

# Thomas Dandekar

## List of Publications by Citations

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348  
papers

13,640  
citations

59  
h-index

108  
g-index

381  
ext. papers

15,650  
ext. citations

6  
avg, IF

6.34  
L-index

#	Paper	IF	Citations
348	Conservation of gene order: a fingerprint of proteins that physically interact. <i>Trends in Biochemical Sciences</i> , <b>1998</b> , 23, 324-8	10.3	865
347	A general definition of metabolic pathways useful for systematic organization and analysis of complex metabolic networks. <i>Nature Biotechnology</i> , <b>2000</b> , 18, 326-32	44.5	762
346	Detection of elementary flux modes in biochemical networks: a promising tool for pathway analysis and metabolic engineering. <i>Trends in Biotechnology</i> , <b>1999</b> , 17, 53-60	15.1	534
345	Predicting function: from genes to genomes and back. <i>Journal of Molecular Biology</i> , <b>1998</b> , 283, 707-25	6.5	370
344	Identifying functional modules in protein-protein interaction networks: an integrated exact approach. <i>Bioinformatics</i> , <b>2008</b> , 24, i223-31	7.2	367
343	5.8S-28S rRNA interaction and HMM-based ITS2 annotation. <i>Gene</i> , <b>2009</b> , 430, 50-7	3.8	331
342	Carbon metabolism of intracellular bacterial pathogens and possible links to virulence. <i>Nature Reviews Microbiology</i> , <b>2010</b> , 8, 401-12	22.2	281
341	4SALE--a tool for synchronous RNA sequence and secondary structure alignment and editing. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 498	3.6	274
340	Long noncoding RNA Chast promotes cardiac remodeling. <i>Science Translational Medicine</i> , <b>2016</b> , 8, 326ra27.5	27.5	250
339	Distinguishing species. <i>Rna</i> , <b>2007</b> , 13, 1469-72	5.8	249
338	Metabolic interdependence of obligate intracellular bacteria and their insect hosts. <i>Microbiology and Molecular Biology Reviews</i> , <b>2004</b> , 68, 745-70	13.2	220
337	Single-cell genomics reveals the lifestyle of Poribacteria, a candidate phylum symbiotically associated with marine sponges. <i>ISME Journal</i> , <b>2011</b> , 5, 61-70	11.9	219
336	Synchronous visual analysis and editing of RNA sequence and secondary structure alignments using 4SALE. <i>BMC Research Notes</i> , <b>2008</b> , 1, 91	2.3	214
335	Re-annotating the <i>Mycoplasma pneumoniae</i> genome sequence: adding value, function and reading frames. <i>Nucleic Acids Research</i> , <b>2000</b> , 28, 3278-88	20.1	194
334	Pathway alignment: application to the comparative analysis of glycolytic enzymes. <i>Biochemical Journal</i> , <b>1999</b> , 343, 115-124	3.8	185
333	Processing of the precursors to small nucleolar RNAs and rRNAs requires common components. <i>Molecular and Cellular Biology</i> , <b>1998</b> , 18, 1181-9	4.8	179
332	BioNet: an R-Package for the functional analysis of biological networks. <i>Bioinformatics</i> , <b>2010</b> , 26, 1129-39	39.2	171

331	The linear chromosome of the plant-pathogenic mycoplasma <i>R. Candidatus Phytoplasma mali</i> . <i>BMC Genomics</i> , <b>2008</b> , 9, 306	4.5	169
330	Exploring the pathway structure of metabolism: decomposition into subnetworks and application to <i>Mycoplasma pneumoniae</i> . <i>Bioinformatics</i> , <b>2002</b> , 18, 351-61	7.2	161
329	Translational regulation of mammalian and <i>Drosophila</i> citric acid cycle enzymes via iron-responsive elements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1996</b> , 93, 4925-30	11.5	159
328	Homology modeling revealed more than 20,000 rRNA internal transcribed spacer 2 (ITS2) secondary structures. <i>Rna</i> , <b>2005</b> , 11, 1616-23	5.8	151
327	Variation and evolution of the citric-acid cycle: a genomic perspective. <i>Trends in Microbiology</i> , <b>1999</b> , 7, 281-91	12.4	150
326	The internal transcribed spacer 2 database--a web server for (not only) low level phylogenetic analyses. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, W704-7	20.1	138
325	Interactions of methylene blue with human disulfide reductases and their orthologues from <i>Plasmodium falciparum</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>2008</b> , 52, 183-91	5.9	125
324	Folding the main chain of small proteins with the genetic algorithm. <i>Journal of Molecular Biology</i> , <b>1994</b> , 236, 844-61	6.5	125
323	Including RNA secondary structures improves accuracy and robustness in reconstruction of phylogenetic trees. <i>Biology Direct</i> , <b>2010</b> , 5, 4	7.2	122
322	Metabolites: a helping hand for pathway evolution?. <i>Trends in Biochemical Sciences</i> , <b>2003</b> , 28, 336-41	10.3	117
321	The ITS2 Database II: homology modelling RNA structure for molecular systematics. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D377-80	20.1	116
320	Isolation and molecular characterization of a surface-bound proteinase of <i>Entamoeba histolytica</i> . <i>Molecular Microbiology</i> , <b>1998</b> , 27, 269-76	4.1	106
319	ProfDistS: (profile-) distance based phylogeny on sequence-structure alignments. <i>Bioinformatics</i> , <b>2008</b> , 24, 2401-2	7.2	105
318	Wall teichoic acid structure governs horizontal gene transfer between major bacterial pathogens. <i>Nature Communications</i> , <b>2013</b> , 4, 2345	17.4	102
317	The nexus between growth and defence signalling: auxin and cytokinin modulate plant immune response pathways. <i>Journal of Experimental Botany</i> , <b>2015</b> , 66, 4885-96	7	94
316	Structure-function characterization of cellulose synthase: relationship to other glycosyltransferases. <i>Phytochemistry</i> , <b>2001</b> , 57, 1135-48	4	94
315	An integrated view of gene expression and solute profiles of <i>Arabidopsis</i> tumors: a genome-wide approach. <i>Plant Cell</i> , <b>2006</b> , 18, 3617-34	11.6	92
314	Integrated systems view on networking by hormones in <i>Arabidopsis</i> immunity reveals multiple crosstalk for cytokinin. <i>Plant Cell</i> , <b>2012</b> , 24, 1793-814	11.6	91

