

# Olaf Wolkenhauer

## List of Publications by Year in descending order

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Version: 2024-02-01

223  
papers

6,740  
citations

57758

44  
h-index

110387

64  
g-index

263  
all docs

263  
docs citations

263  
times ranked

10089  
citing authors

#	ARTICLE	IF	CITATIONS
1	Do simple models lead to generality in ecology?. Trends in Ecology and Evolution, 2013, 28, 578-583.	8.7	215
2	Systems medicine and integrated care to combat chronic noncommunicable diseases. Genome Medicine, 2011, 3, 43.	8.2	181
3	Understanding microRNA-mediated gene regulatory networks through mathematical modelling. Nucleic Acids Research, 2016, 44, 6019-6035.	14.5	135
4	Minimum Information About a Simulation Experiment (MIASE). PLoS Computational Biology, 2011, 7, e1001122.	3.2	133
5	A systematic survey of centrality measures for protein-protein interaction networks. BMC Systems Biology, 2018, 12, 80.	3.0	133
6	Diagnostic Potential of Imaging Flow Cytometry. Trends in Biotechnology, 2018, 36, 649-652.	9.3	130
7	The Atlas of Inflammation Resolution (AIR). Molecular Aspects of Medicine, 2020, 74, 100894.	6.4	110
8	Epigenetic factor EPC1 is a master regulator of DNA damage response by interacting with E2F1 to silence death and activate metastasis-related gene signatures. Nucleic Acids Research, 2016, 44, 117-133.	14.5	102
9	Modeling and Simulation of Intracellular Dynamics: Choosing an Appropriate Framework. IEEE Transactions on Nanobioscience, 2004, 3, 200-207.	3.3	99
10	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. Scientific Data, 2020, 7, 136.	5.3	99
11	Regulation of cell cycle checkpoint kinase WEE1 by miR-195 in malignant melanoma. Oncogene, 2013, 32, 3175-3183.	5.9	85
12	Unraveling a tumor type-specific regulatory core underlying E2F1-mediated epithelial-mesenchymal transition to predict receptor protein signatures. Nature Communications, 2017, 8, 198.	12.8	84
13	Investigations Into the Analysis and Modeling of the TNF $\alpha$ -Mediated NF- $\kappa$ B-Signaling Pathway. Genome Research, 2003, 13, 2413-2422.	5.5	80
14	Feedback dynamics and cell function: Why systems biology is called Systems Biology. Molecular BioSystems, 2005, 1, 14.	2.9	79
15	The road from systems biology to systems medicine. Pediatric Research, 2013, 73, 502-507.	2.3	78
16	E2F1 induces miR-224/452 expression to drive EMT through TXNIP downregulation. EMBO Reports, 2014, 15, 1315-1329.	4.5	78
17	Computational analysis of target hub gene repression regulated by multiple and cooperative miRNAs. Nucleic Acids Research, 2012, 40, 8818-8834.	14.5	77
18	Enabling multiscale modeling in systems medicine. Genome Medicine, 2014, 6, 21.	8.2	76

