

Thomas Dandekar

List of Publications by Year in descending order

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354
papers

17,007
citations

15504

65
h-index

19749

117
g-index

382
all docs

382
docs citations

382
times ranked

18626
citing authors

#	ARTICLE	IF	CITATIONS
1	Conservation of gene order: a fingerprint of proteins that physically interact. Trends in Biochemical Sciences, 1998, 23, 324-328.	7.5	991
2	A general definition of metabolic pathways useful for systematic organization and analysis of complex metabolic networks. Nature Biotechnology, 2000, 18, 326-332.	17.5	860
3	Detection of elementary flux modes in biochemical networks: a promising tool for pathway analysis and metabolic engineering. Trends in Biotechnology, 1999, 17, 53-60.	9.3	609
4	Identifying functional modules in protein-protein interaction networks: an integrated exact approach. Bioinformatics, 2008, 24, i223-i231.	4.1	485
5	Predicting function: from genes to genomes and back 1 Edited by P. E. Wright. Journal of Molecular Biology, 1998, 283, 707-725.	4.2	433
6	5.8S-28S rRNA interaction and HMM-based ITS2 annotation. Gene, 2009, 430, 50-57.	2.2	394
7	Carbon metabolism of intracellular bacterial pathogens and possible links to virulence. Nature Reviews Microbiology, 2010, 8, 401-412.	28.6	338
8	4SALE--a tool for synchronous RNA sequence and secondary structure alignment and editing. BMC Bioinformatics, 2006, 7, 498.	2.6	327
9	Long noncoding RNA <i>Chast</i> promotes cardiac remodeling. Science Translational Medicine, 2016, 8, 326ra22.	12.4	321
10	Distinguishing species. Rna, 2007, 13, 1469-1472.	3.5	284
11	Single-cell genomics reveals the lifestyle of <i>Poribacteria</i> , a candidate phylum symbiotically associated with marine sponges. ISME Journal, 2011, 5, 61-70.	9.8	284
12	Metabolic Interdependence of Obligate Intracellular Bacteria and Their Insect Hosts. Microbiology and Molecular Biology Reviews, 2004, 68, 745-770.	6.6	259
13	Synchronous visual analysis and editing of RNA sequence and secondary structure alignments using 4SALE. BMC Research Notes, 2008, 1, 91.	1.4	253
14	Re-annotating the Mycoplasma pneumoniae genome sequence: adding value, function and reading frames. Nucleic Acids Research, 2000, 28, 3278-3288.	14.5	228
15	BioNet: an R-Package for the functional analysis of biological networks. Bioinformatics, 2010, 26, 1129-1130.	4.1	215
16	Pathway alignment: application to the comparative analysis of glycolytic enzymes. Biochemical Journal, 1999, 343, 115-124.	3.7	208
17	The linear chromosome of the plant-pathogenic mycoplasma 'Candidatus Phytoplasma mali'. BMC Genomics, 2008, 9, 306.	2.8	207
18	Processing of the Precursors to Small Nucleolar RNAs and rRNAs Requires Common Components. Molecular and Cellular Biology, 1998, 18, 1181-1189.	2.3	199

