

Maksim I Sorokin

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

1,686
citations

331670

21
h-index

330143

37
g-index

71
all docs

71
docs citations

71
times ranked

1659
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | 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 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | Atlas of RNA sequencing profiles for normal human tissues. <i>Scientific Data</i> , 2019, 6, 36. | 5.3 | 75 |
| 6 | 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 |
| 7 | RNA sequencing for research and diagnostics in clinical oncology. <i>Seminars in Cancer Biology</i> , 2020, 60, 311-323. | 9.6 | 56 |
| 8 | Quantitation of Molecular Pathway Activation Using RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2020, 2063, 189-206. | 0.9 | 40 |
| 9 | 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 |
| 10 | Gene expression and molecular pathway activation signatures of MYCN-amplified neuroblastomas. <i>Oncotarget</i> , 2017, 8, 83768-83780. | 1.8 | 39 |
| 11 | 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 |
| 12 | 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 |
| 13 | Shambhala: a platform-agnostic data harmonizer for gene expression data. <i>BMC Bioinformatics</i> , 2019, 20, 66. | 2.6 | 31 |
| 14 | 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 |
| 15 | 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 |
| 16 | Algorithmic Annotation of Functional Roles for Components of 3,044 Human Molecular Pathways. <i>Frontiers in Genetics</i> , 2021, 12, 617059. | 2.3 | 30 |
| 17 | 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 |
| 18 | Cytotoxic Potential of the Novel Horseshoe Crab Peptide Polyphemusin III. <i>Marine Drugs</i> , 2018, 16, 466. | 4.6 | 26 |

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|----|---|-----|-----------|
| 19 | 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 |
| 20 | 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 |
| 21 | RNA Sequencing-Based Identification of Ganglioside GD2-Positive Cancer Phenotype. <i>Biomedicines</i> , 2020, 8, 142. | 3.2 | 25 |
| 22 | 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 |
| 23 | 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 |
| 24 | Anticancer Activity of the Goat Antimicrobial Peptide ChMAP-28. <i>Frontiers in Pharmacology</i> , 2018, 9, 1501. | 3.5 | 19 |
| 25 | 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 |
| 26 | Cancer gene expression profiles associated with clinical outcomes to chemotherapy treatments. <i>BMC Medical Genomics</i> , 2020, 13, 111. | 1.5 | 19 |
| 27 | 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 |
| 28 | Growth factor signaling predicts therapy resistance mechanisms and defines neuroblastoma subtypes. <i>Oncogene</i> , 2021, 40, 6258-6272. | 5.9 | 19 |
| 29 | The Role of the Metabolism of Zinc and Manganese Ions in Human Cancerogenesis. <i>Biomedicines</i> , 2022, 10, 1072. | 3.2 | 17 |
| 30 | High FREM2 Gene and Protein Expression Are Associated with Favorable Prognosis of IDH-WT Glioblastomas. <i>Cancers</i> , 2019, 11, 1060. | 3.7 | 16 |
| 31 | 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 |
| 32 | 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 |
| 33 | 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 |
| 34 | 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 |
| 35 | Early manifestations of replicative aging in the yeast <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell</i> , 2014, 1, 37-42. | 3.2 | 14 |
| 36 | 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 |

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|----|---|-----|-----------|
| 37 | 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 |
| 38 | 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 |
| 39 | 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 |
| 40 | Retroelement-Linked Transcription Factor Binding Patterns Point to Quickly Developing Molecular Pathways in Human Evolution. <i>Cells</i> , 2019, 8, 130. | 4.1 | 11 |
| 41 | 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 |
| 42 | 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 |
| 43 | 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 |
| 44 | 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 |
| 45 | 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 |
| 46 | Molecular heterogeneity in breast carcinoma cells with increased invasive capacities. <i>Radiology and Oncology</i> , 2020, 54, 103-118. | 1.7 | 10 |
| 47 | 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 |
| 48 | 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 |
| 49 | Algorithmically Deduced FREM2 Molecular Pathway Is a Potent Grade and Survival Biomarker of Human Gliomas. <i>Cancers</i> , 2021, 13, 4117. | 3.7 | 9 |
| 50 | COVID-19-associated inhibition of energy accumulation pathways in human semen samples. <i>F&S Science</i> , 2021, 2, 355-364. | 0.9 | 8 |
| 51 | 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 |
| 52 | 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 |
| 53 | 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 |
| 54 | Gene Expression-Based Signature Can Predict Sorafenib Response in Kidney Cancer. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 753318. | 3.5 | 7 |

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|----|--|-----|-----------|
| 55 | RNA Sequencing for Personalized Treatment of Metastatic Leiomyosarcoma: Case Report. <i>Frontiers in Oncology</i> , 2021, 11, 666001. | 2.8 | 6 |
| 56 | 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 |
| 57 | 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 |
| 58 | 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 |
| 59 | Simvastatin is effective in killing the radioresistant breast carcinoma cells. <i>Radiology and Oncology</i> , 2021, 55, 305-316. | 1.7 | 5 |
| 60 | 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 |
| 61 | 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 |
| 62 | Shambhala ² : A Protocol for Uniformly Shaped Harmonization of Gene Expression Profiles of Various Formats. <i>Current Protocols</i> , 2022, 2, . | 2.9 | 4 |
| 63 | 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 |
| 64 | 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 |
| 65 | RNA sequencing analysis for profiling activation of cancer-associated molecular pathways.. <i>Journal of Clinical Oncology</i> , 2019, 37, e13032-e13032. | 1.6 | 3 |
| 66 | Transcriptomic Portraits and Molecular Pathway Activation Features of Adult Spinal Intramedullary Astrocytomas. <i>Frontiers in Oncology</i> , 2022, 12, 837570. | 2.8 | 3 |
| 67 | 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 |
| 68 | RetroSpect, a New Method of Measuring Gene Regulatory Evolution Rates Using Co-mapping of Genomic Functional Features with Transposable Elements. , 2019, , 85-111. | | 0 |
| 69 | 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 |