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19	Cooperative gene regulation by microRNA pairs and their identification using a computational workflow. <i>Nucleic Acids Research</i> , 2014, 42, 7539-7552.	14.5	72
20	miR-638 promotes melanoma metastasis and protects melanoma cells from apoptosis and autophagy. <i>Oncotarget</i> , 2015, 6, 2966-2980.	1.8	72
21	MicroRNA-mRNA interactions in colorectal cancer and their role in tumor progression. <i>Genes Chromosomes and Cancer</i> , 2015, 54, 129-141.	2.8	70
22	LoRAS: an oversampling approach for imbalanced datasets. <i>Machine Learning</i> , 2021, 110, 279-301.	5.4	70
23	Quantitative modelling of amyloidogenic processing and its influence by SORLA in Alzheimer's disease. <i>EMBO Journal</i> , 2012, 31, 187-200.	7.8	67
24	Power-law models of signal transduction pathways. <i>Cellular Signalling</i> , 2007, 19, 1531-1541.	3.6	66
25	Label-Free Identification of White Blood Cells Using Machine Learning. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2019, 95, 836-842.	1.5	66
26	Optimal sampling time selection for parameter estimation in dynamic pathway modeling. <i>BioSystems</i> , 2004, 75, 43-55.	2.0	65
27	Gene Expression in Low- and High-Dose-Irradiated Human Peripheral Blood Lymphocytes: Possible Applications for Biodosimetry. <i>Radiation Research</i> , 2012, 178, 304.	1.5	64
28	Why model?. <i>Frontiers in Physiology</i> , 2014, 5, 21.	2.8	64
29	Cardiac Function Improvement and Bone Marrow Response. <i>EBioMedicine</i> , 2017, 22, 208-224.	6.1	64
30	The dynamic systems approach to control and regulation of intracellular networks. <i>FEBS Letters</i> , 2005, 579, 1846-1853.	2.8	62
31	MiR-205-5p and miR-342-3p cooperate in the repression of the E2F1 transcription factor in the context of anticancer chemotherapy resistance. <i>Theranostics</i> , 2018, 8, 1106-1120.	10.0	59
32	LncRNA-SLC16A1-AS1 induces metabolic reprogramming during Bladder Cancer progression as target and co-activator of E2F1. <i>Theranostics</i> , 2020, 10, 9620-9643.	10.0	58
33	Objective assessment of stored blood quality by deep learning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21381-21390.	7.1	57
34	A systems biology approach to investigate the effect of pH-induced gene regulation on solvent production by <i>Clostridium acetobutylicum</i> in continuous culture. <i>BMC Systems Biology</i> , 2011, 5, 10.	3.0	56
35	Kinetic Modeling-Based Detection of Genetic Signatures That Provide Chemoresistance via the E2F1-p73/DNp73-miR-205 Network. <i>Cancer Research</i> , 2013, 73, 3511-3524.	0.9	56
36	Evolution of Centrality Measurements for the Detection of Essential Proteins in Biological Networks. <i>Frontiers in Physiology</i> , 2016, 7, 375.	2.8	56

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37	Analysing the impact of nucleo-cytoplasmic shuttling of $\beta^2$ -catenin and its antagonists APC, Axin and GSK3 on Wnt/ $\beta^2$ -catenin signalling. Cellular Signalling, 2013, 25, 2210-2221.	3.6	53
38	The search for organizing principles as a cure against reductionism in systems medicine. FEBS Journal, 2013, 280, 5938-5948.	4.7	53
39	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
40	Harmonizing semantic annotations for computational models in biology. Briefings in Bioinformatics, 2019, 20, 540-550.	6.5	52
41	MicroRNA-Regulated Networks: The Perfect Storm for Classical Molecular Biology, the Ideal Scenario for Systems Biology. Advances in Experimental Medicine and Biology, 2013, 774, 55-76.	1.6	50
42	Intracellular delay limits cyclic changes in gene expression. Mathematical Biosciences, 2007, 205, 163-179.	1.9	49
43	Clinico-Pathologic Function of Cerebral ABC Transporters – Implications for the Pathogenesis of Alzheimers Disease. Current Alzheimer Research, 2008, 5, 396-405.	1.4	49
44	Whither systems medicine?. Experimental and Molecular Medicine, 2018, 50, e453-e453.	7.7	49
45	Dynamics of biological systems: role of systems biology in medical research. Expert Review of Molecular Diagnostics, 2006, 6, 891-902.	3.1	48
46	Clustering of unevenly sampled gene expression time-series data. Fuzzy Sets and Systems, 2005, 152, 49-66.	2.7	46
47	The systems biology of mitochondrial fission and fusion and implications for disease and aging. Biogerontology, 2014, 15, 1-12.	3.9	46
48	Systems biology of JAK-STAT signalling in human malignancies. Progress in Biophysics and Molecular Biology, 2011, 106, 426-434.	2.9	44
49	A frequency-based gene selection method to identify robust biomarkers for radiation dose prediction. International Journal of Radiation Biology, 2012, 88, 267-276.	1.8	44
50	MicroRNA and Transcription Factor Gene Regulatory Network Analysis Reveals Key Regulatory Elements Associated with Prostate Cancer Progression. PLoS ONE, 2016, 11, e0168760.	2.5	44
51	How Modeling Standards, Software, and Initiatives Support Reproducibility in Systems Biology and Systems Medicine. IEEE Transactions on Biomedical Engineering, 2016, 63, 1999-2006.	4.2	43
52	Mammalian $\beta^2$ AMPK regulates intrinsic heart rate. Nature Communications, 2017, 8, 1258.	12.8	43
53	Level sets and minimum volume sets of probability density functions. International Journal of Approximate Reasoning, 2003, 34, 25-47.	3.3	42
54	Combining computational models, semantic annotations and simulation experiments in a graph database. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	3.0	42

