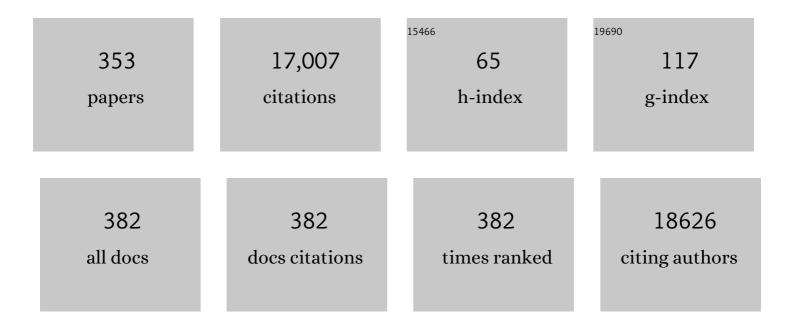
Thomas Dandekar

List of Publications by Year in descending order

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#	Article	lF	CITATIONS
1	A Novel Water-Soluble C60 Fullerene-Based Nano-Platform Enhances Efficiency of Anticancer Chemotherapy. , 2022, , 59-93.		Ο
2	Antibody ligation of CEACAM1, CEACAM3, and CEACAM6, differentially enhance the cytokine release of human neutrophils in responses to Candida albicans. Cellular Immunology, 2022, 371, 104459.	1.4	1
3	Toward Zero Variance in Proteomics Sample Preparation: Positive-Pressure FASP in 96-Well Format (PF96) Enables Highly Reproducible, Time- and Cost-Efficient Analysis of Sample Cohorts. Journal of Proteome Research, 2022, 21, 1181-1188.	1.8	12
4	ACKR3 regulates platelet activation and ischemia-reperfusion tissue injury. Nature Communications, 2022, 13, 1823.	5.8	13
5	Cytokinins: Wide-Spread Signaling Hormones from Plants to Humans with High Medical Potential. Nutrients, 2022, 14, 1495.	1.7	14
6	Influence of breast cancer risk factors on proliferation and DNA damage in human breast glandular tissues: role of intracellular estrogen levels, oxidative stress and estrogen biotransformation. Archives of Toxicology, 2022, 96, 673-687.	1.9	5
7	EMT, Stemness, and Drug Resistance in Biological Context: A 3D Tumor Tissue/In Silico Platform for Analysis of Combinatorial Treatment in NSCLC with Aggressive KRAS-Biomarker Signatures. Cancers, 2022, 14, 2176.	1.7	5
8	Cisplatin-Induced Reproductive Toxicity and Oxidative Stress: Ameliorative Effect of Kinetin. Antioxidants, 2022, 11, 863.	2.2	14
9	A modular systems biological modelling framework studies cyclic nucleotide signaling in platelets. Journal of Theoretical Biology, 2022, , 111222.	0.8	1
10	Kinetin Ameliorates Cisplatin-Induced Hepatotoxicity and Lymphotoxicity via Attenuating Oxidative Damage, Cell Apoptosis and Inflammation in Rats. Biomedicines, 2022, 10, 1620.	1.4	7
11	A systems-biology model of the tumor necrosis factor (TNF) interactions with TNF receptor 1 and 2. Bioinformatics, 2021, 37, 669-676.	1.8	7
12	Magische RNA. , 2021, , 27-38.		0
13	Design-Prinzipien einer Zelle. , 2021, , 155-170.		0
14	Wie ist unser eigenes, extrem leistungsfÄ ¤ iges Gehirn aufgebaut?. , 2021, , 231-242.		0
15	Leben erfindet immer neue Ebenen der Sprache. , 2021, , 189-214.		0
16	Stoffwechsel modellieren und neue Antibiotika finden. , 2021, , 51-60.		0
17	Lösungen zu den Übungsaufgaben. , 2021, , 331-378.		0
18	Komplexe Systeme verhalten sich grundsĿzlich Ĥnlich. , 2021, , 115-135.		0

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19	Signalkaskaden durch Messen der kodierten Information besser verstehen. , 2021, , 93-101.		Ο
20	Bioinformatik verbindet das Leben mit dem Universum und dem ganzen Rest. , 2021, , 243-261.		0
21	An Ebola, Neisseria and Trypanosoma human protein interaction census reveals a conserved human protein cluster targeted by various human pathogens. Computational and Structural Biotechnology Journal, 2021, 19, 5292-5308.	1.9	4
22	Evolution mit dem Computer besser vergleichen. , 2021, , 137-153.		0
23	Genome – molekulare Landkarten von Lebewesen. , 2021, , 39-50.		Ο
24	Modulatory and Toxicological Perspectives on the Effects of the Small Molecule Kinetin. Molecules, 2021, 26, 670.	1.7	15
25	An optimized genetically encoded dual reporter for simultaneous ratio imaging of Ca ²⁺ and H ⁺ reveals new insights into ion signaling in plants. New Phytologist, 2021, 230, 2292-2310.	3.5	42
