

Rainer Breitling

List of Publications by Year in descending order

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Version: 2024-02-01

208
papers

19,891
citations

23879

60
h-index

13635

134
g-index

226
all docs

226
docs citations

226
times ranked

28474
citing authors

#	ARTICLE	IF	CITATIONS
1	What, if anything, is <i>Lycosa accentuata</i> Latreille, 1817? â€œ Review of a nomenclatural conundrum (Araneae: Lycosidae). <i>Zoosystema</i> , 2022, 44, .	0.2	0
2	Host Systems for the Production of Recombinant Spider Silk. <i>Trends in Biotechnology</i> , 2021, 39, 560-573.	4.9	45
3	Investigation of the effects of actinorhodin biosynthetic gene cluster expression and a <i>rpoB</i> point mutation on the metabolome of <i>Streptomyces coelicolor</i> M1146. <i>Journal of Bioscience and Bioengineering</i> , 2021, 131, 525-536.	1.1	6
4	Synthetic biology approaches to actinomycete strain improvement. <i>FEMS Microbiology Letters</i> , 2021, 368, .	0.7	2
5	Multi-omics Study of <i>Planobispora rosea</i> , Producer of the Thiopeptide Antibiotic GE2270A. <i>MSystems</i> , 2021, 6, e0034121.	1.7	2
6	The evolving art of creating genetic diversity: From directed evolution to synthetic biology. <i>Biotechnology Advances</i> , 2021, 50, 107762.	6.0	24
7	Blood, sweat, and tears: extraterrestrial regolith biocomposites with in vivo binders. <i>Materials Today Bio</i> , 2021, 12, 100136.	2.6	12
8	On the authorship and publication dates of Theraphosa and Theraphosidae (Araneae, Mygalomorphae): a clarification. <i>Bionomina</i> , 2021, 24, .	0.2	0
9	Harnessing intercellular signals to engineer the soil microbiome. <i>Natural Product Reports</i> , 2021, , .	5.2	2
10	Unravelling the $\hat{1}^3$ -butyrolactone network in <i>Streptomyces coelicolor</i> by computational ensemble modelling. <i>PLoS Computational Biology</i> , 2020, 16, e1008039.	1.5	6
11	Multi-Omics Analysis of the Effect of cAMP on Actinorhodin Production in <i>Streptomyces coelicolor</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 595552.	2.0	6
12	Engineering <i>Escherichia coli</i> towards de novo production of gatekeeper (2S)-flavanones: naringenin, pinocembrin, eriodictyol and homoeriodictyol. <i>Synthetic Biology</i> , 2020, 5, ysaa012.	1.2	45
13	Exploring novel bacterial terpene synthases. <i>PLoS ONE</i> , 2020, 15, e0232220.	1.1	30
14	The effect of terminal globular domains on the response of recombinant mini-spidroins to fiber spinning triggers. <i>Scientific Reports</i> , 2020, 10, 10671.	1.6	22
15	Rapid prototyping of microbial production strains for the biomanufacture of potential materials monomers. <i>Metabolic Engineering</i> , 2020, 60, 168-182.	3.6	48
16	Towards engineering and production of artificial spider silk using tools of synthetic biology. <i>Engineering Biology</i> , 2020, 4, 1-6.	0.8	9
17	Bioengineering horizon scan 2020. <i>ELife</i> , 2020, 9, .	2.8	19
18	List of German names for the spiders of Germany (Araneae).. <i>Arachnologische Mitteilungen</i> , 2020, 59, 38.	0.4	1

