

# Anatoly A Sorokin

## List of Publications by Year in descending order

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Version: 2024-02-01

74  
papers

3,913  
citations

430442

18  
h-index

128067

60  
g-index

84  
all docs

84  
docs citations

84  
times ranked

5606  
citing authors

#	ARTICLE	IF	CITATIONS
1	Determination of Brain Tissue Samples Storage Conditions for Reproducible Intraoperative Lipid Profiling. <i>Molecules</i> , 2022, 27, 2587.	1.7	2
2	Assessment of variation of inline cartridge extraction mass spectra. <i>Journal of Mass Spectrometry</i> , 2021, 56, e4640.	0.7	14
3	Interactive Estimation of Heterogeneity from Mass Spectrometry Imaging. <i>Analytical Chemistry</i> , 2021, 93, 3706-3709.	3.2	1
4	SBGN Bricks Ontology as a tool to describe recurring concepts in molecular networks. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4
5	Rapid estimation of tumor cell percentage in brain tissue biopsy samples using inline cartridge extraction mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 2913-2922.	1.9	11
6	Comparison of Dimensionality Reduction Methods in Mass Spectra of Astrocytoma and Glioblastoma Tissues. <i>Mass Spectrometry</i> , 2021, 10, A0094-A0094.	0.2	4
7	The Role of Lipids in the Classification of Astrocytoma and Glioblastoma Using Mass Spectrometry Tumor Profiling. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2021, 15, 153-160.	0.2	1
8	Comparative Analysis of Milk Microbiomes and Their Association with Bovine Mastitis in Two Farms in Central Russia. <i>Animals</i> , 2021, 11, 1401.	1.0	9
9	Analysis of Phosphatidylcholines Alterations in Human Glioblastomas Ex Vivo. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2021, 15, 241-247.	0.2	7
10	Lipid Profiles of Human Brain Tumors Obtained by High-Resolution Negative Mode Ambient Mass Spectrometry. <i>Data</i> , 2021, 6, 132.	1.2	3
11	Novel Mass Spectrometric Utilities for Assisting in Oncological Surgery. <i>Russian Journal of Physical Chemistry B</i> , 2020, 14, 483-487.	0.2	7
12	DNA sequence, physics, and promoter function: Analysis of high-throughput data On T7 promoter variants activity. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2040001.	0.3	4
13	Virulence Factors and Phylogeny of <i>Staphylococcus aureus</i> Associated With Bovine Mastitis in Russia Based on Genome Sequences. <i>Frontiers in Veterinary Science</i> , 2020, 7, 135.	0.9	20
14	Using ASAR for Analysis of Electrogenic and Human Gut Microbial Communities. , 2020, , .		0
15	Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	43
16	Metrics for evaluating the stability and reproducibility of mass spectra. <i>Scientific Reports</i> , 2019, 9, 914.	1.6	22
17	Unified representation of high- and low-resolution spectra to facilitate application of mass spectrometric techniques in clinical practice. <i>Clinical Mass Spectrometry</i> , 2019, 12, 37-46.	1.9	16
18	RKappa: Software for Analyzing Rule-Based Models. <i>Methods in Molecular Biology</i> , 2019, 1945, 363-390.	0.4	3

