

# Reka Albert

## List of Publications by Year in descending order

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158  
papers

78,234  
citations

26610

56  
h-index

9579

142  
g-index

170  
all docs

170  
docs citations

170  
times ranked

38032  
citing authors

#	ARTICLE	IF	CITATIONS
1	Emergence of Scaling in Random Networks. <i>Science</i> , 1999, 286, 509-512.	6.0	28,383
2	Statistical mechanics of complex networks. <i>Reviews of Modern Physics</i> , 2002, 74, 47-97.	16.4	16,492
3	Error and attack tolerance of complex networks. <i>Nature</i> , 2000, 406, 378-382.	13.7	7,006
4	The large-scale organization of metabolic networks. <i>Nature</i> , 2000, 407, 651-654.	13.7	4,262
5	Diameter of the World-Wide Web. <i>Nature</i> , 1999, 401, 130-131.	13.7	3,527
6	Near linear time algorithm to detect community structures in large-scale networks. <i>Physical Review E</i> , 2007, 76, 036106.	0.8	2,431
7	Mean-field theory for scale-free random networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 1999, 272, 173-187.	1.2	1,861
8	Scale-free characteristics of random networks: the topology of the world-wide web. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2000, 281, 69-77.	1.2	1,062
9	Topology of Evolving Networks: Local Events and Universality. <i>Physical Review Letters</i> , 2000, 85, 5234-5237.	2.9	1,054
10	Structural vulnerability of the North American power grid. <i>Physical Review E</i> , 2004, 69, 025103.	0.8	1,046
11	Scale-free networks in cell biology. <i>Journal of Cell Science</i> , 2005, 118, 4947-4957.	1.2	1,041
12	The topology of the regulatory interactions predicts the expression pattern of the segment polarity genes in <i>Drosophila melanogaster</i> . <i>Journal of Theoretical Biology</i> , 2003, 223, 1-18.	0.8	827
13	Modeling cascading failures in the North American power grid. <i>European Physical Journal B</i> , 2005, 46, 101-107.	0.6	535
14	Predicting Essential Components of Signal Transduction Networks: A Dynamic Model of Guard Cell Abscisic Acid Signaling. <i>PLoS Biology</i> , 2006, 4, e312.	2.6	356
15	Boolean modeling in systems biology: an overview of methodology and applications. <i>Physical Biology</i> , 2012, 9, 055001.	0.8	353
16	Network model of survival signaling in large granular lymphocyte leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16308-16313.	3.3	337
17	Robustness and fragility of Boolean models for genetic regulatory networks. <i>Journal of Theoretical Biology</i> , 2005, 235, 431-449.	0.8	295
18	Slow Drag in a Granular Medium. <i>Physical Review Letters</i> , 1999, 82, 205-208.	2.9	286