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55	(Epi)genetic Inheritance in <i>Schistosoma mansoni</i> : A Systems Approach. <i>Trends in Parasitology</i> , 2017, 33, 285-294.	3.3	42
56	A systems- and signal-oriented approach to intracellular dynamics. <i>Biochemical Society Transactions</i> , 2005, 33, 507-515.	3.4	41
57	Modeling the Calvin-Benson cycle. <i>BMC Systems Biology</i> , 2011, 5, 185.	3.0	41
58	An abstract cell model that describes the self-organization of cell function in living systems. <i>Journal of Theoretical Biology</i> , 2007, 246, 461-476.	1.7	39
59	The multikinase inhibitor Sorafenib displays significant antiproliferative effects and induces apoptosis via caspase 3, 7 and PARP in B- and T-lymphoblastic cells. <i>BMC Cancer</i> , 2010, 10, 560.	2.6	39
60	Association of RHAMM with E2F1 promotes tumour cell extravasation by transcriptional up-regulation of fibronectin. <i>Journal of Pathology</i> , 2014, 234, 351-364.	4.5	38
61	The RNA workbench: best practices for RNA and high-throughput sequencing bioinformatics in Galaxy. <i>Nucleic Acids Research</i> , 2017, 45, W560-W566.	14.5	38
62	Label-Free Leukemia Monitoring by Computer Vision. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 97, 407-414.	1.5	38
63	A systems biology approach to analyse amplification in the JAK2-STAT5 signalling pathway. <i>BMC Systems Biology</i> , 2008, 2, 38.	3.0	37
64	Single-Nucleus Sequencing of an Entire Mammalian Heart: Cell Type Composition and Velocity. <i>Cells</i> , 2020, 9, 318.	4.1	36
65	Approximations and their consequences for dynamic modelling of signal transduction pathways. <i>Mathematical Biosciences</i> , 2007, 207, 40-57.	1.9	35
66	System approaches of Weiss and Bertalanffy and their relevance for systems biology today. <i>Seminars in Cancer Biology</i> , 2011, 21, 150-155.	9.6	35
67	TRAPLINE: a standardized and automated pipeline for RNA sequencing data analysis, evaluation and annotation. <i>BMC Bioinformatics</i> , 2016, 17, 21.	2.6	35
68	Switching feedback mechanisms realize the dual role of MCIP in the regulation of calcineurin activity. <i>FEBS Letters</i> , 2006, 580, 5965-5973.	2.8	34
69	Investigating the two-moment characterisation of subcellular biochemical networks. <i>Journal of Theoretical Biology</i> , 2009, 260, 340-352.	1.7	34
70	Stochastic approaches in systems biology. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 385-397.	6.6	34
71	Dynamic energy budget approaches for modelling organismal ageing. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 3443-3454.	4.0	33
72	A shift in the dominant phenotype governs the pH-induced metabolic switch of <i>Clostridium acetobutylicum</i> phosphate-limited continuous cultures. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 6451-6466.	3.6	33