313	Phylogeny of Firmicutes with special reference to Mycoplasma (Mollicutes) as inferred from phosphoglycerate kinase amino acid sequence data. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2004</b> , 54, 871-875	2.2	88
312	Potential of genetic algorithms in protein folding and protein engineering simulations. <i>Protein Engineering, Design and Selection</i> , <b>1992</b> , 5, 637-45	1.9	87
311	Iron regulation and the cell cycle: identification of an iron-responsive element in the 3' untranslated region of human cell division cycle 14A mRNA by a refined microarray-based screening strategy. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 22865-74	5.4	85
310	L1Base: from functional annotation to prediction of active LINE-1 elements. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D498-500	20.1	84
309	<sup>13</sup> C isotopologue perturbation studies of <i>Listeria monocytogenes</i> carbon metabolism and its modulation by the virulence regulator PrfA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 2040-5	11.5	83
308	Development of Long Noncoding RNA-Based Strategies to Modulate Tissue Vascularization. <i>Journal of the American College of Cardiology</i> , <b>2015</b> , 66, 2005-2015	15.1	82
307	New molecular data for tardigrade phylogeny, with the erection of <i>Paramacrobiotus</i> gen. nov.. <i>Journal of Zoological Systematics and Evolutionary Research</i> , <b>2009</b> , 47, 315-321	1.9	81
306	The role of auxin-cytokinin antagonism in plant-pathogen interactions. <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1003026	7.6	77
305	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> . <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 7405-15	3.5	77
304	RNA ligands selected by cleavage stimulation factor contain distinct sequence motifs that function as downstream elements in 3' end processing of pre-mRNA. <i>Journal of Biological Chemistry</i> , <b>1997</b> , 272, 26769-79	5.4	76
303	Genome-wide mapping of foamy virus vector integrations into a human cell line. <i>Journal of General Virology</i> , <b>2006</b> , 87, 1339-1347	4.9	76
302	Pathway alignment: application to the comparative analysis of glycolytic enzymes. <i>Biochemical Journal</i> , <b>1999</b> , 343, 115	3.8	75
301	Improving genetic algorithms for protein folding simulations by systematic crossover. <i>BioSystems</i> , <b>1999</b> , 50, 17-25	1.9	73
300	Perforin-like protein PPLP2 permeabilizes the red blood cell membrane during egress of <i>Plasmodium falciparum</i> gametocytes. <i>Cellular Microbiology</i> , <b>2014</b> , 16, 709-33	3.9	71
299	PlateletWeb: a systems biologic analysis of signaling networks in human platelets. <i>Blood</i> , <b>2012</b> , 119, e2234	3.4	71
298	A metabolomics and proteomics study of the adaptation of <i>Staphylococcus aureus</i> to glucose starvation. <i>Molecular BioSystems</i> , <b>2011</b> , 7, 1241-53		71
297	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. <i>Journal of Molecular Biology</i> , <b>1996</b> , 256, 645-60	6.5	71
296	Analysis of SAGE data in human platelets: Features of the transcriptome in an anucleate cell. <i>Thrombosis and Haemostasis</i> , <b>2006</b> , 95, 643-651	7	69

295	Differential genome analysis applied to the species-specific features of <i>Helicobacter pylori</i> . <i>FEBS Letters</i> , <b>1998</b> , 426, 1-5	3.8	66
294	Lysosomal, cytoskeletal, and metabolic alterations in cardiomyopathy of cathepsin L knockout mice. <i>FASEB Journal</i> , <b>2006</b> , 20, 1266-8	0.9	65
293	Platelet protein interactions: map, signaling components, and phosphorylation groundstate. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2008</b> , 28, 1326-31	9.4	63
292	Host-pathogen interactions between the human innate immune system and <i>Candida albicans</i> -understanding and modeling defense and evasion strategies. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 625	5.7	62
291	YANA - a software tool for analyzing flux modes, gene-expression and enzyme activities. <i>BMC Bioinformatics</i> , <b>2005</b> , 6, 135	3.6	62
290	When genetic distance matters: measuring genetic differentiation at microsatellite loci in whole-genome scans of recent and incipient mosquito species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2001</b> , 98, 10769-74	11.5	60
289	Analysis of and function predictions for previously conserved hypothetical or putative proteins in <i>Blochmannia floridanus</i> . <i>BMC Microbiology</i> , <b>2006</b> , 6, 1	4.5	59
288	CBCAnalyzer: inferring phylogenies based on compensatory base changes in RNA secondary structures. <i>In Silico Biology</i> , <b>2005</b> , 5, 291-4	2	59
287	Establishment of a human 3D lung cancer model based on a biological tissue matrix combined with a Boolean in silico model. <i>Molecular Oncology</i> , <b>2014</b> , 8, 351-65	7.9	58
286	Riboswitch finder--a tool for identification of riboswitch RNAs. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, W154-9	20.1	58
285	Revisiting adult neurogenesis and the role of erythropoietin for neuronal and oligodendroglial differentiation in the hippocampus. <i>Molecular Psychiatry</i> , <b>2016</b> , 21, 1752-1767	15.1	55
284	Cytokinins for immunity beyond growth, galls and green islands. <i>Trends in Plant Science</i> , <b>2014</b> , 19, 481-4	13.1	55
283	Integrated network reconstruction, visualization and analysis using YANASquare. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 313	3.6	55
282	Finding the hairpin in the haystack: searching for RNA motifs. <i>Trends in Genetics</i> , <b>1995</b> , 11, 45-50	8.5	55
281	ITS2 data corroborate a monophyletic chlorophycean DO-group (Sphaeropleales). <i>BMC Evolutionary Biology</i> , <b>2008</b> , 8, 218	3	53
280	ProfDist: a tool for the construction of large phylogenetic trees based on profile distances. <i>Bioinformatics</i> , <b>2005</b> , 21, 2108-9	7.2	53
279	Complete genome sequence of the gram-negative probiotic <i>Escherichia coli</i> strain Nissle 1917. <i>Journal of Biotechnology</i> , <b>2014</b> , 187, 106-7	3.7	52
278	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> , <b>2002</b> , 6, 247-58	3.8	50

277	Tardigrade workbench: comparing stress-related proteins, sequence-similar and functional protein clusters as well as RNA elements in tardigrades. <i>BMC Genomics</i> , <b>2009</b> , 10, 469	4.5	48
276	Host insulin stimulates <i>Echinococcus multilocularis</i> insulin signalling pathways and larval development. <i>BMC Biology</i> , <b>2014</b> , 12, 5	7.3	47
275	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> , <b>2012</b> , 7, e50985	3.7	47
274	Software applications toward quantitative metabolic flux analysis and modeling. <i>Briefings in Bioinformatics</i> , <b>2014</b> , 15, 91-107	13.4	45
273	Analysing molecular polar surface descriptors to predict blood-brain barrier permeation. <i>International Journal of Computational Biology and Drug Design</i> , <b>2013</b> , 6, 146-56	0.4	45
272	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> , <b>2009</b> , 282, 417-35 <sup>3.1</sup>		45
271	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> , <b>2010</b> , 10, 287-296	1.7	45
270	Molecular mechanisms of tolerance in tardigrades: new perspectives for preservation and stabilization of biological material. <i>Biotechnology Advances</i> , <b>2009</b> , 27, 348-52	17.8	44
269	Time-resolved in silico modeling of fine-tuned cAMP signaling in platelets: feedback loops, titrated phosphorylations and pharmacological modulation. <i>BMC Systems Biology</i> , <b>2011</b> , 5, 178	3.5	42
268	Deciphering the intracellular metabolism of <i>Listeria monocytogenes</i> by mutant screening and modelling. <i>BMC Genomics</i> , <b>2010</b> , 11, 573	4.5	42
267	Accurate and robust phylogeny estimation based on profile distances: a study of the Chlorophyceae (Chlorophyta). <i>BMC Evolutionary Biology</i> , <b>2004</b> , 4, 20	3	41
266	Proteomic analysis of tardigrades: towards a better understanding of molecular mechanisms by anhydrobiotic organisms. <i>PLoS ONE</i> , <b>2010</b> , 5, e9502	3.7	41
265	<i>Salmonella enterica</i> : a surprisingly well-adapted intracellular lifestyle. <i>Frontiers in Microbiology</i> , <b>2012</b> , 3, 164	5.7	40
264	Pore-forming peptides of <i>Entamoeba dispar</i> . Similarity and divergence to amoebapores in structure, expression and activity. <i>FEBS Journal</i> , <b>1999</b> , 265, 1002-7		40
263	A method for classifying metabolites in topological pathway analyses based on minimization of pathway number. <i>BioSystems</i> , <b>2003</b> , 70, 255-70	1.9	39
262	Toward computer-based cleavage site prediction of cysteine endopeptidases. <i>Biological Chemistry</i> , <b>2003</b> , 384, 899-909	4.5	39
261	Shared components of protein complexes--versatile building blocks or biochemical artefacts?. <i>BioEssays</i> , <b>2004</b> , 26, 1333-43	4.1	38
260	Understanding platelets. Lessons from proteomics, genomics and promises from network analysis. <i>Thrombosis and Haemostasis</i> , <b>2005</b> , 94, 916-25	7	38