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19	Boolean network simulations for life scientists. <i>Source Code for Biology and Medicine</i> , 2008, 3, 16.	1.7	280
20	What keeps sandcastles standing?. <i>Nature</i> , 1997, 387, 765-765.	13.7	273
21	Network Modeling of TGF $\beta$ 2 Signaling in Hepatocellular Carcinoma Epithelial-to-Mesenchymal Transition Reveals Joint Sonic Hedgehog and Wnt Pathway Activation. <i>Cancer Research</i> , 2014, 74, 5963-5977.	0.4	243
22	Dynamics of Complex Systems: Scaling Laws for the Period of Boolean Networks. <i>Physical Review Letters</i> , 2000, 84, 5660-5663.	2.9	217
23	Border Control—A Membrane-Linked Interactome of <i>Arabidopsis</i> . <i>Science</i> , 2014, 344, 711-716.	6.0	213
24	Structure-based control of complex networks with nonlinear dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7234-7239.	3.3	204
25	Common and unique elements of the ABA-regulated transcriptome of <i>Arabidopsis</i> guard cells. <i>BMC Genomics</i> , 2011, 12, 216.	1.2	189
26	Conserved network motifs allow protein-protein interaction prediction. <i>Bioinformatics</i> , 2004, 20, 3346-3352.	1.8	179
27	Cell Fate Reprogramming by Control of Intracellular Network Dynamics. <i>PLoS Computational Biology</i> , 2015, 11, e1004193.	1.5	179
28	Attractor analysis of asynchronous Boolean models of signal transduction networks. <i>Journal of Theoretical Biology</i> , 2010, 266, 641-656.	0.8	163
29	Survivability of Multiagent-Based Supply Networks: A Topological Perspective. <i>IEEE Intelligent Systems</i> , 2004, 19, 24-31.	4.0	162
30	Dynamical and Structural Analysis of a T Cell Survival Network Identifies Novel Candidate Therapeutic Targets for Large Granular Lymphocyte Leukemia. <i>PLoS Computational Biology</i> , 2011, 7, e1002267.	1.5	162
31	Network Inference, Analysis, and Modeling in Systems Biology. <i>Plant Cell</i> , 2007, 19, 3327-3338.	3.1	156
32	Jamming and Fluctuations in Granular Drag. <i>Physical Review Letters</i> , 2000, 84, 5122-5125.	2.9	139
33	An effective network reduction approach to find the dynamical repertoire of discrete dynamic networks. <i>Chaos</i> , 2013, 23, 025111.	1.0	139
34	Maximum angle of stability in wet and dry spherical granular media. <i>Physical Review E</i> , 1997, 56, R6271-R6274.	0.8	133
35	Boolean modeling: a logic-based dynamic approach for understanding signaling and regulatory networks and for making useful predictions. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2014, 6, 353-369.	6.6	122
36	Combinatorial interventions inhibit TGF $\beta$ 2-driven epithelial-to-mesenchymal transition and support hybrid cellular phenotypes. <i>Npj Systems Biology and Applications</i> , 2015, 1, 15014.	1.4	122

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37	Boolean modeling of biological regulatory networks: A methodology tutorial. <i>Methods</i> , 2013, 62, 3-12.	1.9	121
38	Modeling Systems-Level Regulation of Host Immune Responses. <i>PLoS Computational Biology</i> , 2007, 3, e109.	1.5	119
39	Boolean modeling of transcriptome data reveals novel modes of heterotrimeric Gâ€protein action. <i>Molecular Systems Biology</i> , 2010, 6, 372.	3.2	117
40	Inference of Network Dynamics and Metabolic Interactions in the Gut Microbiome. <i>PLoS Computational Biology</i> , 2015, 11, e1004338.	1.5	106
41	Biological switches and clocks. <i>Journal of the Royal Society Interface</i> , 2008, 5, S1-8.	1.5	101
42	Differential gene expression in <i>Arabidopsis wildâ€type</i> and mutant anthers: insights into anther cell differentiation and regulatory networks. <i>Plant Journal</i> , 2007, 52, 14-29.	2.8	98
43	Cooperative development of logical modelling standards and tools with CoLoMoTo. <i>Bioinformatics</i> , 2015, 31, 1154-1159.	1.8	98
44	Stick-slip fluctuations in granular drag. <i>Physical Review E</i> , 2001, 64, 031307.	0.8	94
45	A network model for plantâ€™pollinator community assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 197-202.	3.3	90
46	A Reduction Method for Boolean Network Models Proven to Conserve Attractors. <i>SIAM Journal on Applied Dynamical Systems</i> , 2013, 12, 1997-2011.	0.7	86
47	Abscisic Acidâ€™Responsive Guard Cell Metabolomes of <i>Arabidopsis</i> Wild-Type and <i>gpa1</i> G-Protein Mutants. <i>Plant Cell</i> , 2014, 25, 4789-4811.	3.1	79
48	Multi-level Modeling of Light-Induced Stomatal Opening Offers New Insights into Its Regulation by Drought. <i>PLoS Computational Biology</i> , 2014, 10, e1003930.	1.5	77
49	Systems-level network modeling of Small Cell Lung Cancer subtypes identifies master regulators and destabilizers. <i>PLoS Computational Biology</i> , 2019, 15, e1007343.	1.5	77
50	A new discrete dynamic model of ABA-induced stomatal closure predicts key feedback loops. <i>PLoS Biology</i> , 2017, 15, e2003451.	2.6	75
51	Generating super-shedders: co-infection increases bacterial load and egg production of a gastrointestinal helminth. <i>Journal of the Royal Society Interface</i> , 2013, 10, 20120588.	1.5	74
52	Complex Networks: An Engineering View. <i>IEEE Circuits and Systems Magazine</i> , 2010, 10, 10-25.	2.6	73
53	Elementary signaling modes predict the essentiality of signal transduction network components. <i>BMC Systems Biology</i> , 2011, 5, 44.	3.0	68
54	Variation in host susceptibility and infectiousness generated by co-infection: the myxomaâ€™Trichostrongylus retortaeformis case in wild rabbits. <i>Journal of the Royal Society Interface</i> , 2007, 4, 831-840.	1.5	67