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73	Integrative modelling of pH-dependent enzyme activity and transcriptomic regulation of the acetone-butanol-ethanol fermentation of <i>Clostridium acetobutylicum</i> in continuous culture. <i>Microbial Biotechnology</i> , 2013, 6, 526-539.	4.2	33
74	Chk1 and Wee1 control genotoxic-stress induced G2M arrest in melanoma cells. <i>Cellular Signalling</i> , 2015, 27, 951-960.	3.6	33
75	A Systems Biology Approach to Study MicroRNA-Mediated Gene Regulatory Networks. <i>BioMed Research International</i> , 2013, 2013, 1-15.	1.9	32
76	Mathematical modelling of interferon- $\gamma$ signalling in pancreatic stellate cells reflects and predicts the dynamics of STAT1 pathway activity. <i>Cellular Signalling</i> , 2010, 22, 97-105.	3.6	31
77	Glucose de-repression by yeast AMP-activated protein kinase SNF1 is controlled via at least two independent steps. <i>FEBS Journal</i> , 2014, 281, 1901-1917.	4.7	31
78	Chapter 17 A System Biology Approach to Understand Functional Activity of Cell Communication Systems. <i>Methods in Cell Biology</i> , 2008, 90, 399-415.	1.1	30
79	Mathematical modelling in the post-genome era: understanding genome expression and regulation—a system theoretic approach. <i>BioSystems</i> , 2002, 65, 1-18.	2.0	29
80	Cardiac Cell Therapies for the Treatment of Acute Myocardial Infarction: A Meta-Analysis from Mouse Studies. <i>Cellular Physiology and Biochemistry</i> , 2017, 42, 254-268.	1.6	29
81	Protein-coding variants contribute to the risk of atopic dermatitis and skin-specific gene expression. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 1208-1218.	2.9	29
82	Baccoside A suppresses epileptic-like seizure/convulsion in <i>Caenorhabditis elegans</i> . <i>Seizure: the Journal of the British Epilepsy Association</i> , 2010, 19, 439-442.	2.0	28
83	Comprehensive functional enrichment analysis of male infertility. <i>Scientific Reports</i> , 2017, 7, 15778.	3.3	27
84	Bioinformatic assessment of mass spectrometric chemical derivatisation techniques for proteome database searching. <i>Proteomics</i> , 2001, 1, 1368-1377.	2.2	25
85	2-DE profiling of GDNF overexpression-related proteome changes in differentiating ST14A rat progenitor cells. <i>Proteomics</i> , 2007, 7, 33-46.	2.2	25
86	Dynamic properties of a delayed protein cross talk model. <i>BioSystems</i> , 2008, 91, 51-68.	2.0	25
87	Studies on mechanisms of interferon-gamma action in pancreatic cancer using a data-driven and model-based approach. <i>Molecular Cancer</i> , 2011, 10, 13.	19.2	25
88	Modeling miRNA Regulation in Cancer Signaling Systems: miR-34a Regulation of the p53/Sirt1 Signaling Module. <i>Methods in Molecular Biology</i> , 2012, 880, 87-108.	0.9	25
89	The role of epigenetic modifications for the pathogenesis of Crohn's disease. <i>Clinical Epigenetics</i> , 2021, 13, 108.	4.1	25
90	Systems Epidemiology: What's in a Name?. <i>Online Journal of Public Health Informatics</i> , 2014, 6, e198.	0.7	25

