

# 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	The Prognostic and Predictive Role of Xeroderma Pigmentosum Gene Expression in Melanoma. <i>Frontiers in Oncology</i> , 2022, 12, 810058.	2.8	2
2	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
3	Attention Retrieval Model for Entity Relation Extraction From Biological Literature. <i>IEEE Access</i> , 2022, 10, 22429-22440.	4.2	1
4	Monitoring the maturation of the sarcomere network: a super-resolution microscopy-based approach. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 149.	5.4	4
5	Exploring the evolution of biochemical models at the network level. <i>PLoS ONE</i> , 2022, 17, e0265735.	2.5	0
6	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
7	Network- and enrichment-based inference of phenotypes and targets from large-scale disease maps. <i>Npj Systems Biology and Applications</i> , 2022, 8, 13.	3.0	7
8	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
9	LoRAS: an oversampling approach for imbalanced datasets. <i>Machine Learning</i> , 2021, 110, 279-301.	5.4	70
10	Are all models wrong?. <i>Computational and Systems Oncology</i> , 2021, 1, e1008.	1.5	20
11	Imagining the Future of Learning in Healthcare: The GAME 2019 #FuturistForum. <i>Journal of European CME</i> , 2021, 10, 1984076.	1.6	2
12	The Quest for System-Theoretical Medicine in the COVID-19 Era. <i>Frontiers in Medicine</i> , 2021, 8, 640974.	2.6	13
13	The role of epigenetic modifications for the pathogenesis of Crohn's disease. <i>Clinical Epigenetics</i> , 2021, 13, 108.	4.1	25
14	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
15	Combining uniform manifold approximation with localized affine shadowsampling improves classification of imbalanced datasets. , 2021, , .		1
16	A Metabolic Model of Intestinal Secretions: The Link between Human Microbiota and Colorectal Cancer Progression. <i>Metabolites</i> , 2021, 11, 456.	2.9	11
17	Fibroblast Growth Factor 21 as a Potential Biomarker for Improved Locomotion and Olfaction Detection Ability after Weight Reduction in Obese Mice. <i>Nutrients</i> , 2021, 13, 2916.	4.1	4
18	NaviCenta: Navigate the placenta. <i>Placenta</i> , 2021, 112, e35.	1.5	1

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19	A Multi-Schematic Classifier-Independent Oversampling Approach for Imbalanced Datasets. IEEE Access, 2021, 9, 123358-123374.	4.2	7
20	Structure-function relationships explain CTCF zinc finger mutation phenotypes in cancer. Cellular and Molecular Life Sciences, 2021, 78, 7519-7536.	5.4	12
21	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
22	Self-Attention-Based Models for the Extraction of Molecular Interactions from Biological Texts. Biomolecules, 2021, 11, 1591.	4.0	11
23	Automated annotation of rare-cell types from single-cell RNA-sequencing data through synthetic oversampling. BMC Bioinformatics, 2021, 22, 557.	2.6	6
24	Protein-coding variants contribute to the risk of atopic dermatitis and skin-specific gene expression. Journal of Allergy and Clinical Immunology, 2020, 145, 1208-1218.	2.9	29
25	The Atlas of Inflammation Resolution (AIR). Molecular Aspects of Medicine, 2020, 74, 100894.	6.4	110
26	Cardiomyocyte Transplantation after Myocardial Infarction Alters the Immune Response in the Heart. Cells, 2020, 9, 1825.	4.1	11
27	An integrative network-driven pipeline for systematic identification of lncRNA-associated regulatory network motifs in metastatic melanoma. BMC Bioinformatics, 2020, 21, 329.	2.6	6
28	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. EBioMedicine, 2020, 57, 102862.	6.1	22
29	LncRNA-SLC16A1-AS1 induces metabolic reprogramming during Bladder Cancer progression as target and co-activator of E2F1. Theranostics, 2020, 10, 9620-9643.	10.0	58
30	Objective assessment of stored blood quality by deep learning. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21381-21390.	7.1	57
31	Integrative Cluster Analysis of Whole Hearts Reveals Proliferative Cardiomyocytes in Adult Mice. Cells, 2020, 9, 1144.	4.1	19
32	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. Scientific Data, 2020, 7, 136.	5.3	99
33	Omics Integration Analyses Reveal the Early Evolution of Malignancy in Breast Cancer. Cancers, 2020, 12, 1460.	3.7	1
34	Label-Free Leukemia Monitoring by Computer Vision. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 97, 407-414.	1.5	38
35	RNA-Based Strategies for Cardiac Reprogramming of Human Mesenchymal Stromal Cells. Cells, 2020, 9, 504.	4.1	7
36	TGF- $\beta$ 1 Induces Changes in the Energy Metabolism of White Adipose Tissue-Derived Human Adult Mesenchymal Stem/Stromal Cells In Vitro. Metabolites, 2020, 10, 59.	2.9	2

