

# Andrei Yu Zinovyev

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

133  
papers

4,787  
citations

36  
h-index

67  
g-index

156  
ext. papers

6,547  
ext. citations

6.5  
avg, IF

5.55  
L-index

#	Paper	IF	Citations
133	Fibroblast Heterogeneity and Immunosuppressive Environment in Human Breast Cancer. <i>Cancer Cell</i> , <b>2018</b> , 33, 463-479.e10	24.3	579
132	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. <i>Nature Protocols</i> , <b>2019</b> , 14, 639-702	18.8	385
131	Codon adaptation index as a measure of dominating codon bias. <i>Bioinformatics</i> , <b>2003</b> , 19, 2005-15	7.2	219
130	Control-free calling of copy number alterations in deep-sequencing data using GC-content normalization. <i>Bioinformatics</i> , <b>2011</b> , 27, 268-9	7.2	190
129	Classification of microarray data using gene networks. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 35	3.6	149
128	Single-Cell Analysis Reveals Fibroblast Clusters Linked to Immunotherapy Resistance in Cancer. <i>Cancer Discovery</i> , <b>2020</b> , 10, 1330-1351	24.4	140
127	Mathematical modelling of cell-fate decision in response to death receptor engagement. <i>PLoS Computational Biology</i> , <b>2010</b> , 6, e1000702	5	140
126	The Virtual Metabolic Human database: integrating human and gut microbiome metabolism with nutrition and disease. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D614-D624	20.1	132
125	Independent component analysis uncovers the landscape of the bladder tumor transcriptome and reveals insights into luminal and basal subtypes. <i>Cell Reports</i> , <b>2014</b> , 9, 1235-45	10.6	131
124	The oncogenic EWS-FLI1 protein binds in vivo GGAA microsatellite sequences with potential transcriptional activation function. <i>PLoS ONE</i> , <b>2009</b> , 4, e4932	3.7	121
123	Constructive methods of invariant manifolds for kinetic problems. <i>Physics Reports</i> , <b>2004</b> , 396, 197-403	27.7	112
122	A comprehensive modular map of molecular interactions in RB/E2F pathway. <i>Molecular Systems Biology</i> , <b>2008</b> , 4, 173	12.2	99
121	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. <i>Nature Communications</i> , <b>2019</b> , 10, 1903	17.4	97
120	Atlas of Cancer Signalling Network: a systems biology resource for integrative analysis of cancer data with Google Maps. <i>Oncogenesis</i> , <b>2015</b> , 4, e160	6.6	90
119	Concomitant Notch activation and p53 deletion trigger epithelial-to-mesenchymal transition and metastasis in mouse gut. <i>Nature Communications</i> , <b>2014</b> , 5, 5005	17.4	88
118	BiNoM: a Cytoscape plugin for manipulating and analyzing biological networks. <i>Bioinformatics</i> , <b>2008</b> , 24, 876-7	7.2	87
117	Principal manifolds and graphs in practice: from molecular biology to dynamical systems. <i>International Journal of Neural Systems</i> , <b>2010</b> , 20, 219-32	6.2	84