259	Platelet glycoprotein VI promotes metastasis through interaction with cancer cell-derived galectin-3. <i>Blood</i> , <b>2020</b> , 135, 1146-1160	2.2	38
258	Stress response in tardigrades: differential gene expression of molecular chaperones. <i>Cell Stress and Chaperones</i> , <b>2010</b> , 15, 423-30	4	37
257	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> , <b>2010</b> , 11, 168	4.5	37
256	A novel conserved family of nitric oxide synthase?. <i>Trends in Biochemical Sciences</i> , <b>2004</b> , 29, 224-6	10.3	37
255	Toward a Systemic Understanding of <i>Listeria monocytogenes</i> Metabolism during Infection. <i>Frontiers in Microbiology</i> , <b>2012</b> , 3, 23	5.7	35
254	PlanktoVision--an automated analysis system for the identification of phytoplankton. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 115	3.6	34
253	C fullerene accumulation in human leukemic cells and perspectives of LED-mediated photodynamic therapy. <i>Free Radical Biology and Medicine</i> , <b>2018</b> , 124, 319-327	7.8	33
252	Modelling interaction sites in protein domains with interaction profile hidden Markov models. <i>Bioinformatics</i> , <b>2006</b> , 22, 2851-7	7.2	33
251	ITS-2 and 18S rRNA gene phylogeny of Aplysinidae (Verongida, Demospongiae). <i>Journal of Molecular Evolution</i> , <b>2005</b> , 60, 327-36	3.1	33
250	Systematic Identification of Anti-Fungal Drug Targets by a Metabolic Network Approach. <i>Frontiers in Molecular Biosciences</i> , <b>2016</b> , 3, 22	5.6	33
249	Two nucleus-localized CDK-like kinases with crucial roles for malaria parasite erythrocytic replication are involved in phosphorylation of splicing factor. <i>Journal of Cellular Biochemistry</i> , <b>2011</b> , 112, 1295-310	4.7	32
248	Integration of Boolean models exemplified on hepatocyte signal transduction. <i>Briefings in Bioinformatics</i> , <b>2012</b> , 13, 365-76	13.4	32
247	Modeling system states in liver cells: survival, apoptosis and their modifications in response to viral infection. <i>BMC Systems Biology</i> , <b>2009</b> , 3, 97	3.5	31
246	Exonization of active mouse L1s: a driver of transcriptome evolution?. <i>BMC Genomics</i> , <b>2007</b> , 8, 392	4.5	30
245	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> , <b>2014</b> , 142, 91-101	2.4	29
244	Immune response of the ant <i>Camponotus floridanus</i> against pathogens and its obligate mutualistic endosymbiont. <i>Insect Biochemistry and Molecular Biology</i> , <b>2011</b> , 41, 529-36	4.5	29
243	A software tool-box for analysis of regulatory RNA elements. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3441-5	20.1	29
242	Integrated inference and evaluation of host-fungi interaction networks. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 764	5.7	28

241	Explorative data analysis of MCL reveals gene expression networks implicated in survival and prognosis supported by explorative CGH analysis. <i>BMC Cancer</i> , <b>2008</b> , 8, 106	4.8	28
240	Scrutinizing the immune defence inventory of <i>Camponotus floridanus</i> applying total transcriptome sequencing. <i>BMC Genomics</i> , <b>2015</b> , 16, 540	4.5	27
239	Inhibition of the SR protein-phosphorylating CLK kinases of <i>Plasmodium falciparum</i> impairs blood stage replication and malaria transmission. <i>PLoS ONE</i> , <b>2014</b> , 9, e105732	3.7	27
238	NO-bound myoglobin: structural diversity and dynamics of the NO ligand. <i>Journal of the American Chemical Society</i> , <b>2004</b> , 126, 1930-1	16.4	26
237	TRPM7 Kinase Controls Calcium Responses in Arterial Thrombosis and Stroke in Mice. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2018</b> , 38, 344-352	9.4	26
236	Transcriptome analysis in tardigrade species reveals specific molecular pathways for stress adaptations. <i>Bioinformatics and Biology Insights</i> , <b>2012</b> , 6, 69-96	5.3	25
235	The Plant Hormone Cytokinin Confers Protection against Oxidative Stress in Mammalian Cells. <i>PLoS ONE</i> , <b>2016</b> , 11, e0168386	3.7	25
234	Lipid-Pro: a computational lipid identification solution for untargeted lipidomics on data-independent acquisition tandem mass spectrometry platforms. <i>Bioinformatics</i> , <b>2015</b> , 31, 1150-3	7.2	24
233	Molecular modeling of amoebapore and NK-lysin: a four-alpha-helix bundle motif of cytolytic peptides from distantly related organisms. <i>Folding &amp; Design</i> , <b>1997</b> , 2, 47-52		24
232	Trans-splicing of pre-mRNA is predicted to occur in a wide range of organisms including vertebrates. <i>Nucleic Acids Research</i> , <b>1990</b> , 18, 4719-25	20.1	24
231	Integrative functional genomics decodes herpes simplex virus 1. <i>Nature Communications</i> , <b>2020</b> , 11, 203817.4	17.4	23
230	Eugenol Exerts Apoptotic Effect and Modulates the Sensitivity of HeLa Cells to Cisplatin and Radiation. <i>Molecules</i> , <b>2019</b> , 24,	4.8	23
229	Jimena: efficient computing and system state identification for genetic regulatory networks. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 306	3.6	23
228	Modelling cross-hybridization on phylogenetic DNA microarrays increases the detection power of closely related species. <i>Molecular Ecology Resources</i> , <b>2009</b> , 9, 83-93	8.4	23
227	The 3'-Untranslated Region of the Human Estrogen Receptor $\beta$ Gene Mediates Rapid Messenger Ribonucleic Acid Turnover		23
226	Analysis of SAGE data in human platelets: features of the transcriptome in an anucleate cell. <i>Thrombosis and Haemostasis</i> , <b>2006</b> , 95, 643-51	7	23
225	Applying experimental data to protein fold prediction with the genetic algorithm. <i>Protein Engineering, Design and Selection</i> , <b>1997</b> , 10, 877-93	1.9	22
224	C Fullerene as an Effective Nanoplatfrom of Alkaloid Berberine Delivery into Leukemic Cells. <i>Pharmaceutics</i> , <b>2019</b> , 11,	6.4	21



