

# Borisov Nikolay

## List of Publications by Year in descending order

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Version: 2024-02-01

70  
papers

2,437  
citations

236612

25  
h-index

205818

48  
g-index

73  
all docs

73  
docs citations

73  
times ranked

2332  
citing authors

#	ARTICLE	IF	CITATIONS
1	Pathway Based Analysis of Mutation Data Is Efficient for Scoring Target Cancer Drugs. <i>Frontiers in Pharmacology</i> , 2019, 10, 1.	1.6	303
2	Systems-level interactions between insulin-EGF networks amplify mitogenic signaling. <i>Molecular Systems Biology</i> , 2009, 5, 256.	3.2	205
3	Scaffolding Protein Grb2-associated Binder 1 Sustains Epidermal Growth Factor-induced Mitogenic and Survival Signaling by Multiple Positive Feedback Loops*. <i>Journal of Biological Chemistry</i> , 2006, 281, 19925-19938.	1.6	153
4	In silico Pathway Activation Network Decomposition Analysis (iPANDA) as a method for biomarker development. <i>Nature Communications</i> , 2016, 7, 13427.	5.8	126
5	Oncofinder, a new method for the analysis of intracellular signaling pathway activation using transcriptomic data. <i>Frontiers in Genetics</i> , 2014, 5, 55.	1.1	122
6	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.	4.3	101
7	Data aggregation at the level of molecular pathways improves stability of experimental transcriptomic and proteomic data. <i>Cell Cycle</i> , 2017, 16, 1810-1823.	1.3	96
8	Signaling through Receptors and Scaffolds: Independent Interactions Reduce Combinatorial Complexity. <i>Biophysical Journal</i> , 2005, 89, 951-966.	0.2	91
9	Signaling pathways activation profiles make better markers of cancer than expression of individual genes. <i>Oncotarget</i> , 2014, 5, 10198-10205.	0.8	91
10	Silencing AML1-ETO gene expression leads to simultaneous activation of both pro-apoptotic and proliferation signaling. <i>Leukemia</i> , 2014, 28, 2222-2228.	3.3	77
11	Bioinformatics Meets Biomedicine: OncoFinder, a Quantitative Approach for Interrogating Molecular Pathways Using Gene Expression Data. <i>Methods in Molecular Biology</i> , 2017, 1613, 53-83.	0.4	62
12	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.	1.3	58
13	Mathematical Justification of Expression-Based Pathway Activation Scoring (PAS). <i>Methods in Molecular Biology</i> , 2017, 1613, 31-51.	0.4	56
14	In search for geroprotectors: in silico screening and in vitro validation of signalome-level mimetics of young healthy state. <i>Aging</i> , 2016, 8, 2127-2152.	1.4	56
15	A method of gene expression data transfer from cell lines to cancer patients for machine-learning prediction of drug efficiency. <i>Cell Cycle</i> , 2018, 17, 486-491.	1.3	55
16	A method for predicting target drug efficiency in cancer based on the analysis of signaling pathway activation. <i>Oncotarget</i> , 2015, 6, 29347-29356.	0.8	52
17	Signaling pathway cloud regulation for in silico screening and ranking of the potential geroprotective drugs. <i>Frontiers in Genetics</i> , 2014, 5, 49.	1.1	47
18	Domain-oriented reduction of rule-based network models. <i>IET Systems Biology</i> , 2008, 2, 342-351.	0.8	45

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19	Novel robust biomarkers for human bladder cancer based on activation of intracellular signaling pathways. <i>Oncotarget</i> , 2014, 5, 9022-9032.	0.8	43
20	Quantitation of Molecular Pathway Activation Using RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2020, 2063, 189-206.	0.4	40
21	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.	2.2	38
22	Trading the micro-world of combinatorial complexity for the macro-world of protein interaction domains. <i>BioSystems</i> , 2006, 83, 152-166.	0.9	36
23	Molecular pathway activation features linked with transition from normal skin to primary and metastatic melanomas in human. <i>Oncotarget</i> , 2016, 7, 656-670.	0.8	32
24	Shambhala: a platform-agnostic data harmonizer for gene expression data. <i>BMC Bioinformatics</i> , 2019, 20, 66.	1.2	31
25	Algorithmic Annotation of Functional Roles for Components of 3,044 Human Molecular Pathways. <i>Frontiers in Genetics</i> , 2021, 12, 617059.	1.1	30
26	A NEW GRAPHICAL USER INTERFACE FOR FAST CONSTRUCTION OF COMPUTATION PHANTOMS AND MCNP CALCULATIONS: APPLICATION TO CALIBRATION OF IN VIVO MEASUREMENT SYSTEMS. <i>Health Physics</i> , 2002, 83, 272-279.	0.3	24
27	Combinatorial high-throughput experimental and bioinformatic approach identifies molecular pathways linked with the sensitivity to anticancer target drugs. <i>Oncotarget</i> , 2015, 6, 27227-27238.	0.8	24
28	Application of Monte Carlo calculations to calibration of anthropomorphic phantoms used for activity assessment of actinides in lungs. <i>Radiation Protection Dosimetry</i> , 2003, 105, 403-408.	0.4	21
29	New Paradigm of Machine Learning (ML) in Personalized Oncology: Data Trimming for Squeezing More Biomarkers From Clinical Datasets. <i>Frontiers in Oncology</i> , 2019, 9, 658.	1.3	21
30	Pathway Instability Is an Effective New Mutation-Based Type of Cancer Biomarkers. <i>Frontiers in Oncology</i> , 2018, 8, 658.	1.3	21
31	Oncobox Method for Scoring Efficiencies of Anticancer Drugs Based on Gene Expression Data. <i>Methods in Molecular Biology</i> , 2020, 2063, 235-255.	0.4	21
32	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.	1.1	19
33	Cancer gene expression profiles associated with clinical outcomes to chemotherapy treatments. <i>BMC Medical Genomics</i> , 2020, 13, 111.	0.7	19
34	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.	1.8	19
35	Disparity between Inter-Patient Molecular Heterogeneity and Repertoires of Target Drugs Used for Different Types of Cancer in Clinical Oncology. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1580.	1.8	17
36	The Role of the Metabolism of Zinc and Manganese Ions in Human Cancerogenesis. <i>Biomedicines</i> , 2022, 10, 1072.	1.4	17