116	Kinetic signatures of microRNA modes of action. <i>Rna</i> , <b>2012</b> , 18, 1635-55	5.8	77
115	Robust simplifications of multiscale biochemical networks. <i>BMC Systems Biology</i> , <b>2008</b> , 2, 86	3.5	76
114	Mathematical Modelling of Molecular Pathways Enabling Tumour Cell Invasion and Migration. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004571	5	72
113	Codon bias signatures, organization of microorganisms in codon space, and lifestyle. <i>Molecular Biology and Evolution</i> , <b>2005</b> , 22, 547-61	8.3	63
112	Invariant grids for reaction kinetics. <i>Physica A: Statistical Mechanics and Its Applications</i> , <b>2004</b> , 333, 106-154	5.4	62
111	MaBoSS 2.0: an environment for stochastic Boolean modeling. <i>Bioinformatics</i> , <b>2017</b> , 33, 2226-2228	7.2	59
110	Reduction of dynamical biochemical reactions networks in computational biology. <i>Frontiers in Genetics</i> , <b>2012</b> , 3, 131	4.5	59
109	A Modeling Approach to Explain Mutually Exclusive and Co-Occurring Genetic Alterations in Bladder Tumorigenesis. <i>Cancer Research</i> , <b>2015</b> , 75, 4042-52	10.1	58
108	Systems medicine disease maps: community-driven comprehensive representation of disease mechanisms. <i>Npj Systems Biology and Applications</i> , <b>2018</b> , 4, 21	5	47
107	Computational Systems Biology of Cancer		47
106	Elastic Principal Graphs and Manifolds and their Practical Applications. <i>Computing (Vienna/New York)</i> , <b>2005</b> , 75, 359-379	2.2	45
105	Identification of microRNA clusters cooperatively acting on epithelial to mesenchymal transition in triple negative breast cancer. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 2205-2215	20.1	44
104	Asymptotology of chemical reaction networks. <i>Chemical Engineering Science</i> , <b>2010</b> , 65, 2310-2324	4.4	44
103	PhysiBoSS: a multi-scale agent-based modelling framework integrating physical dimension and cell signalling. <i>Bioinformatics</i> , <b>2019</b> , 35, 1188-1196	7.2	44
102	BiNoM 2.0, a Cytoscape plugin for accessing and analyzing pathways using standard systems biology formats. <i>BMC Systems Biology</i> , <b>2013</b> , 7, 18	3.5	40
101	NaviCell: a web-based environment for navigation, curation and maintenance of large molecular interaction maps. <i>BMC Systems Biology</i> , <b>2013</b> , 7, 100	3.5	39
100	Systems biology of Ewing sarcoma: a network model of EWS-FLI1 effect on proliferation and apoptosis. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 8853-71	20.1	39
99	Transcriptional Programs Define Intratumoral Heterogeneity of Ewing Sarcoma at Single-Cell Resolution. <i>Cell Reports</i> , <b>2020</b> , 30, 1767-1779.e6	10.6	39

98	The second European interdisciplinary Ewing sarcoma research summit--A joint effort to deconstructing the multiple layers of a complex disease. <i>Oncotarget</i> , <b>2016</b> , 7, 8613-24	3.3	38
97	Classification of gene signatures for their information value and functional redundancy. <i>Npj Systems Biology and Applications</i> , <b>2018</b> , 4, 2	5	34
96	Independent Component Analysis for Unraveling the Complexity of Cancer Omics Datasets. <i>International Journal of Molecular Sciences</i> , <b>2019</b> , 20,	6.3	32
95	Determining the optimal number of independent components for reproducible transcriptomic data analysis. <i>BMC Genomics</i> , <b>2017</b> , 18, 712	4.5	32
94	Drug-Driven Synthetic Lethality: Bypassing Tumor Cell Genetics with a Combination of AsiDNA and PARP Inhibitors. <i>Clinical Cancer Research</i> , <b>2017</b> , 23, 1001-1011	12.9	30
93	Dynamical modeling of microRNA action on the protein translation process. <i>BMC Systems Biology</i> , <b>2010</b> , 4, 13	3.5	30
92	Community-driven roadmap for integrated disease maps. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 659-670	13.4	30
91	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. <i>Frontiers in Physiology</i> , <b>2018</b> , 9, 680	4.6	29
90	How much non-coding DNA do eukaryotes require?. <i>Journal of Theoretical Biology</i> , <b>2008</b> , 252, 587-92	2.3	29
89	NaviCell Web Service for network-based data visualization. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, W560-5	20.1	26
88	Topological grammars for data approximation. <i>Applied Mathematics Letters</i> , <b>2007</b> , 20, 382-386	3.5	25
87	ROMA: Representation and Quantification of Module Activity from Target Expression Data. <i>Frontiers in Genetics</i> , <b>2016</b> , 7, 18	4.5	25
86	The shortest path is not the one you know: application of biological network resources in precision oncology research. <i>Mutagenesis</i> , <b>2015</b> , 30, 191-204	2.8	23
85	Network-based approaches for drug response prediction and targeted therapy development in cancer. <i>Biochemical and Biophysical Research Communications</i> , <b>2015</b> , 464, 386-91	3.4	23
84	A multiscale signalling network map of innate immune response in cancer reveals cell heterogeneity signatures. <i>Nature Communications</i> , <b>2019</b> , 10, 4808	17.4	23
83	Mathematical modeling of microRNA-mediated mechanisms of translation repression. <i>Advances in Experimental Medicine and Biology</i> , <b>2013</b> , 774, 189-224	3.6	23
82	Interpreting pathways to discover cancer driver genes with Moonlight. <i>Nature Communications</i> , <b>2020</b> , 11, 69	17.4	23
81	OCSANA: optimal combinations of interventions from network analysis. <i>Bioinformatics</i> , <b>2013</b> , 29, 1571-37.2		21

