# Rainer Breitling

## List of Publications by Year in Descending Order

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|---|---|---|---|
| 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 | 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 |
| 201 | Synthetic biology approaches to actinomycete strain improvement. *FEMS Microbiology Letters*, **2021**, 368, | 2.9 | 1 |
| 200 | Multi-omics Study of Planobispora rosea, Producer of the Thiopeptide Antibiotic GE2270A. *MSystems*, **2021**, 6, e0034121 | 7.6 | 0 |
| 199 | Host Systems for the Production of Recombinant Spider Silk. *Trends in Biotechnology*, **2021**, 39, 560-573 | 15.1 | 10 |
| 198 | The evolving art of creating genetic diversity: From directed evolution to synthetic biology. *Biotechnology Advances*, **2021**, 50, 107762 | 17.8 | 5 |
| 197 | Blood, sweat, and tears: extraterrestrial regolith biocomposites with binders. *Materials Today Bio*, **2021**, 12, 100136 | 9.9 | 2 |
| 196 | Exploring novel bacterial terpene synthases. *PLoS ONE*, **2020**, 15, e0232220 | 3.7 | 9 |
| 195 | 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 |
| 194 | Rapid prototyping of microbial production strains for the biomanufacture of potential materials monomers. *Metabolic Engineering*, **2020**, 60, 168-182 | 9.7 | 25 |
| 193 | South European spiders from the Duffey collection in the Manchester Museum (Arachnida: Araneae) **2020**, 18, 333 | | 0 |
| 192 | Bioengineering horizon scan 2020. *ELife*, **2020**, 9, | 8.9 | 9 |
| 191 | List of German names for the spiders of Germany (Araneae).. *Arachnologische Mitteilungen*, **2020**, 59, 38 | 0.4 | |
| 190 | Unravelling the $\gamma$-butyrolactone network in Streptomyces coelicolor by computational ensemble modelling. *PLoS Computational Biology*, **2020**, 16, e1008039 | 5 | 2 |
| 189 | Multi-Omics Analysis of the Effect of cAMP on Actinorhodin Production in. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 595552 | 5.8 | 5 |
| 188 | Engineering towards production of gatekeeper (2)-flavanones: naringenin, pinocembrin, eriodictyol and homoeriodictyol. *Synthetic Biology*, **2020**, 5, ysaa012 | 3.3 | 17 |
| 187 | Towards engineering and production of artificial spider silk using tools of synthetic biology. *Engineering Biology*, **2020**, 4, 1-6 | 1.1 | 3 |
| 186 | Dynamics of the human skin mediator lipidome in response to dietary $n-3$ fatty acid supplementation. *FASEB Journal*, **2019**, 33, 13014-13027 | 0.9 | 17 |

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| 185 | 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 |
| 184 | Synthetic biology for fibres, adhesives and active camouflage materials in protection and aerospace. *MRS Communications*, **2019**, 9, 486-504 | 2.7 | 13 |
| 183 | SelProm: A Queryable and Predictive Expression Vector Selection Tool for. *ACS Synthetic Biology*, **2019**, 8, 1478-1483 | 5.7 | 26 |
| 182 | Computational identification of co-evolving multi-gene modules in microbial biosynthetic gene clusters. *Communications Biology*, **2019**, 2, 83 | 6.7 | 14 |
| 181 | Highly multiplexed, fast and accurate nanopore sequencing for verification of synthetic DNA constructs and sequence libraries. *Synthetic Biology*, **2019**, 4, ysz025 | 3.3 | 14 |
| 180 | BARCODE TAXONOMY AT THE GENUS LEVEL. *Ecologica Montenegrina*, **2019**, 21, 17-37 | 0.7 | 1 |
| 179 | Efficient learning in metabolic pathway designs through optimal assembling. *IFAC-PapersOnLine*, **2019**, 52, 7-12 | 0.7 | 3 |