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19	Translational regulation of mammalian and <i>Drosophila</i> citric acid cycle enzymes via iron-responsive elements.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 4925-4930.	7.1	188
20	Variation and evolution of the citric-acid cycle: a genomic perspective. Trends in Microbiology, 1999, 7, 281-291.	7.7	184
21	Exploring the pathway structure of metabolism: decomposition into subnetworks and application to <i>Mycoplasma pneumoniae</i> . Bioinformatics, 2002, 18, 351-361.	4.1	179
22	Homology modeling revealed more than 20,000 rRNA internal transcribed spacer 2 (ITS2) secondary structures. Rna, 2005, 11, 1616-1623.	3.5	169
23	The internal transcribed spacer 2 database—a web server for (not only) low level phylogenetic analyses. Nucleic Acids Research, 2006, 34, W704-W707.	14.5	161
24	Including RNA secondary structures improves accuracy and robustness in reconstruction of phylogenetic trees. Biology Direct, 2010, 5, 4.	4.6	154
25	Interactions of Methylene Blue with Human Disulfide Reductases and Their Orthologues from <i>Plasmodium falciparum</i> . Antimicrobial Agents and Chemotherapy, 2008, 52, 183-191.	3.2	153
26	Folding the Main Chain of Small Proteins with the Genetic Algorithm. Journal of Molecular Biology, 1994, 236, 844-861.	4.2	138
27	The ITS2 Database II: homology modelling RNA structure for molecular systematics. Nucleic Acids Research, 2007, 36, D377-D380.	14.5	135
28	Metabolites: a helping hand for pathway evolution?. Trends in Biochemical Sciences, 2003, 28, 336-341.	7.5	133
29	The nexus between growth and defence signalling: auxin and cytokinin modulate plant immune response pathways. Journal of Experimental Botany, 2015, 66, 4885-4896.	4.8	133
30	Wall teichoic acid structure governs horizontal gene transfer between major bacterial pathogens. Nature Communications, 2013, 4, 2345.	12.8	128
31	Isolation and molecular characterization of a surface-bound proteinase of <i>Entamoeba histolytica</i> . Molecular Microbiology, 1998, 27, 269-276.	2.5	122
32	Structure–function characterization of cellulose synthase: relationship to other glycosyltransferases. Phytochemistry, 2001, 57, 1135-1148.	2.9	116
33	ProfDistS: (profile-) distance based phylogeny on sequence–structure alignments. Bioinformatics, 2008, 24, 2401-2402.	4.1	116
34	Integrated Systems View on Networking by Hormones in <i>Arabidopsis</i> Immunity Reveals Multiple Crosstalk for Cytokinin. Plant Cell, 2012, 24, 1793-1814.	6.6	110
35	Potential of genetic algorithms in protein folding and protein engineering simulations. Protein Engineering, Design and Selection, 1992, 5, 637-645.	2.1	106
36	Perforin-like protein <i>PPLP</i> 2 permeabilizes the red blood cell membrane during egress of <i>Plasmodium falciparum</i> gametocytes. Cellular Microbiology, 2014, 16, 709-733.	2.1	106

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37	Phylogeny of Firmicutes with special reference to Mycoplasma (Mollicutes) as inferred from phosphoglycerate kinase amino acid sequence data. International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 871-875.	1.7	105
38	New molecular data for tardigrade phylogeny, with the erection of <i>Paramacrobiotus</i> gen. nov.. Journal of Zoological Systematics and Evolutionary Research, 2009, 47, 315-321.	1.4	104
39	Iron Regulation and the Cell Cycle. Journal of Biological Chemistry, 2006, 281, 22865-22874.	3.4	103
40	Development of Long Noncoding RNA-Based Strategies to Modulate Tissue Vascularization. Journal of the American College of Cardiology, 2015, 66, 2005-2015.	2.8	103
41	An Integrated View of Gene Expression and Solute Profiles of Arabidopsis Tumors: A Genome-Wide Approach. Plant Cell, 2007, 18, 3617-3634.	6.6	101
42	L1Base: from functional annotation to prediction of active LINE-1 elements. Nucleic Acids Research, 2004, 33, D498-D500.	14.5	93
43	The Role of Auxin-Cytokinin Antagonism in Plant-Pathogen Interactions. PLoS Pathogens, 2012, 8, e1003026.	4.7	91
44	Whole-Genome Sequence of <i>Listeria welshimeri</i> Reveals Common Steps in Genome Reduction with <i>Listeria innocua</i> as Compared to <i>Listeria monocytogenes</i> . Journal of Bacteriology, 2006, 188, 7405-7415.	2.2	89
45	¹³ C isotopologue perturbation studies of <i>Listeria monocytogenes</i> carbon metabolism and its modulation by the virulence regulator PrfA. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2040-2045.	7.1	89
46	A metabolomics and proteomics study of the adaptation of <i>Staphylococcus aureus</i> to glucose starvation. Molecular BioSystems, 2011, 7, 1241.	2.9	89
47	Analysis of and function predictions for previously conserved hypothetical or putative proteins in <i>Blochmannia floridanus</i> . BMC Microbiology, 2006, 6, 1.	3.3	87
48	Genome-wide mapping of foamy virus vector integrations into a human cell line. Journal of General Virology, 2006, 87, 1339-1347.	2.9	87
49	Revisiting adult neurogenesis and the role of erythropoietin for neuronal and oligodendroglial differentiation in the hippocampus. Molecular Psychiatry, 2016, 21, 1752-1767.	7.9	86
50	RNA Ligands Selected by Cleavage Stimulation Factor Contain Distinct Sequence Motifs That Function as Downstream Elements in 5'-End Processing of Pre-mRNA. Journal of Biological Chemistry, 1997, 272, 26769-26779.	3.4	85
51	PlateletWeb: a systems biologic analysis of signaling networks in human platelets. Blood, 2012, 119, e22-e34.	1.4	84
52	Improving genetic algorithms for protein folding simulations by systematic crossover. BioSystems, 1999, 50, 17-25.	2.0	83
53	Host-pathogen interactions between the human innate immune system and <i>Candida albicans</i> —understanding and modeling defense and evasion strategies. Frontiers in Microbiology, 2015, 6, 625.	3.5	83
54	Pathway alignment: application to the comparative analysis of glycolytic enzymes. Biochemical Journal, 1999, 343, 115.	3.7	83

