Timothy Ebbels

List of Publications by Citations

Source: https://exaly.com/author-pdf/4010683/timothy-ebbels-publications-by-citations.pdf

Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

134 9,422 48 96 papers citations h-index g-index

151 10,683 6.1 5.64 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
134	Metabolic profiling, metabolomic and metabonomic procedures for NMR spectroscopy of urine, plasma, serum and tissue extracts. <i>Nature Protocols</i> , 2007 , 2, 2692-703	18.8	1536
133	Human metabolic phenotype diversity and its association with diet and blood pressure. <i>Nature</i> , 2008 , 453, 396-400	50.4	847
132	Contemporary issues in toxicology the role of metabonomics in toxicology and its evaluation by the COMET project. <i>Toxicology and Applied Pharmacology</i> , 2003 , 187, 137-46	4.6	342
131	Proposed minimum reporting standards for data analysis in metabolomics. <i>Metabolomics</i> , 2007 , 3, 231-	24.17	317
130	High-resolution magic-angle-spinning NMR spectroscopy for metabolic profiling of intact tissues. <i>Nature Protocols</i> , 2010 , 5, 1019-32	18.8	309
129	Recursive segment-wise peak alignment of biological (1)h NMR spectra for improved metabolic biomarker recovery. <i>Analytical Chemistry</i> , 2009 , 81, 56-66	7.8	258
128	The Consortium for Metabonomic Toxicology (COMET): aims, activities and achievements. <i>Pharmacogenomics</i> , 2005 , 6, 691-9	2.6	255
127	Integrated pathway-level analysis of transcriptomics and metabolomics data with IMPaLA. <i>Bioinformatics</i> , 2011 , 27, 2917-8	7.2	239
126	Analytical reproducibility in (1)H NMR-based metabonomic urinalysis. <i>Chemical Research in Toxicology</i> , 2002 , 15, 1380-6	4	239
125	Optimized preprocessing of ultra-performance liquid chromatography/mass spectrometry urinary metabolic profiles for improved information recovery. <i>Analytical Chemistry</i> , 2011 , 83, 5864-72	7.8	201
124	Improved analysis of multivariate data by variable stability scaling: application to NMR-based metabolic profiling. <i>Analytica Chimica Acta</i> , 2003 , 490, 265-276	6.6	149
123	Prediction and classification of drug toxicity using probabilistic modeling of temporal metabolic data: the consortium on metabonomic toxicology screening approach. <i>Journal of Proteome Research</i> , 2007 , 6, 4407-22	5.6	146
122	Optimization and evaluation of metabolite extraction protocols for untargeted metabolic profiling of liver samples by UPLC-MS. <i>Analytical Chemistry</i> , 2010 , 82, 7779-86	7.8	144
121	Urinary metabolic signatures of human adiposity. Science Translational Medicine, 2015, 7, 285ra62	17.5	141
120	Spectral editing and pattern recognition methods applied to high-resolution magic-angle spinning 1H nuclear magnetic resonance spectroscopy of liver tissues. <i>Analytical Biochemistry</i> , 2003 , 323, 26-32	3.1	134
119	Bayesian deconvolution and quantification of metabolites in complex 1D NMR spectra using BATMAN. <i>Nature Protocols</i> , 2014 , 9, 1416-27	18.8	132
118	Geometric trajectory analysis of metabolic responses to toxicity can define treatment specific profiles. <i>Chemical Research in Toxicology</i> , 2004 , 17, 579-87	4	131

(2003-2003)