223	Salmonella-how a metabolic generalist adopts an intracellular lifestyle during infection. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2014</b> , 4, 191	5.9	21
222	Staphylococcus aureus physiological growth limitations: insights from flux calculations built on proteomics and external metabolite data. <i>Proteomics</i> , <b>2011</b> , 11, 1915-35	4.8	21
221	Developmental profiling by mass spectrometry of phosphocholine containing phospholipids in the rat nervous system reveals temporo-spatial gradients. <i>Journal of Neurochemistry</i> , <b>2010</b> , 114, 1119-34	6	21
220	Systematic genomic screening and analysis of mRNA in untranslated regions and mRNA precursors: combining experimental and computational approaches. <i>Bioinformatics</i> , <b>1998</b> , 14, 271-8	7.2	21
219	Comparative proteome analysis of Milnesium tardigradum in early embryonic state versus adults in active and anhydrobiotic state. <i>PLoS ONE</i> , <b>2012</b> , 7, e45682	3.7	21
218	Plant-Pathogen Maneuvering over Apoplastic Sugars. <i>Trends in Plant Science</i> , <b>2017</b> , 22, 740-743	13.1	20
217	Non-Coding RNAs in Lung Cancer: Contribution of Bioinformatics Analysis to the Development of Non-Invasive Diagnostic Tools. <i>Genes</i> , <b>2016</b> , 8,	4.2	20
216	In search of the prototype of nitric oxide synthase. <i>FEBS Letters</i> , <b>2003</b> , 554, 1-5	3.8	20
215	Modeling antibiotic and cytotoxic effects of the dimeric isoquinoline IQ-143 on metabolism and its regulation in Staphylococcus aureus, Staphylococcus epidermidis and human cells. <i>Genome Biology</i> , <b>2011</b> , 12, R24	18.3	19
214	The ITS2 Database. <i>Journal of Visualized Experiments</i> , <b>2012</b> ,	1.6	19
213	XML schemas for common bioinformatic data types and their application in workflow systems. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 490	3.6	19
212	Proteomics of Conidia-containing Phagolysosomes Identifies Processes Governing Immune Evasion. <i>Molecular and Cellular Proteomics</i> , <b>2018</b> , 17, 1084-1096	7.6	18
211	Complexation with C Fullerene Increases Doxorubicin Efficiency against Leukemic Cells In Vitro. <i>Nanoscale Research Letters</i> , <b>2019</b> , 14, 61	5	18
210	Synergy of Chemo- and Photodynamic Therapies with C Fullerene-Doxorubicin Nanocomplex. <i>Nanomaterials</i> , <b>2019</b> , 9,	5.4	18
209	Robustness and accuracy of functional modules in integrated network analysis. <i>Bioinformatics</i> , <b>2012</b> , 28, 1887-94	7.2	18
208	Use of functional highly purified human platelets for the identification of new proteins of the IPP signaling pathway. <i>Thrombosis Research</i> , <b>2008</b> , 122, 59-68	8.2	18
207	Cloning of Schizosaccharomyces pombe genes encoding the U1, U2, U3 and U4 snRNAs. <i>Gene</i> , <b>1989</b> , 81, 227-35	3.8	18
206	Influence of Platelet-rich Plasma on the immune response of human monocyte-derived dendritic cells and macrophages stimulated with Aspergillus fumigatus. <i>International Journal of Medical Microbiology</i> , <b>2017</b> , 307, 95-107	3.7	17

205	The drug-minded protein interaction database (DrumPID) for efficient target analysis and drug development. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	17
204	Software LS-MIDA for efficient mass isotopomer distribution analysis in metabolic modelling. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 218	3.6	17
203	Microinjected glutathione reductase crystals as indicators of the redox status in living cells. <i>FEBS Letters</i> , <b>1999</b> , 447, 135-8	3.8	17
202	Molecular characterization of antimicrobial peptide genes of the carpenter ant <i>Camponotus floridanus</i> . <i>PLoS ONE</i> , <b>2012</b> , 7, e43036	3.7	17
201	A Combined 3D Tissue Engineered In Vitro/In Silico Lung Tumor Model for Predicting Drug Effectiveness in Specific Mutational Backgrounds. <i>Journal of Visualized Experiments</i> , <b>2016</b> , e53885	1.6	16
200	Analyzing ERK 1/2 signalling and targets. <i>Molecular BioSystems</i> , <b>2016</b> , 12, 2436-46		16
199	A semi-quantitative model of Quorum-Sensing in <i>Staphylococcus aureus</i> , approved by microarray meta-analyses and tested by mutation studies. <i>Molecular BioSystems</i> , <b>2013</b> , 9, 2665-80		16
198	Quality-of-life assessment in the old using the WHOQOL 100: differences between patients with senile dementia and patients with cancer. <i>International Psychogeriatrics</i> , <b>1999</b> , 11, 273-9	3.4	16
197	<i>Schizosaccharomyces pombe</i> U4 small nuclear RNA closely resembles vertebrate U4 and is required for growth. <i>Journal of Molecular Biology</i> , <b>1989</b> , 208, 371-9	6.5	16
196	Bioinformatics of cardiovascular miRNA biology. <i>Journal of Molecular and Cellular Cardiology</i> , <b>2015</b> , 89, 3-10	5.8	15
195	An open source tool for automatic spatiotemporal assessment of calcium transients and local signal-to-noise ratio in calcium imaging data. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1006054	5	15
194	The impact of cytokinin on jasmonate-salicylate antagonism in <i>Arabidopsis</i> immunity against infection with <i>Pst DC3000</i> . <i>Plant Signaling and Behavior</i> , <b>2013</b> , 8, doi: 10.4161/psb.26791	2.5	15
193	Investigating heat shock proteins of tardigrades in active versus anhydrobiotic state using shotgun proteomics. <i>Journal of Zoological Systematics and Evolutionary Research</i> , <b>2011</b> , 49, 111-119	1.9	15
192	Characterization of targeting domains by sequence analysis: glycogen-binding domains in protein phosphatases. <i>Journal of Molecular Medicine</i> , <b>1998</b> , 76, 77-9	5.5	15
191	Mining biomedical images towards valuable information retrieval in biomedical and life sciences. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	15
190	The New Genetic Landscape of Cushing's Disease: Deubiquitinases in the Spotlight. <i>Cancers</i> , <b>2019</b> , 11,	6.6	15
189	Convergence behaviour and Control in Non-Linear Biological Networks. <i>Scientific Reports</i> , <b>2015</b> , 5, 9746	4.9	14
188	A Boolean view separates platelet activatory and inhibitory signalling as verified by phosphorylation monitoring including threshold behaviour and integrin modulation. <i>Molecular BioSystems</i> , <b>2013</b> , 9, 1326-39		14

