Rainer Breitling

List of Publications by Year
in descending order

| 208 papers | 19,891 citations | 20817 60 h-index | 11939 134 g-index |
| 226 all docs | 226 docs citations | 226 times ranked | 25559 citing authors |

#	Article	IF	Citations
1	antiSMASH 3.0â€"a comprehensive resource for the genome mining of biosynthetic gene clusters. Nucleic Acids Research, 2015, 43, W237-W243.	14.5	1,764
2	antiSMASH: rapid identification, annotation and analysis of secondary metabolite biosynthesis gene clusters in bacterial and fungal genome sequences. Nucleic Acids Research, 2011, 39, W339-W346.	14.5	1,622
3	Rank products: a simple, yet powerful, new method to detect differentially regulated genes in replicated microarray experiments. FEBS Letters, 2004, 573, 83-92.	2.8	1,319
4	antiSMASH 4.0â€"improvements in chemistry prediction and gene cluster boundary identification. Nucleic Acids Research, 2017, 45, W36-W41.	14.5	1,196
5	antiSMASH 2.0â€"a versatile platform for genome mining of secondary metabolite producers. Nucleic Acids Research, 2013, 41, W204-W212.	14.5	753
6	Minimum Information about a Biosynthetic Gene cluster. Nature Chemical Biology, 2015, 11, 625-631.	8.0	715
7	RankProd: a bioconductor package for detecting differentially expressed genes in meta-analysis. Bioinformatics, 2006, 22, 2825-2827.	4.1	652
8	Mass appeal: metabolite identification in mass spectrometry-focused untargeted metabolomics. Metabolomics, 2013, 9, 44-66.	3.0	452
9	The Potassium-Dependent Transcriptome of Arabidopsis Reveals a Prominent Role of Jasmonic Acid in Nutrient Signaling. Plant Physiology, 2004, 136, 2556-2576.	4.8	431
10	C. elegans Model Identifies Genetic Modifiers of Î±-Synuclein Inclusion Formation During Aging. PLoS Genetics, 2008, 4, e1000027.	3.5	370
11	Detecting Sequence Homology at the Gene Cluster Level with MultiGeneBlast. Molecular Biology and Evolution, 2013, 30, 1218-1223.	8.9	368
12	Toward Global Metabolomics Analysis with Hydrophilic Interaction Liquid Chromatographyâ€"Mass Spectrometry: Improved Metabolite Identification by Retention Time Prediction. Analytical Chemistry, 2011, 83, 8703-8710.	6.5	326
13	IDEOM: an Excel interface for analysis of LCâ€"MS-based metabolomics data. Bioinformatics, 2012, 28, 1048-1049.	4.1	307
14	PeakML/mzMatch: A File Format, Java Library, R Library, and Tool-Chain for Mass Spectrometry Data Analysis. Analytical Chemistry, 2011, 83, 2786-2793.	6.5	305
15	Regulation of ubiquitin-binding proteins by monoubiquitination. Nature Cell Biology, 2006, 8, 163-169.	10.3	279
16	Mapping Determinants of Gene Expression Plasticity by Genetical Genomics in C. elegans. PLoS Genetics, 2006, 2, e222.	3.5	269
17	System-wide molecular evidence for phenotypic buffering in Arabidopsis. Nature Genetics, 2009, 41, 166-167.	21.4	249
18	GeneRank: using search engine technology for the analysis of microarray experiments. BMC Bioinformatics, 2005, 6, 233.	2.6	214