117	NMR-based metabonomic toxicity classification: hierarchical cluster analysis and k-nearest-neighbour approaches. <i>Analytica Chimica Acta</i> , 2003 , 490, 3-15	6.6	127
116	Design and analysis of metabolomics studies in epidemiologic research: a primer on -omic technologies. <i>American Journal of Epidemiology</i> , 2014 , 180, 129-39	3.8	123
115	Correction of mass calibration gaps in liquid chromatography-mass spectrometry metabolomics data. <i>Bioinformatics</i> , 2010 , 26, 2488-9	7.2	119
114	BATMANan R package for the automated quantification of metabolites from nuclear magnetic resonance spectra using a Bayesian model. <i>Bioinformatics</i> , 2012 , 28, 2088-90	7.2	118
113	Opening up the "Black Box": metabolic phenotyping and metabolome-wide association studies in epidemiology. <i>Journal of Clinical Epidemiology</i> , 2010 , 63, 970-9	5.7	113
112	COordination of Standards in MetabOlomicS (COSMOS): facilitating integrated metabolomics data access. <i>Metabolomics</i> , 2015 , 11, 1587-1597	4.7	109
111	Comparative metabonomics of differential hydrazine toxicity in the rat and mouse. <i>Toxicology and Applied Pharmacology</i> , 2005 , 204, 135-51	4.6	107
110	Metabolome-wide association study identifies multiple biomarkers that discriminate north and south Chinese populations at differing risks of cardiovascular disease: INTERMAP study. <i>Journal of Proteome Research</i> , 2010 , 9, 6647-54	5.6	106
109	Optimizing the use of quality control samples for signal drift correction in large-scale urine metabolic profiling studies. <i>Analytical Chemistry</i> , 2012 , 84, 2670-7	7.8	104
108	The evolution of partial least squares models and related chemometric approaches in metabonomics and metabolic phenotyping. <i>Journal of Chemometrics</i> , 2010 , 24, 636-649	1.6	104
107	Metabolic profiling and the metabolome-wide association study: significance level for biomarker identification. <i>Journal of Proteome Research</i> , 2010 , 9, 4620-7	5.6	102
106	Meeting-in-the-middle using metabolic profiling - a strategy for the identification of intermediate biomarkers in cohort studies. <i>Biomarkers</i> , 2011 , 16, 83-8	2.6	88
105	Data standards can boost metabolomics research, and if there is a will, there is a way. <i>Metabolomics</i> , 2016 , 12, 14	4.7	85
104	Bioinformatic methods in NMR-based metabolic profiling. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2009 , 55, 361-374	10.4	82
103	Batch statistical processing of 1H NMR-derived urinary spectral data. <i>Journal of Chemometrics</i> , 2002 , 16, 461-468	1.6	80
102	Applying 'omics technologies in chemicals risk assessment: Report of an ECETOC workshop. <i>Regulatory Toxicology and Pharmacology</i> , 2017 , 91 Suppl 1, S3-S13	3.4	74
101	Power Analysis and Sample Size Determination in Metabolic Phenotyping. <i>Analytical Chemistry</i> , 2016 , 88, 5179-88	7.8	70
100	Toxicity classification from metabonomic data using a density superposition approach: [ILOUDS] <i>Analytica Chimica Acta</i> , 2003 , 490, 109-122	6.6	69