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37	Application of new imaging and calculation techniques to activity and dose assessment in the case of a <sup>106</sup> Ru contaminated wound. <i>Radiation Protection Dosimetry</i> , 2003, 105, 219-223.	0.4	16
38	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.	1.3	16
39	OncoboxPD: human 51 672 molecular pathways database with tools for activity calculating and visualization. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2280-2291.	1.9	16
40	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.	0.8	14
41	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.	0.9	13
42	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.	1.0	13
43	Early stage of cytomegalovirus infection suppresses host microRNA expression regulation in human fibroblasts. <i>Cell Cycle</i> , 2016, 15, 3378-3389.	1.3	12
44	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.	0.4	8
45	Development of voxelised numerical phantoms using MCNP Monte Carlo code: Application to in vivo measurement. <i>Radioprotection</i> , 2001, 36, 77-86.	0.5	7
46	Individual Drug Treatment Prediction in Oncology Based on Machine Learning Using Cell Culture Gene Expression Data. , 2017, , .		7
47	Gene Expression-Based Signature Can Predict Sorafenib Response in Kidney Cancer. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 753318.	1.6	7
48	Prediction of Drug Efficiency by Transferring Gene Expression Data from Cell Lines to Cancer Patients. <i>Lecture Notes in Computer Science</i> , 2018, , 201-212.	1.0	6
49	FNC: An Advanced Anticancer Therapeutic or Just an Underdog?. <i>Frontiers in Oncology</i> , 2022, 12, 820647.	1.3	6
50	Adjoint Importance Monte Carlo Simulation for Gamma Ray Deep Penetration Problem. <i>Monte Carlo Methods and Applications</i> , 1997, 3, .	0.3	5
51	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.	1.8	4
52	Shambhala <sup>2</sup> : A Protocol for Uniformly Shaped Harmonization of Gene Expression Profiles of Various Formats. <i>Current Protocols</i> , 2022, 2, .	1.3	4
53	Generalized Particle Concept for Adjoint Monte Carlo Calculations of Coupled Gamma-Ray <sup>+</sup> Electron <sup>-</sup> Positron Transport. <i>Nuclear Science and Engineering</i> , 2005, 150, 284-298.	0.5	3
54	New Method Based on Monte Carlo Calculation and Voxelized Phantoms for Realistic Internal Dosimetry: Application to a Complex and Old Actinide Contamination. <i>Nuclear Technology</i> , 2009, 168, 824-831.	0.7	3

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55	Adjoint Monte Carlo Calculations of Pulse-Height-Spectrum. Monte Carlo Methods and Applications, 1998, 4, .	0.3	2
56	System, Method and Software for Calculation of a Cannabis Drug Efficiency Index for the Reduction of Inflammation. International Journal of Molecular Sciences, 2021, 22, 388.	1.8	2
57	Generalized Particle Concept for Adjoint Monte Carlo Calculations of Coupled Gamma Ray $\beta^-$ Electron Transport. Monte Carlo Methods and Applications, 1998, 4, .	0.3	1
58	Model for estimating the angular distribution of gamma-ray flux of an isotropic point source in an infinite geometry. Atomic Energy, 1998, 85, 761-764.	0.1	0
59	Simulation of singular collision kernels in adjoint random walk. Atomic Energy, 1999, 86, 177-182.	0.1	0
60	A performance criterion for value simulation based on contribution transport theory. Atomic Energy, 1999, 86, 105-110.	0.1	0
61	Modern internal-irradiation dosimetry. Atomic Energy, 2004, 97, 713-719.	0.1	0
62	Check of the Application of the Monte Carlo Method for Spectrometry of Human Body Radiation in an Experiment on Large Animals. Atomic Energy, 2005, 99, 503-510.	0.1	0
63	Prevalence Of Hypoactive Sexual Desire Disorder in us Women 30 to 70 Years Old Based on a Random-Digit Dial Survey. American Journal of Epidemiology, 2006, 163, S149-S49.	1.6	0
64	Semi-Empirical Model of X-ray Tube Facility. , 2010, , .		0
65	1518 poster SYSTEMS BIOLOGY OF MITOGENIC SIGNALING: A MOLECULAR BASIS FOR ONCOLOGY AND RADIOLOGY. Radiotherapy and Oncology, 2011, 99, S565.	0.3	0
66	Adjoint Monte Carlo Simulation of Fixed-Energy Secondary Radiation. , 2001, , 181-186.		0
67	Importance Biasing Quality Criterion Based on Contribution Response Theory. , 2001, , 193-198.		0
68	The Method for Analysis of Expression Data Homogeneity Based On the Student Test. Mathematical Biology and Bioinformatics, 2018, 13, 50-67.	0.1	0
69	Problems of creating an online scientific journal with multimedia content. , 2019, , .		0
70	Flexible Data Trimming for Different Machine Learning Methods in Omics-Based Personalized Oncology. Lecture Notes in Computer Science, 2019, , 62-71.	1.0	0