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55	Constraint-based network model of pathogen-immune system interactions. <i>Journal of the Royal Society Interface</i> , 2009, 6, 599-612.	1.5	59
56	Discrete Dynamic Modeling of Cellular Signaling Networks. <i>Methods in Enzymology</i> , 2009, 467, 281-306.	0.4	56
57	Stabilization of perturbed Boolean network attractors through compensatory interactions. <i>BMC Systems Biology</i> , 2014, 8, 53.	3.0	53
58	Bacteriophage-mediated competition in <i>Bordetella</i> bacteria. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006, 273, 1843-1848.	1.2	52
59	A Novel Method for Signal Transduction Network Inference from Indirect Experimental Evidence. <i>Journal of Computational Biology</i> , 2007, 14, 927-949.	0.8	52
60	Discrete dynamic network modeling of oncogenic signaling: Mechanistic insights for personalized treatment of cancer. <i>Current Opinion in Systems Biology</i> , 2018, 9, 1-10.	1.3	52
61	Systems-level insights into cellular regulation: inferring, analysing, and modelling intracellular networks. <i>IET Systems Biology</i> , 2007, 1, 61-77.	0.8	51
62	Target Control in Logical Models Using the Domain of Influence of Nodes. <i>Frontiers in Physiology</i> , 2018, 9, 454.	1.3	51
63	A network modeling approach to elucidate drug resistance mechanisms and predict combinatorial drug treatments in breast cancer. <i>Cancer Convergence</i> , 2017, 1, 5.	8.0	50
64	Computational and Experimental Analysis Reveals a Requirement for Eosinophil-Derived IL-13 for the Development of Allergic Airway Responses in C57BL/6 Mice. <i>Journal of Immunology</i> , 2011, 186, 2936-2949.	0.4	48
65	Rapid and asymmetric divergence of duplicate genes in the human gene coexpression network. <i>BMC Bioinformatics</i> , 2006, 7, 46.	1.2	45
66	Topological implications of negative curvature for biological and social networks. <i>Physical Review E</i> , 2014, 89, 032811.	0.8	45
67	Search in weighted complex networks. <i>Physical Review E</i> , 2005, 72, 066128.	0.8	44
68	Towards control of cellular decision-making networks in the epithelial-to-mesenchymal transition. <i>Physical Biology</i> , 2019, 16, 031002.	0.8	44
69	Topology of plant-pollinator networks that are vulnerable to collapse from species extinction. <i>Physical Review E</i> , 2012, 86, 021924.	0.8	43
70	Parity and time reversal elucidate both decision-making in empirical models and attractor scaling in critical Boolean networks. <i>Science Advances</i> , 2021, 7, .	4.7	43
71	Boolean Modeling of Genetic Regulatory Networks. <i>Lecture Notes in Physics</i> , 0, , 459-481.	0.3	42
72	Network Model of Immune Responses Reveals Key Effectors to Single and Co-infection Dynamics by a Respiratory Bacterium and a Gastrointestinal Helminth. <i>PLoS Computational Biology</i> , 2012, 8, e1002345.	1.5	42