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19	A comparison of meta-analysis methods for detecting differentially expressed genes in microarray experiments. Bioinformatics, 2008, 24, 374-382.	4.1	208
20	Computational tools for the synthetic design of biochemical pathways. Nature Reviews Microbiology, 2012, 10, 191-202.	28.6	206
21	The Sequence of a 1.8-Mb Bacterial Linear Plasmid Reveals a Rich Evolutionary Reservoir of Secondary Metabolic Pathways. Genome Biology and Evolution, 2010, 2, 212-224.	2.5	193
22	DiffCoEx: a simple and sensitive method to find differentially coexpressed gene modules. BMC Bioinformatics, 2010, 11, 497.	2.6	190
23	Genetical Genomics: Spotlight on QTL Hotspots. PLoS Genetics, 2008, 4, e1000232.	3.5	172
24	The dynamic architecture of the metabolic switch in Streptomyces coelicolor. BMC Genomics, 2010, 11, 10.	2.8	171
25	Stable isotope-labeling studies in metabolomics: new insights into structure and dynamics of metabolic networks. Bioanalysis, 2014, 6, 511-524.	1.5	171
26	An automated Design-Build-Test-Learn pipeline for enhanced microbial production of fine chemicals. Communications Biology, 2018, 1, 66.	4.4	159
27	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. Cell Death and Disease, 2011, 2, e243-e243.	6.3	157
28	Exploiting plug-and-play synthetic biology for drug discovery and production in microorganisms. Nature Reviews Microbiology, 2011, 9, 131-137.	28.6	152
29	Iterative Group Analysis (iGA): a simple tool to enhance sensitivity and facilitate interpretation of microarray experiments. BMC Bioinformatics, 2004, 5, 34.	2.6	139
30	Stable Isotope-Assisted Metabolomics for Network-Wide Metabolic Pathway Elucidation. Analytical Chemistry, 2012, 84, 8442-8447.	6.5	132
31	Phytoestrogens inhibit human 17Î²-hydroxysteroid dehydrogenase type 5. Molecular and Cellular Endocrinology, 2001, 171, 151-162.	3.2	130
32	RANK-BASED METHODS AS A NON-PARAMETRIC ALTERNATIVE OF THE T-STATISTIC FOR THE ANALYSIS OF BIOLOGICAL MICROARRAY DATA. Journal of Bioinformatics and Computational Biology, 2005, 03, 1171-1189.	0.8	128
33	Probing the Metabolic Network in Bloodstream-Form Trypanosoma brucei Using Untargeted Metabolomics with Stable Isotope Labelled Glucose. PLoS Pathogens, 2015, 11, e1004689.	4.7	128
34	Precision mapping of the metabolome. Trends in Biotechnology, 2006, 24, 543-548.	9.3	125
35	Closing the Gap: Identification of Human 3-Ketosteroid Reductase, the Last Unknown Enzyme of Mammalian Cholesterol Biosynthesis. Molecular Endocrinology, 2003, 17, 1715-1725.	3.7	121
36	Ab initio prediction of metabolic networks using Fourier transform mass spectrometry data. Metabolomics, 2006, 2, 155-164.	3.0	117

#	Article	IF	Citations
37	Sequence Polymorphisms Cause Many False cis eQTLs. PLoS ONE, 2007, 2, e622.	2.5	113
38	RankProd 2.0: a refactored bioconductor package for detecting differentially expressed features in molecular profiling datasets. Bioinformatics, 2017, 33, 2774-2775.	4.1	113
39	Determination of cDNA, gene structure and chromosomal localization of the novel human 17β-hydroxysteroid dehydrogenase type 7. FEBS Letters, 1999, 460, 373-379.	2.8	104
40	Anti-cancer effects of artesunate in a panel of chemoresistant neuroblastoma cell lines. Biochemical Pharmacology, 2010, 79, 130-136.	4.4	100
41	Feature Selection and the Class Imbalance Problem in Predicting Protein Function from Sequence. Applied Bioinformatics, 2005, 4, 195-203.	1.6	94
42	Graph-based iterative Group Analysis enhances microarray interpretation. BMC Bioinformatics, 2004, 5, 100.	2.6	92
43	Metabolomics to Unveil and Understand Phenotypic Diversity between Pathogen Populations. PLoS Neglected Tropical Diseases, 2010, 4, e904.	3.0	91
44	mzMatch–ISO: an R tool for the annotation and relative quantification of isotope-labelled mass spectrometry data. Bioinformatics, 2013, 29, 281-283.	4.1	91
45	Towards synthesis of monoterpenes and derivatives using synthetic biology. Current Opinion in Chemical Biology, 2016, 34, 37-43.	6.1	89
46	Machine Learning of Designed Translational Control Allows Predictive Pathway Optimization in <i>Escherichia coli</i>. ACS Synthetic Biology, 2019, 8, 127-136.	3.8	88
47	A lock-and-key model for protein-protein interactions. Bioinformatics, 2006, 22, 2012-2019.	4.1	86
48	Expression Quantitative Trait Loci Are Highly Sensitive to Cellular Differentiation State. PLoS Genetics, 2009, 5, e1000692.	3.5	85
49	Metabolic modeling and analysis of the metabolic switch in Streptomyces coelicolor. BMC Genomics, 2010, 11, 202.	2.8	84
50	What is systems biology?. Frontiers in Physiology, 2010, 1, 9.	2.8	84
51	Metabolomic Characterization of the Salt Stress Response in <i>Streptomyces coelicolor</i>. Applied and Environmental Microbiology, 2010, 76, 2574-2581.	3.1	84
52	New surveyor tools for charting microbial metabolic maps. Nature Reviews Microbiology, 2008, 6, 156-161.	28.6	83
53	Probabilistic assignment of formulas to mass peaks in metabolomics experiments. Bioinformatics, 2009, 25, 512-518.	4.1	82
54	Pep2Path: Automated Mass Spectrometry-Guided Genome Mining of Peptidic Natural Products. PLoS Computational Biology, 2014, 10, e1003822.	3.2	81