26	Population-Predicted MHC Class II Epitope Presentation of SARS-CoV-2 Structural Proteins Correlates to the Case Fatality Rates of COVID-19 in Different Countries. International Journal of Molecular Sciences, 2021, 22, 2630.	1.8	10
27	Modeling of stringent-response reflects nutrient stress induced growth impairment and essential amino acids in different Staphylococcus aureus mutants. Scientific Reports, 2021, 11, 9651.	1.6	1
28	Design, Synthesis, and Anticancer Screening for Repurposed Pyrazolo[3,4-d]pyrimidine Derivatives on Four Mammalian Cancer Cell Lines. Molecules, 2021, 26, 2961.	1.7	9
29	RhoA/Cdc42 signaling drives cytoplasmic maturation but not endomitosis in megakaryocytes. Cell Reports, 2021, 35, 109102.	2.9	13
30	Rapid proliferation due to better metabolic adaptation results in full virulence of a filament-deficient Candida albicans strain. Nature Communications, 2021, 12, 3899.	5.8	31
31	An effective model of endogenous clocks and external stimuli determining circadian rhythms. Scientific Reports, 2021, 11, 16165.	1.6	4
32	Aspergillus fumigatus versus Genus Aspergillus: Conservation, Adaptive Evolution and Specific Virulence Genes. Microorganisms, 2021, 9, 2014.	1.6	4
33	Wir können über uns nachdenken – der Computer nicht. , 2021, , 215-229.		0
34	Modeling Immune Dynamics in Plants Using JIMENA-Package. Methods in Molecular Biology, 2021, 2328, 183-189.	0.4	2
35	Pathogen and Host-Pathogen Protein Interactions Provide a Key to Identify Novel Drug Targets. , 2021, , 543-553.		3
36	Staphylococcus aureus Transcriptome Data and Metabolic Modelling Investigate the Interplay of Ser/Thr Kinase PknB, Its Phosphatase Stp, the glmR/yvcK Regulon and the cdaA Operon for Metabolic Adaptation. Microorganisms, 2021, 9, 2148.	1.6	4

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37	Alveolar Regeneration in COVID-19 Patients: A Network Perspective. International Journal of Molecular Sciences, 2021, 22, 11279.	1.8	7
38	Topological Analysis of the Carbon-Concentrating CETCH Cycle and a Photorespiratory Bypass Reveals Boosted CO2-Sequestration by Plants. Frontiers in Bioengineering and Biotechnology, 2021, 9, 708417.	2.0	4
39	Scaffold Searching of FDA and EMA-Approved Drugs Identifies Lead Candidates for Drug Repurposing in Alzheimer's Disease. Frontiers in Chemistry, 2021, 9, 736509.	1.8	11
40	An In Vitro and In Silico Study of the Enhanced Antiproliferative and Pro-Oxidant Potential of Olea europaea L. cv. Arbosana Leaf Extract via Elastic Nanovesicles (Spanlastics). Antioxidants, 2021, 10, 1860.	2.2	7
41	Editorial: Innovative Strategies From Synthetic Biology and Bacterial Pathways to Master Biochemical Environmental Challenges. Frontiers in Bioengineering and Biotechnology, 2021, 9, 828632.	2.0	Ο
42	CoxBase: an Online Platform for Epidemiological Surveillance, Visualization, Analysis, and Typing of Coxiella burnetii Genomic Sequences. MSystems, 2021, 6, e0040321.	1.7	5
43	In silico signaling modeling to understand cancer pathways and treatment responses. Briefings in Bioinformatics, 2020, 21, 1115-1117.	3.2	6
44	A comprehensive method protocol for annotation and integrated functional understanding of IncRNAs. Briefings in Bioinformatics, 2020, 21, 1391-1396.	3.2	5
45	Bacterial Shoot Apical Meristem Inoculation Assay. Methods in Molecular Biology, 2020, 2094, 17-22.	0.4	Ο
46	Molecular Modeling of the Interaction Between Stem Cell Peptide and Immune Receptor in Plants. Methods in Molecular Biology, 2020, 2094, 67-77.	0.4	0