99	NMR-based metabolic profiling identifies biomarkers of liver regeneration following partial hepatectomy in the rat. <i>Journal of Proteome Research</i> , 2010 , 9, 59-69	5.6	68
98	Consensus-phenotype integration of transcriptomic and metabolomic data implies a role for metabolism in the chemosensitivity of tumour cells. <i>PLoS Computational Biology</i> , 2011 , 7, e1001113	5	65
97	Subset optimization by reference matching (STORM): an optimized statistical approach for recovery of metabolic biomarker structural information from 1H NMR spectra of biofluids. <i>Analytical Chemistry</i> , 2012 , 84, 10694-701	7.8	64
96	Use cases, best practice and reporting standards for metabolomics in regulatory toxicology. <i>Nature Communications</i> , 2019 , 10, 3041	17.4	62
95	Serum metabolic signatures of coronary and carotid atherosclerosis and subsequent cardiovascular disease. <i>European Heart Journal</i> , 2019 , 40, 2883-2896	9.5	58
94	Statistical experimental design and partial least squares regression analysis of biofluid metabonomic NMR and clinical chemistry data for screening of adverse drug effects. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2004 , 73, 139-149	3.8	57
93	Computational tools and workflows in metabolomics: An international survey highlights the opportunity for harmonisation through Galaxy. <i>Metabolomics</i> , 2017 , 13, 12	4.7	52
92	Robust algorithms for automated chemical shift calibration of 1D 1H NMR spectra of blood serum. <i>Analytical Chemistry</i> , 2008 , 80, 7158-62	7.8	52
91	Analytic properties of statistical total correlation spectroscopy based information recovery in 1H NMR metabolic data sets. <i>Analytical Chemistry</i> , 2009 , 81, 2075-84	7.8	51
90	Genetic algorithms for simultaneous variable and sample selection in metabonomics. <i>Bioinformatics</i> , 2009 , 25, 112-8	7.2	50
89	The carcinoGENOMICS project: critical selection of model compounds for the development of omics-based in vitro carcinogenicity screening assays. <i>Mutation Research - Reviews in Mutation Research</i> , 2008 , 659, 202-10	7	50
88	Temporal metabonomic modeling of l-arginine-induced exocrine pancreatitis. <i>Journal of Proteome Research</i> , 2008 , 7, 4435-45	5.6	49
87	Metabolic response to low-level toxicant exposure in a novel renal tubule epithelial cell system. <i>Molecular BioSystems</i> , 2011 , 7, 247-57		48
86	Intra- and inter-omic fusion of metabolic profiling data in a systems biology framework. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2010 , 104, 121-131	3.8	48
85	Time-resolved metabolic footprinting for nonlinear modeling of bacterial substrate utilization. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 2453-63	4.8	46
84	Validation of metabolomics for toxic mechanism of action screening with the earthworm Lumbricus rubellus. <i>Metabolomics</i> , 2009 , 5, 72-83	4.7	46
83	Identification of a gravitationally lensed z = 2.515 star-forming galaxy. <i>Monthly Notices of the Royal Astronomical Society</i> , 1996 , 281, L75-L81	4.3	45
82	Correlation Network Analysis reveals a sequential reorganization of metabolic and transcriptional states during germination and gene-metabolite relationships in developing seedlings of Arabidonsis BMC Systems Biology 2010 4 62	3.5	41

(2008-2019)

81	PhenoMeNal: processing and analysis of metabolomics data in the cloud. GigaScience, 2019, 8,	7.6	41
80	Reliability of plasma polar metabolite concentrations in a large-scale cohort study using capillary electrophoresis-mass spectrometry. <i>PLoS ONE</i> , 2018 , 13, e0191230	3.7	40
79	nmrML: A Community Supported Open Data Standard for the Description, Storage, and Exchange of NMR Data. <i>Analytical Chemistry</i> , 2018 , 90, 649-656	7.8	37
78	Statistical total correlation spectroscopy editing of 1H NMR spectra of biofluids: application to drug metabolite profile identification and enhanced information recovery. <i>Analytical Chemistry</i> , 2009 , 81, 6458-66	7.8	37
77	Intra- and interlaboratory reproducibility of ultra performance liquid chromatography-time-of-flight mass spectrometry for urinary metabolic profiling. <i>Analytical Chemistry</i> , 2012 , 84, 2424-32	7.8	36
76	Metabolic profiling and population screening of analgesic usage in nuclear magnetic resonance spectroscopy-based large-scale epidemiologic studies. <i>Analytical Chemistry</i> , 2009 , 81, 5119-29	7.8	36
75	A statistical framework for biomarker discovery in metabolomic time course data. <i>Bioinformatics</i> , 2011 , 27, 1979-85	7.2	36
74	Data-driven approach for metabolite relationship recovery in biological 1H NMR data sets using iterative statistical total correlation spectroscopy. <i>Analytical Chemistry</i> , 2011 , 83, 2075-82	7.8	35
73	A Bayesian Model of NMR Spectra for the Deconvolution and Quantification of Metabolites in Complex Biological Mixtures. <i>Journal of the American Statistical Association</i> , 2012 , 107, 1259-1271	2.8	34
72	Evaluation of metabolic variation in normal rat strains from a statistical analysis of 1H NMR spectra of urine. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2004 , 36, 823-33	3.5	32
71	Cluster analysis statistical spectroscopy using nuclear magnetic resonance generated metabolic data sets from perturbed biological systems. <i>Analytical Chemistry</i> , 2009 , 81, 6581-9	7.8	30
70	Workflow for Integrated Processing of Multicohort Untargeted H NMR Metabolomics Data in Large-Scale Metabolic Epidemiology. <i>Journal of Proteome Research</i> , 2016 , 15, 4188-4194	5.6	28
69	diXa: a data infrastructure for chemical safety assessment. <i>Bioinformatics</i> , 2015 , 31, 1505-7	7.2	27
68	Bidirectional correlation of NMR and capillary electrophoresis fingerprints: a new approach to investigating Schistosoma mansoni infection in a mouse model. <i>Analytical Chemistry</i> , 2010 , 82, 203-10	7.8	27
67	A differential network approach to exploring differences between biological states: an application to prediabetes. <i>PLoS ONE</i> , 2011 , 6, e24702	3.7	27
66	Modelling the acid/base H NMR chemical shift limits of metabolites in human urine. <i>Metabolomics</i> , 2016 , 12, 152	4.7	24
65	Untargeted metabolome quantitative trait locus mapping associates variation in urine glycerate to mutant glycerate kinase. <i>Journal of Proteome Research</i> , 2012 , 11, 631-42	5.6	23
64	Piecewise multivariate modelling of sequential metabolic profiling data. <i>BMC Bioinformatics</i> , 2008 , 9, 105	3.6	23