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55	YANA - a software tool for analyzing flux modes, gene-expression and enzyme activities. BMC Bioinformatics, 2005, 6, 135.	2.6	80
56	Analysis of SAGE data in human platelets: Features of the transcriptome in an anucleate cell. Thrombosis and Haemostasis, 2006, 95, 643-651.	3.4	79
57	Differential genome analysis applied to the species-specific features of <i>Helicobacter pylori</i> . FEBS Letters, 1998, 426, 1-5.	2.8	76
58	Complete genome sequence of the Gram-negative probiotic <i>Escherichia coli</i> strain Nissle 1917. Journal of Biotechnology, 2014, 187, 106-107.	3.8	76
59	Integrated network reconstruction, visualization and analysis using YANASquare. BMC Bioinformatics, 2007, 8, 313.	2.6	75
60	Identifying the Tertiary Fold of Small Proteins with Different Topologies from Sequence and Secondary Structure using the Genetic Algorithm and Extended Criteria Specific for Strand Regions. Journal of Molecular Biology, 1996, 256, 645-660.	4.2	74
61	Lysosomal, cytoskeletal, and metabolic alterations in cardiomyopathy of cathepsin L knockout mice. FASEB Journal, 2006, 20, 1266-1268.	0.5	74
62	Establishment of a human 3D lung cancer model based on a biological tissue matrix combined with a Boolean <i>in silico</i> model. Molecular Oncology, 2014, 8, 351-365.	4.6	74
63	Cytokinins for immunity beyond growth, galls and green islands. Trends in Plant Science, 2014, 19, 481-484.	8.8	73
64	When genetic distance matters: Measuring genetic differentiation at microsatellite loci in whole-genome scans of recent and incipient mosquito species. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 10769-10774.	7.1	72
65	Platelet glycoprotein VI promotes metastasis through interaction with cancer cell-derived Galectin-3. Blood, 2020, 135, 1146-1160.	1.4	71
66	Platelet Protein Interactions. Arteriosclerosis, Thrombosis, and Vascular Biology, 2008, 28, 1326-1331.	2.4	70
67	Host insulin stimulates <i>Echinococcus multilocularis</i> insulin signalling pathways and larval development. BMC Biology, 2014, 12, 5.	3.8	70
68	Riboswitch finder—a tool for identification of riboswitch RNAs. Nucleic Acids Research, 2004, 32, W154-W159.	14.5	66
69	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
70	CBCAnalyzer: inferring phylogenies based on compensatory base changes in RNA secondary structures. In Silico Biology, 2005, 5, 291-4.	0.9	65
71	Finding the hairpin in the haystack: searching for RNA motifs. Trends in Genetics, 1995, 11, 45-50.	6.7	63
72	Integrated inference and evaluation of host–fungi interaction networks. Frontiers in Microbiology, 2015, 6, 764.	3.5	63