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55	The Yeast Vacuolar Membrane Proteome. Molecular and Cellular Proteomics, 2009, 8, 380-392.	3.8	77
56	Selenzyme: enzyme selection tool for pathway design. Bioinformatics, 2018, 34, 2153-2154.	4.1	75
57	Neurodegenerative diseases: Lessons from genome‐wide screens in small model organisms. EMBO Molecular Medicine, 2009, 1, 360-370.	6.9	72
58	Steps towards the synthetic biology of polyketide biosynthesis. FEMS Microbiology Letters, 2014, 351, 116-125.	1.8	69
59	The Latent Process Decomposition of cDNA Microarray Data Sets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 143-156.	3.0	66
60	Microarray challenges in ecology. Trends in Ecology and Evolution, 2007, 22, 273-279.	8.7	65
61	Metabolomics methods for the synthetic biology of secondary metabolism. FEBS Letters, 2012, 586, 2177-2183.	2.8	63
62	MetAssign: probabilistic annotation of metabolites from LC‐MS data using a Bayesian clustering approach. Bioinformatics, 2014, 30, 2764-2771.	4.1	63
63	Coronatine-Insensitive 1 (COI1) Mediates Transcriptional Responses of Arabidopsis thaliana to External Potassium Supply. Molecular Plant, 2010, 3, 390-405.	8.3	62
64	A structured approach for the engineering of biochemical network models, illustrated for signalling pathways. Briefings in Bioinformatics, 2008, 9, 404-421.	6.5	61
65	Metabolomics for Secondary Metabolite Research. Metabolites, 2013, 3, 1076-1083.	2.9	59
66	Synthetic biology advances for pharmaceutical production. Current Opinion in Biotechnology, 2015, 35, 46-51.	6.6	59
67	Bioinformatics for the synthetic biology of natural products: integrating across the Design‐Build‐Test cycle. Natural Product Reports, 2016, 33, 925-932.	10.3	58
68	Origin of the paired domain. Development Genes and Evolution, 2000, 210, 644-650.	0.9	57
69	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.	2.2	56
70	MetaNetter: inference and visualization of high-resolution metabolomic networks. Bioinformatics, 2008, 24, 143-145.	4.1	56
71	Global Genetic Robustness of the Alternative Splicing Machinery in *Caenorhabditis elegans*. Genetics, 2010, 186, 405-410.	2.9	55
72	Evolution of 17β-HSD type 4, a multifunctional protein of β-oxidation. Molecular and Cellular Endocrinology, 2001, 171, 205-210.	3.2	54