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19	South European spiders from the Duffey collection in the Manchester Museum (Arachnida: Araneae). , 2020, 18, 333.		6
20	Highly multiplexed, fast and accurate nanopore sequencing for verification of synthetic DNA constructs and sequence libraries. <i>Synthetic Biology</i> , 2019, 4, ysz025.	1.2	35
21	Dynamics of the human skin mediator lipidome in response to dietary ω -3 fatty acid supplementation. <i>FASEB Journal</i> , 2019, 33, 13014-13027.	0.2	29
22	Integrated Probabilistic Annotation: A Bayesian-Based Annotation Method for Metabolomic Profiles Integrating Biochemical Connections, Isotope Patterns, and Adduct Relationships. <i>Analytical Chemistry</i> , 2019, 91, 12799-12807.	3.2	17
23	Synthetic biology for fibers, adhesives, and active camouflage materials in protection and aerospace. <i>MRS Communications</i> , 2019, 9, 486-504.	0.8	21
24	SelProm: A Queryable and Predictive Expression Vector Selection Tool for <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2019, 8, 1478-1483.	1.9	37
25	Computational identification of co-evolving multi-gene modules in microbial biosynthetic gene clusters. <i>Communications Biology</i> , 2019, 2, 83.	2.0	20
26	Efficient learning in metabolic pathway designs through optimal assembling. <i>IFAC-PapersOnLine</i> , 2019, 52, 7-12.	0.5	5
27	Machine Learning of Designed Translational Control Allows Predictive Pathway Optimization in <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2019, 8, 127-136.	1.9	88
28	Orthogonal Regulatory Circuits for <i>Escherichia coli</i> Based on the $\hat{\text{I}}^3$ -Butyrolactone System of <i>Streptomyces coelicolor</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 1043-1055.	1.9	25
29	Rational cell culture optimization enhances experimental reproducibility in cancer cells. <i>Scientific Reports</i> , 2018, 8, 3029.	1.6	25
30	Output ordering and prioritisation system (OOPS): ranking biosynthetic gene clusters to enhance bioactive metabolite discovery. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2018, 45, 615-619.	1.4	1
31	Selenzyme: enzyme selection tool for pathway design. <i>Bioinformatics</i> , 2018, 34, 2153-2154.	1.8	75
32	Metabolomics tools for the synthetic biology of natural products. <i>Current Opinion in Biotechnology</i> , 2018, 54, 114-120.	3.3	25
33	Detection and Quantification of Butyrolactones from <i>Streptomyces</i> . <i>Methods in Molecular Biology</i> , 2018, 1673, 117-128.	0.4	3
34	Defining informative priors for ensemble modeling in systems biology. <i>Nature Protocols</i> , 2018, 13, 2643-2663.	5.5	16
35	Translation Stress Positively Regulates MscL-Dependent Excretion of Cytoplasmic Proteins. <i>MBio</i> , 2018, 9, .	1.8	19
36	Development and validation of an updated computational model of <i>Streptomyces coelicolor</i> primary and secondary metabolism. <i>BMC Genomics</i> , 2018, 19, 519.	1.2	20