80	Blind source separation methods for deconvolution of complex signals in cancer biology. <i>Biochemical and Biophysical Research Communications</i> , <b>2013</b> , 430, 1182-7	3.4	20
79	Synthetic lethality between gene defects affecting a single non-essential molecular pathway with reversible steps. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1003016	5	19
78	Inferring hidden causal relations between pathway members using reduced Google matrix of directed biological networks. <i>PLoS ONE</i> , <b>2018</b> , 13, e0190812	3.7	19
77	DeDaL: Cytoscape 3 app for producing and morphing data-driven and structure-driven network layouts. <i>BMC Systems Biology</i> , <b>2015</b> , 9, 46	3.5	16
76	Robust and Scalable Learning of Complex Intrinsic Dataset Geometry via ELPiGraph. <i>Entropy</i> , <b>2020</b> , 22,	2.8	16
75	NetNorM: Capturing cancer-relevant information in somatic exome mutation data with gene networks for cancer stratification and prognosis. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005573	5	16
74	Predicting genetic interactions from Boolean models of biological networks. <i>Integrative Biology (United Kingdom)</i> , <b>2015</b> , 7, 921-9	3.7	15
73	Assessing reproducibility of matrix factorization methods in independent transcriptomes. <i>Bioinformatics</i> , <b>2019</b> , 35, 4307-4313	7.2	14
72	Model composition through model reduction: a combined model of CD95 and NF- $\kappa$ B signaling pathways. <i>BMC Systems Biology</i> , <b>2013</b> , 7, 13	3.5	14
71	Deconvolution of transcriptomes and miRNomes by independent component analysis provides insights into biological processes and clinical outcomes of melanoma patients. <i>BMC Medical Genomics</i> , <b>2019</b> , 12, 132	3.7	13
70	Data complexity measured by principal graphs. <i>Computers and Mathematics With Applications</i> , <b>2013</b> , 65, 1471-1482	2.7	12
69	Detection of miRNA regulatory effect on triple negative breast cancer transcriptome. <i>BMC Genomics</i> , <b>2015</b> , 16, S4	4.5	11
68	Fast and user-friendly non-linear principal manifold learning by method of elastic maps <b>2015</b> ,		11
67	Self-Organizing Approach for Automated Gene Identification. <i>Open Systems and Information Dynamics</i> , <b>2003</b> , 10, 321-333	0.4	11
66	Codon usage trajectories and 7-cluster structure of 143 complete bacterial genomic sequences. <i>Physica A: Statistical Mechanics and Its Applications</i> , <b>2005</b> , 353, 365-387	3.3	11
65	Applications of single-cell and bulk RNA sequencing in onco-immunology. <i>European Journal of Cancer</i> , <b>2021</b> , 149, 193-210	7.5	11
64	A review of computational approaches detecting microRNAs involved in cancer. <i>Frontiers in Bioscience - Landmark</i> , <b>2017</b> , 22, 1774-1791	2.8	10
63	Estimating the effective dimension of large biological datasets using Fisher separability analysis <b>2019</b> ,		10