187	Mucorales spores induce a proinflammatory cytokine response in human mononuclear phagocytes and harbor no rodlet hydrophobins. <i>Virulence</i> , <b>2017</b> , 8, 1708-1718	4.7	14
186	Modelling antibiotic and cytotoxic isoquinoline effects in <i>Staphylococcus aureus</i> , <i>Staphylococcus epidermidis</i> and mammalian cells. <i>International Journal of Medical Microbiology</i> , <b>2015</b> , 305, 96-109	3.7	14
185	IsotopoPa database application for facile analysis and management of mass isotopomer data. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2014</b> , 2014,	5	14
184	Protecs, a comprehensive and powerful storage and analysis system for OMICS data, applied for profiling the anaerobiosis response of <i>Staphylococcus aureus</i> COL. <i>Proteomics</i> , <b>2010</b> , 10, 2982-3000	4.8	14
183	Refined Genetic Algorithm Simulations to Model Proteins. <i>Journal of Molecular Modeling</i> , <b>1999</b> , 5, 317-324		14
182	Optimality principles reveal a complex interplay of intermediate toxicity and kinetic efficiency in the regulation of prokaryotic metabolism. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005371	5	13
181	Use of pathway analysis and genome context methods for functional genomics of <i>Mycoplasma pneumoniae</i> nucleotide metabolism. <i>Gene</i> , <b>2007</b> , 396, 215-25	3.8	13
180	RIP death domain structural interactions implicated in TNF-mediated proliferation and survival. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2006</b> , 63, 413-23	4.2	13
179	Solvent entropy-driven searching for protein modeling examined and tested in simplified models. <i>Protein Engineering, Design and Selection</i> , <b>2001</b> , 14, 329-35	1.9	13
178	Comparative genome analysis and pathway reconstruction. <i>Pharmacogenomics</i> , <b>2002</b> , 3, 245-56	2.6	13
177	DNA recognition, strand selectivity, and cleavage mode during integrase family site-specific recombination. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 22255-67	5.4	13
176	Fine mapping of the antigen-antibody interaction of scFv215, a recombinant antibody inhibiting RNA polymerase II from <i>Drosophila melanogaster</i> . <i>Journal of Molecular Recognition</i> , <b>1999</b> , 12, 103-11	2.6	13
175	Identification and functional analysis of a novel yeast small nucleolar RNA. <i>Nucleic Acids Research</i> , <b>1993</b> , 21, 5386-90	20.1	13
174	An antibiotic target ranking and prioritization pipeline combining sequence, structure and network-based approaches exemplified for <i>Serratia marcescens</i> . <i>Gene</i> , <b>2016</b> , 591, 268-278	3.8	13
173	An optimized genetically encoded dual reporter for simultaneous ratio imaging of Ca and H reveals new insights into ion signaling in plants. <i>New Phytologist</i> , <b>2021</b> , 230, 2292-2310	9.8	13
172	LONELY-GUY Knocks Every Door: Crosskingdom Microbial Pathogenesis. <i>Trends in Plant Science</i> , <b>2015</b> , 20, 781-783	13.1	12
171	MicroRNA-21 versus microRNA-34: Lung cancer promoting and inhibitory microRNAs analysed in silico and in vitro and their clinical impact. <i>Tumor Biology</i> , <b>2017</b> , 39, 1010428317706430	2.9	12
170	Modelling the host-pathogen interactions of macrophages and using Game Theory and dynamic optimization. <i>Journal of the Royal Society Interface</i> , <b>2017</b> , 14,	4.1	12

169	Diagnostic value of preoperative CT scan to stratify colon cancer for neoadjuvant therapy. <i>International Journal of Colorectal Disease</i> , <b>2015</b> , 30, 1067-73	3	12
168	Pharmacogenomic strategies against microbial resistance: from bright to bleak to innovative. <i>Pharmacogenomics</i> , <b>2010</b> , 11, 1193-6	2.6	12
167	Detecting species-site dependencies in large multiple sequence alignments. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, 5959-68	20.1	12
166	Probing F1p: a new approach to analyze the structure of a DNA recognizing protein by combining the genetic algorithm, mutagenesis and non-canonical DNA target sites. <i>BBA - Proteins and Proteomics</i> , <b>1997</b> , 1340, 187-204		12
165	Modelling phagosomal lipid networks that regulate actin assembly. <i>BMC Systems Biology</i> , <b>2008</b> , 2, 107	3.5	12
164	Comparative Genome Analysis of the Mollicutes <b>2002</b> , 255-278		12
163	Ab initio tertiary-fold prediction of helical and non-helical protein chains using a genetic algorithm. <i>International Journal of Biological Macromolecules</i> , <b>1996</b> , 18, 1-4	7.9	12
162	Developing sustainable software solutions for bioinformatics by the " Butterfly" paradigm. <i>F1000Research</i> , <b>2014</b> , 3, 71	3.6	12
161	Transcriptomic buffering of cryptic genetic variation contributes to meningococcal virulence. <i>BMC Genomics</i> , <b>2017</b> , 18, 282	4.5	11
160	Probing the Unknowns in Cytokinin-Mediated Immune Defense in Arabidopsis with Systems Biology Approaches. <i>Bioinformatics and Biology Insights</i> , <b>2014</b> , 8, BBI.S13462	5.3	11
159	Characterization of a novel interaction between vasodilator-stimulated phosphoprotein and Abelson interactor 1 in human platelets: a concerted computational and experimental approach. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2010</b> , 30, 843-50	9.4	11
158	B-Raf and C-Raf signaling investigated in a simplified model of the mitogenic kinase cascade. <i>Biological Chemistry</i> , <b>2005</b> , 386, 1165-71	4.5	11
157	Lead expansion and virtual screening of Indinavir derivate HIV-1 protease inhibitors using pharmacophoric - shape similarity scoring function. <i>Bioinformation</i> , <b>2010</b> , 4, 295-9	1.1	11
156	In Silico Designed Axl Receptor Blocking Drug Candidates Against Zika Virus Infection. <i>ACS Omega</i> , <b>2018</b> , 3, 5281-5290	3.9	11
155	Challenged by Human Dendritic Cells: Metabolic and Regulatory Pathway Responses Testify a Tight Battle. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2019</b> , 9, 168	5.9	10
154	Identification of Antifungal Targets Based on Computer Modeling. <i>Journal of Fungi (Basel, Switzerland)</i> , <b>2018</b> , 4,	5.6	10
153	Dynamical modelling of prostaglandin signalling in platelets reveals individual receptor contributions and feedback properties. <i>Molecular BioSystems</i> , <b>2013</b> , 9, 2520-9		10
152	High-throughput microarray technology in diagnostics of enterobacteria based on genome-wide probe selection and regression analysis. <i>BMC Genomics</i> , <b>2010</b> , 11, 591	4.5	10

151	Improving Protein Structure Prediction by New Strategies: Experimental Insights and the Genetic Algorithm. <i>Journal of Molecular Modeling</i> , <b>1997</b> , 3, 312-314	2	10
150	A versatile structural domain analysis server using profile weight matrices. <i>Journal of Chemical Information and Computer Sciences</i> , <b>2002</b> , 42, 405-7		10
149	Rapid proliferation due to better metabolic adaptation results in full virulence of a filament-deficient <i>Candida albicans</i> strain. <i>Nature Communications</i> , <b>2021</b> , 12, 3899	17.4	10
148	Comprehensive Flux Modeling of Proteome and qRT-PCR Data Indicate Biphasic Metabolic Differences Between Elementary Bodies and Reticulate Bodies During Infection. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 2350	5.7	9
147	Gene expression profiles and protein-protein interaction network analysis in AIDS patients with HIV-associated encephalitis and dementia. <i>HIV/AIDS - Research and Palliative Care</i> , <b>2015</b> , 7, 265-76	1.2	9
146	New trends in pharmacogenomic strategies against resistance development in microbial infections. <i>Pharmacogenomics</i> , <b>2008</b> , 9, 1711-23	2.6	9
145	Placozoa: at least two. <i>Biologia (Poland)</i> , <b>2007</b> , 62, 641-645	1.5	9
144	Exogenous administration of a recombinant variant of TWEAK impairs healing after myocardial infarction by aggravation of inflammation. <i>PLoS ONE</i> , <b>2013</b> , 8, e78938	3.7	9
143	Draft genome of the Eutardigrade <i>Milnesium tardigradum</i> sheds light on ecdysozoan evolution		9
142	Synthetic Rewiring of Plant CO Sequestration Galvanizes Plant Biomass Production. <i>Trends in Biotechnology</i> , <b>2020</b> , 38, 354-359	15.1	8
141	Omics and bioinformatics applied to vaccine development against <i>Borrelia</i> . <i>Molecular Omics</i> , <b>2018</b> , 14, 330-340	4.4	8
140	Integrated pathway modules using time-course metabolic profiles and EST data from <i>Milnesium tardigradum</i> . <i>BMC Systems Biology</i> , <b>2012</b> , 6, 72	3.5	8
139	Pharmacogenomic strategies against resistance development in microbial infections. <i>Pharmacogenomics</i> , <b>2004</b> , 5, 361-79	2.6	8
138	Current efforts in the analysis of RNAi and RNAi target genes. <i>Briefings in Bioinformatics</i> , <b>2005</b> , 6, 72-85	13.4	8
137	Opiates induce long-term increases in prodynorphin-derived peptide levels in the guinea-pig myenteric plexus. <i>Naunyn-Schmiedeberg's Archives of Pharmacology</i> , <b>1986</b> , 333, 381-6	3.4	8
136	Affinity purification of $\delta$ -endorphin-like material from NG108CC15 hybrid cells by means of the monoclonal $\delta$ -endorphin antibody 3-E7. <i>Neurochemistry International</i> , <b>1985</b> , 7, 247-53	4.4	8
135	FIJI Macro 3D ART VeSelect: 3D Automated Reconstruction Tool for Vesicle Structures of Electron Tomograms. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005317	5	8
134	Delaying memory decline: different options and emerging solutions. <i>Translational Psychiatry</i> , <b>2020</b> , 10, 13	8.6	7