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37	The "Three Cs" of Novel Antibiotic Discovery and Production through Synthetic Biology: Biosynthetic Gene Clusters, Heterologous Chassis, and Synthetic Microbial Consortia. <i>Advanced Biology</i> , 2018, 2, 1800064.	3.0	4
38	Mobilising ion mobility mass spectrometry for metabolomics. <i>Analyst, The</i> , 2018, 143, 4783-4788.	1.7	29
39	An automated Design-Build-Test-Learn pipeline for enhanced microbial production of fine chemicals. <i>Communications Biology</i> , 2018, 1, 66.	2.0	159
40	Respectful Modeling: Addressing Uncertainty in Dynamic System Models for Molecular Biology. <i>Trends in Biotechnology</i> , 2017, 35, 518-529.	4.9	19
41	antiSMASH 4.0's improvements in chemistry prediction and gene cluster boundary identification. <i>Nucleic Acids Research</i> , 2017, 45, W36-W41.	6.5	1,196
42	RankProd 2.0: a refactored bioconductor package for detecting differentially expressed features in molecular profiling datasets. <i>Bioinformatics</i> , 2017, 33, 2774-2775.	1.8	113
43	A transatlantic perspective on 20 emerging issues in biological engineering. <i>ELife</i> , 2017, 6, .	2.8	49
44	biochem4j: Integrated and extensible biochemical knowledge through graph databases. <i>PLoS ONE</i> , 2017, 12, e0179130.	1.1	31
45	reGenotyper: Detecting mislabeled samples in genetic data. <i>PLoS ONE</i> , 2017, 12, e0171324.	1.1	25
46	Public DNA barcoding data resolve the status of the genus <i>Arboricaria</i> (Araneae: Gnaphosidae). <i>Arachnologische Mitteilungen</i> , 2017, 54, 24-27.	0.4	6
47	Bioinformatics for the synthetic biology of natural products: integrating across the Design-Build-Test cycle. <i>Natural Product Reports</i> , 2016, 33, 925-932.	5.2	58
48	SYNBIOCHEM—a SynBio foundry for the biosynthesis and sustainable production of fine and speciality chemicals. <i>Biochemical Society Transactions</i> , 2016, 44, 675-677.	1.6	7
49	Synthetic Biology of Natural Products. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a023994.	2.3	22
50	SYNBIOCHEM Synthetic Biology Research Centre, Manchester — A UK foundry for fine and speciality chemicals production. <i>Synthetic and Systems Biotechnology</i> , 2016, 1, 271-275.	1.8	6
51	Towards synthesis of monoterpenes and derivatives using synthetic biology. <i>Current Opinion in Chemical Biology</i> , 2016, 34, 37-43.	2.8	89
52	Phantom spiders 2: More notes on dubious spider species from Europe. <i>Arachnologische Mitteilungen</i> , 2016, 52, 50-77.	0.4	12
53	Epigeal Spiders at Abisko Scientific Research Station in Swedish Lapland (Arachnida: Araneae). <i>Arachnology</i> , 2015, 16, 287-293.	0.4	0
54	Bacterial Microcompartments: Biomaterials for Synthetic Biology-Based Compartmentalization Strategies. <i>ACS Biomaterials Science and Engineering</i> , 2015, 1, 345-351.	2.6	36

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55	Judging synthetic biology risks. <i>Science</i> , 2015, 347, 107-107.	6.0	18
56	Butyrolactone signalling circuits for synthetic biology. <i>Current Opinion in Chemical Biology</i> , 2015, 28, 91-98.	2.8	54
57	antiSMASH 3.0—a comprehensive resource for the genome mining of biosynthetic gene clusters. <i>Nucleic Acids Research</i> , 2015, 43, W237-W243.	6.5	1,764
58	Probing the Metabolic Network in Bloodstream-Form <i>Trypanosoma brucei</i> Using Untargeted Metabolomics with Stable Isotope Labelled Glucose. <i>PLoS Pathogens</i> , 2015, 11, e1004689.	2.1	128
59	Synthetic biology advances for pharmaceutical production. <i>Current Opinion in Biotechnology</i> , 2015, 35, 46-51.	3.3	59
60	Incorporating peak grouping information for alignment of multiple liquid chromatography-mass spectrometry datasets. <i>Bioinformatics</i> , 2015, 31, 1999-2006.	1.8	10
61	Remarks on Synonyms of European <i>Larinioides</i> Species (Arachnida: Araneae: Araneidae). <i>Arachnology</i> , 2015, 16, 305-310.	0.4	1
62	LC-MS-based absolute metabolite quantification: application to metabolic flux measurement in trypanosomes. <i>Metabolomics</i> , 2015, 11, 1721-1732.	1.4	36
63	Minimum Information about a Biosynthetic Gene cluster. <i>Nature Chemical Biology</i> , 2015, 11, 625-631.	3.9	715
64	TrypanoCyc: a community-led biochemical pathways database for <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 2015, 43, D637-D644.	6.5	35
65	Phantom spiders: notes on dubious spider species from Europe. <i>Arachnologische Mitteilungen</i> , 2015, 50, 65-80.	0.4	6
66	antiSMASH. , 2015, , 33-38.		0
67	Pep2Path: Automated Mass Spectrometry-Guided Genome Mining of Peptidic Natural Products. <i>PLoS Computational Biology</i> , 2014, 10, e1003822.	1.5	81
68	Phosphoenolpyruvate Carboxylase Identified as a Key Enzyme in Erythrocytic <i>Plasmodium falciparum</i> Carbon Metabolism. <i>PLoS Pathogens</i> , 2014, 10, e1003876.	2.1	32
69	MetAssign: probabilistic annotation of metabolites from LC-MS data using a Bayesian clustering approach. <i>Bioinformatics</i> , 2014, 30, 2764-2771.	1.8	63
70	A fast algorithm for determining bounds and accurate approximate p-values of the rank product statistic for replicate experiments. <i>BMC Bioinformatics</i> , 2014, 15, 367.	1.2	23
71	Stable isotope-labeling studies in metabolomics: new insights into structure and dynamics of metabolic networks. <i>Bioanalysis</i> , 2014, 6, 511-524.	0.6	171
72	The Silicon Trypanosome. <i>Advances in Microbial Physiology</i> , 2014, 64, 115-143.	1.0	5