| 178 | Machine Learning of Designed Translational Control Allows Predictive Pathway Optimization in Escherichia coli. *ACS Synthetic Biology*, **2019**, 8, 127-136 | 5.7 | 53 |
| 177 | Orthogonal Regulatory Circuits for Escherichia coli Based on the ꝫButyrolactone System of Streptomyces coelicolor. *ACS Synthetic Biology*, **2018**, 7, 1043-1055 | 5.7 | 16 |
| 176 | Rational cell culture optimization enhances experimental reproducibility in cancer cells. *Scientific Reports*, **2018**, 8, 3029 | 4.9 | 18 |
| 175 | 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 |
| 174 | Selenzyme: enzyme selection tool for pathway design. *Bioinformatics*, **2018**, 34, 2153-2154 | 7.2 | 41 |
| 173 | Metabolomics tools for the synthetic biology of natural products. *Current Opinion in Biotechnology*, **2018**, 54, 114-120 | 11.4 | 17 |
| 172 | Development and validation of an updated computational model of Streptomyces coelicolor primary and secondary metabolism. *BMC Genomics*, **2018**, 19, 519 | 4.5 | 14 |
| 171 | The ꝫThree Csꝫof 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 |
| 170 | Mobilising ion mobility mass spectrometry for metabolomics. *Analyst, The*, **2018**, 143, 4783-4788 | 5 | 26 |
| 169 | An automated Design-Build-Test-Learn pipeline for enhanced microbial production of fine chemicals. *Communications Biology*, **2018**, 1, 66 | 6.7 | 97 |
| 168 | Detection and Quantification of Butyrolactones from Streptomyces. *Methods in Molecular Biology*, **2018**, 1673, 117-128 | 1.4 | 3 |

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| 167 | Defining informative priors for ensemble modeling in systems biology. *Nature Protocols*, **2018**, 13, 2643-2663 | 10.0 | 9 |
| 166 | Translation Stress Positively Regulates MscL-Dependent Excretion of Cytoplasmic Proteins. *MBio*, **2018**, 9, | 7.8 | 14 |
| 165 | Respectful Modeling: Addressing Uncertainty in Dynamic System Models for Molecular Biology. *Trends in Biotechnology*, **2017**, 35, 518-529 | 15.1 | 14 |
| 164 | antiSMASH 4.0-improvements in chemistry prediction and gene cluster boundary identification. *Nucleic Acids Research*, **2017**, 45, W36-W41 | 20.1 | 834 |
| 163 | A transatlantic perspective on 20 emerging issues in biological engineering. *ELife*, **2017**, 6, | 8.9 | 36 |
| 162 | biochem4j: Integrated and extensible biochemical knowledge through graph databases. *PLoS ONE*, **2017**, 12, e0179130 | 3.7 | 18 |
| 161 | RankProd 2.0: a refactored bioconductor package for detecting differentially expressed features in molecular profiling datasets. *Bioinformatics*, **2017**, 33, 2774-2775 | 7.2 | 57 |
| 160 | reGenotyper: Detecting mislabeled samples in genetic data. *PLoS ONE*, **2017**, 12, e0171324 | 3.7 | 13 |
| 159 | Public DNA barcoding data resolve the status of the genus Arboricaria (Araneae: Gnaphosidae). *Arachnologische Mitteilungen*, **2017**, 54, 24-27 | 0.4 | 2 |
| 158 | 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 |
| 157 | Towards synthesis of monoterpenes and derivatives using synthetic biology. *Current Opinion in Chemical Biology*, **2016**, 34, 37-43 | 9.7 | 66 |
| 156 | Phantom spiders 2: More notes on dubious spider species from Europe. *Arachnologische Mitteilungen*, **2016**, 52, 50-77 | 0.4 | 3 |
| 155 | Bioinformatics for the synthetic biology of natural products: integrating across the Design-Build-Test cycle. *Natural Product Reports*, **2016**, 33, 925-32 | 15.1 | 48 |
| 154 | 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 |