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73	Butyrolactone signalling circuits for synthetic biology. Current Opinion in Chemical Biology, 2015, 28, 91-98.	6.1	54
74	17β-hydroxysteroid dehydrogenase type 7 â€" an ancient 3-ketosteroid reductase of cholesterogenesis. Molecular and Cellular Endocrinology, 2001, 171, 199-204.	3.2	52
75	Simple data-reduction method for high-resolution LCâ€"MS data in metabolomics. Bioanalysis, 2009, 1, 1551-1557.	1.5	52
76	Expression of Muscarinic Receptor Types in the Primate Ovary and Evidence for Nonneuronal Acetylcholine Synthesis. Journal of Clinical Endocrinology and Metabolism, 2001, 86, 349-354.	3.6	52
77	Synthetic Biology in Streptomyces Bacteria. Methods in Enzymology, 2011, 497, 485-502.	1.0	50
78	Separating the wheat from the chaff: a prioritisation pipeline for the analysis of metabolomics datasets. Metabolomics, 2012, 8, 29-36.	3.0	50
79	Genomeâ€wide gene expression changes in an industrial clavulanic acid overproduction strain of <i>Streptomyces clavuligerus</i>. Microbial Biotechnology, 2011, 4, 300-305.	4.2	49
80	The future of industrial antibiotic production: From random mutagenesis to synthetic biology. Bioengineered Bugs, 2011, 2, 230-233.	1.7	49
81	A transatlantic perspective on 20 emerging issues in biological engineering. ELife, 2017, 6, .	6.0	49
82	Towards an unbiased metabolic profiling of protozoan parasites: optimisation of a Leishmania sampling protocol for HILIC-orbitrap analysis. Analytical and Bioanalytical Chemistry, 2010, 398, 2059-2069.	3.7	48
83	Metabolic adaptations of <i><scp>L</scp>eishmania donovani</i> in relation to differentiation, drug resistance, and drug pressure. Molecular Microbiology, 2013, 90, 428-442.	2.5	48
84	Rapid prototyping of microbial production strains for the biomanufacture of potential materials monomers. Metabolic Engineering, 2020, 60, 168-182.	7.0	48
85	Engineering Escherichia coli towards de novo production of gatekeeper (2S)-flavanones: naringenin, pinocembrin, eriodictyol and homoeriodictyol. Synthetic Biology, 2020, 5, ysaa012.	2.2	45
86	Host Systems for the Production of Recombinant Spider Silk. Trends in Biotechnology, 2021, 39, 560-573.	9.3	45
87	Generalizing genetical genomics: getting added value from environmental perturbation. Trends in Genetics, 2008, 24, 518-524.	6.7	41
88	Biological microarray interpretation: The rules of engagement. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2006, 1759, 319-327.	2.4	40
89	Genome-based phylogenetic analysis of Streptomyces and its relatives. Molecular Phylogenetics and Evolution, 2010, 54, 763-772.	2.7	40
90	Handling Uncertainty in Dynamic Models: The Pentose Phosphate Pathway in Trypanosoma brucei. PLoS Computational Biology, 2013, 9, e1003371.	3.2	40

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91	msCompare: A Framework for Quantitative Analysis of Label-free LC-MS Data for Comparative Candidate Biomarker Studies. Molecular and Cellular Proteomics, 2012, 11, M111.015974.	3.8	39
92	LC-MS METABOLOMICS FROM STUDY DESIGN TO DATA-ANALYSIS â€" USING A VERSATILE PATHOGEN AS A TEST CASE. Computational and Structural Biotechnology Journal, 2013, 4, e201301002.	4.1	39
93	The potential of metabolomics for <i>Leishmania</i> research in the post-genomics era. Parasitology, 2010, 137, 1291-1302.	1.5	38
94	SelProm: A Queryable and Predictive Expression Vector Selection Tool for <i>Escherichia coli</i>. ACS Synthetic Biology, 2019, 8, 1478-1483.	3.8	37
95	Bacterial Microcompartments: Biomaterials for Synthetic Biology-Based Compartmentalization Strategies. ACS Biomaterials Science and Engineering, 2015, 1, 345-351.	5.2	36
96	LCâ€"MS-based absolute metabolite quantification: application to metabolic flux measurement in trypanosomes. Metabolomics, 2015, 11, 1721-1732.	3.0	36
97	TrypanoCyc: a community-led biochemical pathways database for Trypanosoma brucei. Nucleic Acids Research, 2015, 43, D637-D644.	14.5	35
98	Highly multiplexed, fast and accurate nanopore sequencing for verification of synthetic DNA constructs and sequence libraries. Synthetic Biology, 2019, 4, ysz025.	2.2	35
99	Network Theory to Understand Microarray Studies of Complex Diseases. Current Molecular Medicine, 2006, 6, 695-701.	1.3	34
100	The exact probability distribution of the rank product statistics for replicated experiments. FEBS Letters, 2013, 587, 677-682.	2.8	33
101	Loss of Compartmentalization Causes Misregulation of Lysine Biosynthesis in Peroxisome-Deficient Yeast Cells. Eukaryotic Cell, 2002, 1, 978-986.	3.4	32
102	Biologically valid linear factor models of gene expression. Bioinformatics, 2004, 20, 3021-3033.	4.1	32
103	Design-based re-engineering of biosynthetic gene clusters: plug-and-play in practice. Current Opinion in Biotechnology, 2013, 24, 1144-1150.	6.6	32
104	Phosphoenolpyruvate Carboxylase Identified as a Key Enzyme in Erythrocytic Plasmodium falciparum Carbon Metabolism. PLoS Pathogens, 2014, 10, e1003876.	4.7	32
105	Structure-based Phylogenetic Analysis of Short-chain Alcohol Dehydrogenases and Reclassification of the 17beta-Hydroxysteroid Dehydrogenase Family. Molecular Biology and Evolution, 2001, 18, 2154-2161.	8.9	31
106	Inhibition of 17beta-hydroxysteroid dehydrogenases by phytoestrogens: Comparison with other steroid metabolizing enzymes. Journal of Steroid Biochemistry and Molecular Biology, 2005, 93, 285-292.	2.5	31
107	biochem4j: Integrated and extensible biochemical knowledge through graph databases. PLoS ONE, 2017, 12, e0179130.	2.5	31
108	MultiMetEval: Comparative and Multi-Objective Analysis of Genome-Scale Metabolic Models. PLoS ONE, 2012, 7, e51511.	2.5	31