133	HPLC-ESI-MS method for C fullerene mitochondrial content quantification. <i>Data in Brief</i> , <b>2018</b> , 19, 2047-2052	2052	7
132	MOLECULAR DYNAMICS SIMULATION OF POPC AND POPE LIPID MEMBRANE BILAYERS ENFORCED BY AN INTERCALATED SINGLE-WALL CARBON NANOTUBE. <i>Nano</i> , <b>2011</b> , 06, 19-29	1.1	7
131	Thirty-three nucleotides of 5Rflanking sequence including the TATABox are necessary and sufficient for efficient U2 snRNA transcription in <i>Schizosaccharomyces pombe</i> . <i>Molecular Microbiology</i> , <b>1991</b> , 5, 1621-5	4.1	7
130	Novel Approach for Characterizing Propofol Binding Affinities to Serum Albumins from Different Species. <i>ACS Omega</i> , <b>2020</b> , 5, 25543-25551	3.9	7
129	Integrated structural and functional analysis of the protective effects of kinetin against oxidative stress in mammalian cellular systems. <i>Scientific Reports</i> , <b>2020</b> , 10, 13330	4.9	7
128	A Proteome Overview: Shared and Specific Proteins and Protein Complexes from Representative Strains of All Three Clades. <i>Proteomes</i> , <b>2016</b> , 4,	4.6	7
127	Evaluation of Aspergillus and Mucorales specific T-cells and peripheral blood mononuclear cell cytokine signatures as biomarkers of environmental mold exposure. <i>International Journal of Medical Microbiology</i> , <b>2018</b> , 308, 1018-1026	3.7	7
126	A combined tissue-engineered/inSilico signature tool patient stratification in lung cancer. <i>Molecular Oncology</i> , <b>2018</b> , 12, 1264-1285	7.9	7
125	How to Steer and Control ERK and the ERK Signaling Cascade Exemplified by Looking at Cardiac Insufficiency. <i>International Journal of Molecular Sciences</i> , <b>2019</b> , 20,	6.3	6
124	The Cytokinin-Activating LOG-Family Proteins Are Not Lysine Decarboxylases. <i>Trends in Biochemical Sciences</i> , <b>2018</b> , 43, 232-236	10.3	6
123	C. elegans protein interaction network analysis probes RNAi validated pro-longevity effect of nhr-6, a human homolog of tumor suppressor Nr4a1. <i>Scientific Reports</i> , <b>2019</b> , 9, 15711	4.9	6
122	A comparative analysis of the bistability switch for platelet aggregation by logic ODE based dynamical modeling. <i>Molecular BioSystems</i> , <b>2014</b> , 10, 2082-9		6
121	Integration of boolean models on hormonal interactions and prospects of cytokinin-auxin crosstalk in plant immunity. <i>Plant Signaling and Behavior</i> , <b>2013</b> , 8, e23890	2.5	6
120	Bioinformatics identifies tardigrade molecular adaptations including the DNA-j family and first steps towards dynamical modelling. <i>Journal of Zoological Systematics and Evolutionary Research</i> , <b>2011</b> , 49, 120-126	1.9	6
119	Computational methods for the prediction of protein folds. <i>BBA - Proteins and Proteomics</i> , <b>1997</b> , 1343, 1-15		6
118	Rational Drug Design of Axl Tyrosine Kinase Type I Inhibitors as Promising Candidates Against Cancer. <i>Frontiers in Chemistry</i> , <b>2019</b> , 7, 920	5	6
117	Connecting Cancer Pathways to Tumor Engines: A Stratification Tool for Colorectal Cancer Combining Human In Vitro Tissue Models with Boolean In Silico Models. <i>Cancers</i> , <b>2019</b> , 12,	6.6	6
116	Functional genomics identifies AMPD2 as a new prognostic marker for undifferentiated pleomorphic sarcoma. <i>International Journal of Cancer</i> , <b>2019</b> , 144, 859-867	7.5	6

115	A new triple system DNA-Nanosilver-Berberine for cancer therapy. <i>Applied Nanoscience (Switzerland)</i> , <b>2019</b> , 9, 945-956	3.3	6
114	JANE: efficient mapping of prokaryotic ESTs and variable length sequence reads on related template genomes. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 391	3.6	5
113	Analyzing Thiol-Dependent Redox Networks in the Presence of Methylene Blue and Other Antimalarial Agents with RT-PCR-Supported in silico Modeling. <i>Bioinformatics and Biology Insights</i> , <b>2012</b> , 6, 287-302	5.3	5
112	Ribosomal RNA phylogenetics: the third dimension. <i>Biologia (Poland)</i> , <b>2010</b> , 65, 388-391	1.5	5
111	inGeno--an integrated genome and ortholog viewer for improved genome to genome comparisons. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 461	3.6	5
110	DNA and mRNA sequence of the immune protective DNA ligase I gene match the rev response element of HIV. <i>DNA Sequence</i> , <b>1996</b> , 6, 119-21		5
109	Mutational analysis of Schizosaccharomyces pombe U4 snRNA by plasmid exchange. <i>Yeast</i> , <b>1992</b> , 8, 647-53		5
108	Probing the unknowns in cytokinin-mediated immune defense in Arabidopsis with systems biology approaches. <i>Bioinformatics and Biology Insights</i> , <b>2014</b> , 8, 35-44	5.3	5
107	Systems Biology Analysis to Understand Regulatory miRNA Networks in Lung Cancer. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1819, 235-247	1.4	5
106	Deep metazoan phylogeny. <i>In Silico Biology</i> , <b>2007</b> , 7, 151-4	2	5
105	Vaccinia virus injected human tumors: oncolytic virus efficiency predicted by antigen profiling analysis fitted boolean models. <i>Bioengineered</i> , <b>2019</b> , 10, 190-196	5.7	4
104	Comparison of the central human and mouse platelet signaling cascade by systems biological analysis. <i>BMC Genomics</i> , <b>2020</b> , 21, 897	4.5	4
103	Genome-wide inference of the Camponotus floridanus protein-protein interaction network using homologous mapping and interacting domain profile pairs. <i>Scientific Reports</i> , <b>2020</b> , 10, 2334	4.9	4
102	Functional module search in protein networks based on semantic similarity improves the analysis of proteomics data. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 1877-89	7.6	4
101	DNAseq Workflow in a Diagnostic Context and an Example of a User Friendly Implementation. <i>BioMed Research International</i> , <b>2015</b> , 2015, 403497	3	4
100	Metabolic adaptation and protein complexes in prokaryotes. <i>Metabolites</i> , <b>2012</b> , 2, 940-58	5.6	4
99	Medical target prediction from genome sequence: combining different sequence analysis algorithms with expert knowledge and input from artificial intelligence approaches. <i>Computers &amp; Chemistry</i> , <b>2001</b> , 26, 15-21		4
98	Integrative functional genomics decodes herpes simplex virus 1		4