| 153 | Synthetic Biology of Natural Products. *Cold Spring Harbor Perspectives in Biology*, **2016**, 8, | 10.2 | 20 |
| 152 | Butyrolactone signalling circuits for synthetic biology. *Current Opinion in Chemical Biology*, **2015**, 28, 91-8 | 9.7 | 40 |
| 151 | antiSMASH 3.0-a comprehensive resource for the genome mining of biosynthetic gene clusters. *Nucleic Acids Research*, **2015**, 43, W237-43 | 20.1 | 1403 |
| 150 | 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 |

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| 149 | Advanced LC-MS applications for identification and quantification of the metabolome **2015**, 84-93 | | |
| 148 | Synthetic biology advances for pharmaceutical production. *Current Opinion in Biotechnology*, **2015**, 35, 46-51 | 11.4 | 49 |
| 147 | Incorporating peak grouping information for alignment of multiple liquid chromatography-mass spectrometry datasets. *Bioinformatics*, **2015**, 31, 1999-2006 | 7.2 | 10 |
| 146 | Remarks on Synonyms of EuropeanLarinioidesSpecies (Arachnida: Araneae: Araneidae). *Arachnology*, **2015**, 16, 305-310 | | 0 |
| 145 | LC-MS-based absolute metabolite quantification: application to metabolic flux measurement in trypanosomes. *Metabolomics*, **2015**, 11, 1721-1732 | 4.7 | 27 |
| 144 | Minimum Information about a Biosynthetic Gene cluster. *Nature Chemical Biology*, **2015**, 11, 625-31 | 11.7 | 498 |
| 143 | TrypanoCyc: a community-led biochemical pathways database for Trypanosoma brucei. *Nucleic Acids Research*, **2015**, 43, D637-44 | 20.1 | 28 |
| 142 | Epigean Spiders at Abisko Scientific Research Station in Swedish Lapland (Arachnida: Araneae). *Arachnology*, **2015**, 16, 287-293 | | |
| 141 | Bacterial Microcompartments: Biomaterials for Synthetic Biology-Based Compartmentalization Strategies. *ACS Biomaterials Science and Engineering*, **2015**, 1, 345-351 | 5.5 | 26 |
| 140 | Phantom spiders: notes on dubious spider species from Europe. *Arachnologische Mitteilungen*, **2015**, 50, 65-80 | 0.4 | 4 |
| 139 | Stable isotope-labeling studies in metabolomics: new insights into structure and dynamics of metabolic networks. *Bioanalysis*, **2014**, 6, 511-24 | 2.1 | 123 |
| 138 | The silicon trypanosome: a test case of iterative model extension in systems biology. *Advances in Microbial Physiology*, **2014**, 64, 115-43 | 4.4 | 4 |
| 137 | Steps towards the synthetic biology of polyketide biosynthesis. *FEMS Microbiology Letters*, **2014**, 351, 116-25 | 2.9 | 59 |
| 136 | Synthetic Biology of Natural Products **2014**, 357-369 | | |
| 135 | Theridion zonulatum Thorell 1890, a senior synonym of Theridion zebrinusum Zhu 1998. *Acta Arachnologica*, **2014**, 63, 79-82 | 0.1 | |
| 134 | Synthetic Biology of Antibiotic Production **2014**, 1-24 | | |
| 133 | Pep2Path: automated mass spectrometry-guided genome mining of peptidic natural products. *PLoS Computational Biology*, **2014**, 10, e1003822 | 5 | 68 |
| 132 | Phosphoenolpyruvate carboxylase identified as a key enzyme in erythrocytic Plasmodium falciparum carbon metabolism. *PLoS Pathogens*, **2014**, 10, e1003876 | 7.6 | 29 |

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| 131 | MetAssign: probabilistic annotation of metabolites from LC-MS data using a Bayesian clustering approach. *Bioinformatics*, **2014**, 30, 2764-71 | 7.2 | 54 |
| 130 | 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 |
| 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 | 3.6 | 14 |
