Rainer Breitling

List of Publications by Citations

202 papers	15,611 citations
57 h-index	122 g-index
226 ext. papers	18,453 ext. citations
6.5 avg, IF	6.52 L-index

#	Paper	IF	Citations
202	antiSMASH 3.0-a comprehensive resource for the genome mining of biosynthetic gene clusters. *Nucleic Acids Research*, **2015**, 43, W237-43	20.1	1403
201	Rank products: a simple, yet powerful, new method to detect differentially regulated genes in replicated microarray experiments. *FEBS Letters*, **2004**, 573, 83-92	3.8	1155
200	antiSMASH: rapid identification, annotation and analysis of secondary metabolite biosynthesis gene clusters in bacterial and fungal genome sequences. *Nucleic Acids Research*, **2011**, 39, W339-46	20.1	1153
199	antiSMASH 4.0-improvements in chemistry prediction and gene cluster boundary identification. *Nucleic Acids Research*, **2017**, 45, W36-W41	20.1	834
198	antiSMASH 2.0--a versatile platform for genome mining of secondary metabolite producers. *Nucleic Acids Research*, **2013**, 41, W204-12	20.1	654
197	RankProd: a bioconductor package for detecting differentially expressed genes in meta-analysis. *Bioinformatics*, **2006**, 22, 2825-7	7.2	566
196	Minimum Information about a Biosynthetic Gene cluster. *Nature Chemical Biology*, **2015**, 11, 625-31	11.7	498
195	The potassium-dependent transcriptome of Arabidopsis reveals a prominent role of jasmonic acid in nutrient signaling. *Plant Physiology*, **2004**, 136, 2556-76	6.6	381
194	Mass appeal: metabolite identification in mass spectrometry-focused untargeted metabolomics. *Metabolomics*, **2013**, 9, 44-66	4.7	369
193	C. elegans model identifies genetic modifiers of alpha-synuclein inclusion formation during aging. *PLoS Genetics*, **2008**, 4, e1000027	6	295
192	Toward global metabolomics analysis with hydrophilic interaction liquid chromatography-mass spectrometry: improved metabolite identification by retention time prediction. *Analytical Chemistry*, **2011**, 83, 8703-10	7.8	266
191	Regulation of ubiquitin-binding proteins by monoubiquitination. *Nature Cell Biology*, **2006**, 8, 163-9	23.4	254
190	Detecting sequence homology at the gene cluster level with MultiGeneBlast. *Molecular Biology and Evolution*, **2013**, 30, 1218-23	8.3	235
189	IDEOM: an Excel interface for analysis of LC-MS-based metabolomics data. *Bioinformatics*, **2012**, 28, 1048-9	7.2	214
188	PeakML/mzMatch: a file format, Java library, R library, and tool-chain for mass spectrometry data analysis. *Analytical Chemistry*, **2011**, 83, 2786-93	7.8	210
187	Mapping determinants of gene expression plasticity by genetical genomics in C. elegans. *PLoS Genetics*, **2006**, 2, e222	6	210
186	System-wide molecular evidence for phenotypic buffering in Arabidopsis. *Nature Genetics*, **2009**, 41, 166-7	36.3	205