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91	Microarray data clustering based on temporal variation: FCV with TSD preclustering. <i>Applied Bioinformatics</i> , 2003, 2, 35-45.	1.6	25
92	Investigating dynamics of inhibitory and feedback loops in ERK signalling using power-law models. <i>Molecular BioSystems</i> , 2010, 6, 2174.	2.9	24
93	Identification of immunogenic consensus T-cell epitopes in globally distributed influenza-A H1N1 neuraminidase. <i>Infection, Genetics and Evolution</i> , 2011, 11, 308-319.	2.3	23
94	An algorithm to detect and communicate the differences in computational models describing biological systems. <i>Bioinformatics</i> , 2016, 32, 563-570.	4.1	23
95	Personalized cancer immunotherapy using Systems Medicine approaches. <i>Briefings in Bioinformatics</i> , 2016, 17, 453-467.	6.5	23
96	Systems biology to battle vascular disease. <i>Nephrology Dialysis Transplantation</i> , 2010, 25, 1019-1022.	0.7	22
97	Naïve Bayes classifier predicts functional microRNA target interactions in colorectal cancer. <i>Molecular BioSystems</i> , 2015, 11, 2126-2134.	2.9	22
98	Hematopoietic stem-cell senescence and myocardial repair - Coronary artery disease genotype/phenotype analysis of post-MI myocardial regeneration response induced by CABG/CD133+ bone marrow hematopoietic stem cell treatment in RCT PERFECT Phase 3. <i>EBioMedicine</i> , 2020, 57, 102862.	6.1	22
99	Improving the reuse of computational models through version control. <i>Bioinformatics</i> , 2013, 29, 742-748.	4.1	21
100	Hybrid modeling of the crosstalk between signaling and transcriptional networks using ordinary differential equations and multi-valued logic. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 289-298.	2.3	21
101	Systems approach to the study of brain damage in the very preterm newborn. <i>Frontiers in Systems Neuroscience</i> , 2015, 9, 58.	2.5	21
102	A hybrid systems framework for cellular processes. <i>BioSystems</i> , 2005, 80, 273-282.	2.0	20
103	Parameter Identifiability and Sensitivity Analysis Predict Targets for Enhancement of STAT1 Activity in Pancreatic Cancer and Stellate Cells. <i>PLoS Computational Biology</i> , 2012, 8, e1002815.	3.2	20
104	Diagrams as locality aids for explanation and model construction in cell biology. <i>Biology and Philosophy</i> , 2012, 27, 705-721.	1.4	20
105	Are all models wrong?. <i>Computational and Systems Oncology</i> , 2021, 1, e1008.	1.5	20
106	Essay: Defining Systems Biology: An Engineering Perspective. <i>IET Systems Biology</i> , 2007, 1, 204-206.	1.5	19
107	Phosphoglycerate Mutases Function as Reverse Regulated Isoenzymes in <i>Synechococcus elongatus</i> PCC 7942. <i>PLoS ONE</i> , 2013, 8, e58281.	2.5	19
108	The RNA world in the 21st century – a systems approach to finding non-coding keys to clinical questions. <i>Briefings in Bioinformatics</i> , 2016, 17, 380-392.	6.5	19

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109	Integrative Cluster Analysis of Whole Hearts Reveals Proliferative Cardiomyocytes in Adult Mice. <i>Cells</i> , 2020, 9, 1144.	4.1	19
110	A multi-level model accounting for the effects of JAK2-STAT5 signal modulation in erythropoiesis. <i>Computational Biology and Chemistry</i> , 2009, 33, 312-324.	2.3	18
111	A model-based strategy to investigate the role of microRNA regulation in cancer signalling networks. <i>Theory in Biosciences</i> , 2011, 130, 55-69.	1.4	18
112	A web platform for the network analysis of high-throughput data in melanoma and its use to investigate mechanisms of resistance to anti-PD1 immunotherapy. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 2315-2328.	3.8	18
113	Dynamical effects of epigenetic silencing of 14-3-3 $\beta$ expression. <i>Molecular BioSystems</i> , 2009, 6, 264-273.	2.9	17
114	Non-coding RNA detection methods combined to improve usability, reproducibility and precision. <i>BMC Bioinformatics</i> , 2010, 11, 491.	2.6	17
115	Integration of sensitivity and bifurcation analysis to detect critical processes in a model combining signalling and cell population dynamics. <i>International Journal of Systems Science</i> , 2010, 41, 81-105.	5.5	17
116	Analysis of cell adhesion during early stages of colon cancer based on an extended multi-valued logic approach. <i>Molecular BioSystems</i> , 2012, 8, 1230.	2.9	17
117	Inbred mouse strains reveal biomarkers that are pro-longevity, antilongevity or role switching. <i>Aging Cell</i> , 2014, 13, 729-738.	6.7	17
118	Tumors as chaotic attractors. <i>Molecular BioSystems</i> , 2014, 10, 172-179.	2.9	17
119	Unveiling network-based functional features through integration of gene expression into protein networks. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 2349-2359.	3.8	17
120	A unified framework for unraveling the functional interaction structure of a biomolecular network based on stimulus-response experimental data. <i>FEBS Letters</i> , 2005, 579, 4520-4528.	2.8	16
121	Web Resources for microRNA Research. <i>Advances in Experimental Medicine and Biology</i> , 2013, 774, 225-250.	1.6	16
122	Customized workflow development and data modularization concepts for RNA-Sequencing and metatranscriptome experiments. <i>Journal of Biotechnology</i> , 2017, 261, 85-96.	3.8	16
123	Age-Dependent Effects of UCP2 Deficiency on Experimental Acute Pancreatitis in Mice. <i>PLoS ONE</i> , 2014, 9, e94494.	2.5	16
124	The role of theorem proving in systems biology. <i>Journal of Theoretical Biology</i> , 2012, 300, 57-61.	1.7	15
125	Simulations of stressosome activation emphasize allosteric interactions between RsbR and RsbT. <i>BMC Systems Biology</i> , 2013, 7, 3.	3.0	15
126	COMODI: an ontology to characterise differences in versions of computational models in biology. <i>Journal of Biomedical Semantics</i> , 2016, 7, 46.	1.6	15