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73	Steps towards the synthetic biology of polyketide biosynthesis. FEMS Microbiology Letters, 2014, 351, 116-125.	0.7	69
74	Theridion zonulatum Thorell 1890, a senior synonym of Theridion zebrinusum Zhu 1998. Acta Arachnologica, 2014, 63, 79-82.	0.0	0
75	A fast algorithm for determining bounds and accurate approximate p-values of the rank product statistic for replicate experiments. BMC Bioinformatics, 2014, 15, 367.	1.2	19
76	Natural Products: Tools and More Special Issue. ACS Synthetic Biology, 2013, 2, 352-353.	1.9	0
77	Mass appeal: metabolite identification in mass spectrometry-focused untargeted metabolomics. Metabolomics, 2013, 9, 44-66.	1.4	452
78	Metabolic adaptations of <i>Eishmania donovani</i> in relation to differentiation, drug resistance, and drug pressure. Molecular Microbiology, 2013, 90, 428-442.	1.2	48
79	antiSMASH 2.0 – a versatile platform for genome mining of secondary metabolite producers. Nucleic Acids Research, 2013, 41, W204-W212.	6.5	753
80	The exact probability distribution of the rank product statistics for replicated experiments. FEBS Letters, 2013, 587, 677-682.	1.3	33
81	Design-based re-engineering of biosynthetic gene clusters: plug-and-play in practice. Current Opinion in Biotechnology, 2013, 24, 1144-1150.	3.3	32
82	Modeling Challenges in the Synthetic Biology of Secondary Metabolism. ACS Synthetic Biology, 2013, 2, 373-378.	1.9	30
83	LC-MS METABOLOMICS FROM STUDY DESIGN TO DATA-ANALYSIS – USING A VERSATILE PATHOGEN AS A TEST CASE. Computational and Structural Biotechnology Journal, 2013, 4, e201301002.	1.9	39
84	mzMatch – ISO: an R tool for the annotation and relative quantification of isotope-labelled mass spectrometry data. Bioinformatics, 2013, 29, 281-283.	1.8	91
85	Handling Uncertainty in Dynamic Models: The Pentose Phosphate Pathway in Trypanosoma brucei. PLoS Computational Biology, 2013, 9, e1003371.	1.5	40
86	Detecting Sequence Homology at the Gene Cluster Level with MultiGeneBlast. Molecular Biology and Evolution, 2013, 30, 1218-1223.	3.5	368
87	Metabolomics for Secondary Metabolite Research. Metabolites, 2013, 3, 1076-1083.	1.3	59
88	Computation: A New Open Access Journal of Computational Chemistry, Computational Biology and Computational Engineering. Computation, 2013, 1, 27-30.	1.0	1
89	Explicit consideration of topological and parameter uncertainty gives new insights into a well-established model of glycolysis. FEBS Journal, 2013, 280, 4640-4651.	2.2	15
90	Human neuroblastoma cells with acquired resistance to the p53 activator RITA retain functional p53 and sensitivity to other p53 activating agents. Cell Death and Disease, 2012, 3, e294-e294.	2.7	24