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37	Single-Nucleus Sequencing of an Entire Mammalian Heart: Cell Type Composition and Velocity. <i>Cells</i> , 2020, 9, 318.	4.1	36
38	GEMtractor: extracting views into genome-scale metabolic models. <i>Bioinformatics</i> , 2020, 36, 3281-3282.	4.1	1
39	The role of cooperativity in a p53-miR34 dynamical mathematical model. <i>Journal of Theoretical Biology</i> , 2020, 495, 110252.	1.7	2
40	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
41	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
42	Towards biomarkers for outcomes after pancreatic ductal adenocarcinoma and ischaemic stroke, with focus on (co)-morbidity and ageing/cellular senescence (SASKit): protocol for a prospective cohort study. <i>BMJ Open</i> , 2020, 10, e039560.	1.9	5
43	Envisioning the Application of Systems Biology in Cancer Immunology. , 2020, , 599-624.		0
44	Vom Anfang und Ende der Systembiologie. <i>BioSpektrum</i> , 2019, 25, 507-509.	0.0	1
45	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
46	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
47	Harmonizing semantic annotations for computational models in biology. <i>Briefings in Bioinformatics</i> , 2019, 20, 540-550.	6.5	52
48	Computational Approaches in microRNA Biology. , 2019, , 317-330.		1
49	Workflow Development for the Functional Characterization of ncRNAs. <i>Methods in Molecular Biology</i> , 2019, 1912, 111-132.	0.9	7
50	Tools for Understanding miRNA-mRNA Interactions for Reproducible RNA Analysis. <i>Methods in Molecular Biology</i> , 2019, 1912, 199-214.	0.9	3
51	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
52	Whither systems medicine?. <i>Experimental and Molecular Medicine</i> , 2018, 50, e453-e453.	7.7	49
53	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
54	Diagnostic Potential of Imaging Flow Cytometry. <i>Trends in Biotechnology</i> , 2018, 36, 649-652.	9.3	130

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55	Impact of graphene-based nanomaterials (GBNMs) on the structural and functional conformations of hepcidin peptide. <i>Journal of Computer-Aided Molecular Design</i> , 2018, 32, 487-496.	2.9	4
56	Evolution of computational models in BioModels Database and the Physiome Model Repository. <i>BMC Systems Biology</i> , 2018, 12, 53.	3.0	3
57	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
58	Model-Based Phenotypic Signatures Governing the Dynamics of the Stem and Semi-differentiated Cell Populations in Dysplastic Colonic Crypts. <i>Bulletin of Mathematical Biology</i> , 2018, 80, 360-384.	1.9	3
59	A Network-Based Integrative Workflow to Unravel Mechanisms Underlying Disease Progression. <i>Methods in Molecular Biology</i> , 2018, 1702, 247-276.	0.9	6
60	Identifying frequent patterns in biochemical reaction networks: a workflow. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	8
61	Integrative workflows for network analysis. <i>Essays in Biochemistry</i> , 2018, 62, 549-561.	4.7	6
62	A systematic survey of centrality measures for protein-protein interaction networks. <i>BMC Systems Biology</i> , 2018, 12, 80.	3.0	133
63	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
64	Quick tips for creating effective and impactful biological pathways using the Systems Biology Graphical Notation. <i>PLoS Computational Biology</i> , 2018, 14, e1005740.	3.2	6
65	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
66	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
67	(Epi)genetic Inheritance in <i>Schistosoma mansoni</i> : A Systems Approach. <i>Trends in Parasitology</i> , 2017, 33, 285-294.	3.3	42
68	Unraveling a tumor type-specific regulatory core underlying E2F1-mediated epithelial-mesenchymal transition to predict receptor protein signatures. <i>Nature Communications</i> , 2017, 8, 198.	12.8	84
69	Cardiac Function Improvement and Bone Marrow Response "â". <i>EBioMedicine</i> , 2017, 22, 208-224.	6.1	64
70	Comprehensive functional enrichment analysis of male infertility. <i>Scientific Reports</i> , 2017, 7, 15778.	3.3	27
71	Mammalian Î³2 AMPK regulates intrinsic heart rate. <i>Nature Communications</i> , 2017, 8, 1258.	12.8	43
72	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