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109	Modeling Challenges in the Synthetic Biology of Secondary Metabolism. ACS Synthetic Biology, 2013, 2, 373-378.	3.8	30
110	Exploring novel bacterial terpene synthases. PLoS ONE, 2020, 15, e0232220.	2.5	30
111	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). Microbial Biotechnology, 2011, 4, 239-251.	4.2	29
112	Comparative genome-scale metabolic modeling of actinomycetes: The topology of essential core metabolism. FEBS Letters, 2011, 585, 2389-2394.	2.8	29
113	Mobilising ion mobility mass spectrometry for metabolomics. Analyst, The, 2018, 143, 4783-4788.	3.5	29
114	Dynamics of the human skin mediator lipidome in response to dietary Ï‰â€3 fatty acid supplementation. FASEB Journal, 2019, 33, 13014-13027.	0.5	29
115	Predicting protein function by machine learning on amino acid sequences â€" a critical evaluation. BMC Genomics, 2007, 8, 78.	2.8	28
116	Dynamic Modelling under Uncertainty: The Case of Trypanosoma brucei Energy Metabolism. PLoS Computational Biology, 2012, 8, e1002352.	3.2	28
117	FIVA: Functional Information Viewer and Analyzer extracting biological knowledge from transcriptome data of prokaryotes. Bioinformatics, 2007, 23, 1161-1163.	4.1	26
118	FRANKSUM: NEW FEATURE SELECTION METHOD FOR PROTEIN FUNCTION PREDICTION. International Journal of Neural Systems, 2005, 15, 259-275.	5.2	25
119	Current challenges in quantitative modeling of epidermal growth factor signaling. FEBS Letters, 2005, 579, 6289-6294.	2.8	25
120	Chemoresistance acquisition induces a global shift of expression of aniogenesis-associated genes and increased pro-angogenic activity in neuroblastoma cells. Molecular Cancer, 2009, 8, 80.	19.2	25
121	The silicon trypanosome. Parasitology, 2010, 137, 1333-1341.	1.5	25
122	Orthogonal Regulatory Circuits for <i>Escherichia coli</i> Based on the Î³-Butyrolactone System of <i>Streptomyces coelicolor</i>. ACS Synthetic Biology, 2018, 7, 1043-1055.	3.8	25
123	Rational cell culture optimization enhances experimental reproducibility in cancer cells. Scientific Reports, 2018, 8, 3029.	3.3	25
124	Metabolomics tools for the synthetic biology of natural products. Current Opinion in Biotechnology, 2018, 54, 114-120.	6.6	25
125	reGenotyper: Detecting mislabeled samples in genetic data. PLoS ONE, 2017, 12, e0171324.	2.5	25
126	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.	6.3	24