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91	Selection of a highly invasive neuroblastoma cell population through long-term human cytomegalovirus infection. <i>Oncogenesis</i> , 2012, 1, e10-e10.	2.1	6
92	msCompare: A Framework for Quantitative Analysis of Label-free LC-MS Data for Comparative Candidate Biomarker Studies. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.015974.	2.5	39
93	IDEOM: an Excel interface for analysis of LC-MS-based metabolomics data. <i>Bioinformatics</i> , 2012, 28, 1048-1049.	1.8	307
94	Computational tools for the synthetic design of biochemical pathways. <i>Nature Reviews Microbiology</i> , 2012, 10, 191-202.	13.6	206
95	Stable Isotope-Assisted Metabolomics for Network-Wide Metabolic Pathway Elucidation. <i>Analytical Chemistry</i> , 2012, 84, 8442-8447.	3.2	132
96	Dynamic Modelling under Uncertainty: The Case of <i>Trypanosoma brucei</i> Energy Metabolism. <i>PLoS Computational Biology</i> , 2012, 8, e1002352.	1.5	28
97	Separating the wheat from the chaff: a prioritisation pipeline for the analysis of metabolomics datasets. <i>Metabolomics</i> , 2012, 8, 29-36.	1.4	50
98	Effect of iTRAQ Labeling on the Relative Abundance of Peptide Fragment Ions Produced by MALDI-MS/MS. <i>Journal of Proteome Research</i> , 2012, 11, 4044-4051.	1.8	1
99	A turning point for natural product discovery – ESF-EMBO research conference: synthetic biology of antibiotic production. <i>Molecular Microbiology</i> , 2012, 83, 884-893.	1.2	4
100	Metabolomics methods for the synthetic biology of secondary metabolism. <i>FEBS Letters</i> , 2012, 586, 2177-2183.	1.3	63
101	Metabolomic Systems Biology of Protozoan Parasites. , 2012, , 73-84.		8
102	antiSMASH. , 2012, , 1-6.		1
103	MultiMetEval: Comparative and Multi-Objective Analysis of Genome-Scale Metabolic Models. <i>PLoS ONE</i> , 2012, 7, e51511.	1.1	31
104	antiSMASH: rapid identification, annotation and analysis of secondary metabolite biosynthesis gene clusters in bacterial and fungal genome sequences. <i>Nucleic Acids Research</i> , 2011, 39, W339-W346.	6.5	1,622
105	PeakML/mzMatch: A File Format, Java Library, R Library, and Tool-Chain for Mass Spectrometry Data Analysis. <i>Analytical Chemistry</i> , 2011, 83, 2786-2793.	3.2	305
106	Synthetic Biology in <i>Streptomyces</i> Bacteria. <i>Methods in Enzymology</i> , 2011, 497, 485-502.	0.4	50
107	Exploring the metabolic state of microorganisms using metabolomics. <i>Bioanalysis</i> , 2011, 3, 2443-2458.	0.6	19
108	Toward Global Metabolomics Analysis with Hydrophilic Interaction Liquid Chromatography-Mass Spectrometry: Improved Metabolite Identification by Retention Time Prediction. <i>Analytical Chemistry</i> , 2011, 83, 8703-8710.	3.2	326