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19	Inline cartridge extraction for rapid brain tumor tissue identification by molecular profiling. <i>Scientific Reports</i> , 2019, 9, 18960.	1.6	18
20	Untangling the Metabolic Reprogramming in Brain Cancer: Discovering Key Molecular Players Using Mass Spectrometry. <i>Current Topics in Medicinal Chemistry</i> , 2019, 19, 1521-1534.	1.0	20
21	Rule-based modelling provides an extendable framework for comparing candidate mechanisms underpinning clathrin polymerisation. <i>Scientific Reports</i> , 2018, 8, 5658.	1.6	2
22	Bacterial promoter prediction: Selection of dynamic and static physical properties of DNA for reliable sequence classification. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840003.	0.3	9
23	ASAR: visual analysis of metagenomes in R. <i>Bioinformatics</i> , 2018, 34, 1404-1405.	1.8	5
24	Comparative Analysis of <i>Mycoplasma gallisepticum</i> vH A Promoters. <i>Frontiers in Genetics</i> , 2018, 9, 569.	1.1	4
25	Destabilization of the DNA Duplex of Actively Replicating Promoters of T7-Like Bacteriophages. <i>Molecular Biology</i> , 2018, 52, 686-692.	0.4	2
26	Multi-omics analysis of meningioma samples. <i>Journal of Biotechnology</i> , 2018, 280, S42.	1.9	0
27	ASAR Database: An R Tool for Visual Analysis and Storage of Metagenomes. , 2018, , .		0
28	Feature selection algorithm for spray-from-tissue mass spectrometry. <i>European Journal of Mass Spectrometry</i> , 2017, 23, 237-241.	0.5	7
29	Bioinformatic analysis of bacterial composition and metabolic mapping of selectively enriched microbial community within Microbial Fuel Cells. , 2017, , .		0
30	A novel computational method to analyse metagenome for understanding of microbial community composition and functional potential. , 2017, , .		0
31	Multi-label classification of brain tumor mass spectrometry data In pursuit of tumor boundary detection method. , 2017, , .		5
32	High-resolution mass spectra processing for the identification of different pathological tissue types of brain tumors. <i>European Journal of Mass Spectrometry</i> , 2017, 23, 213-216.	0.5	10
33	Comparative Metagenomic Analysis of Electrogenic Microbial Communities in Differentially Inoculated Swine Wastewater-Fed Microbial Fuel Cells. <i>Scientifica</i> , 2017, 2017, 1-10.	0.6	7
34	Structural distinctions of fast and slow bacterial luciferases revealed by phylogenetic analysis. <i>Bioinformatics</i> , 2016, 32, 3053-3057.	1.8	12
35	Systems Biology Graphical Notation: Entity Relationship language Level 1 Version 2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 281-339.	1.0	21
36	Systems Biology Graphical Notation: Activity Flow language Level 1 Version 1.2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 340-381.	1.0	35

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37	Dynamics of Elongation Factor 2 Kinase Regulation in Cortical Neurons in Response to Synaptic Activity. <i>Journal of Neuroscience</i> , 2015, 35, 3034-3047.	1.7	33
38	RKappa: Statistical Sampling Suite for Kappa Models. <i>Lecture Notes in Computer Science</i> , 2015, , 128-142.	1.0	3
39	Systems Biology Graphical Notation: Entity Relationship language Level 1 Version 2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 264.	1.0	21
40	Systems Biology Graphical Notation: Activity Flow language Level 1 Version 1.2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 265.	1.0	17
41	Electrostatic map of T7 DNA: comparative analysis of functional and electrostatic properties of T7 RNA polymerase-specific promoters. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 1184-1192.	2.0	11
42	A community-driven global reconstruction of human metabolism. <i>Nature Biotechnology</i> , 2013, 31, 419-425.	9.4	920
43	A simulator for spatially extended kappa models. <i>Bioinformatics</i> , 2013, 29, 3105-3106.	1.8	22
44	SBSI: an extensible distributed software infrastructure for parameter estimation in systems biology. <i>Bioinformatics</i> , 2013, 29, 664-665.	1.8	20
45	Software support for SBGN maps: SBGN-ML and LibSBGN. <i>Bioinformatics</i> , 2012, 28, 2016-2021.	1.8	74
46	Wiring diagrams in biology: towards the standardized representation of biological information. <i>Trends in Biotechnology</i> , 2012, 30, 555-557.	4.9	13
47	Model-based global sensitivity analysis as applied to identification of anti-cancer drug targets and biomarkers of drug resistance in the ErbB2/3 network. <i>European Journal of Pharmaceutical Sciences</i> , 2012, 46, 244-258.	1.9	35
48	A user-defined data type for the storage of time series data allowing efficient similarity screening. <i>European Journal of Pharmaceutical Sciences</i> , 2012, 46, 272-274.	1.9	1
49	Towards a quantitative model of the post-synaptic proteome. <i>Molecular BioSystems</i> , 2011, 7, 2813.	2.9	32
50	Conceptual model of E. coli transcriptional machinery. <i>Nature Precedings</i> , 2011, , .	0.1	0
51	Meeting report from the first meetings of the Computational Modeling in Biology Network (COMBINE). <i>Standards in Genomic Sciences</i> , 2011, 5, 230-242.	1.5	7
52	Microarray data can predict diurnal changes of starch content in the picoalga <i>Ostreococcus</i> . <i>BMC Systems Biology</i> , 2011, 5, 36.	3.0	37
53	Systems Biology Graphical Notation: Entity Relationship language Level 1. <i>Nature Precedings</i> , 2010, , .	0.1	2
54	LibSBGN: Electronic Processing of SBGN maps. <i>Nature Precedings</i> , 2010, , .	0.1	0