| 128 | Stoffwechselwege vom Reißbrett: neue Ansätze der Naturstoffbiochemie. *BioSpektrum*, **2013**, 19, 30-32 | 0.1 | |
| 127 | Mass appeal: metabolite identification in mass spectrometry-focused untargeted metabolomics. *Metabolomics*, **2013**, 9, 44-66 | 4.7 | 369 |
| 126 | Metabolic adaptations of Leishmania donovani in relation to differentiation, drug resistance, and drug pressure. *Molecular Microbiology*, **2013**, 90, 428-42 | 4.1 | 42 |
| 125 | antiSMASH 2.0--a versatile platform for genome mining of secondary metabolite producers. *Nucleic Acids Research*, **2013**, 41, W204-12 | 20.1 | 654 |
| 124 | The exact probability distribution of the rank product statistics for replicated experiments. *FEBS Letters*, **2013**, 587, 677-82 | 3.8 | 22 |
| 123 | Design-based re-engineering of biosynthetic gene clusters: plug-and-play in practice. *Current Opinion in Biotechnology*, **2013**, 24, 1144-50 | 11.4 | 31 |
| 122 | Modeling challenges in the synthetic biology of secondary metabolism. *ACS Synthetic Biology*, **2013**, 2, 373-8 | 5.7 | 20 |
| 121 | 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 |
| 120 | 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 |
| 119 | Handling uncertainty in dynamic models: the pentose phosphate pathway in Trypanosoma brucei. *PLoS Computational Biology*, **2013**, 9, e1003371 | 5 | 34 |
| 118 | Detecting sequence homology at the gene cluster level with MultiGeneBlast. *Molecular Biology and Evolution*, **2013**, 30, 1218-23 | 8.3 | 235 |
| 117 | Metabolomics for secondary metabolite research. *Metabolites*, **2013**, 3, 1076-83 | 5.6 | 42 |
| 116 | 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 |
| 115 | IDEOM: an Excel interface for analysis of LC-MS-based metabolomics data. *Bioinformatics*, **2012**, 28, 1048-9 | 7.2 | 214 |
| 114 | Computational tools for the synthetic design of biochemical pathways. *Nature Reviews Microbiology*, **2012**, 10, 191-202 | 22.2 | 181 |

| # | Reference | IF | Cit |
|---|---|---|---|
| 113 | Stable isotope-assisted metabolomics for network-wide metabolic pathway elucidation. *Analytical Chemistry*, **2012**, 84, 8442-7 | 7.8 | 98 |
| 112 | Dynamic modelling under uncertainty: the case of Trypanosoma brucei energy metabolism. *PLoS Computational Biology*, **2012**, 8, e1002352 | 5 | 25 |
| 111 | Separating the wheat from the chaff: a prioritisation pipeline for the analysis of metabolomics datasets. *Metabolomics*, **2012**, 8, 29-36 | 4.7 | 38 |
| 110 | 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 |
| 109 | A turning point for natural product discovery--ESF-EMBO research conference: synthetic biology of antibiotic production. *Molecular Microbiology*, **2012**, 83, 884-93 | 4.1 | 2 |
| 108 | Metabolomics methods for the synthetic biology of secondary metabolism. *FEBS Letters*, **2012**, 586, 2177-83 | 3.83 | 57 |
| 107 | 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 |
| 106 | Selection of a highly invasive neuroblastoma cell population through long-term human cytomegalovirus infection. *Oncogenesis*, **2012**, 1, e10 | 6.6 | 4 |
| 105 | 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 | 7.6 | 34 |
| 104 | MultiMetEval: comparative and multi-objective analysis of genome-scale metabolic models. *PLoS ONE*, **2012**, 7, e51511 | 3.7 | 28 |
| 103 | Metabolomic Systems Biology of Protozoan Parasites **2012**, 73-84 | | 8 |
| 102 | Exploring the metabolic state of microorganisms using metabolomics. *Bioanalysis*, **2011**, 3, 2443-58 | 2.1 | 18 |
| 101 | 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 |