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73	Identification of Antineoplastic Targets with Systems Approaches, Using Resveratrol as an In-Depth Case Study. <i>Current Pharmaceutical Design</i> , 2017, 23, 4773-4793.	1.9	7
74	Evolution of Centrality Measurements for the Detection of Essential Proteins in Biological Networks. <i>Frontiers in Physiology</i> , 2016, 7, 375.	2.8	56
75	How Modeling Standards, Software, and Initiatives Support Reproducibility in Systems Biology and Systems Medicine. <i>IEEE Transactions on Biomedical Engineering</i> , 2016, 63, 1999-2006.	4.2	43
76	Understanding microRNA-mediated gene regulatory networks through mathematical modelling. <i>Nucleic Acids Research</i> , 2016, 44, 6019-6035.	14.5	135
77	Deciphering hallmark processes of aging from interaction networks. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2706-2715.	2.4	11
78	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
79	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
80	Epigenetic factor EPC1 is a master regulator of DNA damage response by interacting with E2F1 to silence death and activate metastasis-related gene signatures. <i>Nucleic Acids Research</i> , 2016, 44, 117-133.	14.5	102
81	TRAPLINE: a standardized and automated pipeline for RNA sequencing data analysis, evaluation and annotation. <i>BMC Bioinformatics</i> , 2016, 17, 21.	2.6	35
82	An algorithm to detect and communicate the differences in computational models describing biological systems. <i>Bioinformatics</i> , 2016, 32, 563-570.	4.1	23
83	Network-Assisted Disease Classification and Biomarker Discovery. <i>Methods in Molecular Biology</i> , 2016, 1386, 353-374.	0.9	11
84	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
85	Personalized cancer immunotherapy using Systems Medicine approaches. <i>Briefings in Bioinformatics</i> , 2016, 17, 453-467.	6.5	23
86	RNA Systems Biology for Cancer: From Diagnosis to Therapy. <i>Methods in Molecular Biology</i> , 2016, 1386, 305-330.	0.9	1
87	MicroRNA and Transcription Factor Gene Regulatory Network Analysis Reveals Key Regulatory Elements Associated with Prostate Cancer Progression. <i>PLoS ONE</i> , 2016, 11, e0168760.	2.5	44
88	Combining computational models, semantic annotations and simulation experiments in a graph database. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	3.0	42
89	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
90	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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91	Annotation-based feature extraction from sets of SBML models. <i>Journal of Biomedical Semantics</i> , 2015, 6, 20.	1.6	13
92	Envisioning the Application of Systems Biology in Cancer Immunology. , 2015, , 429-449.		3
93	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
94	Chk1 and Wee1 control genotoxic-stress induced G2-M arrest in melanoma cells. <i>Cellular Signalling</i> , 2015, 27, 951-960.	3.6	33
95	Naïve Bayes classifier predicts functional microRNA target interactions in colorectal cancer. <i>Molecular BioSystems</i> , 2015, 11, 2126-2134.	2.9	22
96	An explicit numerical scheme to efficiently simulate molecular diffusion in environments with dynamically changing barriers. <i>Mathematical and Computer Modelling of Dynamical Systems</i> , 2015, 21, 535-559.	2.2	0
97	miR-638 promotes melanoma metastasis and protects melanoma cells from apoptosis and autophagy. <i>Oncotarget</i> , 2015, 6, 2966-2980.	1.8	72
98	Dissecting Long-Term Glucose Metabolism Identifies New Susceptibility Period for Metabolic Dysfunction in Aged Mice. <i>PLoS ONE</i> , 2015, 10, e0140858.	2.5	2
99	Why model?. <i>Frontiers in Physiology</i> , 2014, 5, 21.	2.8	64
100	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
101	Inbred mouse strains reveal biomarkers that are pro-longevity, antilongevity or role switching. <i>Aging Cell</i> , 2014, 13, 729-738.	6.7	17
102	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
103	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
104	The systems biology of mitochondrial fission and fusion and implications for disease and aging. <i>Biogerontology</i> , 2014, 15, 1-12.	3.9	46
105	Systems Biology Approaches in Aging Research. <i>Interdisciplinary Topics in Gerontology</i> , 2014, 40, 155-176.	3.6	7
106	E2F1 induces miR-224/452 expression to drive EMT through TXNIP downregulation. <i>EMBO Reports</i> , 2014, 15, 1315-1329.	4.5	78
107	Enabling multiscale modeling in systems medicine. <i>Genome Medicine</i> , 2014, 6, 21.	8.2	76
108	Tumors as chaotic attractors. <i>Molecular BioSystems</i> , 2014, 10, 172-179.	2.9	17