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73	NET-SYNTHESIS: a software for synthesis, inference and simplification of signal transduction networks. <i>Bioinformatics</i> , 2008, 24, 293-295.	1.8	39
74	Networks in motion. <i>Physics Today</i> , 2012, 65, 43-48.	0.3	39
75	The physics of sand castles: maximum angle of stability in wet and dry granular media. <i>Physica A: Statistical Mechanics and Its Applications</i> , 1999, 266, 366-371.	1.2	36
76	pystablemotifs: Python library for attractor identification and control in Boolean networks. <i>Bioinformatics</i> , 2022, 38, 1465-1466.	1.8	35
77	Model-driven discovery of calcium-related protein-phosphatase inhibition in plant guard cell signaling. <i>PLoS Computational Biology</i> , 2019, 15, e1007429.	1.5	34
78	USING GRAPH CONCEPTS TO UNDERSTAND THE ORGANIZATION OF COMPLEX SYSTEMS. <i>International Journal of Bifurcation and Chaos in Applied Sciences and Engineering</i> , 2007, 17, 2201-2214.	0.7	33
79	A comparative study of qualitative and quantitative dynamic models of biological regulatory networks. <i>EPJ Nonlinear Biomedical Physics</i> , 2016, 4, .	0.8	32
80	A framework to find the logic backbone of a biological network. <i>BMC Systems Biology</i> , 2017, 11, 122.	3.0	32
81	Disease dynamics in a dynamic social network. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2010, 389, 2663-2674.	1.2	31
82	synergy: a Python library for calculating, analyzing and visualizing drug combination synergy. <i>Bioinformatics</i> , 2021, 37, 1473-1474.	1.8	31
83	Driven Interfaces in Disordered Media: Determination of Universality Classes from Experimental Data. <i>Physical Review Letters</i> , 1998, 81, 2926-2929.	2.9	30
84	miR-200b restoration and DNA methyltransferase inhibitor block lung metastasis of mesenchymal-phenotype hepatocellular carcinoma. <i>Oncogenesis</i> , 2012, 1, e15-e15.	2.1	29
85	Transience and constancy of interactions in a plant-frugivore network. <i>Ecosphere</i> , 2013, 4, 1-25.	1.0	29
86	Boolean models of within-host immune interactions. <i>Current Opinion in Microbiology</i> , 2010, 13, 377-381.	2.3	28
87	A Guard Cell Abscisic Acid (ABA) Network Model That Captures the Stomatal Resting State. <i>Frontiers in Physiology</i> , 2020, 11, 927.	1.3	28
88	Discrete Dynamic Modeling with Asynchronous Update, or How to Model Complex Systems in the Absence of Quantitative Information. <i>Methods in Molecular Biology</i> , 2009, 553, 207-225.	0.4	28
89	Search in spatial scale-free networks. <i>New Journal of Physics</i> , 2007, 9, 190-190.	1.2	27
90	Identifying (un)controllable dynamical behavior in complex networks. <i>PLoS Computational Biology</i> , 2018, 14, e1006630.	1.5	27

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91	Computationally efficient measure of topological redundancy of biological and social networks. <i>Physical Review E</i> , 2011, 84, 036117.	0.8	26
92	Elucidation of directionality for co-expressed genes: predicting intra-operon termination sites. <i>Bioinformatics</i> , 2006, 22, 209-214.	1.8	25
93	Introduction to Focus Issue: Quantitative Approaches to Genetic Networks. <i>Chaos</i> , 2013, 23, 025001.	1.0	25
94	General method to find the attractors of discrete dynamic models of biological systems. <i>Physical Review E</i> , 2018, 97, 042308.	0.8	25
95	Network model and analysis of the spread of Covid-19 with social distancing. <i>Applied Network Science</i> , 2020, 5, 100.	0.8	24
96	Dynamic Receptor Team Formation Can Explain the High Signal Transduction Gain in <i>Escherichia coli</i> . <i>Biophysical Journal</i> , 2004, 86, 2650-2659.	0.2	23
97	Clustering social networks using ant colony optimization. <i>Operational Research</i> , 2013, 13, 47-65.	1.3	23
98	Plant-pollinator community network response to species invasion depends on both invader and community characteristics. <i>Oikos</i> , 2015, 124, 406-413.	1.2	22
99	A feedback loop of conditionally stable circuits drives the cell cycle from checkpoint to checkpoint. <i>Scientific Reports</i> , 2019, 9, 16430.	1.6	22
100	Large-scale inference and graph-theoretical analysis of gene-regulatory networks in <i>B. Subtilis</i> . <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007, 373, 796-810.	1.2	21
101	Inferring (Biological) Signal Transduction Networks via Transitive Reductions of Directed Graphs. <i>Algorithmica</i> , 2008, 51, 129-159.	1.0	20
102	Dynamic models of immune responses: what is the ideal level of detail?. <i>Theoretical Biology and Medical Modelling</i> , 2010, 7, 35.	2.1	19
103	Global versus local extinction in a network model of plant-pollinator communities. <i>Theoretical Ecology</i> , 2013, 6, 495-503.	0.4	18
104	Effects of community structure on the dynamics of random threshold networks. <i>Physical Review E</i> , 2013, 87, 012810.	0.8	18
105	Restoration of plant-pollinator interaction networks via species translocation. <i>Theoretical Ecology</i> , 2014, 7, 209-220.	0.4	17
106	Topological constraints on network control profiles. <i>Scientific Reports</i> , 2016, 5, 18693.	1.6	16
107	Experimental species introduction shapes network interactions in a plant-pollinator community. <i>Biological Invasions</i> , 2019, 21, 3505-3519.	1.2	16
108	Mathematical modeling of the <i>Candida albicans</i> yeast to hyphal transition reveals novel control strategies. <i>PLoS Computational Biology</i> , 2021, 17, e1008690.	1.5	16