185	Computational tools for the synthetic design of biochemical pathways. *Nature Reviews Microbiology*, **2012**, 10, 191-202	22.2	181
184	A comparison of meta-analysis methods for detecting differentially expressed genes in microarray experiments. *Bioinformatics*, **2008**, 24, 374-82	7.2	171
183	GeneRank: using search engine technology for the analysis of microarray experiments. *BMC Bioinformatics*, **2005**, 6, 233	3.6	170
182	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, 212-24	3.9	150
181	Genetical genomics: spotlight on QTL hotspots. *PLoS Genetics*, **2008**, 4, e1000232	6	146
180	Exploiting plug-and-play synthetic biology for drug discovery and production in microorganisms. *Nature Reviews Microbiology*, **2011**, 9, 131-7	22.2	144
179	The dynamic architecture of the metabolic switch in Streptomyces coelicolor. *BMC Genomics*, **2010**, 11, 10	4.5	137
178	DiffCoEx: a simple and sensitive method to find differentially coexpressed gene modules. *BMC Bioinformatics*, **2010**, 11, 497	3.6	135
177	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	9.8	127
176	Stable isotope-labeling studies in metabolomics: new insights into structure and dynamics of metabolic networks. *Bioanalysis*, **2014**, 6, 511-24	2.1	123
175	Phytoestrogens inhibit human 17beta-hydroxysteroid dehydrogenase type 5. *Molecular and Cellular Endocrinology*, **2001**, 171, 151-62	4.4	116
174	Precision mapping of the metabolome. *Trends in Biotechnology*, **2006**, 24, 543-8	15.1	113
173	Iterative Group Analysis (iGA): a simple tool to enhance sensitivity and facilitate interpretation of microarray experiments. *BMC Bioinformatics*, **2004**, 5, 34	3.6	109
172	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**, 3, 1171-89	1	109
171	Sequence polymorphisms cause many false cis eQTLs. *PLoS ONE*, **2007**, 2, e622	3.7	105
170	Closing the gap: identification of human 3-ketosteroid reductase, the last unknown enzyme of mammalian cholesterol biosynthesis. *Molecular Endocrinology*, **2003**, 17, 1715-25		104
169	prediction of metabolic networks using Fourier transform mass spectrometry data. *Metabolomics*, **2006**, 2, 155-164	4.7	99
168	Stable isotope-assisted metabolomics for network-wide metabolic pathway elucidation. *Analytical Chemistry*, **2012**, 84, 8442-7	7.8	98

167	An automated Design-Build-Test-Learn pipeline for enhanced microbial production of fine chemicals. *Communications Biology*, **2018**, 1, 66	6.7	97
166	Determination of cDNA, gene structure and chromosomal localization of the novel human 17beta-hydroxysteroid dehydrogenase type 7(1). *FEBS Letters*, **1999**, 460, 373-9	3.8	91
165	Anti-cancer effects of artesunate in a panel of chemoresistant neuroblastoma cell lines. *Biochemical Pharmacology*, **2010**, 79, 130-6	6	89
164	Metabolomics to unveil and understand phenotypic diversity between pathogen populations. *PLoS Neglected Tropical Diseases*, **2010**, 4, e904	4.8	85
163	Probing the metabolic network in bloodstream-form Trypanosoma brucei using untargeted metabolomics with stable isotope labelled glucose. *PLoS Pathogens*, **2015**, 11, e1004689	7.6	79
162	Feature selection and the class imbalance problem in predicting protein function from sequence. *Applied Bioinformatics*, **2005**, 4, 195-203		79
161	New surveyor tools for charting microbial metabolic maps. *Nature Reviews Microbiology*, **2008**, 6, 156-61	22.2	78
160	Probabilistic assignment of formulas to mass peaks in metabolomics experiments. *Bioinformatics*, **2009**, 25, 512-8	7.2	75
159	Metabolic modeling and analysis of the metabolic switch in Streptomyces coelicolor. *BMC Genomics* , **2010**, 11, 202	4.5	75
158	Expression quantitative trait loci are highly sensitive to cellular differentiation state. *PLoS Genetics*, **2009**, 5, e1000692	6	74
157	A lock-and-key model for protein-protein interactions. *Bioinformatics*, **2006**, 22, 2012-9	7.2	72
156	Pep2Path: automated mass spectrometry-guided genome mining of peptidic natural products. *PLoS Computational Biology*, **2014**, 10, e1003822	5	68
155	Graph-based iterative Group Analysis enhances microarray interpretation. *BMC Bioinformatics*, **2004** , 5, 100	3.6	68
154	mzMatch-ISO: an R tool for the annotation and relative quantification of isotope-labelled mass spectrometry data. *Bioinformatics*, **2013**, 29, 281-3	7.2	67
153	Towards synthesis of monoterpenes and derivatives using synthetic biology. *Current Opinion in Chemical Biology*, **2016**, 34, 37-43	9.7	66
152	The yeast vacuolar membrane proteome. *Molecular and Cellular Proteomics*, **2009**, 8, 380-92	7.6	66
151	Neurodegenerative diseases: Lessons from genome-wide screens in small model organisms. *EMBO Molecular Medicine*, **2009**, 1, 360-70	12	65
150	Metabolomic characterization of the salt stress response in Streptomyces coelicolor. *Applied and Environmental Microbiology*, **2010**, 76, 2574-81	4.8	62