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73	Molecular mechanisms of tolerance in tardigrades: New perspectives for preservation and stabilization of biological material. <i>Biotechnology Advances</i> , 2009, 27, 348-352.	11.7	61
74	Software applications toward quantitative metabolic flux analysis and modeling. <i>Briefings in Bioinformatics</i> , 2014, 15, 91-107.	6.5	61
75	Integrative functional genomics decodes herpes simplex virus 1. <i>Nature Communications</i> , 2020, 11, 2038.	12.8	61
76	Systematic Identification of Anti-Fungal Drug Targets by a Metabolic Network Approach. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 22.	3.5	60
77	Suspected Utility of Enzymes with Multiple Activities in the Small Genome <i>Mycoplasma</i> Species: The Replacement of the Missing "Household" Nucleoside Diphosphate Kinase Gene and Activity by Glycolytic Kinases. <i>OMICS A Journal of Integrative Biology</i> , 2002, 6, 247-258.	2.0	59
78	Tardigrade workbench: comparing stress-related proteins, sequence-similar and functional protein clusters as well as RNA elements in tardigrades. <i>BMC Genomics</i> , 2009, 10, 469.	2.8	59
79	ProfDist: a tool for the construction of large phylogenetic trees based on profile distances. <i>Bioinformatics</i> , 2005, 21, 2108-2109.	4.1	58
80	Using compensatory base change analysis of internal transcribed spacer 2 secondary structures to identify three new species in <i>Paramacrobiotus</i> (Tardigrada). <i>Organisms Diversity and Evolution</i> , 2010, 10, 287-296.	1.6	58
81	Proteomic Analysis of Tardigrades: Towards a Better Understanding of Molecular Mechanisms by Anhydrobiotic Organisms. <i>PLoS ONE</i> , 2010, 5, e9502.	2.5	58
82	ITS2 data corroborate a monophyletic chlorophycean DO-group (Sphaeropleales). <i>BMC Evolutionary Biology</i> , 2008, 8, 218.	3.2	56
83	Eugenol Exerts Apoptotic Effect and Modulates the Sensitivity of HeLa Cells to Cisplatin and Radiation. <i>Molecules</i> , 2019, 24, 3979.	3.8	56
84	Identification of New Therapeutic Targets by Genome-Wide Analysis of Gene Expression in the Ipsilateral Cortex of Aged Rats after Stroke. <i>PLoS ONE</i> , 2012, 7, e50985.	2.5	53
85	<i>Salmonella enterica</i> : a surprisingly well-adapted intracellular lifestyle. <i>Frontiers in Microbiology</i> , 2012, 3, 164.	3.5	53
86	Stress response in tardigrades: differential gene expression of molecular chaperones. <i>Cell Stress and Chaperones</i> , 2010, 15, 423-430.	2.9	52
87	PlanktoVision - an automated analysis system for the identification of phytoplankton. <i>BMC Bioinformatics</i> , 2013, 14, 115.	2.6	52
88	A method for classifying metabolites in topological pathway analyses based on minimization of pathway number. <i>BioSystems</i> , 2003, 70, 255-270.	2.0	51
89	The highly attenuated oncolytic recombinant vaccinia virus GLV-1h68: comparative genomic features and the contribution of F14.5L inactivation. <i>Molecular Genetics and Genomics</i> , 2009, 282, 417-435.	2.1	51
90	Deciphering the intracellular metabolism of <i>Listeria monocytogenes</i> by mutant screening and modelling. <i>BMC Genomics</i> , 2010, 11, 573.	2.8	51

