, 12, 837570.	2.8	3
4	Gene Expression-Based Signature Can Predict Sorafenib Response in Kidney Cancer. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 753318.	3.5	7
5	The Role of the Metabolism of Zinc and Manganese Ions in Human Cancerogenesis. <i>Biomedicines</i> , 2022, 10, 1072.	3.2	17
6	Shambhalaâ€²: A Protocol for Uniformly Shaped Harmonization of Gene Expression Profiles of Various Formats. <i>Current Protocols</i> , 2022, 2, .	2.9	4
7	Next-Generation Grade and Survival Expression Biomarkers of Human Gliomas Based on Algorithmically Reconstructed Molecular Pathways. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7330.	4.1	6
8	Subtype of Neuroblastoma Cells with High KIT Expression Are Dependent on KIT and Its Knockdown Induces Compensatory Activation of Pro-Survival Signaling. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7724.	4.1	4
9	Using proteomic and transcriptomic data to assess activation of intracellular molecular pathways. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021, 127, 1-53.	2.3	13
10	Algorithmic Annotation of Functional Roles for Components of 3,044 Human Molecular Pathways. <i>Frontiers in Genetics</i> , 2021, 12, 617059.	2.3	30
11	DNA repair pathway activation features in follicular and papillary thyroid tumors, interrogated using 95 experimental RNA sequencing profiles. <i>Heliyon</i> , 2021, 7, e06408.	3.2	10
12	Human blood serum can donor-specifically antagonize effects of EGFR-targeted drugs on squamous carcinoma cell growth. <i>Heliyon</i> , 2021, 7, e06394.	3.2	9
13	Gene Expression Signature of Endometrial Samples from Women with and without Endometriosis. <i>Journal of Minimally Invasive Gynecology</i> , 2021, 28, 1774-1785.	0.6	11
14	Machine Learning Applicability for Classification of PAD/VCD Chemotherapy Response Using 53 Multiple Myeloma RNA Sequencing Profiles. <i>Frontiers in Oncology</i> , 2021, 11, 652063.	2.8	16
15	Simvastatin is effective in killing the radioresistant breast carcinoma cells. <i>Radiology and Oncology</i> , 2021, 55, 305-316.	1.7	5
16	Large-Scale Transcriptomics-Driven Approach Revealed Overexpression of CRNDE as a Poor Survival Prognosis Biomarker in Glioblastoma. <i>Cancers</i> , 2021, 13, 3419.	3.7	14
17	COVID-19â€²-associated inhibition of energy accumulation pathways in human semen samples. <i>F&S Science</i> , 2021, 2, 355-364.	0.9	8
18	RNA Sequencing for Personalized Treatment of Metastatic Leiomyosarcoma: Case Report. <i>Frontiers in Oncology</i> , 2021, 11, 666001.	2.8	6

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19	Case of multifocal glioblastoma with four fusion transcripts of ALK, FGFR2, NTRK2, and NTRK3 genes stresses the need for tumor tissue multisampling for transcriptomic analysis. <i>Journal of Physical Education and Sports Management</i> , 2021, 7, a006100.	1.2	8
20	Algorithmically Deduced FREM2 Molecular Pathway Is a Potent Grade and Survival Biomarker of Human Gliomas. <i>Cancers</i> , 2021, 13, 4117.	3.7	9
21	Growth factor signaling predicts therapy resistance mechanisms and defines neuroblastoma subtypes. <i>Oncogene</i> , 2021, 40, 6258-6272.	5.9	19
22	RNA Sequencing Data for FFPE Tumor Blocks Can Be Used for Robust Estimation of Tumor Mutation Burden in Individual Biosamples. <i>Frontiers in Oncology</i> , 2021, 11, 732644.	2.8	6
23	Experimental and Meta-Analytic Validation of RNA Sequencing Signatures for Predicting Status of Microsatellite Instability. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 737821.	3.5	4
24	EGFR Pathway-Based Gene Signatures of Druggable Gene Mutations in Melanoma, Breast, Lung, and Thyroid Cancers. <i>Biochemistry (Moscow)</i> , 2021, 86, 1477-1488.	1.5	1
25	RNA sequencing for research and diagnostics in clinical oncology. <i>Seminars in Cancer Biology</i> , 2020, 60, 311-323.	9.6	56