131	Synthetic biology in Streptomyces bacteria. *Methods in Enzymology*, **2011**, 497, 485-502	1.7	46
130	Simple data-reduction method for high-resolution LC-MS data in metabolomics. *Bioanalysis*, **2009**, 1, 1551-7	2.1	46
129	MetaNetter: inference and visualization of high-resolution metabolomic networks. *Bioinformatics*, **2008**, 24, 143-5	7.2	46
128	Global genetic robustness of the alternative splicing machinery in Caenorhabditis elegans. *Genetics*, **2010**, 186, 405-10	4	43
127	Metabolic adaptations of Leishmania donovani in relation to differentiation, drug resistance, and drug pressure. *Molecular Microbiology*, **2013**, 90, 428-42	4.1	42
126	Metabolomics for secondary metabolite research. *Metabolites*, **2013**, 3, 1076-83	5.6	42
125	Selenzyme: enzyme selection tool for pathway design. *Bioinformatics*, **2018**, 34, 2153-2154	7.2	41
124	Butyrolactone signalling circuits for synthetic biology. *Current Opinion in Chemical Biology*, **2015**, 28, 91-8	9.7	40
123	Separating the wheat from the chaff: a prioritisation pipeline for the analysis of metabolomics datasets. *Metabolomics*, **2012**, 8, 29-36	4.7	38
122	Genome-wide gene expression changes in an industrial clavulanic acid overproduction strain of Streptomyces clavuligerus. *Microbial Biotechnology*, **2011**, 4, 300-5	6.3	37
121	A transatlantic perspective on 20 emerging issues in biological engineering. *ELife*, **2017**, 6,	8.9	36
120	The potential of metabolomics for Leishmania research in the post-genomics era. *Parasitology*, **2010**, 137, 1291-302	2.7	35
119	Biological microarray interpretation: the rules of engagement. *Biochimica Et Biophysica Acta Gene Regulatory Mechanisms*, **2006**, 1759, 319-27		35
118	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	6.8	34
117	Handling uncertainty in dynamic models: the pentose phosphate pathway in Trypanosoma brucei. *PLoS Computational Biology*, **2013**, 9, e1003371	5	34
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114	Network theory to understand microarray studies of complex diseases. *Current Molecular Medicine*, **2006**, 6, 695-701	2.5	33

113	Design-based re-engineering of biosynthetic gene clusters: plug-and-play in practice. *Current Opinion in Biotechnology*, **2013**, 24, 1144-50	11.4	31
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111	Phosphoenolpyruvate carboxylase identified as a key enzyme in erythrocytic Plasmodium falciparum carbon metabolism. *PLoS Pathogens*, **2014**, 10, e1003876	7.6	29
110	Inhibition of 17beta-hydroxysteroid dehydrogenases by phytoestrogens: comparison with other steroid metabolizing enzymes. *Journal of Steroid Biochemistry and Molecular Biology*, **2005**, 93, 285-92	5.1	29
109	TrypanoCyc: a community-led biochemical pathways database for Trypanosoma brucei. *Nucleic Acids Research*, **2015**, 43, D637-44	20.1	28
108	MultiMetEval: comparative and multi-objective analysis of genome-scale metabolic models. *PLoS ONE*, **2012**, 7, e51511	3.7	28
107	LC-MS-based absolute metabolite quantification: application to metabolic flux measurement in trypanosomes. *Metabolomics*, **2015**, 11, 1721-1732	4.7	27
106	Comparative genome-scale metabolic modeling of actinomycetes: the topology of essential core metabolism. *FEBS Letters*, **2011**, 585, 2389-94	3.8	27
105	Structure-based phylogenetic analysis of short-chain alcohol dehydrogenases and reclassification of the 17beta-hydroxysteroid dehydrogenase family. *Molecular Biology and Evolution*, **2001**, 18, 2154-61	8.3	27
104	SelProm: A Queryable and Predictive Expression Vector Selection Tool for. *ACS Synthetic Biology*, **2019**, 8, 1478-1483	5.7	26
103	Mobilising ion mobility mass spectrometry for metabolomics. *Analyst, The*, **2018**, 143, 4783-4788	5	26
102	Bacterial Microcompartments: Biomaterials for Synthetic Biology-Based Compartmentalization Strategies. *ACS Biomaterials Science and Engineering*, **2015**, 1, 345-351	5.5	26
101	FIVA: Functional Information Viewer and Analyzer extracting biological knowledge from transcriptome data of prokaryotes. *Bioinformatics*, **2007**, 23, 1161-3	7.2	26
100	Biologically valid linear factor models of gene expression. *Bioinformatics*, **2004**, 20, 3021-33	7.2	26
99	Rapid prototyping of microbial production strains for the biomanufacture of potential materials monomers. *Metabolic Engineering*, **2020**, 60, 168-182	9.7	25
98	Dynamic modelling under uncertainty: the case of Trypanosoma brucei energy metabolism. *PLoS Computational Biology*, **2012**, 8, e1002352	5	25
97	Deletion of the signalling molecule synthase ScbA has pleiotropic effects on secondary metabolite biosynthesis, morphological differentiation and primary metabolism in Streptomyces coelicolor A3(2). *Microbial Biotechnology*, **2011**, 4, 239-51	6.3	25
96	The future of industrial antibiotic production: From random mutagenesis to synthetic biology. *Bioengineered Bugs*, **2011**, 2, 230-233		25