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91	C60 fullerene accumulation in human leukemic cells and perspectives of LED-mediated photodynamic therapy. <i>Free Radical Biology and Medicine</i> , 2018, 124, 319-327.	2.9	50
92	Transcriptome survey of the anhydrobiotic tardigrade <i>Milnesium tardigradum</i> in comparison with <i>Hypsibius dujardini</i> and <i>Richtersius coronifer</i> . <i>BMC Genomics</i> , 2010, 11, 168.	2.8	49
93	Time-resolved in silico modeling of fine-tuned cAMP signaling in platelets: feedback loops, titrated phosphorylations and pharmacological modulation. <i>BMC Systems Biology</i> , 2011, 5, 178.	3.0	49
94	Toward a Systemic Understanding of <i>Listeria monocytogenes</i> Metabolism during Infection. <i>Frontiers in Microbiology</i> , 2012, 3, 23.	3.5	45
95	Pore-forming peptides of <i>Entamoeba dispar</i> . <i>FEBS Journal</i> , 2001, 265, 1002-1007.	0.2	44
96	Two nucleus-located CDK-like kinases with crucial roles for malaria parasite erythrocytic replication are involved in phosphorylation of splicing factor. <i>Journal of Cellular Biochemistry</i> , 2011, 112, 1295-1310.	2.6	44
97	Accurate and robust phylogeny estimation based on profile distances: a study of the Chlorophyceae (Chlorophyta). <i>BMC Evolutionary Biology</i> , 2004, 4, 20.	3.2	43
98	Understanding platelets. <i>Thrombosis and Haemostasis</i> , 2005, 94, 916-925.	3.4	43
99	Toward Computer-Based Cleavage Site Prediction of Cysteine Endopeptidases. <i>Biological Chemistry</i> , 2003, 384, 899-909.	2.5	42
100	TRPM7 Kinase Controls Calcium Responses in Arterial Thrombosis and Stroke in Mice. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018, 38, 344-352.	2.4	42
101	An optimized genetically encoded dual reporter for simultaneous ratio imaging of Ca^{2+} and H^{+} reveals new insights into ion signaling in plants. <i>New Phytologist</i> , 2021, 230, 2292-2310.	7.3	42
102	A novel conserved family of nitric oxide synthase?. <i>Trends in Biochemical Sciences</i> , 2004, 29, 224-226.	7.5	41
103	Exonization of active mouse L1s: a driver of transcriptome evolution?. <i>BMC Genomics</i> , 2007, 8, 392.	2.8	41
104	Shared components of protein complexes? versatile building blocks or biochemical artefacts?. <i>BioEssays</i> , 2004, 26, 1333-1343.	2.5	40
105	Modelling interaction sites in protein domains with interaction profile hidden Markov models. <i>Bioinformatics</i> , 2006, 22, 2851-2857.	4.1	40
106	Transcriptome Analysis in Tardigrade Species Reveals Specific Molecular Pathways for Stress Adaptations. <i>Bioinformatics and Biology Insights</i> , 2012, 6, BBI.S9150.	2.0	39
107	Inhibition of the SR Protein-Phosphorylating CLK Kinases of <i>Plasmodium falciparum</i> Impairs Blood Stage Replication and Malaria Transmission. <i>PLoS ONE</i> , 2014, 9, e105732.	2.5	39
108	Plant "Pathogen Maneuvering over Apoplastic Sugars. <i>Trends in Plant Science</i> , 2017, 22, 740-743.	8.8	38