62	NaviCom: a web application to create interactive molecular network portraits using multi-level omics data. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2017</b> , 2017,	5	9
61	Conceptual and computational framework for logical modelling of biological networks deregulated in diseases. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 1238-1249	13.4	9
60	The inconvenience of data of convenience: computational research beyond post-mortem analyses. <i>Nature Methods</i> , <b>2017</b> , 14, 937-938	21.6	8
59	Lizard Brain: Tackling Locally Low-Dimensional Yet Globally Complex Organization of Multi-Dimensional Datasets. <i>Frontiers in Neurorobotics</i> , <b>2019</b> , 13, 110	3.4	8
58	Signalling maps in cancer research: construction and data analysis. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2018</b> , 2018,	5	8
57	ETS Proteins Bind with Glucocorticoid Receptors: Relevance for Treatment of Ewing Sarcoma. <i>Cell Reports</i> , <b>2019</b> , 29, 104-117.e4	10.6	7
56	Piece-wise quadratic approximations of arbitrary error functions for fast and robust machine learning. <i>Neural Networks</i> , <b>2016</b> , 84, 28-38	9.1	7
55	Overcoming Complexity of Biological Systems: from Data Analysis to Mathematical Modeling. <i>Mathematical Modelling of Natural Phenomena</i> , <b>2015</b> , 10, 186-205	3	7
54	Antagonism pattern detection between microRNA and target expression in Ewing's sarcoma. <i>PLoS ONE</i> , <b>2012</b> , 7, e41770	3.7	7
53	From a biological hypothesis to the construction of a mathematical model. <i>Methods in Molecular Biology</i> , <b>2013</b> , 1021, 107-25	1.4	7
52	Invariant Grids: Method of Complexity Reduction in Reaction Networks. <i>Complexus</i> , <b>2004</b> , 2, 110-127		7
51	Network analysis of gene lists for finding reproducible prognostic breast cancer gene signatures. <i>Bioinformatics</i> , <b>2012</b> , 8, 773-6	1.1	7
50	cd2sbgmml: bidirectional conversion between CellDesigner and SBGN formats. <i>Bioinformatics</i> , <b>2020</b> , 36, 2620-2622	7.2	7
49	Trajectories, bifurcations, and pseudo-time in large clinical datasets: applications to myocardial infarction and diabetes data. <i>GigaScience</i> , <b>2020</b> , 9,	7.6	7
48	Application of Atlas of Cancer Signalling Network in preclinical studies. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 701-716	13.4	7
47	Molecular Inverse Comorbidity between Alzheimer's Disease and Lung Cancer: New Insights from Matrix Factorization. <i>International Journal of Molecular Sciences</i> , <b>2019</b> , 20,	6.3	6
46	Prediction of Mutations to Control Pathways Enabling Tumor Cell Invasion with the CoLoMoTo Interactive Notebook (Tutorial). <i>Frontiers in Physiology</i> , <b>2018</b> , 9, 787	4.6	6
45	Logical versus kinetic modeling of biological networks: applications in cancer research. <i>Current Opinion in Chemical Engineering</i> , <b>2018</b> , 21, 22-31	5.4	5

44	Cell death and life in cancer: mathematical modeling of cell fate decisions. <i>Advances in Experimental Medicine and Biology</i> , <b>2012</b> , 736, 261-74	3.6	5
43	Practical use of BiNoM: a biological network manager software. <i>Methods in Molecular Biology</i> , <b>2013</b> , 1021, 127-46	1.4	5
42	Scikit-Dimension: A Python Package for Intrinsic Dimension Estimation. <i>Entropy</i> , <b>2021</b> , 23,	2.8	5
41	Geometrical Complexity of Data Approximators. <i>Lecture Notes in Computer Science</i> , <b>2013</b> , 500-509	0.9	5
40	Moonlight: a tool for biological interpretation and driver genes discovery		5
39	Metabolic and signalling network maps integration: application to cross-talk studies and omics data analysis in cancer. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 140	3.6	4
38	The mystery of two straight lines in bacterial genome statistics. <i>Bulletin of Mathematical Biology</i> , <b>2007</b> , 69, 2429-42	2.1	4
37	Synthesis and Simulation of Ensembles of Boolean Networks for Cell Fate Decision. <i>Lecture Notes in Computer Science</i> , <b>2020</b> , 193-209	0.9	4
36	STREAM: Single-cell Trajectories Reconstruction, Exploration And Mapping of omics data		4
35	Modelling of Immune Checkpoint Network Explains Synergistic Effects of Combined Immune Checkpoint Inhibitor Therapy and the Impact of Cytokines in Patient Response. <i>Cancers</i> , <b>2020</b> , 12,	6.6	4
34	Identification of shortened 3Suntranslated regions from expression arrays. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2012</b> , 10, 1241001	1	3
33	Application of Independent Component Analysis to Tumor Transcriptomes Reveals Specific and Reproducible Immune-Related Signals. <i>Lecture Notes in Computer Science</i> , <b>2018</b> , 501-513	0.9	2
32	Calculating Biological Module Enrichment or Depletion and Visualizing Data on Large-scale Molecular Maps with ACSNMiner and RNavicell Packages. <i>R Journal</i> , <b>2016</b> , 8, 293	3.3	2
31	Calculating Biological Module Enrichment or Depletion and Visualizing Data on Large-scale Molecular Maps with ACSNMiner and RNavicell R packages		2
30	PhysiBoSS: a multi-scale agent based modelling framework integrating physical dimension and cell signalling		2
29	Independent component analysis provides clinically relevant insights into the biology of melanoma patients		2
28	Minimum Spanning vs. Principal Trees for Structured Approximations of Multi-Dimensional Datasets. <i>Entropy</i> , <b>2020</b> , 22,	2.8	2
27	Data analysis with arbitrary error measures approximated by piece-wise quadratic PQSQ functions <b>2018</b> ,		2