| 100 | Physiological Adaptation of the Bacterium Lactococcus lactis in Response to the Production of Human CFTR. *Molecular and Cellular Proteomics*, **2011**, 10, M000052-MCP200 | 7.6 | 11 |
| 99 | Bayesian Approaches for Mass Spectrometry-Based Metabolomics **2011**, 467-476 | | 1 |
| 98 | Exploiting plug-and-play synthetic biology for drug discovery and production in microorganisms. *Nature Reviews Microbiology*, **2011**, 9, 131-7 | 22.2 | 144 |
| 97 | Genome-wide gene expression changes in an industrial clavulanic acid overproduction strain of Streptomyces clavuligerus. *Microbial Biotechnology*, **2011**, 4, 300-5 | 6.3 | 37 |
| 96 | 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 |

| # | Reference | IF | Cit |
|---|---|---|---|
| 95 | Prioritizing orphan proteins for further study using phylogenomics and gene expression profiles in Streptomyces coelicolor. *BMC Research Notes*, **2011**, 4, 325 | 2.3 | 2 |
| 94 | Comparative genome-scale metabolic modeling of actinomycetes: the topology of essential core metabolism. *FEBS Letters*, **2011**, 585, 2389-94 | 3.8 | 27 |
| 93 | Metabolomic analysis of a synthetic metabolic switch in Streptomyces coelicolor A3(2). *Proteomics*, **2011**, 11, 4622-31 | 4.8 | 20 |
| 92 | 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 |
| 91 | 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 |
| 90 | Synthetic biology in Streptomyces bacteria. *Methods in Enzymology*, **2011**, 497, 485-502 | 1.7 | 46 |
| 89 | 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 |
| 88 | The future of industrial antibiotic production: From random mutagenesis to synthetic biology. *Bioengineered Bugs*, **2011**, 2, 230-233 | | 25 |
| 87 | 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 |
| 86 | Genome-based phylogenetic analysis of Streptomyces and its relatives. *Molecular Phylogenetics and Evolution*, **2010**, 54, 763-72 | 4.1 | 31 |
| 85 | What is systems biology?. *Frontiers in Physiology*, **2010**, 1, 9 | 4.6 | 57 |
| 84 | Metabolomic characterization of the salt stress response in Streptomyces coelicolor. *Applied and Environmental Microbiology*, **2010**, 76, 2574-81 | 4.8 | 62 |
| 83 | Global genetic robustness of the alternative splicing machinery in Caenorhabditis elegans. *Genetics*, **2010**, 186, 405-10 | 4 | 43 |
| 82 | The potential of metabolomics for Leishmania research in the post-genomics era. *Parasitology*, **2010**, 137, 1291-302 | 2.7 | 35 |
| 81 | Metabolomics to unveil and understand phenotypic diversity between pathogen populations. *PLoS Neglected Tropical Diseases*, **2010**, 4, e904 | 4.8 | 85 |
| 80 | Coronatine-insensitive 1 (COI1) mediates transcriptional responses of Arabidopsis thaliana to external potassium supply. *Molecular Plant*, **2010**, 3, 390-405 | 14.4 | 51 |
| 79 | 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 |
| 78 | The silicon trypanosome. *Parasitology*, **2010**, 137, 1333-41 | 2.7 | 24 |

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|---|---|---|---|
| 77 | Metabolomic systems biology of trypanosomes. *Parasitology*, **2010**, 137, 1285-90 | 2.7 | 17 |
| 76 | 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 |
| 75 | Towards an unbiased metabolic profiling of protozoan parasites: optimisation of a Leishmania sampling protocol for HILIC-orbitrap analysis. *Analytical and Bioanalytical Chemistry*, **2010**, 398, 2059-69 | 4.4 | 47 |
