

# Anatoly A Sorokin

## List of Publications by Year in descending order

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Version: 2024-02-01

74  
papers

3,913  
citations

430874

18  
h-index

128289

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.  | 3.8 | 2         |
| 2  | Assessment of variation of inline cartridge extraction mass spectra. <i>Journal of Mass Spectrometry</i> , 2021, 56, e4640.   | 1.6 | 14        |
| 3  | Interactive Estimation of Heterogeneity from Mass Spectrometry Imaging. <i>Analytical Chemistry</i> , 2021, 93, 3706-3709.  | 6.5 | 1         |
| 4  | SBGN Bricks Ontology as a tool to describe recurring concepts in molecular networks. <i>Briefings in Bioinformatics</i> , 2021, 22, .   | 6.5 | 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.           | 3.7 | 11        |
| 6  | Comparison of Dimensionality Reduction Methods in Mass Spectra of Astrocytoma and Glioblastoma Tissues. <i>Mass Spectrometry</i> , 2021, 10, A0094-A0094.   | 0.6 | 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. | 0.4 | 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.  | 2.3 | 9         |
| 9  | Analysis of Phosphatidylcholines Alterations in Human Glioblastomas Ex Vivo. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2021, 15, 241-247.                                      | 0.4 | 7         |
| 10 | Lipid Profiles of Human Brain Tumors Obtained by High-Resolution Negative Mode Ambient Mass Spectrometry. <i>Data</i> , 2021, 6, 132.   | 2.3 | 3         |
| 11 | Novel Mass Spectrometric Utilities for Assisting in Oncological Surgery. <i>Russian Journal of Physical Chemistry B</i> , 2020, 14, 483-487.  | 1.3 | 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.              | 0.8 | 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.                   | 2.2 | 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, .  | 1.5 | 43        |
| 16 | Metrics for evaluating the stability and reproducibility of mass spectra. <i>Scientific Reports</i> , 2019, 9, 914.   | 3.3 | 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.  | 0.9 | 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.   | 3.3 | 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.                          | 2.1 | 20        |
| 21 | Rule-based modelling provides an extendable framework for comparing candidate mechanisms underpinning clathrin polymerisation. <i>Scientific Reports</i> , 2018, 8, 5658.                                       | 3.3 | 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. | 0.8 | 9         |
| 23 | ASAR: visual analysis of metagenomes in R. <i>Bioinformatics</i> , 2018, 34, 1404-1405.   | 4.1 | 5         |
| 24 | Comparative Analysis of <i>Mycoplasma gallisepticum</i> vH A Promoters. <i>Frontiers in Genetics</i> , 2018, 9, 569.  | 2.3 | 4         |
| 25 | Destabilization of the DNA Duplex of Actively Replicating Promoters of T7-Like Bacteriophages. <i>Molecular Biology</i> , 2018, 52, 686-692.  | 1.3 | 2         |
| 26 | Multi-omics analysis of meningioma samples. <i>Journal of Biotechnology</i> , 2018, 280, S42.   | 3.8 | 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.  | 1.0 | 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.                        | 1.0 | 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.                           | 1.7 | 7         |
| 34 | Structural distinctions of fast and slow bacterial luciferases revealed by phylogenetic analysis. <i>Bioinformatics</i> , 2016, 32, 3053-3057.  | 4.1 | 12        |
| 35 | Systems Biology Graphical Notation: Entity Relationship language Level 1 Version 2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 281-339.   | 1.5 | 21        |
| 36 | Systems Biology Graphical Notation: Activity Flow language Level 1 Version 1.2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 340-381.   | 1.5 | 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.  | 3.6  | 33        |
| 38 | RKappa: Statistical Sampling Suite for Kappa Models. <i>Lecture Notes in Computer Science</i> , 2015, , 128-142.   | 1.3  | 3         |
| 39 | Systems Biology Graphical Notation: Entity Relationship language Level 1 Version 2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 264.  | 1.5  | 21        |
| 40 | Systems Biology Graphical Notation: Activity Flow language Level 1 Version 1.2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 265.  | 1.5  | 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.                 | 3.5  | 11        |
| 42 | A community-driven global reconstruction of human metabolism. <i>Nature Biotechnology</i> , 2013, 31, 419-425.   | 17.5 | 920       |
| 43 | A simulator for spatially extended kappa models. <i>Bioinformatics</i> , 2013, 29, 3105-3106.  | 4.1  | 22        |
| 44 | SBSI: an extensible distributed software infrastructure for parameter estimation in systems biology. <i>Bioinformatics</i> , 2013, 29, 664-665.  | 4.1  | 20        |
| 45 | Software support for SBGN maps: SBGN-ML and LibSBGN. <i>Bioinformatics</i> , 2012, 28, 2016-2021.  | 4.1  | 74        |
| 46 | Wiring diagrams in biology: towards the standardized representation of biological information. <i>Trends in Biotechnology</i> , 2012, 30, 555-557.   | 9.3  | 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. | 4.0  | 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.  | 4.0  | 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.   | 17.5 | 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.                   | 0.9  | 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.   | 7.2  | 364       |
| 61 | Analysis of the nucleotide sequence and electrostatic potential distribution in the Escherichia coli genome. Biophysics (Russian Federation), 2007, 52, 168-171.                             | 0.7  | 3         |
| 62 | Regulation of promoter activity through electrostatic interactions with RNA polymerase. Biophysics (Russian Federation), 2007, 52, 172-178.  | 0.7  | 1         |
| 63 | A Graphical Notation to Describe the Logical Interactions of Biological Pathways. Journal of Integrative Bioinformatics, 2006, 3, 177-187.   | 1.5  | 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.   | 3.1  | 25        |
| 66 | ELECTROSTATIC PROPERTIES OF PROMOTER RECOGNIZED BYE. COLIRNA POLYMERASE Eİf70. Journal of Bioinformatics and Computational Biology, 2006, 04, 455-467.                                       | 0.8  | 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. | 3.5  | 15        |
| 68 | Automated analysis of interatomic contacts in proteins. Bioinformatics, 1999, 15, 327-332.   | 4.1  | 759       |
| 69 | Electrostatic Potentials of DNA. Comparative Analysis of Promoter and Nonpromoter Nucleotide Sequences. Journal of Biomolecular Structure and Dynamics, 1999, 16, 1135-1143.                 | 3.5  | 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.             | 1.6  | 0         |
| 72 | Analysis of ion currents in mass spectrometric profiles using glioblastoma tissue. F1000Research, 0, 10, 37.   | 1.6  | 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. | 1.6 | 0         |