95	Current challenges in quantitative modeling of epidermal growth factor signaling. *FEBS Letters*, **2005**, 579, 6289-94	3.8	25
94	Loss of compartmentalization causes misregulation of lysine biosynthesis in peroxisome-deficient yeast cells. *Eukaryotic Cell*, **2002**, 1, 978-86		25
93	The silicon trypanosome. *Parasitology*, **2010**, 137, 1333-41	2.7	24
92	FrankSum: new feature selection method for protein function prediction. *International Journal of Neural Systems*, **2005**, 15, 259-75	6.2	24
91	The exact probability distribution of the rank product statistics for replicated experiments. *FEBS Letters*, **2013**, 587, 677-82	3.8	22
90	Robust signaling networks of the adipose secretome. *Trends in Endocrinology and Metabolism*, **2009**, 20, 1-7	8.8	22
89	Predicting protein function by machine learning on amino acid sequences--a critical evaluation. *BMC Genomics*, **2007**, 8, 78	4.5	21
88	Modeling challenges in the synthetic biology of secondary metabolism. *ACS Synthetic Biology*, **2013**, 2, 373-8	5.7	20
87	Metabolomic analysis of a synthetic metabolic switch in Streptomyces coelicolor A3(2). *Proteomics*, **2011**, 11, 4622-31	4.8	20
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85	Synthetic Biology of Natural Products. *Cold Spring Harbor Perspectives in Biology*, **2016**, 8,	10.2	20
84	biochem4j: Integrated and extensible biochemical knowledge through graph databases. *PLoS ONE*, **2017**, 12, e0179130	3.7	18
83	Rational cell culture optimization enhances experimental reproducibility in cancer cells. *Scientific Reports*, **2018**, 8, 3029	4.9	18
82	Exploring the metabolic state of microorganisms using metabolomics. *Bioanalysis*, **2011**, 3, 2443-58	2.1	18
81	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	9.8	18
80	Dynamics of the human skin mediator lipidome in response to dietary ꞵ fatty acid supplementation. *FASEB Journal*, **2019**, 33, 13014-13027	0.9	17
79	Metabolomics tools for the synthetic biology of natural products. *Current Opinion in Biotechnology*, **2018**, 54, 114-120	11.4	17
78	A fast algorithm for determining bounds and accurate approximate p-values of the rank product statistic for replicate experiments. *BMC Bioinformatics*, **2014**, 15, 367	3.6	17