| 74 | DiffCoEx: a simple and sensitive method to find differentially coexpressed gene modules. *BMC Bioinformatics*, **2010**, 11, 497 | 3.6 | 135 |
| 73 | The dynamic architecture of the metabolic switch in Streptomyces coelicolor. *BMC Genomics*, **2010**, 11, 10 | 4.5 | 137 |
| 72 | Metabolic modeling and analysis of the metabolic switch in Streptomyces coelicolor. *BMC Genomics*, **2010**, 11, 202 | 4.5 | 75 |
| 71 | A circuit model of the temporal pattern generator of Caenorhabditis egg-laying behavior. *BMC Systems Biology*, **2010**, 4, 81 | 3.5 | 7 |
| 70 | Anti-cancer effects of artesunate in a panel of chemoresistant neuroblastoma cell lines. *Biochemical Pharmacology*, **2010**, 79, 130-6 | 6 | 89 |
| 69 | Biomodel Engineering From Structure to Behavior. *Lecture Notes in Computer Science*, **2010**, 1-12 | 0.9 | 5 |
| 68 | Computational modelling of kinase signalling cascades. *Methods in Molecular Biology*, **2010**, 661, 369-84 | 1.4 | 2 |
| 67 | Simple data-reduction method for high-resolution LC-MS data in metabolomics. *Bioanalysis*, **2009**, 1, 1551-7 | 2.1 | 46 |
| 66 | Probabilistic assignment of formulas to mass peaks in metabolomics experiments. *Bioinformatics*, **2009**, 25, 512-8 | 7.2 | 75 |
| 65 | Expression quantitative trait loci are highly sensitive to cellular differentiation state. *PLoS Genetics*, **2009**, 5, e1000692 | 6 | 74 |
| 64 | The yeast vacuolar membrane proteome. *Molecular and Cellular Proteomics*, **2009**, 8, 380-92 | 7.6 | 66 |
| 63 | designGG: an R-package and web tool for the optimal design of genetical genomics experiments. *BMC Bioinformatics*, **2009**, 10, 188 | 3.6 | 6 |
| 62 | Neurodegenerative diseases: Lessons from genome-wide screens in small model organisms. *EMBO Molecular Medicine*, **2009**, 1, 360-70 | 12 | 65 |
| 61 | System-wide molecular evidence for phenotypic buffering in Arabidopsis. *Nature Genetics*, **2009**, 41, 166-7 | 36.3 | 205 |
| 60 | Robust signaling networks of the adipose secretome. *Trends in Endocrinology and Metabolism*, **2009**, 20, 1-7 | 8.8 | 22 |

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| 59 | 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 | 42.1 | 20 |
| 58 | An Introduction to BioModel Engineering, Illustrated for Signal Transduction Pathways. *Lecture Notes in Computer Science*, **2009**, 13-28 | 0.9 | 7 |
| 57 | New surveyor tools for charting microbial metabolic maps. *Nature Reviews Microbiology*, **2008**, 6, 156-61 | 22.2 | 78 |
| 56 | 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 |
| 55 | Generalizing genetical genomics: getting added value from environmental perturbation. *Trends in Genetics*, **2008**, 24, 518-24 | 8.5 | 33 |
| 54 | A comparison of meta-analysis methods for detecting differentially expressed genes in microarray experiments. *Bioinformatics*, **2008**, 24, 374-82 | 7.2 | 171 |
| 53 | A structured approach for the engineering of biochemical network models, illustrated for signalling pathways. *Briefings in Bioinformatics*, **2008**, 9, 404-21 | 13.4 | 53 |
| 52 | MetaNetter: inference and visualization of high-resolution metabolomic networks. *Bioinformatics*, **2008**, 24, 143-5 | 7.2 | 46 |
| 51 | Genetical genomics: spotlight on QTL hotspots. *PLoS Genetics*, **2008**, 4, e1000232 | 6 | 146 |
| 50 | C. elegans model identifies genetic modifiers of alpha-synuclein inclusion formation during aging. *PLoS Genetics*, **2008**, 4, e1000027 | 6 | 295 |
| 49 | Increasing the mass accuracy of high-resolution LC-MS data using background ions: a case study on the LTQ-Orbitrap. *Proteomics*, **2008**, 8, 4647-56 | 4.8 | 51 |