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109	A software tool-box for analysis of regulatory RNA elements. <i>Nucleic Acids Research</i> , 2003, 31, 3441-3445.	14.5	36
110	ITS-2 and 18S rRNA Gene Phylogeny of Aplysiniidae (Verongida, Demospongiae). <i>Journal of Molecular Evolution</i> , 2005, 60, 327-336.	1.8	36
111	Modeling antibiotic and cytotoxic effects of the dimeric isoquinoline IQ-143 on metabolism and its regulation in <i>Staphylococcus aureus</i> , <i>Staphylococcus epidermidis</i> and human cells. <i>Genome Biology</i> , 2011, 12, R24.	9.6	36
112	Immune response of the ant <i>Camponotus floridanus</i> against pathogens and its obligate mutualistic endosymbiont. <i>Insect Biochemistry and Molecular Biology</i> , 2011, 41, 529-536.	2.7	36
113	Proteomics of <i>Aspergillus fumigatus</i> Conidia-containing Phagolysosomes Identifies Processes Governing Immune Evasion. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1084-1096.	3.8	36
114	Explorative data analysis of MCL reveals gene expression networks implicated in survival and prognosis supported by explorative CGH analysis. <i>BMC Cancer</i> , 2008, 8, 106.	2.6	35
115	Integration of Boolean models exemplified on hepatocyte signal transduction. <i>Briefings in Bioinformatics</i> , 2012, 13, 365-376.	6.5	35
116	Quantitative single-molecule localization microscopy combined with rule-based modeling reveals ligand-induced TNF-R1 reorganization toward higher-order oligomers. <i>Histochemistry and Cell Biology</i> , 2014, 142, 91-101.	1.7	35
117	Influence of Platelet-rich Plasma on the immune response of human monocyte-derived dendritic cells and macrophages stimulated with <i>Aspergillus fumigatus</i> . <i>International Journal of Medical Microbiology</i> , 2017, 307, 95-107.	3.6	35
118	An open source tool for automatic spatiotemporal assessment of calcium transients and local "signal-close-to-noise" activity in calcium imaging data. <i>PLoS Computational Biology</i> , 2018, 14, e1006054.	3.2	35
119	Complexation with C60 Fullerene Increases Doxorubicin Efficiency against Leukemic Cells In Vitro. <i>Nanoscale Research Letters</i> , 2019, 14, 61.	5.7	35
120	Scrutinizing the immune defence inventory of <i>Camponotus floridanus</i> applying total transcriptome sequencing. <i>BMC Genomics</i> , 2015, 16, 540.	2.8	33
121	The Plant Hormone Cytokinin Confers Protection against Oxidative Stress in Mammalian Cells. <i>PLoS ONE</i> , 2016, 11, e0168386.	2.5	33
122	Trans-splicing of pre-mRNA is predicted to occur in a wide range of organisms including vertebrates. <i>Nucleic Acids Research</i> , 1990, 18, 4719-4725.	14.5	32
123	Synergy of Chemo- and Photodynamic Therapies with C60 Fullerene-Doxorubicin Nanocomplex. <i>Nanomaterials</i> , 2019, 9, 1540.	4.1	32
124	Modeling system states in liver cells: Survival, apoptosis and their modifications in response to viral infection. <i>BMC Systems Biology</i> , 2009, 3, 97.	3.0	31
125	<i>Salmonella</i> —how a metabolic generalist adopts an intracellular lifestyle during infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2014, 4, 191.	3.9	31
126	Rapid proliferation due to better metabolic adaptation results in full virulence of a filament-deficient <i>Candida albicans</i> strain. <i>Nature Communications</i> , 2021, 12, 3899.	12.8	31

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127	Comparative proteome analysis of <i>Milnesium tardigradum</i> in early embryonic state versus adults in active and anhydrobiotic state. PLoS ONE, 2012, 7, e45682.	2.5	31
128	The ITS2 Database. Journal of Visualized Experiments, 2012, , .	0.3	30
129	Modelling antibiotic and cytotoxic isoquinoline effects in <i>Staphylococcus aureus</i> , <i>Staphylococcus epidermidis</i> and mammalian cells. International Journal of Medical Microbiology, 2015, 305, 96-109.	3.6	30
130	Robustness and accuracy of functional modules in integrated network analysis. Bioinformatics, 2012, 28, 1887-1894.	4.1	29
131	<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.	4.1	29
132	C60 Fullerene as an Effective Nanoplatform of Alkaloid Berberine Delivery into Leukemic Cells. Pharmaceutics, 2019, 11, 586.	4.5	29
133	Molecular modeling of amoebapore and NK-lysin: a four- α -helix bundle motif of cytolytic peptides from distantly related organisms. Folding & Design, 1997, 2, 47-52.	4.5	28
134	Non-Coding RNAs in Lung Cancer: Contribution of Bioinformatics Analysis to the Development of Non-Invasive Diagnostic Tools. Genes, 2017, 8, 8.	2.4	28
135	<i>Staphylococcus aureus</i> physiological growth limitations: Insights from flux calculations built on proteomics and external metabolite data. Proteomics, 2011, 11, 1915-1935.	2.2	27
136	The New Genetic Landscape of Cushing's Disease: Deubiquitinases in the Spotlight. Cancers, 2019, 11, 1761.	3.7	27
137	NO-Bound Myoglobin: Structural Diversity and Dynamics of the NO Ligand. Journal of the American Chemical Society, 2004, 126, 1930-1931.	13.7	26
138	Jimena: efficient computing and system state identification for genetic regulatory networks. BMC Bioinformatics, 2013, 14, 306.	2.6	26
139	Analysis of SAGE data in human platelets: features of the transcriptome in an anucleate cell. Thrombosis and Haemostasis, 2006, 95, 643-51.	3.4	26
140	Applying experimental data to protein fold prediction with the genetic algorithm. Protein Engineering, Design and Selection, 1997, 10, 877-893.	2.1	25
141	Systematic genomic screening and analysis of mRNA in untranslated regions and mRNA precursors: combining experimental and computational approaches. Bioinformatics, 1998, 14, 271-278.	4.1	25
142	XML schemas for common bioinformatic data types and their application in workflow systems. BMC Bioinformatics, 2006, 7, 490.	2.6	25
143	Investigating heat shock proteins of tardigrades in active versus anhydrobiotic state using shotgun proteomics. Journal of Zoological Systematics and Evolutionary Research, 2011, 49, 111-119.	1.4	25
144	Mucorales spores induce a proinflammatory cytokine response in human mononuclear phagocytes and harbor no rodlet hydrophobins. Virulence, 2017, 8, 1708-1718.	4.4	25