26	Systems Biology Analysis for Ewing Sarcoma. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2226, 303-333	1.4	2
25	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1007652	5	1
24	Understanding Different Types of Cell Death Using Systems Biology <b>2012</b> , 125-143		1
23	Analysis of the Growth Control Network Specific for Human Lung Adenocarcinoma Cells. <i>Mathematical Modelling of Natural Phenomena</i> , <b>2012</b> , 7, 337-368	3	1
22	Branching Principal Components: Elastic Graphs, Topological Grammars and Metro Maps. <i>Neural Networks (IJCNN), International Joint Conference on</i> , <b>2007</b> ,		1
21	The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks		1
20	Stabilized Independent Component Analysis outperforms other methods in finding reproducible signals in tumoral transcriptomes		1
19	Basic, simple and extendable kinetic model of protein synthesis. <i>Mathematical Biosciences and Engineering</i> , <b>2019</b> , 16, 6602-6622	2.1	1
18	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network		1
17	How Cell Decides Between Life and Death: Mathematical Modeling of Epigenetic Landscapes of Cellular Fates. <i>Springer Proceedings in Mathematics</i> , <b>2013</b> , 191-204		1
16	Metabolic and signalling network map integration: application to cross-talk studies and omics data analysis in cancer		1
15	Hubness reduction improves clustering and trajectory inference in single-cell transcriptomic data		1
14	Modeling Progression of Single Cell Populations Through the Cell Cycle as a Sequence of Switches		1
13	Adaptation through the lens of single-cell multi-omics data: Comment on "Dynamic and thermodynamic models of adaptation" by A.N. Gorban et al. <i>Physics of Life Reviews</i> , <b>2021</b> , 38, 132-134	2.1	1
12	Exact solving and sensitivity analysis of stochastic continuous time Boolean models. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 241	3.6	0
11	Modeling Progression of Single Cell Populations Through the Cell Cycle as a Sequence of Switches.. <i>Frontiers in Molecular Biosciences</i> , <b>2021</b> , 8, 793912	5.6	0
10	WebMaBoSS: A Web Interface for Simulating Boolean Models Stochastically. <i>Frontiers in Molecular Biosciences</i> , <b>2021</b> , 8, 754444	5.6	0
9	Meta-Analysis of Esophageal Cancer Transcriptomes Using Independent Component Analysis. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 683632	4.5	0



- 8 The multilayer community structure of medulloblastoma. *IScience*, **2021**, 24, 102365 6.1 o
- 7 . *IEEE Transactions on Geoscience and Remote Sensing*, **2021**, 1-15 8.1 o
- 6 Atlas of Cancer Signaling Network: A Resource of Multi-Scale Biological Maps to Study Disease Mechanisms **2021**, 490-506
- 5 LNetReduce: Tool for Reducing Linear Dynamic Networks with Separated Timescales. *Lecture Notes in Computer Science*, **2021**, 238-244 0.9
- 4 Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network **2020**, 16, e1007652
- 3 Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network **2020**, 16, e1007652
- 2 Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network **2020**, 16, e1007652
- 1 Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network **2020**, 16, e1007652