47	Mapping a Transcriptome-Guided Arabidopsis SAM Interactome. Methods in Molecular Biology, 2020, 2094, 113-118.	0.4	Ο
48	Connecting Cancer Pathways to Tumor Engines: A Stratification Tool for Colorectal Cancer Combining Human In Vitro Tissue Models with Boolean In Silico Models. Cancers, 2020, 12, 28.	1.7	14
49	Integrated structural and functional analysis of the protective effects of kinetin against oxidative stress in mammalian cellular systems. Scientific Reports, 2020, 10, 13330.	1.6	18
50	Integrated Framework of the Immune-Defense Transcriptional Signatures in the Arabidopsis Shoot Apical Meristem. International Journal of Molecular Sciences, 2020, 21, 5745.	1.8	0
51	Comparison of the central human and mouse platelet signaling cascade by systems biological analysis. BMC Genomics, 2020, 21, 897.	1.2	12
52	Modeling of shotgun sequencing of DNA plasmids using experimental and theoretical approaches. BMC Bioinformatics, 2020, 21, 132.	1.2	1
53	Genome-wide inference of the Camponotus floridanus protein-protein interaction network using homologous mapping and interacting domain profile pairs. Scientific Reports, 2020, 10, 2334.	1.6	9
54	Delaying memory decline: different options and emerging solutions. Translational Psychiatry, 2020, 10, 13.	2.4	15

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55	Synthetic Rewiring of Plant CO2 Sequestration Galvanizes Plant Biomass Production. Trends in Biotechnology, 2020, 38, 354-359.	4.9	13
56	Integrative functional genomics decodes herpes simplex virus 1. Nature Communications, 2020, 11, 2038.	5.8	61
57	Platelet glycoprotein VI promotes metastasis through interaction with cancer cell-derived Galectin-3. Blood, 2020, 135, 1146-1160.	0.6	71
58	Novel Approach for Characterizing Propofol Binding Affinities to Serum Albumins from Different Species. ACS Omega, 2020, 5, 25543-25551.	1.6	13
59	Chagas Disease: Detection of Trypanosoma cruzi by a New, High-Specific Real Time PCR. Journal of Clinical Medicine, 2020, 9, 1517.	1.0	12
60	Modular micro-physiological human tumor/tissue models based on decellularized tissue for improved preclinical testing. ALTEX: Alternatives To Animal Experimentation, 2020, 38, 289-306.	0.9	3
61	Analyzing pharmacological intervention points: A method to calculate external stimuli to switch between steady states in regulatory networks. PLoS Computational Biology, 2019, 15, e1007075.	1.5	11
62	Complexation with C60 Fullerene Increases Doxorubicin Efficiency against Leukemic Cells In Vitro. Nanoscale Research Letters, 2019, 14, 61.	3.1	35
63	C. elegans protein interaction network analysis probes RNAi validated pro-longevity effect of nhr-6, a human homolog of tumor suppressor Nr4a1. Scientific Reports, 2019, 9, 15711.	1.6	7
64	Comprehensive Flux Modeling of Chlamydia trachomatis Proteome and qRT-PCR Data Indicate Biphasic Metabolic Differences Between Elementary Bodies and Reticulate Bodies During Infection. Frontiers in Microbiology, 2019, 10, 2350.	1.5	15
65	Synergy of Chemo- and Photodynamic Therapies with C60 Fullerene-Doxorubicin Nanocomplex. Nanomaterials, 2019, 9, 1540.	1.9	32
66	C60 Fullerene as an Effective Nanoplatform of Alkaloid Berberine Delivery into Leukemic Cells. Pharmaceutics, 2019, 11, 586.	2.0	29
67	Eugenol Exerts Apoptotic Effect and Modulates the Sensitivity of HeLa Cells to Cisplatin and Radiation. Molecules, 2019, 24, 3979.	1.7	56