26	Analysis of miR-9-5p, miR-124-3p, miR-21-5p, miR-138-5p, and miR-1-3p in Glioblastoma Cell Lines and Extracellular Vesicles. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8491.	4.1	25
27	Cancer gene expression profiles associated with clinical outcomes to chemotherapy treatments. <i>BMC Medical Genomics</i> , 2020, 13, 111.	1.5	19
28	Reciprocal Dysregulation of MiR-146b and MiR-451 Contributes in Malignant Phenotype of Follicular Thyroid Tumor. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5950.	4.1	12
29	Large-Scale Profiling of Signaling Pathways Reveals a Distinct Demarcation between Normal and Extended Liver Resection. <i>Cells</i> , 2020, 9, 1149.	4.1	3
30	RNA Sequencing in Comparison to Immunohistochemistry for Measuring Cancer Biomarkers in Breast Cancer and Lung Cancer Specimens. <i>Biomedicines</i> , 2020, 8, 114.	3.2	22
31	RNA Sequencing-Based Identification of Ganglioside GD2-Positive Cancer Phenotype. <i>Biomedicines</i> , 2020, 8, 142.	3.2	25
32	Diversity of Clinically Relevant Outcomes Resulting from Hypofractionated Radiation in Human Glioma Stem Cells Mirrors Distinct Patterns of Transcriptomic Changes. <i>Cancers</i> , 2020, 12, 570.	3.7	10
33	Intratumoral Heterogeneity and Longitudinal Changes in Gene Expression Predict Differential Drug Sensitivity in Newly Diagnosed and Recurrent Glioblastoma. <i>Cancers</i> , 2020, 12, 520.	3.7	38
34	RNA sequencing profiles and diagnostic signatures linked with response to ramucirumab in gastric cancer. <i>Journal of Physical Education and Sports Management</i> , 2020, 6, a004945.	1.2	26
35	Molecular heterogeneity in breast carcinoma cells with increased invasive capacities. <i>Radiology and Oncology</i> , 2020, 54, 103-118.	1.7	10
36	Flexible Data Trimming Improves Performance of Global Machine Learning Methods in Omics-Based Personalized Oncology. <i>International Journal of Molecular Sciences</i> , 2020, 21, 713.	4.1	19

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37	Quantitation of Molecular Pathway Activation Using RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2020, 2063, 189-206.	0.9	40
38	Molecular Pathway Analysis of Mutation Data for Biomarkers Discovery and Scoring of Target Cancer Drugs. <i>Methods in Molecular Biology</i> , 2020, 2063, 207-234.	0.9	8
39	Oncobox Method for Scoring Efficiencies of Anticancer Drugs Based on Gene Expression Data. <i>Methods in Molecular Biology</i> , 2020, 2063, 235-255.	0.9	21
40	Clinical use of RNA sequencing and onco-box analytics to predict personalized targeted therapeutic efficacy. <i>Journal of Clinical Oncology</i> , 2020, 38, e13676-e13676.	1.6	7
41	Constitutive interferon signaling maintains critical threshold of MLKL expression to license necroptosis. <i>Cell Death and Differentiation</i> , 2019, 26, 332-347.	11.2	129
42	High FREM2 Gene and Protein Expression Are Associated with Favorable Prognosis of IDH-WT Glioblastomas. <i>Cancers</i> , 2019, 11, 1060.	3.7	16
43	Retroelement-Linked H3K4me1 Histone Tags Uncover Regulatory Evolution Trends of Gene Enhancers and Feature Quickly Evolving Molecular Processes in Human Physiology. <i>Cells</i> , 2019, 8, 1219.	4.1	5
44	Atlas of RNA sequencing profiles for normal human tissues. <i>Scientific Data</i> , 2019, 6, 36.	5.3	75
45	Shambhala: a platform-agnostic data harmonizer for gene expression data. <i>BMC Bioinformatics</i> , 2019, 20, 66.	2.6	31
46	High-Throughput Mutation Data Now Complement Transcriptomic Profiling: Advances in Molecular Pathway Activation Analysis Approach in Cancer Biology. <i>Cancer Informatics</i> , 2019, 18, 117693511983884.	1.9	13
47	Retroelement-Linked Transcription Factor Binding Patterns Point to Quickly Developing Molecular Pathways in Human Evolution. <i>Cells</i> , 2019, 8, 130.	4.1	11