97	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. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	4
96	Modulatory and Toxicological Perspectives on the Effects of the Small Molecule Kinetin. <i>Molecules</i> , <b>2021</b> , 26,	4.8	4
95	Automated classification of synaptic vesicles in electron tomograms of <i>C. elegans</i> using machine learning. <i>PLoS ONE</i> , <b>2018</b> , 13, e0205348	3.7	4
94	Analyzing pharmacological intervention points: A method to calculate external stimuli to switch between steady states in regulatory networks. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1007075	5	3
93	Antigen profiling analysis of vaccinia virus injected canine tumors: oncolytic virus efficiency predicted by boolean models. <i>Bioengineered</i> , <b>2014</b> , 5, 319-25	5.7	3
92	GoSynthetic database tool to analyse natural and engineered molecular processes. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2013</b> , 2013, bat043	5	3
91	CA/C1 peptidases of the malaria parasites <i>Plasmodium falciparum</i> and <i>P. berghei</i> and their mammalian hosts--a bioinformatical analysis. <i>Biological Chemistry</i> , <b>2009</b> , 390, 1185-97	4.5	3
90	Different evolutionary modifications as a guide to rewire two-component systems. <i>Bioinformatics and Biology Insights</i> , <b>2012</b> , 6, 97-128	5.3	3
89	The IronChip evaluation package: a package of perl modules for robust analysis of custom microarrays. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 112	3.6	3
88	MSL: Facilitating automatic and physical analysis of published scientific literature in PDF format. <i>F1000Research</i> , <b>2015</b> , 4, 1453	3.6	3
87	Chagas Disease: Detection of by a New, High-Specific Real Time PCR. <i>Journal of Clinical Medicine</i> , <b>2020</b> , 9,	5.1	3
86	MSL: Facilitating automatic and physical analysis of published scientific literature in PDF format. <i>F1000Research</i> , <b>2015</b> , 4, 1453	3.6	3
85	Ant-App-DB: a smart solution for monitoring arthropods activities, experimental data management and solar calculations without GPS in behavioral field studies. <i>F1000Research</i> , <b>2014</b> , 3, 311	3.6	3
84	In silico signaling modeling to understand cancer pathways and treatment responses. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 1115-1117	13.4	3
83	A comprehensive method protocol for annotation and integrated functional understanding of lncRNAs. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 1391-1396	13.4	3
82	A Systems Biology Methodology Combining Transcriptome and Interactome Datasets to Assess the Implications of Cytokinin Signaling for Plant Immune Networks. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1569, 165-173	1.4	2
81	Improving Re-annotation of Annotated Eukaryotic Genomes <b>2016</b> , 171-195		2
80	Stem-cell-triggered immunity safeguards cytokinin enriched plant shoot apices from pathogen infection. <i>Frontiers in Plant Science</i> , <b>2014</b> , 5, 588	6.2	2



79	G244E in the canine factor IX gene leads to severe haemophilia B in Rhodesian Ridgebacks. <i>Veterinary Journal</i> , <b>2011</b> , 187, 113-8	2.5	2
78	Unsupervised meta-analysis on diverse gene expression datasets allows insight into gene function and regulation. <i>Bioinformatics and Biology Insights</i> , <b>2008</b> , 2, 265-80	5.3	2
77	A java applet for exploring the new higher level classification of eukaryotes with emphasis on the taxonomy of protists. <i>Journal of Eukaryotic Microbiology</i> , <b>2006</b> , 53, 315	3.6	2
76	An open source protein gel documentation system for proteome analyses. <i>Journal of Chemical Information and Computer Sciences</i> , <b>2004</b> , 44, 168-9		2
75	Yeast U3 localization and correct sequence (snR17a) and promotor activity (snR17b) identified by homology search. <i>DNA Sequence</i> , <b>1991</b> , 1, 217-8		2
74	Alveolar Regeneration in COVID-19 Patients: A Network Perspective. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	2
73	Topological Analysis of the Carbon-Concentrating CETCH Cycle and a Photorespiratory Bypass Reveals Boosted CO-Sequestration by Plants. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2021</b> , 9, 708417	5.8	2
72	Recent Developments in Metabolic Pathway Analysis and Their Potential Implications for Biotechnology and Medicine <b>2000</b> , 57-66		2
71	Computational Feature Performance and Domain Specific Architecture Evaluation of Software Applications Towards Metabolic Flux Analysis. <i>Recent Patents on Computer Science</i> , <b>2012</b> , 5, 165-176	1	2
70	Design, Synthesis, and Anticancer Screening for Repurposed Pyrazolo[3,4-d]pyrimidine Derivatives on Four Mammalian Cancer Cell Lines. <i>Molecules</i> , <b>2021</b> , 26,	4.8	2
69	A systems-biology model of the tumor necrosis factor (TNF) interactions with TNF receptor 1 and 2. <i>Bioinformatics</i> , <b>2021</b> , 37, 669-676	7.2	2
68	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.. <i>Journal of Proteome Research</i> , <b>2022</b> , 21, 1181-1188	5.6	2
67	Reconstruction of an Immune Dynamic Model to Simulate the Contrasting Role of Auxin and Cytokinin in Plant Immunity. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1569, 83-92	1.4	1
66	Modeling of shotgun sequencing of DNA plasmids using experimental and theoretical approaches. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 132	3.6	1
65	Draft Genome Sequence of the Moderately Heat-Tolerant <i>Lactococcus lactis</i> subsp. <i>lactis</i> bv. <i>diacetylactis</i> Strain GL2 from Algerian Dromedary Milk. <i>Genome Announcements</i> , <b>2015</b> , 3,		1
64	Evaluation and prediction of the HIV-1 central polypurine tract influence on foamy viral vectors to transduce dividing and growth-arrested cells. <i>Scientific World Journal, The</i> , <b>2014</b> , 2014, 487969	2.2	1
63	Integrated Platelet Networks for the Analysis of Different System States. <i>Current Proteomics</i> , <b>2011</b> , 8, 229-236	0.7	1
62	Evidence for the expression of peptides derived from three opioid precursors in NG 108CC15 hybrid cells. <i>Neuropeptides</i> , <b>1987</b> , 9, 25-32	3.3	1