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55	Systems Biology Graphical Notation: Process Description language Level 1. Nature Precedings, 2009, , .	0.1	3
56	A fragile metabolic network adapted for cooperation in the symbiotic bacterium Buchnera aphidicola. BMC Systems Biology, 2009, 3, 24.	3.0	98
57	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	9.4	828
58	Systems Biology Reveals New Strategies for Personalizing Cancer Medicine and Confirms the Role of PTEN in Resistance to Trastuzumab. Cancer Research, 2009, 69, 6713-6720.	0.4	152
59	Systems Biology Graphical Notation: Process Diagram Level 1. Nature Precedings, 2008, , .	0.1	7
60	The Edinburgh human metabolic network reconstruction and its functional analysis. Molecular Systems Biology, 2007, 3, 135.	3.2	364
61	Analysis of the nucleotide sequence and electrostatic potential distribution in the Escherichia coli genome. Biophysics (Russian Federation), 2007, 52, 168-171.	0.2	3
62	Regulation of promoter activity through electrostatic interactions with RNA polymerase. Biophysics (Russian Federation), 2007, 52, 172-178.	0.2	1
63	A Graphical Notation to Describe the Logical Interactions of Biological Pathways. Journal of Integrative Bioinformatics, 2006, 3, 177-187.	1.0	14
64	Comparative Analysis of Electrostatic Patterns for Promoter and Nonpromoter DNA in E. Coli Genome. , 2006, , 67-74.		4
65	The Pathway Editor: A tool for managing complex biological networks. IBM Journal of Research and Development, 2006, 50, 561-573.	3.2	25
66	ELECTROSTATIC PROPERTIES OF PROMOTER RECOGNIZED BYE. COLIRNA POLYMERASE Eİf70. Journal of Bioinformatics and Computational Biology, 2006, 04, 455-467.	0.3	14
67	RNA Polymeraseâ€”Promoter Recognition. Specific Features of Electrostatic Potential of â€œEarlyâ€•T4 Phage DNA Promoters. Journal of Biomolecular Structure and Dynamics, 2000, 18, 325-334.	2.0	15
68	Automated analysis of interatomic contacts in proteins. Bioinformatics, 1999, 15, 327-332.	1.8	759
69	Electrostatic Potentials of DNA. Comparative Analysis of Promoter and Nonpromoter Nucleotide Sequences. Journal of Biomolecular Structure and Dynamics, 1999, 16, 1135-1143.	2.0	21
70	Systems Biology Graphical Notation: Activity Flow language Level 1. Nature Precedings, 0, , .	0.1	11
71	Comparison of different machine learning methods and dimensionality reduction for classification astrocytoma and glioblastoma tissues by mass spectra. F1000Research, 0, 10, 39.	0.8	0
72	Analysis of ion currents in mass spectrometric profiles using glioblastoma tissue. F1000Research, 0, 10, 37.	0.8	0

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73	Systems Biology Graphical Notation: Entity Relationship language Level 1. Nature Precedings, 0, , .	0.1	3
74	The software for interactive evaluation of mass spectrometric imaging heterogeneity. F1000Research, 0, 11, 92.	0.8	0