68	How to Steer and Control ERK and the ERK Signaling Cascade Exemplified by Looking at Cardiac Insufficiency. International Journal of Molecular Sciences, 2019, 20, 2179.	1.8	17
69	Vaccinia virus injected human tumors: oncolytic virus efficiency predicted by antigen profiling analysis fitted boolean models. Bioengineered, 2019, 10, 190-196.	1.4	5
70	Aspergillus fumigatus Challenged by Human Dendritic Cells: Metabolic and Regulatory Pathway Responses Testify a Tight Battle. Frontiers in Cellular and Infection Microbiology, 2019, 9, 168.	1.8	19
71	The New Genetic Landscape of Cushing's Disease: Deubiquitinases in the Spotlight. Cancers, 2019, 11, 1761.	1.7	27
72	Functional genomics identifies AMPD2 as a new prognostic marker for undifferentiated pleomorphic sarcoma. International Journal of Cancer, 2019, 144, 859-867.	2.3	10

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73	A new triple system DNA-Nanosilver-Berberine for cancer therapy. Applied Nanoscience (Switzerland), 2019, 9, 945-956.	1.6	9
74	Rational Drug Design of Axl Tyrosine Kinase Type I Inhibitors as Promising Candidates Against Cancer. Frontiers in Chemistry, 2019, 7, 920.	1.8	9
75	Proteomics of Aspergillus fumigatus Conidia-containing Phagolysosomes Identifies Processes Governing Immune Evasion. Molecular and Cellular Proteomics, 2018, 17, 1084-1096.	2.5	36
76	The Cytokinin-Activating LOG-Family Proteins Are Not Lysine Decarboxylases. Trends in Biochemical Sciences, 2018, 43, 232-236.	3.7	13
77	TRPM7 Kinase Controls Calcium Responses in Arterial Thrombosis and Stroke in Mice. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 344-352.	1.1	42
78	Systems Biology Analysis to Understand Regulatory miRNA Networks in Lung Cancer. Methods in Molecular Biology, 2018, 1819, 235-247.	0.4	5
79	Automated classification of synaptic vesicles in electron tomograms of C. elegans using machine learning. PLoS ONE, 2018, 13, e0205348.	1.1	8
80	Evaluation of Aspergillus and Mucorales specific T-cells and peripheral blood mononuclear cell cytokine signatures as biomarkers of environmental mold exposure. International Journal of Medical Microbiology, 2018, 308, 1018-1026.	1.5	13
81	Nanocellulose: A New Multifunctional Tool for RNA Systems Biology Research. RNA Technologies, 2018, , 373-401.	0.2	0
82	A combined tissueâ€engineered/ inÂsilico signature tool patient stratification in lung cancer. Molecular Oncology, 2018, 12, 1264-1285.	2.1	8
83	In Silico Designed Axl Receptor Blocking Drug Candidates Against Zika Virus Infection. ACS Omega, 2018, 3, 5281-5290.	1.6	14
84	C60 fullerene accumulation in human leukemic cells and perspectives of LED-mediated photodynamic therapy. Free Radical Biology and Medicine, 2018, 124, 319-327.	1.3	50
85	Omics and bioinformatics applied to vaccine development against <i>Borrelia</i> . Molecular Omics, 2018, 14, 330-340.	1.4	11
86	Meta-Alignment: Combining Sequence Aligners for Better Results. Lecture Notes in Computer Science, 2018, , 395-404.	1.0	0
87	Bioinformatics in Leishmania Drug Design. , 2018, , 297-317.		0
88	Identification of Antifungal Targets Based on Computer Modeling. Journal of Fungi (Basel,) Tj ETQq0 0 0 rgBT /O	verlock 10) Tf 50 142 Td

89	HPLC-ESI-MS method for C60 fullerene mitochondrial content quantification. Data in Brief, 2018, 19, 2047-2052.	0.5	8
90	An open source tool for automatic spatiotemporal assessment of calcium transients and local	15	35

90 †signal-close-to-noise' activity in calcium imaging data. PLoS Computational Biology, 2018, 14, e1006054.

