

# 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	A community-driven global reconstruction of human metabolism. <i>Nature Biotechnology</i> , 2013, 31, 419-425.	9.4	920
2	The Systems Biology Graphical Notation. <i>Nature Biotechnology</i> , 2009, 27, 735-741.	9.4	828
3	Automated analysis of interatomic contacts in proteins. <i>Bioinformatics</i> , 1999, 15, 327-332.	1.8	759
4	The Edinburgh human metabolic network reconstruction and its functional analysis. <i>Molecular Systems Biology</i> , 2007, 3, 135.	3.2	364
5	Systems Biology Reveals New Strategies for Personalizing Cancer Medicine and Confirms the Role of PTEN in Resistance to Trastuzumab. <i>Cancer Research</i> , 2009, 69, 6713-6720.	0.4	152
6	A fragile metabolic network adapted for cooperation in the symbiotic bacterium <i>Buchnera aphidicola</i> . <i>BMC Systems Biology</i> , 2009, 3, 24.	3.0	98
7	Software support for SBGN maps: SBGN-ML and LibSBGN. <i>Bioinformatics</i> , 2012, 28, 2016-2021.	1.8	74
8	Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	43
9	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
10	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
11	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
12	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
13	Towards a quantitative model of the post-synaptic proteome. <i>Molecular BioSystems</i> , 2011, 7, 2813.	2.9	32
14	The Pathway Editor: A tool for managing complex biological networks. <i>IBM Journal of Research and Development</i> , 2006, 50, 561-573.	3.2	25
15	A simulator for spatially extended kappa models. <i>Bioinformatics</i> , 2013, 29, 3105-3106.	1.8	22
16	Metrics for evaluating the stability and reproducibility of mass spectra. <i>Scientific Reports</i> , 2019, 9, 914.	1.6	22
17	Electrostatic Potentials of DNA. Comparative Analysis of Promoter and Nonpromoter Nucleotide Sequences. <i>Journal of Biomolecular Structure and Dynamics</i> , 1999, 16, 1135-1143.	2.0	21
18	Systems Biology Graphical Notation: Entity Relationship language Level 1 Version 2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 281-339.	1.0	21

#	ARTICLE	IF	CITATIONS
19	Systems Biology Graphical Notation: Entity Relationship language Level 1 Version 2. Journal of Integrative Bioinformatics, 2015, 12, 264.	1.0	21
20	SBSI: an extensible distributed software infrastructure for parameter estimation in systems biology. Bioinformatics, 2013, 29, 664-665.	1.8	20
21	Virulence Factors and Phylogeny of Staphylococcus aureus Associated With Bovine Mastitis in Russia Based on Genome Sequences. Frontiers in Veterinary Science, 2020, 7, 135.	0.9	20
22	Untangling the Metabolic Reprogramming in Brain Cancer: Discovering Key Molecular Players Using Mass Spectrometry. Current Topics in Medicinal Chemistry, 2019, 19, 1521-1534.	1.0	20
23	Inline cartridge extraction for rapid brain tumor tissue identification by molecular profiling. Scientific Reports, 2019, 9, 18960.	1.6	18
24	Systems Biology Graphical Notation: Activity Flow language Level 1 Version 1.2. Journal of Integrative Bioinformatics, 2015, 12, 265.	1.0	17
25	Unified representation of high- and low-resolution spectra to facilitate application of mass spectrometric techniques in clinical practice. Clinical Mass Spectrometry, 2019, 12, 37-46.	1.9	16
26	RNA Polymerase- $\sigma$ Promoter Recognition. Specific Features of Electrostatic Potential of $\sigma$ Early T4 Phage DNA Promoters. Journal of Biomolecular Structure and Dynamics, 2000, 18, 325-334.	2.0	15
27	A Graphical Notation to Describe the Logical Interactions of Biological Pathways. Journal of Integrative Bioinformatics, 2006, 3, 177-187.	1.0	14
28	ELECTROSTATIC PROPERTIES OF PROMOTER RECOGNIZED BY $\sigma$ 70. COLIRNA POLYMERASE $\sigma$ 70. Journal of Bioinformatics and Computational Biology, 2006, 04, 455-467.	0.3	14
29	Assessment of variation of inline cartridge extraction mass spectra. Journal of Mass Spectrometry, 2021, 56, e4640.	0.7	14
30	Wiring diagrams in biology: towards the standardized representation of biological information. Trends in Biotechnology, 2012, 30, 555-557.	4.9	13
31	Structural distinctions of fast and slow bacterial luciferases revealed by phylogenetic analysis. Bioinformatics, 2016, 32, 3053-3057.	1.8	12
32	Systems Biology Graphical Notation: Activity Flow language Level 1. Nature Precedings, 0, , .	0.1	11
33	Electrostatic map of T7 DNA: comparative analysis of functional and electrostatic properties of T7 RNA polymerase-specific promoters. Journal of Biomolecular Structure and Dynamics, 2014, 32, 1184-1192.	2.0	11
34	Rapid estimation of tumor cell percentage in brain tissue biopsy samples using inline cartridge extraction mass spectrometry. Analytical and Bioanalytical Chemistry, 2021, 413, 2913-2922.	1.9	11
35	High-resolution mass spectra processing for the identification of different pathological tissue types of brain tumors. European Journal of Mass Spectrometry, 2017, 23, 213-216.	0.5	10
36	Bacterial promoter prediction: Selection of dynamic and static physical properties of DNA for reliable sequence classification. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840003.	0.3	9