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109	Physiological Adaptation of the Bacterium <i>Lactococcus lactis</i> in Response to the Production of Human CFTR. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M000052-MCP200.	2.5	12
110	Exploiting plug-and-play synthetic biology for drug discovery and production in microorganisms. <i>Nature Reviews Microbiology</i> , 2011, 9, 131-137.	13.6	152
111	Genome-wide gene expression changes in an industrial clavulanic acid overproduction strain of <i>Streptomyces clavuligerus</i> . <i>Microbial Biotechnology</i> , 2011, 4, 300-305.	2.0	49
112	Deletion of the signalling molecule synthase ScbA has pleiotropic effects on secondary metabolite biosynthesis, morphological differentiation and primary metabolism in <i>Streptomyces coelicolor</i> A3(2). <i>Microbial Biotechnology</i> , 2011, 4, 239-251.	2.0	29
113	Prioritizing orphan proteins for further study using phylogenomics and gene expression profiles in <i>Streptomyces coelicolor</i> . <i>BMC Research Notes</i> , 2011, 4, 325.	0.6	2
114	Comparative genome-scale metabolic modeling of actinomycetes: The topology of essential core metabolism. <i>FEBS Letters</i> , 2011, 585, 2389-2394.	1.3	29
115	Metabolomic analysis of a synthetic metabolic switch in <i>Streptomyces coelicolor</i> A3(2). <i>Proteomics</i> , 2011, 11, 4622-4631.	1.3	20
116	Adaptation of cancer cells from different entities to the MDM2 inhibitor nutlin-3 results in the emergence of p53-mutated multi-drug-resistant cancer cells. <i>Cell Death and Disease</i> , 2011, 2, e243-e243.	2.7	157
117	The future of industrial antibiotic production: From random mutagenesis to synthetic biology. <i>Bioengineered Bugs</i> , 2011, 2, 230-233.	2.0	49
118	Physiological Adaptation of the Bacterium <i>Lactococcus lactis</i> in Response to the Production of Human CFTR. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M000052-MCP200-M000052-MCP200.	2.5	13
119	Metabolomic systems biology of trypanosomes. <i>Parasitology</i> , 2010, 137, 1285-1290.	0.7	19
120	The Sequence of a 1.8-Mb Bacterial Linear Plasmid Reveals a Rich Evolutionary Reservoir of Secondary Metabolic Pathways. <i>Genome Biology and Evolution</i> , 2010, 2, 212-224.	1.1	193
121	Towards an unbiased metabolic profiling of protozoan parasites: optimisation of a <i>Leishmania</i> sampling protocol for HILIC-orbitrap analysis. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 398, 2059-2069.	1.9	48
122	DiffCoEx: a simple and sensitive method to find differentially coexpressed gene modules. <i>BMC Bioinformatics</i> , 2010, 11, 497.	1.2	190
123	The dynamic architecture of the metabolic switch in <i>Streptomyces coelicolor</i> . <i>BMC Genomics</i> , 2010, 11, 10.	1.2	171
124	Metabolic modeling and analysis of the metabolic switch in <i>Streptomyces coelicolor</i> . <i>BMC Genomics</i> , 2010, 11, 202.	1.2	84
125	A circuit model of the temporal pattern generator of <i>Caenorhabditis</i> egg-laying behavior. <i>BMC Systems Biology</i> , 2010, 4, 81.	3.0	14
126	Anti-cancer effects of artesunate in a panel of chemoresistant neuroblastoma cell lines. <i>Biochemical Pharmacology</i> , 2010, 79, 130-136.	2.0	100

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127	Genome-based phylogenetic analysis of <i>Streptomyces</i> and its relatives. <i>Molecular Phylogenetics and Evolution</i> , 2010, 54, 763-772.	1.2	40
128	What is systems biology?. <i>Frontiers in Physiology</i> , 2010, 1, 9.	1.3	84
129	Metabolomic Characterization of the Salt Stress Response in <i>Streptomyces coelicolor</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 2574-2581.	1.4	84
130	Global Genetic Robustness of the Alternative Splicing Machinery in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2010, 186, 405-410.	1.2	55
131	The potential of metabolomics for <i>Leishmania</i> research in the post-genomics era. <i>Parasitology</i> , 2010, 137, 1291-1302.	0.7	38
132	Metabolomics to Unveil and Understand Phenotypic Diversity between Pathogen Populations. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e904.	1.3	91
133	Coronatine-Insensitive 1 (COI1) Mediates Transcriptional Responses of <i>Arabidopsis thaliana</i> to External Potassium Supply. <i>Molecular Plant</i> , 2010, 3, 390-405.	3.9	62
134	Apex Peptide Elution Chain Selection: A New Strategy for Selecting Precursors in 2D-LC ^{MS} MALDI-TOF/TOF Experiments on Complex Biological Samples. <i>Journal of Proteome Research</i> , 2010, 9, 5922-5928.	1.8	3
135	The silicon trypanosome. <i>Parasitology</i> , 2010, 137, 1333-1341.	0.7	25
136	Biomodel Engineering – From Structure to Behavior. <i>Lecture Notes in Computer Science</i> , 2010, , 1-12.	1.0	7
137	Computational Modelling of Kinase Signalling Cascades. <i>Methods in Molecular Biology</i> , 2010, 661, 369-384.	0.4	3
138	Simple data-reduction method for high-resolution LC-MS data in metabolomics. <i>Bioanalysis</i> , 2009, 1, 1551-1557.	0.6	52
139	Probabilistic assignment of formulas to mass peaks in metabolomics experiments. <i>Bioinformatics</i> , 2009, 25, 512-518.	1.8	82
140	Expression Quantitative Trait Loci Are Highly Sensitive to Cellular Differentiation State. <i>PLoS Genetics</i> , 2009, 5, e1000692.	1.5	85
141	The Yeast Vacuolar Membrane Proteome. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 380-392.	2.5	77
142	designGG: an R-package and web tool for the optimal design of genetical genomics experiments. <i>BMC Bioinformatics</i> , 2009, 10, 188.	1.2	10
143	Neurodegenerative diseases: Lessons from genome-wide screens in small model organisms. <i>EMBO Molecular Medicine</i> , 2009, 1, 360-370.	3.3	72
144	System-wide molecular evidence for phenotypic buffering in <i>Arabidopsis</i> . <i>Nature Genetics</i> , 2009, 41, 166-167.	9.4	249