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91	A Systems Biology Methodology Combining Transcriptome and Interactome Datasets to Assess the Implications of Cytokinin Signaling for Plant Immune Networks. Methods in Molecular Biology, 2017, 1569, 165-173.	0.4	3
92	Reconstruction of an Immune Dynamic Model to Simulate the Contrasting Role of Auxin and Cytokinin in Plant Immunity. Methods in Molecular Biology, 2017, 1569, 83-92.	0.4	2
93	Influence of Platelet-rich Plasma on the immune response of human monocyte-derived dendritic cells and macrophages stimulated with Aspergillus fumigatus. International Journal of Medical Microbiology, 2017, 307, 95-107.	1.5	35
94	MicroRNA-21 versus microRNA-34: Lung cancer promoting and inhibitory microRNAs analysed in silico and in vitro and their clinical impact. Tumor Biology, 2017, 39, 101042831770643.	0.8	16
95	Plant–Pathogen Maneuvering over Apoplastic Sugars. Trends in Plant Science, 2017, 22, 740-743.	4.3	38
96	Mucorales spores induce a proinflammatory cytokine response in human mononuclear phagocytes and harbor no rodlet hydrophobins. Virulence, 2017, 8, 1708-1718.	1.8	25
97	Modelling the host–pathogen interactions of macrophages and <i>Candida albicans</i> using Game Theory and dynamic optimization. Journal of the Royal Society Interface, 2017, 14, 20170095.	1.5	16
98	Transcriptomic buffering of cryptic genetic variation contributes to meningococcal virulence. BMC Genomics, 2017, 18, 282.	1.2	14
99	Non-Coding RNAs in Lung Cancer: Contribution of Bioinformatics Analysis to the Development of Non-Invasive Diagnostic Tools. Genes, 2017, 8, 8.	1.0	28
100	Optimality principles reveal a complex interplay of intermediate toxicity and kinetic efficiency in the regulation of prokaryotic metabolism. PLoS Computational Biology, 2017, 13, e1005371.	1.5	15
101	FIJI Macro 3D ART VeSElecT: 3D Automated Reconstruction Tool for Vesicle Structures of Electron Tomograms. PLoS Computational Biology, 2017, 13, e1005317.	1.5	13
102	Komplexe Systeme verhalten sich grundsĿlich Ĥnlich. , 2017, , 107-129.		0
103	Bioinformatik verbindet das Leben mit dem Universum und dem ganzen Rest. , 2017, , 225-241.		0
104	Wir können über uns nachdenken – der Computer nicht. , 2017, , 203-212.		0
105	Signalkaskaden durch Messen der kodierten Information besser verstehen. , 2017, , 89-95.		0
106	Wie ist unser eigenes, extrem leistungsfäiges Gehirn aufgebaut?. , 2017, , 213-224.		0
107	Evolution mit dem Computer besser vergleichen. , 2017, , 131-146.		0
108	Systembiologie und Krankheitsursachen aufdecken. , 2017, , 57-75.		0

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109	Design-Prinzipien einer Zelle. , 2017, , 147-160.		0
110	Systematic Identification of Anti-Fungal Drug Targets by a Metabolic Network Approach. Frontiers in Molecular Biosciences, 2016, 3, 22.	1.6	60
111	A Staphylococcus aureus Proteome Overview: Shared and Specific Proteins and Protein Complexes from Representative Strains of All Three Clades. Proteomes, 2016, 4, 8.	1.7	10
112	Mining biomedical images towards valuable information retrieval in biomedical and life sciences. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw118.	1.4	19
113	GNATY: Optimized NGS Variant Calling and Coverage Analysis. Lecture Notes in Computer Science, 2016, , 446-454.	1.0	Ο
114	An antibiotic target ranking and prioritization pipeline combining sequence, structure and network-based approaches exemplified for Serratia marcescens. Gene, 2016, 591, 268-278.	1.0	17