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70	Respectful Modeling: Addressing Uncertainty in Dynamic System Models for Molecular Biology. *Trends in Biotechnology*, **2017**, 35, 518-529	15.1	14
69	Computational identification of co-evolving multi-gene modules in microbial biosynthetic gene clusters. *Communications Biology*, **2019**, 2, 83	6.7	14
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67	Highly multiplexed, fast and accurate nanopore sequencing for verification of synthetic DNA constructs and sequence libraries. *Synthetic Biology*, **2019**, 4, ysz025	3.3	14
66	A fast algorithm for determining bounds and accurate approximate p -values of the rank product statistic for replicate experiments. *BMC Bioinformatics*, **2014**, 15, 367	3.6	14
65	Translation Stress Positively Regulates MscL-Dependent Excretion of Cytoplasmic Proteins. *MBio*, **2018**, 9,	7.8	14
64	Synthetic biology for fibres, adhesives and active camouflage materials in protection and aerospace. *MRS Communications*, **2019**, 9, 486-504	2.7	13
63	Analyses of intricate kinetics of the serum proteome during and after colon surgery by protein expression time series. *Proteomics*, **2007**, 7, 3219-28	4.8	13
62	reGenotyper: Detecting mislabeled samples in genetic data. *PLoS ONE*, **2017**, 12, e0171324	3.7	13
61	Explicit consideration of topological and parameter uncertainty gives new insights into a well-established model of glycolysis. *FEBS Journal*, **2013**, 280, 4640-51	5.7	12
60	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	7.8	11

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58	Physiological adaptation of the bacterium Lactococcus lactis in response to the production of human CFTR. *Molecular and Cellular Proteomics*, **2011**, 10, M000052MCP200	7.6	11
57	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	3.6	11
56	Pathogenesis of peroxisomal deficiency disorders (Zellweger syndrome) may be mediated by misregulation of the GABAergic system via the diazepam binding inhibitor. *BMC Pediatrics*, **2004**, 4, 5	2.6	11
55	Incorporating peak grouping information for alignment of multiple liquid chromatography-mass spectrometry datasets. *Bioinformatics*, **2015**, 31, 1999-2006	7.2	10
54	Host Systems for the Production of Recombinant Spider Silk. *Trends in Biotechnology*, **2021**, 39, 560-573	15.1	10
53	Exploring novel bacterial terpene synthases. *PLoS ONE*, **2020**, 15, e0232220	3.7	9
52	Isopentenyl-diphosphate isomerases in human and mouse: evolutionary analysis of a mammalian gene duplication. *Journal of Molecular Evolution*, **2003**, 57, 282-91	3.1	9
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49	CodonGenie: optimised ambiguous codon design tools. *PeerJ Computer Science*, 3, e120	2.7	9
48	Defining informative priors for ensemble modeling in systems biology. *Nature Protocols*, **2018**, 13, 2643-2663	26.6	9
47	The effect of terminal globular domains on the response of recombinant mini-spidroins to fiber spinning triggers. *Scientific Reports*, **2020**, 10, 10671	4.9	8
46	Metabolomic Systems Biology of Protozoan Parasites **2012**, 73-84		8
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43	designGG: an R-package and web tool for the optimal design of genetical genomics experiments. *BMC Bioinformatics*, **2009**, 10, 188	3.6	6
42	Analysis of Tiling Microarray Data by Learning Vector Quantization and Relevance Learning **2007**, 880-889		6