61	Scaffold Searching of FDA and EMA-Approved Drugs Identifies Lead Candidates for Drug Repurposing in Alzheimer's Disease. <i>Frontiers in Chemistry</i> , <b>2021</b> , 9, 736509	5	1
60	An In Vitro and In Silico Study of the Enhanced Antiproliferative and Pro-Oxidant Potential of <i>L. cv. Arbosana</i> Leaf Extract via Elastic Nanovesicles (Spanlastics).. <i>Antioxidants</i> , <b>2021</b> , 10,	7.1	1
59	Bioinformatical approaches to detect and analyze protein interactions. <i>Methods in Molecular Biology</i> , <b>2009</b> , 564, 401-31	1.4	1
58	RhoA/Cdc42 signaling drives cytoplasmic maturation but not endomitosis in megakaryocytes. <i>Cell Reports</i> , <b>2021</b> , 35, 109102	10.6	1
57	An Ebola, human protein interaction census reveals a conserved human protein cluster targeted by various human pathogens. <i>Computational and Structural Biotechnology Journal</i> , <b>2021</b> , 19, 5292-5308	6.8	1
56	Antibody ligation of carcinoembryonic antigen-related cell adhesion molecule 1 (CEACAM1), CEACAM3, and CEACAM6, differentially enhance the cytokine release of human neutrophils in responses to <i>Candida albicans</i>		1
55	Pathogen and Host-Pathogen Protein Interactions Provide a Key to Identify Novel Drug Targets <b>2021</b> , 543-553		1
54	CoxBase: an Online Platform for Epidemiological Surveillance, Visualization, Analysis, and Typing of <i>Coxiella burnetii</i> Genomic Sequences.. <i>MSystems</i> , <b>2021</b> , 6, e0040321	7.6	1
53	Cisplatin-Induced Reproductive Toxicity and Oxidative Stress: Ameliorative Effect of Kinetin. <i>Antioxidants</i> , <b>2022</b> , 11, 863	7.1	1
52	Modular micro-physiological human tumor/tissue models based on decellularized tissue for improved preclinical testing. <i>ALTEX: Alternatives To Animal Experimentation</i> , <b>2020</b> , 38, 289-306	4.3	0
51	An effective model of endogenous clocks and external stimuli determining circadian rhythms. <i>Scientific Reports</i> , <b>2021</b> , 11, 16165	4.9	0
50	Modeling Immune Dynamics in Plants Using JIMENA-Package. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2328, 183-189	1.4	0
49	ACKR3 regulates platelet activation and ischemia-reperfusion tissue injury.. <i>Nature Communications</i> , <b>2022</b> , 13, 1823	17.4	0
48	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.. <i>Archives of Toxicology</i> , <b>2021</b> , 96, 673	5.8	0
47	Application of Biotechnology and Bioinformatics Tools in Plant-Fungus Interactions <b>2015</b> , 49-64		
46	Meta-Alignment: Combining Sequence Aligners for Better Results. <i>Lecture Notes in Computer Science</i> , <b>2018</b> , 395-404	0.9	
45	Bioinformatics in Leishmania Drug Design <b>2018</b> , 297-317		
44	New Bioinformatic Strategies against Apicomplexan Parasites <b>2011</b> , 21-33		

- 43 Bioinformatics: Data Mining Among Genome Sequences **2006**, 1-19
- 42 The Genetic Algorithm Applied as a Modelling Tool to Predict the Fold of Small Proteins with Different Topologies. *Journal of Molecular Modeling*, **1996**, 2, 304-306 2
- 41 Olbers Paradox. *Nature*, **1991**, 351, 21-21 50.4
- 40 Antibody ligation of CEACAM1, CEACAM3, and CEACAM6, differentially enhance the cytokine release of human neutrophils in responses to *Candida albicans*. *Cellular Immunology*, **2021**, 371, 104459 4.4
- 39 Klimapflanzen und biologische Wege zu negativen Kohlendioxidemissionen. *BioSpektrum*, **2021**, 27, 769-772
- 38 An Introduction to Regulatory RNA Motifs **1998**, 1-18
- 37 Computer Based and Theoretical Identification of Regulatory RNA **1998**, 105-131
- 36 Functional RNA Interactions **1998**, 133-163
- 35 Instances of Functional RNA (An Overview) **1998**, 19-84
- 34 Experimental Identification of New Functional RNA **1998**, 85-104
- 33 Areas of Research on Regulatory RNA and Functional RNA Motifs **1998**, 165-220
- 32 Komplexe Systeme verhalten sich grundsätzlich ähnlich **2017**, 107-129
- 31 Bioinformatik verbindet das Leben mit dem Universum und dem ganzen Rest **2017**, 225-241
- 30 Wir können über uns nachdenken über Computer nicht **2017**, 203-212
- 29 Signalkaskaden durch Messen der kodierten Information besser verstehen **2017**, 89-95
- 28 Wie ist unser eigenes, extrem leistungsfähiges Gehirn aufgebaut? **2017**, 213-224
- 27 Stoffwechsel modellieren und neue Antibiotika finden **2017**, 47-55
- 26 Übungen zu den Übungsaufgaben **2017**, 307-350

- 25 Evolution mit dem Computer besser vergleichen **2017**, 131-146
- 24 Magische RNA **2017**, 25-35
- 23 Systembiologie und Krankheitsursachen aufdecken **2017**, 57-75
- 22 Design-Prinzipien einer Zelle **2017**, 147-160
- 21 Bacterial Shoot Apical Meristem Inoculation Assay. *Methods in Molecular Biology*, **2020**, 2094, 17-22 1.4
- 20 Molecular Modeling of the Interaction Between Stem Cell Peptide and Immune Receptor in Plants. *Methods in Molecular Biology*, **2020**, 2094, 67-77 1.4
- 19 Mapping a Transcriptome-Guided Arabidopsis SAM Interactome. *Methods in Molecular Biology*, **2020**, 2094, 113-118 1.4
- 18 Modeling of stringent-response reflects nutrient stress induced growth impairment and essential amino acids in different *Staphylococcus aureus* mutants. *Scientific Reports*, **2021**, 11, 9651 4.9
- 17 GNATY: Optimized NGS Variant Calling and Coverage Analysis. *Lecture Notes in Computer Science*, **2016**, 446-454 0.9
- 16 Magische RNA **2021**, 27-38
- 15 Design-Prinzipien einer Zelle **2021**, 155-170
- 14 Wie ist unser eigenes, extrem leistungsfähiges Gehirn aufgebaut? **2021**, 231-242
- 13 Leben erfindet immer neue Ebenen der Sprache **2021**, 189-214
- 12 Stoffwechsel modellieren und neue Antibiotika finden **2021**, 51-60
- 11 Übungen zu den Übungsaufgaben **2021**, 331-378
- 10 Komplexe Systeme verhalten sich grundsätzlich ähnlich **2021**, 115-135
- 9 Signalkaskaden durch Messen der kodierten Information besser verstehen **2021**, 93-101
- 8 Bioinformatik verbindet das Leben mit dem Universum und dem ganzen Rest **2021**, 243-261

7 Systembiologie und Krankheitsursachen aufdecken **2021**, 61-80

6 Evolution mit dem Computer besser vergleichen **2021**, 137-153

5 Genome ¶molekulare Landkarten von Lebewesen **2021**, 39-50

4 Nanocellulose: A New Multifunctional Tool for RNA Systems Biology Research. *RNA Technologies*, **2018**, 373-401 0.2

3 A Novel Water-Soluble C60 Fullerene-Based Nano-Platform Enhances Efficiency of Anticancer Chemotherapy **2022**, 59-93

2 Wir können über uns nachdenken ¶der Computer nicht **2021**, 215-229

1 Metabolites and pathway flexibility. *In Silico Biology*, **2005**, 5, 103-110 2