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127	The evolving art of creating genetic diversity: From directed evolution to synthetic biology. Biotechnology Advances, 2021, 50, 107762.	11.7	24
128	Robust signaling networks of the adipose secretome. Trends in Endocrinology and Metabolism, 2009, 20, 1-7.	7.1	23
129	A fast algorithm for determining bounds and accurate approximate p-values of the rank product statistic for replicate experiments. BMC Bioinformatics, 2014, 15, 367.	2.6	23
130	Synthetic Biology of Natural Products. Cold Spring Harbor Perspectives in Biology, 2016, 8, a023994.	5.5	22
131	The effect of terminal globular domains on the response of recombinant mini-spidroins to fiber spinning triggers. Scientific Reports, 2020, 10, 10671.	3.3	22
132	Synthetic biology for fibers, adhesives, and active camouflage materials in protection and aerospace. MRS Communications, 2019, 9, 486-504.	1.8	21
133	Metabolomic analysis of a synthetic metabolic switch in *Streptomyces coelicolor* A3(2). Proteomics, 2011, 11, 4622-4631.	2.2	20
134	Development and validation of an updated computational model of Streptomyces coelicolor primary and secondary metabolism. BMC Genomics, 2018, 19, 519.	2.8	20
135	Computational identification of co-evolving multi-gene modules in microbial biosynthetic gene clusters. Communications Biology, 2019, 2, 83.	4.4	20
136	A second gene for peroxisomal HMG-CoA reductase? A genomic reassessment. Journal of Lipid Research, 2002, 43, 2031-2036.	4.2	19
137	Metabolomic systems biology of trypanosomes. Parasitology, 2010, 137, 1285-1290.	1.5	19
138	Exploring the metabolic state of microorganisms using metabolomics. Bioanalysis, 2011, 3, 2443-2458.	1.5	19
139	Respectful Modeling: Addressing Uncertainty in Dynamic System Models for Molecular Biology. Trends in Biotechnology, 2017, 35, 518-529.	9.3	19
140	Translation Stress Positively Regulates MscL-Dependent Excretion of Cytoplasmic Proteins. MBio, 2018, 9, .	4.1	19
141	Bioengineering horizon scan 2020. ELife, 2020, 9, .	6.0	19
142	A fast algorithm for determining bounds and accurate approximate p -values of the rank product statistic for replicate experiments. BMC Bioinformatics, 2014, 15, 367.	2.6	19
143	Greased hedgehogs: New links between hedgehog signaling and cholesterol metabolism. BioEssays, 2007, 29, 1085-1094.	2.5	18
144	Judging synthetic biology risks. Science, 2015, 347, 107-107.	12.6	18

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145	Embryonic expression of cholesterogenic genes is restricted to distinct domains and colocalizes with apoptotic regions in mice. Molecular Brain Research, 2003, 115, 87-92.	2.3	17
146	Integrated Probabilistic Annotation: A Bayesian-Based Annotation Method for Metabolomic Profiles Integrating Biochemical Connections, Isotope Patterns, and Adduct Relationships. Analytical Chemistry, 2019, 91, 12799-12807.	6.5	17
147	Vector analysis as a fast and easy method to compare gene expression responses between different experimental backgrounds. BMC Bioinformatics, 2005, 6, 181.	2.6	16
148	Defining informative priors for ensemble modeling in systems biology. Nature Protocols, 2018, 13, 2643-2663.	12.0	16
149	Analyses of intricate kinetics of the serum proteome during and after colon surgery by protein expression time series. Proteomics, 2007, 7, 3219-3228.	2.2	15
150	Explicit consideration of topological and parameter uncertainty gives new insights into a wellâ€established model of glycolysis. FEBS Journal, 2013, 280, 4640-4651.	4.7	15
151	A circuit model of the temporal pattern generator of Caenorhabditis egg-laying behavior. BMC Systems Biology, 2010, 4, 81.	3.0	14
152	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.	2.6	13
153	Physiological Adaptation of the Bacterium Lactococcus lactis in Response to the Production of Human CFTR. Molecular and Cellular Proteomics, 2011, 10, M000052-MCP200-M000052-MCP200.	3.8	13
154	Pathogenesis of peroxisomal deficiency disorders (Zellweger syndrome) may be mediated by misregulation of the GABAergic system viathe diazepam binding inhibitor. BMC Pediatrics, 2004, 4, 5.	1.7	12
155	Physiological Adaptation of the Bacterium Lactococcus lactis in Response to the Production of Human CFTR. Molecular and Cellular Proteomics, 2011, 10, M000052-MCP200.	3.8	12
156	Blood, sweat, and tears: extraterrestrial regolith biocomposites with in vivo binders. Materials Today Bio, 2021, 12, 100136.	5.5	12
157	Phantom spiders 2: More notes on dubious spider species from Europe. Arachnologische Mitteilungen, 2016, 52, 50-77.	0.3	12
158	CodonGenie: optimised ambiguous codon design tools. PeerJ Computer Science, 0, 3, e120.	4.5	12
159	Isopentenyl-Diphosphate Isomerases in Human and Mouse: Evolutionary Analysis of a Mammalian Gene Duplication. Journal of Molecular Evolution, 2003, 57, 282-291.	1.8	11
160	designGG: an R-package and web tool for the optimal design of genetical genomics experiments. BMC Bioinformatics, 2009, 10, 188.	2.6	10
161	Incorporating peak grouping information for alignment of multiple liquid chromatography-mass spectrometry datasets. Bioinformatics, 2015, 31, 1999-2006.	4.1	10
162	An Introduction to BioModel Engineering, Illustrated for Signal Transduction Pathways. Lecture Notes in Computer Science, 2009, , 13-28.	1.3	10