48	Exploration of the Transcriptional Landscape of ALPPS Reveals the Pathways of Accelerated Liver Regeneration. <i>Frontiers in Oncology</i> , 2019, 9, 1206.	2.8	30
49	Plasma exosomes stimulate breast cancer metastasis through surface interactions and activation of FAK signaling. <i>Breast Cancer Research and Treatment</i> , 2019, 174, 129-141.	2.5	39
50	RNA sequencing analysis for profiling activation of cancer-associated molecular pathways. <i>Journal of Clinical Oncology</i> , 2019, 37, e13032-e13032.	1.6	3
51	Oncobox, gene expression-based second opinion system for predicting response to treatment in advanced solid tumors. <i>Journal of Clinical Oncology</i> , 2019, 37, e13143-e13143.	1.6	11
52	RetroSpect, a New Method of Measuring Gene Regulatory Evolution Rates Using Co-mapping of Genomic Functional Features with Transposable Elements. , 2019, , 85-111.		0
53	RNA-sequencing and bioinformatic analysis to pre-assess sensitivity to targeted therapeutics in recurrent glioblastoma. <i>Journal of Clinical Oncology</i> , 2019, 37, e13533-e13533.	1.6	0
54	Anticancer Activity of the Goat Antimicrobial Peptide ChMAP-28. <i>Frontiers in Pharmacology</i> , 2018, 9, 1501.	3.5	19

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55	Cytotoxic Potential of the Novel Horseshoe Crab Peptide Polyphemusin III. <i>Marine Drugs</i> , 2018, 16, 466.	4.6	26
56	Oncobox Bioinformatical Platform for Selecting Potentially Effective Combinations of Target Cancer Drugs Using High-Throughput Gene Expression Data. <i>Cancers</i> , 2018, 10, 365.	3.7	27
57	Profiling of Human Molecular Pathways Affected by Retrotransposons at the Level of Regulation by Transcription Factor Proteins. <i>Frontiers in Immunology</i> , 2018, 9, 30.	4.8	38
58	Acquired resistance to tyrosine kinase inhibitors may be linked with the decreased sensitivity to X-ray irradiation. <i>Oncotarget</i> , 2018, 9, 5111-5124.	1.8	30
59	Molecular pathway activation – New type of biomarkers for tumor morphology and personalized selection of target drugs. <i>Seminars in Cancer Biology</i> , 2018, 53, 110-124.	9.6	101
60	FLOating-Window Projective Separator (FloWPS): A Data Trimming Tool for Support Vector Machines (SVM) to Improve Robustness of the Classifier. <i>Frontiers in Genetics</i> , 2018, 9, 717.	2.3	19
61	Functional Properties of Circulating Exosomes Mediated by Surface-Attached Plasma Proteins. <i>Journal of Hematology (Brossard, Quebec)</i> , 2018, 7, 149-153.	1.0	11
62	Cutting Edge: Activation of STING in T Cells Induces Type I IFN Responses and Cell Death. <i>Journal of Immunology</i> , 2017, 199, 397-402.	0.8	237
63	Data aggregation at the level of molecular pathways improves stability of experimental transcriptomic and proteomic data. <i>Cell Cycle</i> , 2017, 16, 1810-1823.	2.6	96
64	Activation of intracellular signaling pathways as a new type of biomarkers for selection of target anticancer drugs. <i>Journal of Clinical Oncology</i> , 2017, 35, e23142-e23142.	1.6	14
65	Gene expression and molecular pathway activation signatures of MYCN-amplified neuroblastomas. <i>Oncotarget</i> , 2017, 8, 83768-83780.	1.8	39
66	Molecular pathway activation features of pediatric acute myeloid leukemia (AML) and acute lymphoblast leukemia (ALL) cells. <i>Aging</i> , 2016, 8, 2936-2947.	3.1	15
67	MiRImpact, a new bioinformatic method using complete microRNA expression profiles to assess their overall influence on the activity of intracellular molecular pathways. <i>Cell Cycle</i> , 2016, 15, 689-698.	2.6	58
68	Mitochondrial retrograde signaling inhibits the survival during prolong S/G2 arrest in <i>Saccharomyces cerevisiae</i> . <i>Oncotarget</i> , 2015, 6, 44084-44094.	1.8	11
69	Early manifestations of replicative aging in the yeast <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell</i> , 2014, 1, 37-42.	3.2	14