115	Improving Re-annotation of Annotated Eukaryotic Genomes. , 2016, , 171-195.		2
116	A Combined 3D Tissue Engineered In Vitro / In Silico Lung Tumor Model for Predicting Drug Effectiveness in Specific Mutational Backgrounds. Journal of Visualized Experiments, 2016, , e53885.	0.2	20
117	The drug-minded protein interaction database (DrumPID) for efficient target analysis and drug development. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw041.	1.4	21
118	Analyzing ERK 1/2 signalling and targets. Molecular BioSystems, 2016, 12, 2436-2446.	2.9	17
119	Long noncoding RNA <i>Chast</i> promotes cardiac remodeling. Science Translational Medicine, 2016, 8, 326ra22.	5.8	321
120	Revisiting adult neurogenesis and the role of erythropoietin for neuronal and oligodendroglial differentiation in the hippocampus. Molecular Psychiatry, 2016, 21, 1752-1767.	4.1	86
121	The Plant Hormone Cytokinin Confers Protection against Oxidative Stress in Mammalian Cells. PLoS ONE, 2016, 11, e0168386.	1.1	33
122	Development of Long Noncoding RNA-Based Strategies to Modulate TissueÂVascularization. Journal of the American College of Cardiology, 2015, 66, 2005-2015.	1.2	103
123	Draft Genome Sequence of the Moderately Heat-Tolerant <i>Lactococcus lactis</i> subsp. <i>lactis</i> bv. diacetylactis Strain GL2 from Algerian Dromedary Milk. Genome Announcements, 2015, 3, .	0.8	4
124	Gene expression profiles and protein–protein interaction network analysis in AIDS patients with HIV-associated encephalitis and dementia. HIV/AIDS - Research and Palliative Care, 2015, 7, 265.	0.4	12
125	DNAseq Workflow in a Diagnostic Context and an Example of a User Friendly Implementation. BioMed Research International, 2015, 2015, 1-11.	0.9	10
126	Host-adapted metabolism and its regulation in bacterial pathogens. Frontiers in Cellular and Infection Microbiology, 2015, 5, 28.	1.8	8

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127	Host-pathogen interactions between the human innate immune system and Candida albicans—understanding and modeling defense and evasion strategies. Frontiers in Microbiology, 2015, 6, 625.	1.5	83
128	Integrated inference and evaluation of host–fungi interaction networks. Frontiers in Microbiology, 2015, 6, 764.	1.5	63
129	Diagnostic value of preoperative CT scan to stratify colon cancer for neoadjuvant therapy. International Journal of Colorectal Disease, 2015, 30, 1067-1073.	1.0	16
130	Scrutinizing the immune defence inventory of Camponotus floridanus applying total transcriptome sequencing. BMC Genomics, 2015, 16, 540.	1.2	33
131	Modelling antibiotic and cytotoxic isoquinoline effects in Staphylococcus aureus, Staphylococcus epidermidis and mammalian cells. International Journal of Medical Microbiology, 2015, 305, 96-109.	1.5	30
132	Convergence behaviour and Control in Non-Linear Biological Networks. Scientific Reports, 2015, 5, 9746.	1.6	17
133	The nexus between growth and defence signalling: auxin and cytokinin modulate plant immune response pathways. Journal of Experimental Botany, 2015, 66, 4885-4896.	2.4	133
134	Application of Biotechnology and Bioinformatics Tools in Plant–Fungus Interactions. , 2015, , 49-64.		0
135	LONELY-GUY Knocks Every Door: Crosskingdom Microbial Pathogenesis. Trends in Plant Science, 2015, 20, 781-783.	4.3	16