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37	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
38	Systems Biology Graphical Notation: Process Diagram Level 1. <i>Nature Precedings</i> , 2008, , .	0.1	7
39	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
40	Feature selection algorithm for spray-from-tissue mass spectrometry. <i>European Journal of Mass Spectrometry</i> , 2017, 23, 237-241.	0.5	7
41	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
42	Novel Mass Spectrometric Utilities for Assisting in Oncological Surgery. <i>Russian Journal of Physical Chemistry B</i> , 2020, 14, 483-487.	0.2	7
43	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
44	Multi-label classification of brain tumor mass spectrometry data In pursuit of tumor boundary detection method. , 2017, , .		5
45	ASAR: visual analysis of metagenomes in R. <i>Bioinformatics</i> , 2018, 34, 1404-1405.	1.8	5
46	Comparative Analysis of Electrostatic Patterns for Promoter and Nonpromoter DNA in E. Coli Genome. , 2006, , 67-74.		4
47	Comparative Analysis of Mycoplasma gallisepticum vlhA Promoters. <i>Frontiers in Genetics</i> , 2018, 9, 569.	1.1	4
48	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
49	SBGN Bricks Ontology as a tool to describe recurring concepts in molecular networks. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4
50	Comparison of Dimensionality Reduction Methods in Mass Spectra of Astrocytoma and Glioblastoma Tissues. <i>Mass Spectrometry</i> , 2021, 10, A0094-A0094.	0.2	4
51	Analysis of the nucleotide sequence and electrostatic potential distribution in the Escherichia coli genome. <i>Biophysics (Russian Federation)</i> , 2007, 52, 168-171.	0.2	3
52	Systems Biology Graphical Notation: Process Description language Level 1. <i>Nature Precedings</i> , 2009, , .	0.1	3
53	RKappa: Software for Analyzing Rule-Based Models. <i>Methods in Molecular Biology</i> , 2019, 1945, 363-390.	0.4	3
54	RKappa: Statistical Sampling Suite for Kappa Models. <i>Lecture Notes in Computer Science</i> , 2015, , 128-142.	1.0	3

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55	Systems Biology Graphical Notation: Entity Relationship language Level 1. Nature Precedings, 0, , .	0.1	3
56	Lipid Profiles of Human Brain Tumors Obtained by High-Resolution Negative Mode Ambient Mass Spectrometry. Data, 2021, 6, 132.	1.2	3
57	Systems Biology Graphical Notation: Entity Relationship language Level 1. Nature Precedings, 2010, , .	0.1	2
58	Rule-based modelling provides an extendable framework for comparing candidate mechanisms underpinning clathrin polymerisation. Scientific Reports, 2018, 8, 5658.	1.6	2
59	Destabilization of the DNA Duplex of Actively Replicating Promoters of T7-Like Bacteriophages. Molecular Biology, 2018, 52, 686-692.	0.4	2
60	Determination of Brain Tissue Samples Storage Conditions for Reproducible Intraoperative Lipid Profiling. Molecules, 2022, 27, 2587.	1.7	2
61	Regulation of promoter activity through electrostatic interactions with RNA polymerase. Biophysics (Russian Federation), 2007, 52, 172-178.	0.2	1
62	A user-defined data type for the storage of time series data allowing efficient similarity screening. European Journal of Pharmaceutical Sciences, 2012, 46, 272-274.	1.9	1
63	Interactive Estimation of Heterogeneity from Mass Spectrometry Imaging. Analytical Chemistry, 2021, 93, 3706-3709.	3.2	1
64	The Role of Lipids in the Classification of Astrocytoma and Glioblastoma Using Mass Spectrometry Tumor Profiling. Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry, 2021, 15, 153-160.	0.2	1
65	LibSBGN: Electronic Processing of SBGN maps. Nature Precedings, 2010, , .	0.1	0
66	Conceptual model of E. coli transcriptional machinery. Nature Precedings, 2011, , .	0.1	0
67	Bioinformatic analysis of bacterial composition and metabolic mapping of selectively enriched microbial community within Microbial Fuel Cells. , 2017, , .		0
68	A novel computational method to analyse metagenome for understanding of microbial community composition and functional potential. , 2017, , .		0
69	Multi-omics analysis of meningioma samples. Journal of Biotechnology, 2018, 280, S42.	1.9	0
70	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
71	Analysis of ion currents in mass spectrometric profiles using glioblastoma tissue. F1000Research, 0, 10, 37.	0.8	0
72	ASAR Database: An R Tool for Visual Analysis and Storage of Metagenomes. , 2018, , .		0

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73	Using ASAR for Analysis of Electrogenic and Human Gut Microbial Communities. , 2020, , .		0
74	The software for interactive evaluation of mass spectrometric imaging heterogeneity. F1000Research, 0, 11, 92.	0.8	0