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109	ER+ Breast Cancer Strongly Depends on MCL-1 and BCL-xL Anti-Apoptotic Proteins. <i>Cells</i> , 2021, 10, 1659.	1.8	16
110	Discrete Dynamic Modeling of Signal Transduction Networks. <i>Methods in Molecular Biology</i> , 2012, 880, 255-272.	0.4	15
111	Studying the effect of cell division on expression patterns of the segment polarity genes. <i>Journal of the Royal Society Interface</i> , 2008, 5, S71-84.	1.5	14
112	A voxelwise approach to determine consensus regions-of-interest for the study of brain network plasticity. <i>Frontiers in Neuroanatomy</i> , 2015, 9, 97.	0.9	14
113	Analysis of a dynamic model of guard cell signaling reveals the stability of signal propagation. <i>BMC Systems Biology</i> , 2016, 10, 78.	3.0	14
114	Network analysis reveals cross-links of the immune pathways activated by bacteria and allergen. <i>Physical Review E</i> , 2011, 84, 031929.	0.8	13
115	Edgetic perturbations to eliminate fixed-point attractors in Boolean regulatory networks. <i>Chaos</i> , 2019, 29, 023130.	1.0	13
116	Cell Line-Specific Network Models of ER+ Breast Cancer Identify Potential PI3K Inhibitor Resistance Mechanisms and Drug Combinations. <i>Cancer Research</i> , 2021, 81, 4603-4617.	0.4	13
117	Signaling Networks. , 2015, , 65-91.		13
118	Correlations in the degeneracy of structurally controllable topologies for networks. <i>Scientific Reports</i> , 2017, 7, 46251.	1.6	12
119	Self-sustaining positive feedback loops in discrete and continuous systems. <i>Journal of Theoretical Biology</i> , 2018, 459, 36-44.	0.8	12
120	Comment on "Control profiles of complex networks". <i>Science</i> , 2014, 346, 561-561.	6.0	11
121	Shaping specificity in signaling networks. <i>Nature Genetics</i> , 2007, 39, 286-287.	9.4	10
122	Node-independent elementary signaling modes: A measure of redundancy in Boolean signaling transduction networks. <i>Network Science</i> , 2016, 4, 273-292.	0.8	10
123	Data-Driven Math Model of FLT3-ITD Acute Myeloid Leukemia Reveals Potential Therapeutic Targets. <i>Journal of Personalized Medicine</i> , 2021, 11, 193.	1.1	10
124	Structure-based approach to identifying small sets of driver nodes in biological networks. <i>Chaos</i> , 2022, 32, .	1.0	10
125	Minimal functional routes in directed graphs with dependent edges. <i>International Transactions in Operational Research</i> , 2013, 20, 391-409.	1.8	8
126	Top-down network analysis characterizes hidden termite-termite interactions. <i>Ecology and Evolution</i> , 2016, 6, 6178-6188.	0.8	7