136	Bioinformatics of cardiovascular miRNA biology. Journal of Molecular and Cellular Cardiology, 2015, 89, 3-10.	0.9	20
137	<i>Lipid-Pro:</i> a computational lipid identification solution for untargeted lipidomics on data-independent acquisition tandem mass spectrometry platforms. Bioinformatics, 2015, 31, 1150-1153.	1.8	29
138	MSL: Facilitating automatic and physical analysis of published scientific literature in PDF format. F1000Research, 2015, 4, 1453.	0.8	3
139	MSL: Facilitating automatic and physical analysis of published scientific literature in PDF format. F1000Research, 2015, 4, 1453.	0.8	3
140	Evaluation and Prediction of the HIV-1 Central Polypurine Tract Influence on Foamy Viral Vectors to Transduce Dividing and Growth-Arrested Cells. Scientific World Journal, The, 2014, 2014, 1-11.	0.8	1
141	Antigen profiling analysis of vaccinia virus injected canine tumors. Bioengineered, 2014, 5, 319-325.	1.4	3
142	'Isotopo' a database application for facile analysis and management of mass isotopomer data. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau077-bau077.	1.4	24
143	Perforinâ€like protein <scp>PPLP</scp> 2 permeabilizes the red blood cell membrane during egress of <scp> <i>P</i> </scp> <i>lasmodium falciparum</i> gametocytes. Cellular Microbiology, 2014, 16, 709-733.	1.1	106
144	Stem-cell-triggered immunity safeguards cytokinin enriched plant shoot apexes from pathogen infection. Frontiers in Plant Science, 2014, 5, 588.	1.7	2

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145	Probing the Unknowns in Cytokinin-Mediated Immune Defense in <i>Arabidopsis</i> with Systems Biology Approaches. Bioinformatics and Biology Insights, 2014, 8, BBI.S13462.	1.0	14
146	Cytokinins for immunity beyond growth, galls and green islands. Trends in Plant Science, 2014, 19, 481-484.	4.3	73
147	Host insulin stimulates Echinococcus multilocularisinsulin signalling pathways and larval development. BMC Biology, 2014, 12, 5.	1.7	70
148	Quantitative single-molecule localization microscopy combined with rule-based modeling reveals ligand-induced TNF-R1 reorganization toward higher-order oligomers. Histochemistry and Cell Biology, 2014, 142, 91-101.	0.8	35
149	A comparative analysis of the bistability switch for platelet aggregation by logic ODE based dynamical modeling. Molecular BioSystems, 2014, 10, 2082.	2.9	8
150	Complete genome sequence of the Gram-negative probiotic Escherichia coli strain Nissle 1917. Journal of Biotechnology, 2014, 187, 106-107.	1.9	76
151	Functional Module Search in Protein Networks based on Semantic Similarity Improves the Analysis of Proteomics Data. Molecular and Cellular Proteomics, 2014, 13, 1877-1889.	2.5	4
152	Establishment of a human 3D lung cancer model based on a biological tissue matrix combined with a Boolean <i>inÂsilico</i> model. Molecular Oncology, 2014, 8, 351-365.	2.1	74
153	Software applications toward quantitative metabolic flux analysis and modeling. Briefings in Bioinformatics, 2014, 15, 91-107.	3.2	61
154	Salmonellaââ,¬â€how a metabolic generalist adopts an intracellular lifestyle during infection. Frontiers in Cellular and Infection Microbiology, 2014, 4, 191.	1.8	31
155	Developing sustainable software solutions for bioinformatics by the "Butterfly―paradigm. F1000Research, 2014, 3, 71.	0.8	22
156	Inhibition of the SR Protein-Phosphorylating CLK Kinases of Plasmodium falciparum Impairs Blood Stage Replication and Malaria Transmission. PLoS ONE, 2014, 9, e105732.	1.1	39