41	SYNBIOCHEM Synthetic Biology Research Centre, Manchester - A UK foundry for fine and speciality chemicals production. *Synthetic and Systems Biotechnology*, **2016**, 1, 271-275	4.2	5
40	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	4.5	5
39	Biomodel Engineering From Structure to Behavior. *Lecture Notes in Computer Science*, **2010**, 1-12	0.9	5
38	Multi-Omics Analysis of the Effect of cAMP on Actinorhodin Production in. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 595552	5.8	5
37	SYNBIOCHEM-a SynBio foundry for the biosynthesis and sustainable production of fine and speciality chemicals. *Biochemical Society Transactions*, **2016**, 44, 675-7	5.1	5
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35	The silicon trypanosome: a test case of iterative model extension in systems biology. *Advances in Microbial Physiology*, **2014**, 64, 115-43	4.4	4
34	Selection of a highly invasive neuroblastoma cell population through long-term human cytomegalovirus infection. *Oncogenesis*, **2012**, 1, e10	6.6	4
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32	Phantom spiders: notes on dubious spider species from Europe. *Arachnologische Mitteilungen*, **2015**, 50, 65-80	0.4	4
31	Apex peptide elution chain selection: a new strategy for selecting precursors in 2D-LC-MALDI-TOF/TOF experiments on complex biological samples. *Journal of Proteome Research*, **2010**, 9, 5922-8	5.6	3
30	A BARCODE-BASED PHYLOGENETIC SCAFFOLD FOR XYSTICUS AND ITS RELATIVES (ARANEAE: THOMISIDAE: CORIARACHNINI). *Ecologica Montenegrina*,20, 198-206	0.7	3
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28	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	3.3	3
27	Efficient learning in metabolic pathway designs through optimal assembling. *IFAC-PapersOnLine*, **2019**, 52, 7-12	0.7	3
26	Towards engineering and production of artificial spider silk using tools of synthetic biology. *Engineering Biology*, **2020**, 4, 1-6	1.1	3
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24	The Three Cs of Novel Antibiotic Discovery and Production through Synthetic Biology: Biosynthetic Gene Clusters, Heterologous Chassis, and Synthetic Microbial Consortia. *Advanced Biology*, **2018**, 2, 1800064	3.5	2

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22	Prioritizing orphan proteins for further study using phylogenomics and gene expression profiles in Streptomyces coelicolor. *BMC Research Notes*, **2011**, 4, 325	2.3	2
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19	Computational modelling of kinase signalling cascades. *Methods in Molecular Biology*, **2010**, 661, 369-84	1.4	2
18	Unravelling the γ-butyrolactone network in Streptomyces coelicolor by computational ensemble modelling. *PLoS Computational Biology*, **2020**, 16, e1008039	5	2
17	Blood, sweat, and tears: extraterrestrial regolith biocomposites with binders. *Materials Today Bio*, **2021**, 12, 100136	9.9	2
16	Effect of iTRAQ labeling on the relative abundance of peptide fragment ions produced by MALDI-MS/MS. *Journal of Proteome Research*, **2012**, 11, 4044-51	5.6	1
15	Bayesian Approaches for Mass Spectrometry-Based Metabolomics **2011**, 467-476		1
14	Synthetic biology approaches to actinomycete strain improvement. *FEMS Microbiology Letters*, **2021**, 368,	2.9	1
13	BARCODE TAXONOMY AT THE GENUS LEVEL. *Ecologica Montenegrina*, **2019**, 21, 17-37	0.7	1
12	Remarks on Synonyms of European Larinioides Species (Arachnida: Araneae: Araneidae). *Arachnology*, **2015**, 16, 305-310		0
11	Output ordering and prioritisation system (OOPS): ranking biosynthetic gene clusters to enhance bioactive metabolite discovery. *Journal of Industrial Microbiology and Biotechnology*, **2018**, 45, 615-619	4.2	0
10	South European spiders from the Duffey collection in the Manchester Museum (Arachnida: Araneae) **2020**, 18, 333		0
9	Multi-omics Study of Planobispora rosea, Producer of the Thiopeptide Antibiotic GE2270A. *MSystems*, **2021**, 6, e0034121	7.6	0
8	Advanced LC-MS applications for identification and quantification of the metabolome **2015**, 84-93		
7	Synthetic Biology of Natural Products **2014**, 357-369		
6	Theridion zonulatum Thorell 1890, a senior synonym of Theridion zebrinusum Zhu 1998. *Acta Arachnologica*, **2014**, 63, 79-82	0.1	

5   Stoffwechselwege vom Reißbrett: neue Ansätze der Naturstoffbiochemie. *BioSpektrum*, **2013**, 19, 30-32   0.1

4   Epigean Spiders at Abisko Scientific Research Station in Swedish Lapland (Arachnida: Araneae). *Arachnology*, **2015**, 16, 287-293   13

3   Synthetic Biology of Antibiotic Production **2014**, 1-24

2   Discriminating Microbial Species Using Protein Sequence Properties and Machine Learning **2007**, 890-897

1   List of German names for the spiders of Germany (Araneae).. *Arachnologische Mitteilungen*, **2020**, 59, 38   0.4