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163	Biological Master Games: Using Biologists' Reasoning to Guide Algorithm Development for Integrated Functional Genomics. OMICS A Journal of Integrative Biology, 2005, 9, 225-232.	2.0	9
164	Towards engineering and production of artificial spider silk using tools of synthetic biology. Engineering Biology, 2020, 4, 1-6.	1.8	9
165	Metabolomic Systems Biology of Protozoan Parasites. , 2012, , 73-84.		8
166	Analysis of Tiling Microarray Data by Learning Vector Quantization and Relevance Learning. , 2007, , 880-889.		8
167	A BARCODE-BASED PHYLOGENETIC SCAFFOLD FOR XYSTICUS AND ITS RELATIVES (ARANEAE: THOMISIDAE:) Tj ETQq1 1 0.784314 rgBT	0.5	8
168	SYNBIOCHEMâ€"a SynBio foundry for the biosynthesis and sustainable production of fine and speciality chemicals. Biochemical Society Transactions, 2016, 44, 675-677.	3.4	7
169	Biomodel Engineering â€" From Structure to Behavior. Lecture Notes in Computer Science, 2010, , 1-12.	1.3	7
170	Selection of a highly invasive neuroblastoma cell population through long-term human cytomegalovirus infection. Oncogenesis, 2012, 1, e10-e10.	4.9	6
171	SYNBIOCHEM Synthetic Biology Research Centre, Manchester â€" A UK foundry for fine and speciality chemicals production. Synthetic and Systems Biotechnology, 2016, 1, 271-275.	3.7	6
172	BARCODE TAXONOMY AT THE GENUS LEVEL. Ecologica Montenegrina, 0, 21, 17-37.	0.5	6
173	Unravelling the Î³-butyrolactone network in Streptomyces coelicolor by computational ensemble modelling. PLoS Computational Biology, 2020, 16, e1008039.	3.2	6
174	Multi-Omics Analysis of the Effect of cAMP on Actinorhodin Production in Streptomyces coelicolor. Frontiers in Bioengineering and Biotechnology, 2020, 8, 595552.	4.1	6
175	Investigation of the effects of actinorhodin biosynthetic gene cluster expression and a rpoB point mutation on the metabolome of Streptomyces coelicolor M1146. Journal of Bioscience and Bioengineering, 2021, 131, 525-536.	2.2	6
176	Phantom spiders: notes on dubious spider species from Europe. Arachnologische Mitteilungen, 2015, 50, 65-80.	0.3	6
177	Public DNA barcoding data resolve the status of the genus Arboricaria (Araneae: Gnaphosidae). Arachnologische Mitteilungen, 2017, 54, 24-27.	0.3	6
178	South European spiders from the Duffey collection in the Manchester Museum (Arachnida: Araneae). , 2020, 18, 333.		6
179	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.	2.8	5
180	The Silicon Trypanosome. Advances in Microbial Physiology, 2014, 64, 115-143.	2.4	5

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181	Efficient learning in metabolic pathway designs through optimal assembling. IFAC-PapersOnLine, 2019, 52, 7-12.	0.9	5
182	A turning point for natural product discovery â€" ESFâ€EMBO research conference: synthetic biology of antibiotic production. Molecular Microbiology, 2012, 83, 884-893.	2.5	4
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