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127	Detecting network anomalies using Formanâ€™Ricci curvature and a case study for human brain networks. Scientific Reports, 2021, 11, 8121.	1.6	7
128	Whole community invasions and the integration of novel ecosystems. PLoS Computational Biology, 2022, 18, e1010151.	1.5	7
129	Compensatory interactions to stabilize multiple steady states or mitigate the effects of multiple deregulations in biological networks. Physical Review E, 2016, 94, 062316.	0.8	6
130	Exploring phospholipase C-coupled Ca <sup>2+</sup> signalling networks using boolean modelling. IET Systems Biology, 2011, 5, 174-184.	0.8	5
131	Some Perspectives on Network Modeling in Therapeutic Target Prediction. Biomedical Engineering and Computational Biology, 2013, 5, BECB.S10793.	0.8	5
132	CONTROLLING THE CELL CYCLE RESTRICTION SWITCH ACROSS THE INFORMATION GRADIENT. International Journal of Modeling, Simulation, and Scientific Computing, 2019, 22, 1950020.	0.9	5
133	Inference of Signal Transduction Networks from Double Causal Evidence. Methods in Molecular Biology, 2010, 673, 239-251.	0.4	5
134	Inference of a Boolean Network From Causal Logic Implications. Frontiers in Genetics, 0, 13, .	1.1	5
135	Motif profile dynamics and transient species in a Boolean model of mutualistic ecological communities. Journal of Complex Networks, 2016, 4, 127-139.	1.1	4
136	A survey of some tensor analysis techniques for biological systems. Quantitative Biology, 2019, 7, 266-277.	0.3	4
137	Relationships among generalized positive feedback loops determine possible community outcomes in plant-pollinator interaction networks. Physical Review E, 2021, 104, 054304.	0.8	4
138	Why Do CD8+ T Cells become Indifferent to Tumors: A Dynamic Modeling Approach. Frontiers in Physiology, 2011, 2, 32.	1.3	3
139	Context-specific regulation of lysosomal lipolysis through network-level diverting of transcription factor interactions. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	3
140	Structure and timescale analysis in genetic regulatory networks. , 2006, , .		2
141	Boolean Models of Cellular Signaling Networks. , 2013, , 197-210.		2
142	Discrete Dynamic Modeling: A Network Approach for Systems Pharmacology. AAPS Advances in the Pharmaceutical Sciences Series, 2016, , 81-103.	0.2	2
143	Introduction to the Special Issue on Approaches to Control Biological and Biologically Inspired Networks. IEEE Transactions on Control of Network Systems, 2018, 5, 690-693.	2.4	2
144	Spatial Pattern Formation and Morphogenesis in Development: Recent Progress for Two Model Systems. , 2003, , 21-32.		2

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145	Toward Understanding the Structure and Function of Cellular Interaction Networks. Bolyai Society Mathematical Studies, 2008, , 239-275.	0.3	1
146	Boolean Networks in Inference and Dynamic Modeling of Biological Systems at the Molecular and Physiological Level. World Scientific Lecture Notes in Complex Systems, 2009, , 59-78.	0.1	1
147	Complexity and Large-Scale Networks. Operations Research Series, 2008, , 319-351.	0.0	1
148	A Novel Method for Signal Transduction Network Inference from Indirect Experimental Evidence. Lecture Notes in Computer Science, 2007, , 407-419.	1.0	1
149	Modeling of Molecular Networks. Mathematics of Planet Earth, 2019, , 35-62.	0.1	1
150	Abstract 675: Network modeling of drug resistance mechanisms and drug combinations in breast cancer. , 2019, , .		1
151	An Overview of Systems Biology. , 0, , 41-66.		1
152	An Experimental Study of the Fluctuations in Granular Drag. Materials Research Society Symposia Proceedings, 2000, 627, 1.	0.1	0
153	Effects of Noise on Ecological Invasion Processes: Bacteriophage-Mediated Competition in Bacteria. Journal of Statistical Physics, 2007, 128, 229-256.	0.5	0
154	Dynamic Network Modeling of Epithelial-to-Mesenchymal Transition Determines Snail1 as Critical Driver of Stemness in Liver Cancer. Gastroenterology, 2011, 140, S-14.	0.6	0
155	Internet Based Service Networks. Springer Optimization and Its Applications, 2012, , 263-303.	0.6	0
156	Introduction to the Special Section on Network Science in Biological and Bio-Inspired Systems. IEEE Transactions on Network Science and Engineering, 2020, 7, 409-410.	4.1	0
157	Abstract 1465: Metastatic potential of hepatocellular carcinoma determined by dynamic modeling of EMT network and Snail1 expression. , 2011, , .		0
158	Quantification of Regulation in Networks with Positive and Negative Interaction Weights. , 2016, , 1642-1646.		0