157	Ant-App-DB: a smart solution for monitoring arthropods activities, experimental data management and solar calculations without GPS in behavioral field studies. F1000Research, 2014, 3, 311.	0.8	3
158	Probing the unknowns in cytokinin-mediated immune defense in Arabidopsis with systems biology approaches. Bioinformatics and Biology Insights, 2014, 8, 35-44.	1.0	6
159	Software LS-MIDA for efficient mass isotopomer distribution analysis in metabolic modelling. BMC Bioinformatics, 2013, 14, 218.	1.2	21
160	PlanktoVision - an automated analysis system for the identification of phytoplankton. BMC Bioinformatics, 2013, 14, 115.	1.2	52
161	Analysing molecular polar surface descriptors to predict blood-brain barrier permeation. International Journal of Computational Biology and Drug Design, 2013, 6, 146.	0.3	65
162	A semi-quantitative model of Quorum-Sensing in Staphylococcus aureus, approved by microarray meta-analyses and tested by mutation studies. Molecular BioSystems, 2013, 9, 2665.	2.9	16

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163	Dynamical modelling of prostaglandin signalling in platelets reveals individual receptor contributions and feedback properties. Molecular BioSystems, 2013, 9, 2520.	2.9	11
164	A Boolean view separates platelet activatory and inhibitory signalling as verified by phosphorylation monitoring including threshold behaviour and integrin modulation. Molecular BioSystems, 2013, 9, 1326.	2.9	16
165	Integration of boolean models on hormonal interactions and prospects of cytokinin-auxin crosstalk in plant immunity. Plant Signaling and Behavior, 2013, 8, e23890.	1.2	6
166	Wall teichoic acid structure governs horizontal gene transfer between major bacterial pathogens. Nature Communications, 2013, 4, 2345.	5.8	128
167	CoSynthetic database tool to analyse natural and engineered molecular processes. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat043.	1.4	4
168	The impact of cytokinin on jasmonate-salicylate antagonism in Arabidopsis immunity against infection with <i>Pst </i> DC3000. Plant Signaling and Behavior, 2013, 8, e26791.	1.2	18
169	Jimena: efficient computing and system state identification for genetic regulatory networks. BMC Bioinformatics, 2013, 14, 306.	1.2	26
170	Exogenous Administration of a Recombinant Variant of TWEAK Impairs Healing after Myocardial Infarction by Aggravation of Inflammation. PLoS ONE, 2013, 8, e78938.	1.1	10
171	The Role of Auxin-Cytokinin Antagonism in Plant-Pathogen Interactions. PLoS Pathogens, 2012, 8, e1003026.	2.1	91
172	Robustness and accuracy of functional modules in integrated network analysis. Bioinformatics, 2012, 28, 1887-1894.	1.8	29
173	Analyzing Thiol-Dependent Redox Networks in the Presence of Methylene Blue and Other Antimalarial Agents with RT-PCR-Supported in silico Modeling. Bioinformatics and Biology Insights, 2012, 6, BBI.S10193.	1.0	17
174	Different Evolutionary Modifications as a Guide to Rewire Two-Component Systems. Bioinformatics and Biology Insights, 2012, 6, BBI.S9356.	1.0	8
175	Integration of Boolean models exemplified on hepatocyte signal transduction. Briefings in Bioinformatics, 2012, 13, 365-376.	3.2	35
176	The ITS2 Database. Journal of Visualized Experiments, 2012, , .	0.2	30
177	PlateletWeb: a systems biologic analysis of signaling networks in human platelets. Blood, 2012, 119, e22-e34.	0.6	84
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