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127	Drug Repositioning Inferred from E2F1-Coregulator Interactions Studies for the Prevention and Treatment of Metastatic Cancers. <i>Theranostics</i> , 2019, 9, 1490-1509.	10.0	15
128	Coenzyme A-transferase-independent butyrate re-assimilation in <i>Clostridium acetobutylicum</i> —evidence from a mathematical model. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 9059-9072.	3.6	14
129	On the role of data, statistics and decisions in a pandemic. <i>AStA Advances in Statistical Analysis</i> , 2022, 106, 349-382.	0.9	14
130	Nucleo-cytoplasmic shuttling of APC can maximize $\beta$ -catenin/TCF concentration. <i>Journal of Theoretical Biology</i> , 2011, 279, 132-142.	1.7	13
131	Annotation-based feature extraction from sets of SBML models. <i>Journal of Biomedical Semantics</i> , 2015, 6, 20.	1.6	13
132	Single nuclei sequencing of entire mammalian hearts: strain-dependent cell-type composition and velocity. <i>Cardiovascular Research</i> , 2020, 116, 1249-1251.	3.8	13
133	The Quest for System-Theoretical Medicine in the COVID-19 Era. <i>Frontiers in Medicine</i> , 2021, 8, 640974.	2.6	13
134	Insights into erlotinib action in pancreatic cancer cells using a combined experimental and mathematical approach. <i>World Journal of Gastroenterology</i> , 2012, 18, 6226.	3.3	13
135	Multi-compartmental modeling of SORLA's influence on amyloidogenic processing in Alzheimer's disease. <i>BMC Systems Biology</i> , 2012, 6, 74.	3.0	12
136	A benchmark of hemoglobin blocking during library preparation for mRNA-Sequencing of human blood samples. <i>Scientific Reports</i> , 2020, 10, 5630.	3.3	12
137	Structure–function relationships explain CTCF zinc finger mutation phenotypes in cancer. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 7519-7536.	5.4	12
138	Cross-tissue transcriptome-wide association studies identify susceptibility genes shared between schizophrenia and inflammatory bowel disease. <i>Communications Biology</i> , 2022, 5, 80.	4.4	12
139	Principal difference between stability and structural stability (robustness) as used in systems biology. <i>Nonlinear Dynamics, Psychology, and Life Sciences</i> , 2007, 11, 413-33.	0.2	12
140	Identification and epidemiological characterization of Type-2 diabetes sub-population using an unsupervised machine learning approach. <i>Nutrition and Diabetes</i> , 2022, 12, .	3.2	12
141	How mathematical modelling elucidates signalling in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2010, 77, 1083-1095.	2.5	11
142	Deciphering hallmark processes of aging from interaction networks. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2706-2715.	2.4	11
143	Network-Assisted Disease Classification and Biomarker Discovery. <i>Methods in Molecular Biology</i> , 2016, 1386, 353-374.	0.9	11
144	Mathematical analysis of the influence of brain metabolism on the BOLD signal in Alzheimer's disease. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2018, 38, 304-316.	4.3	11