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109	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
110	Glucose deacetylase repression by yeast <i>AMP</i> -activated protein kinase <i>SNF1</i> is controlled via at least two independent steps. <i>FEBS Journal</i> , 2014, 281, 1901-1917.	4.7	31
111	Pushing limits by embracing complexity. <i>IET Systems Biology</i> , 2014, 8, 244-250.	1.5	3
112	Age-Dependent Effects of UCP2 Deficiency on Experimental Acute Pancreatitis in Mice. <i>PLoS ONE</i> , 2014, 9, e94494.	2.5	16
113	Systems Epidemiology: What's in a Name?. <i>Online Journal of Public Health Informatics</i> , 2014, 6, e198.	0.7	25
114	Accounting for randomness in measurement and sampling in studying cancer cell population dynamics. <i>IET Systems Biology</i> , 2014, 8, 230-241.	1.5	0
115	Simulations of stressosome activation emphasize allosteric interactions between RsbR and RsbT. <i>BMC Systems Biology</i> , 2013, 7, 3.	3.0	15
116	A shift in the dominant phenotype governs the pH-induced metabolic switch of <i>Clostridium acetobutylicum</i> in phosphate-limited continuous cultures. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 6451-6466.	3.6	33
117	Analysing the impact of nucleo-cytoplasmic shuttling of $\beta$ -catenin and its antagonists APC, Axin and GSK3 on Wnt/ $\beta$ -catenin signalling. <i>Cellular Signalling</i> , 2013, 25, 2210-2221.	3.6	53
118	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
119	Improving the reuse of computational models through version control. <i>Bioinformatics</i> , 2013, 29, 742-748.	4.1	21
120	Web Resources for microRNA Research. <i>Advances in Experimental Medicine and Biology</i> , 2013, 774, 225-250.	1.6	16
121	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
122	The road from systems biology to systems medicine. <i>Pediatric Research</i> , 2013, 73, 502-507.	2.3	78
123	MicroRNA-Regulated Networks: The Perfect Storm for Classical Molecular Biology, the Ideal Scenario for Systems Biology. <i>Advances in Experimental Medicine and Biology</i> , 2013, 774, 55-76.	1.6	50
124	Reverse Engineering of Biochemical Reaction Networks Using Co-evolution with Eng-Genes. <i>Cognitive Computation</i> , 2013, 5, 106-118.	5.2	4
125	Systems biology and pediatric research. <i>Pediatric Research</i> , 2013, 73, 499-501.	2.3	3
126	Do simple models lead to generality in ecology?. <i>Trends in Ecology and Evolution</i> , 2013, 28, 578-583.	8.7	215