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145	In search of the prototype of nitric oxide synthase. FEBS Letters, 2003, 554, 1-5.	2.8	24
146	Modelling cross-hybridization on phylogenetic DNA microarrays increases the detection power of closely related species. Molecular Ecology Resources, 2009, 9, 83-93.	4.8	24
147	'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.	3.0	24
148	The 3'-Untranslated Region of the Human Estrogen Receptor α Gene Mediates Rapid Messenger Ribonucleic Acid Turnover. Endocrinology, 2000, 141, 2805-2813.	2.8	24
149	Use of functional highly purified human platelets for the identification of new proteins of the IPP signaling pathway. Thrombosis Research, 2008, 122, 59-68.	1.7	23
150	Developmental profiling by mass spectrometry of phosphocholine containing phospholipids in the rat nervous system reveals temporal-spatial gradients. Journal of Neurochemistry, 2010, 114, 1119-1134.	3.9	23
151	Developing sustainable software solutions for bioinformatics by the "Butterfly"-paradigm. F1000Research, 2014, 3, 71.	1.6	22
152	Cloning of Schizosaccharomyces pombe genes encoding the U1, U2, U3 and U4 snRNAs. Gene, 1989, 81, 227-235.	2.2	21
153	Software LS-MIDA for efficient mass isotopomer distribution analysis in metabolic modelling. BMC Bioinformatics, 2013, 14, 218.	2.6	21
154	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.	3.0	21
155	Molecular Characterization of Antimicrobial Peptide Genes of the Carpenter Ant Camponotus floridanus. PLoS ONE, 2012, 7, e43036.	2.5	21
156	Quality-of-Life Assessment in the Old Using the WHOQOL 100: Differences Between Patients With Senile Dementia and Patients With Cancer. International Psychogeriatrics, 1999, 11, 273-279.	1.0	20
157	Bioinformatics of cardiovascular miRNA biology. Journal of Molecular and Cellular Cardiology, 2015, 89, 3-10.	1.9	20
158	A Combined 3D Tissue Engineered <i>In Vitro</i> / <i>In Silico</i> Lung Tumor Model for Predicting Drug Effectiveness in Specific Mutational Backgrounds. Journal of Visualized Experiments, 2016,, e53885.	0.3	20
159	Refined Genetic Algorithm Simulations to Model Proteins. Journal of Molecular Modeling, 1999, 5, 317-324.	1.8	19
160	Mining biomedical images towards valuable information retrieval in biomedical and life sciences. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw118.	3.0	19
161	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.	3.9	19
162	Schizosaccharomyces pombe U4 small nuclear RNA closely resembles vertebrate U4 and is required for growth. Journal of Molecular Biology, 1989, 208, 371-379.	4.2	18

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163	Microinjected glutathione reductase crystals as indicators of the redox status in living cells. FEBS Letters, 1999, 447, 135-138.	2.8	18
164	Comparative Genome Analysis of the Mollicutes. , 2002, , 255-278.		18
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