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145	Cardiomyocyte Transplantation after Myocardial Infarction Alters the Immune Response in the Heart. <i>Cells</i> , 2020, 9, 1825.	4.1	11
146	Exploring the Metabolic Heterogeneity of Cancers: A Benchmark Study of Context-Specific Models. <i>Journal of Personalized Medicine</i> , 2021, 11, 496.	2.5	11
147	A Metabolic Model of Intestinal Secretions: The Link between Human Microbiota and Colorectal Cancer Progression. <i>Metabolites</i> , 2021, 11, 456.	2.9	11
148	Self-Attention-Based Models for the Extraction of Molecular Interactions from Biological Texts. <i>Biomolecules</i> , 2021, 11, 1591.	4.0	11
149	Random set system identification. <i>IEEE Transactions on Fuzzy Systems</i> , 2002, 10, 287-296.	9.8	10
150	Information-Theoretic Analysis of Protein Sequences Shows that Amino Acids Self-cluster. <i>Journal of Theoretical Biology</i> , 2002, 218, 409-418.	1.7	10
151	The Curse of Normalization. <i>Comparative and Functional Genomics</i> , 2002, 3, 375-379.	2.0	10
152	Thresholds in transient dynamics of signal transduction pathways. <i>Journal of Theoretical Biology</i> , 2010, 264, 334-346.	1.7	10
153	Dynamics of a miRNA Model with Two Delays. <i>Biotechnology and Biotechnological Equipment</i> , 2012, 26, 3315-3320.	1.3	10
154	Autocrine TGF- $\beta$ 2/ZEB/microRNA-200 signal transduction drives epithelial-mesenchymal transition: Kinetic models predict minimal drug dose to inhibit metastasis. <i>Cellular Signalling</i> , 2016, 28, 861-870.	3.6	10
155	Advanced significance analysis of microarray data based on weighted resampling: a comparative study and application to gene deletions in <i>Mycobacterium bovis</i> . <i>Bioinformatics</i> , 2004, 20, 357-363.	4.1	9
156	Interpreting Rosen. <i>Artificial Life</i> , 2007, 13, 291-292.	1.3	9
157	The role of dynamic stimulation pattern in the analysis of bistable intracellular networks. <i>BioSystems</i> , 2008, 92, 270-281.	2.0	9
158	Dynamics of receptor and protein transducer homodimerisation. <i>BMC Systems Biology</i> , 2008, 2, 92.	3.0	9
159	The role of theory and modeling in medical research. <i>Frontiers in Physiology</i> , 2013, 4, 377.	2.8	9
160	SBML export interface for the systems biology toolbox for MATLAB. <i>Bioinformatics</i> , 2007, 23, 1297-1298.	4.1	8
161	A mathematical analysis of nuclear intensity dynamics for Mig1-GFP under consideration of bleaching effects and background noise in <i>Saccharomyces cerevisiae</i> . <i>Molecular BioSystems</i> , 2011, 7, 215-223.	2.9	8
162	Reduced Adolescent-Age Spatial Learning Ability Associated with Elevated Juvenile-Age Superoxide Levels in Complex I Mouse Mutants. <i>PLoS ONE</i> , 2015, 10, e0123863.	2.5	8

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163	Identifying frequent patterns in biochemical reaction networks: a workflow. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	8
164	All models are wrong. , 2007, , 163-179.		7
165	How quantitative measures unravel design principles in multi-stage phosphorylation cascades. Journal of Theoretical Biology, 2008, 254, 27-36.	1.7	7
166	A stem cell niche dominance theorem. BMC Systems Biology, 2011, 5, 4.	3.0	7
167	Nonlinear modelling of curvature by bi-linear metamodelling. Chemometrics and Intelligent Laboratory Systems, 2012, 117, 2-12.	3.5	7
168	Systems Biology Approaches in Aging Research. Interdisciplinary Topics in Gerontology, 2014, 40, 155-176.	3.6	7
169	Workflow Development for the Functional Characterization of ncRNAs. Methods in Molecular Biology, 2019, 1912, 111-132.	0.9	7
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