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127	A Systemsâ€™ Biology Approach to Study MicroRNA-Mediated Gene Regulatory Networks. <i>BioMed Research International</i> , 2013, 2013, 1-15.	1.9	32
128	The role of theory and modeling in medical research. <i>Frontiers in Physiology</i> , 2013, 4, 377.	2.8	9
129	Phosphoglycerate Mutases Function as Reverse Regulated Isoenzymes in <i>Synechococcus elongatus</i> PCC 7942. <i>PLoS ONE</i> , 2013, 8, e58281.	2.5	19
130	The search for organizing principles as a cure against reductionism in systems medicine. <i>FEBS Journal</i> , 2013, 280, 5938-5948.	4.7	53
131	Regulation of cell cycle checkpoint kinase WEE1 by miR-195 in malignant melanoma. <i>Oncogene</i> , 2013, 32, 3175-3183.	5.9	85
132	Reproducibility of Model-Based Results in Systems Biology. , 2013, , 301-320.		7
133	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
134	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
135	Computational analysis of target hub gene repression regulated by multiple and cooperative miRNAs. <i>Nucleic Acids Research</i> , 2012, 40, 8818-8834.	14.5	77
136	Dynamics of a miRNA Model with Two Delays. <i>Biotechnology and Biotechnological Equipment</i> , 2012, 26, 3315-3320.	1.3	10
137	Diagrams as locality aids for explanation and model construction in cell biology. <i>Biology and Philosophy</i> , 2012, 27, 705-721.	1.4	20
138	Nonlinear modelling of curvature by bi-linear metamodelling. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2012, 117, 2-12.	3.5	7
139	A frequency-based gene selection method to identify robust biomarkers for radiation dose prediction. <i>International Journal of Radiation Biology</i> , 2012, 88, 267-276.	1.8	44
140	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
141	Proteolysis of beta-galactosidase following SigmaB activation in <i>Bacillus subtilis</i> . <i>Molecular BioSystems</i> , 2012, 8, 1806.	2.9	5
142	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
143	Multi-compartmental modeling of SORLAâ€™s influence on amyloidogenic processing in Alzheimerâ€™s disease. <i>BMC Systems Biology</i> , 2012, 6, 74.	3.0	12
144	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

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145	The role of theorem proving in systems biology. <i>Journal of Theoretical Biology</i> , 2012, 300, 57-61.	1.7	15
146	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
147	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
148	Systems medicine and integrated care to combat chronic noncommunicable diseases. <i>Genome Medicine</i> , 2011, 3, 43.	8.2	181
149	The Complexity of Cell-Biological Systems. , 2011, , 355-385.		6
150	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
151	Systems biology of JAK-STAT signalling in human malignancies. <i>Progress in Biophysics and Molecular Biology</i> , 2011, 106, 426-434.	2.9	44
152	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
153	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
154	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
155	Modeling the Calvin-Benson cycle. <i>BMC Systems Biology</i> , 2011, 5, 185.	3.0	41
156	A stem cell niche dominance theorem. <i>BMC Systems Biology</i> , 2011, 5, 4.	3.0	7
157	Nucleo-cytoplasmic shuttling of APC can maximize $\beta$ -catenin/TCF concentration. <i>Journal of Theoretical Biology</i> , 2011, 279, 132-142.	1.7	13
158	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
159	Computational analysis and modeling the effectiveness of Zanamivir™ targeting neuraminidase protein in pandemic H1N1 strains. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1072-1082.	2.3	4
160	Minimum Information About a Simulation Experiment (MIASE). <i>PLoS Computational Biology</i> , 2011, 7, e1001122.	3.2	133
161	Modeling of Cellular Processes: Methods, Data, and Requirements. <i>Methods in Molecular Biology</i> , 2011, 696, 429-447.	0.9	2
162	Mathematical Tools in Cancer Signalling Systems Biology. , 2011, , 185-212.		5

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163	Systems biology to battle vascular disease. <i>Nephrology Dialysis Transplantation</i> , 2010, 25, 1019-1022.	0.7	22
164	Thresholds in transient dynamics of signal transduction pathways. <i>Journal of Theoretical Biology</i> , 2010, 264, 334-346.	1.7	10
165	Non-coding RNA detection methods combined to improve usability, reproducibility and precision. <i>BMC Bioinformatics</i> , 2010, 11, 491.	2.6	17
166	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
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