| 48 | Sequence polymorphisms cause many false cis eQTLs. *PLoS ONE*, **2007**, 2, e622 | 3.7 | 105 |
| 47 | Greased hedgehogs: new links between hedgehog signaling and cholesterol metabolism. *BioEssays*, **2007**, 29, 1085-94 | 4.1 | 15 |
| 46 | 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 |
| 45 | 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 |
| 44 | Predicting protein function by machine learning on amino acid sequences--a critical evaluation. *BMC Genomics*, **2007**, 8, 78 | 4.5 | 21 |
| 43 | FIVA: Functional Information Viewer and Analyzer extracting biological knowledge from transcriptome data of prokaryotes. *Bioinformatics*, **2007**, 23, 1161-3 | 7.2 | 26 |
| 42 | Microarray challenges in ecology. *Trends in Ecology and Evolution*, **2007**, 22, 273-9 | 10.9 | 57 |

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| 41 | Discriminating Microbial Species Using Protein Sequence Properties and Machine Learning **2007**, 890-897 | | |
| 40 | Analysis of Tiling Microarray Data by Learning Vector Quantization and Relevance Learning **2007**, 880-889 | | 6 |
| 39 | Biological microarray interpretation: the rules of engagement. *Biochimica Et Biophysica Acta Gene Regulatory Mechanisms*, **2006**, 1759, 319-27 | | 35 |
| 38 | Precision mapping of the metabolome. *Trends in Biotechnology*, **2006**, 24, 543-8 | 15.1 | 113 |
| 37 | Network theory to understand microarray studies of complex diseases. *Current Molecular Medicine*, **2006**, 6, 695-701 | 2.5 | 33 |
| 36 | Mapping determinants of gene expression plasticity by genetical genomics in C. elegans. *PLoS Genetics*, **2006**, 2, e222 | 6 | 210 |
| 35 | RankProd: a bioconductor package for detecting differentially expressed genes in meta-analysis. *Bioinformatics*, **2006**, 22, 2825-7 | 7.2 | 566 |
| 34 | A lock-and-key model for protein-protein interactions. *Bioinformatics*, **2006**, 22, 2012-9 | 7.2 | 72 |
| 33 | Interspecies comparison of gene structure and computational analysis of gene regulation of 17beta-hydroxysteroid dehydrogenase type 1. *Molecular and Cellular Endocrinology*, **2006**, 248, 168-71 | 4.4 | 2 |
| 32 | Regulation of ubiquitin-binding proteins by monoubiquitination. *Nature Cell Biology*, **2006**, 8, 163-9 | 23.4 | 254 |
| 31 | prediction of metabolic networks using Fourier transform mass spectrometry data. *Metabolomics*, **2006**, 2, 155-164 | 4.7 | 99 |
| 30 | The latent process decomposition of cDNA microarray data sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2005**, 2, 143-56 | 3 | 54 |
| 29 | 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 |
| 28 | Current challenges in quantitative modeling of epidermal growth factor signaling. *FEBS Letters*, **2005**, 579, 6289-94 | 3.8 | 25 |
| 27 | Feature selection and the class imbalance problem in predicting protein function from sequence. *Applied Bioinformatics*, **2005**, 4, 195-203 | | 79 |
| 26 | Vector analysis as a fast and easy method to compare gene expression responses between different experimental backgrounds. *BMC Bioinformatics*, **2005**, 6, 181 | 3.6 | 15 |
| 25 | GeneRank: using search engine technology for the analysis of microarray experiments. *BMC Bioinformatics*, **2005**, 6, 233 | 3.6 | 170 |
| 24 | FrankSum: new feature selection method for protein function prediction. *International Journal of Neural Systems*, **2005**, 15, 259-75 | 6.2 | 24 |

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