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145	Robust signaling networks of the adipose secretome. Trends in Endocrinology and Metabolism, 2009, 20, 1-7.	3.1	23
146	Chemoresistance acquisition induces a global shift of expression of angiogenesis-associated genes and increased pro-angiogenic activity in neuroblastoma cells. Molecular Cancer, 2009, 8, 80.	7.9	25
147	An Introduction to BioModel Engineering, Illustrated for Signal Transduction Pathways. Lecture Notes in Computer Science, 2009, , 13-28.	1.0	10
148	Increasing the mass accuracy of high-resolution LC-MS data using background ions – a case study on the LTQ-Orbitrap. Proteomics, 2008, 8, 4647-4656.	1.3	56
149	New surveyor tools for charting microbial metabolic maps. Nature Reviews Microbiology, 2008, 6, 156-161.	13.6	83
150	Prosecutor: parameter-free inference of gene function for prokaryotes using DNA microarray data, genomic context and multiple gene annotation sources. BMC Genomics, 2008, 9, 495.	1.2	5
151	Generalizing genetical genomics: getting added value from environmental perturbation. Trends in Genetics, 2008, 24, 518-524.	2.9	41
152	A comparison of meta-analysis methods for detecting differentially expressed genes in microarray experiments. Bioinformatics, 2008, 24, 374-382.	1.8	208
153	A structured approach for the engineering of biochemical network models, illustrated for signalling pathways. Briefings in Bioinformatics, 2008, 9, 404-421.	3.2	61
154	MetaNetter: inference and visualization of high-resolution metabolomic networks. Bioinformatics, 2008, 24, 143-145.	1.8	56
155	Genetical Genomics: Spotlight on QTL Hotspots. PLoS Genetics, 2008, 4, e1000232.	1.5	172
156	C. elegans Model Identifies Genetic Modifiers of α -Synuclein Inclusion Formation During Aging. PLoS Genetics, 2008, 4, e1000027.	1.5	370
157	FIVA: Functional Information Viewer and Analyzer extracting biological knowledge from transcriptome data of prokaryotes. Bioinformatics, 2007, 23, 1161-1163.	1.8	26
158	Microarray challenges in ecology. Trends in Ecology and Evolution, 2007, 22, 273-279.	4.2	65
159	Sequence Polymorphisms Cause Many False cis eQTLs. PLoS ONE, 2007, 2, e622.	1.1	113
160	Greased hedgehogs: New links between hedgehog signaling and cholesterol metabolism. BioEssays, 2007, 29, 1085-1094.	1.2	18
161	Analyses of intricate kinetics of the serum proteome during and after colon surgery by protein expression time series. Proteomics, 2007, 7, 3219-3228.	1.3	15
162	A verification protocol for the probe sequences of Affymetrix genome arrays reveals high probe accuracy for studies in mouse, human and rat. BMC Bioinformatics, 2007, 8, 132.	1.2	13

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163	Predicting protein function by machine learning on amino acid sequences – a critical evaluation. BMC Genomics, 2007, 8, 78.	1.2	28
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