63	Processing and modeling of nuclear magnetic resonance (NMR) metabolic profiles. <i>Methods in Molecular Biology</i> , 2011 , 708, 365-88	1.4	23
62	Dietary and urinary metabonomic factors possibly accounting for higher blood pressure of black compared with white Americans: results of International Collaborative Study on macro-/micronutrients and blood pressure. <i>Hypertension</i> , 2013 , 62, 1074-80	8.5	22
61	A statistically rigorous test for the identification of parent-fragment pairs in LC-MS datasets. <i>Analytical Chemistry</i> , 2010 , 82, 1766-78	7.8	21
60	Synergistic and Antagonistic Mutation Responses of Human MCL-5 Cells to Mixtures of Benzo[a]pyrene and 2-Amino-1-Methyl-6-Phenylimidazo[4,5-b]pyridine: Dose-Related Variation in the Joint Effects of Common Dietary Carcinogens. <i>Environmental Health Perspectives</i> , 2016 , 124, 88-96	8.4	21
59	Framework for the quality assurance of 'omics technologies considering GLP requirements. Regulatory Toxicology and Pharmacology, 2017 , 91 Suppl 1, S27-S35	3.4	20
58	Optimized Phenotypic Biomarker Discovery and Confounder Elimination via Covariate-Adjusted Projection to Latent Structures from Metabolic Spectroscopy Data. <i>Journal of Proteome Research</i> , 2018 , 17, 1586-1595	5.6	20
57	A comparison of human serum and plasma metabolites using untargeted H NMR spectroscopy and UPLC-MS. <i>Metabolomics</i> , 2018 , 14, 32	4.7	20
56	Statistical Correlations between NMR Spectroscopy and Direct Infusion FT-ICR Mass Spectrometry Aid Annotation of Unknowns in Metabolomics. <i>Analytical Chemistry</i> , 2016 , 88, 2583-9	7.8	20
55	1H NMR-based profiling reveals differential immune-metabolic networks during influenza virus infection in obese mice. <i>PLoS ONE</i> , 2014 , 9, e97238	3.7	20
54	Genome metabolome integrated network analysis to uncover connections between genetic variants and complex traits: an application to obesity. <i>Journal of the Royal Society Interface</i> , 2014 , 11, 20130908	4.1	18
53	Bayesian inference for multiple Gaussian graphical models with application to metabolic association networks. <i>Annals of Applied Statistics</i> , 2017 , 11,	2.1	18
52	Combining spectral ordering with peak fitting for one-dimensional NMR quantitative metabolomics. <i>Analytical Chemistry</i> , 2013 , 85, 4605-12	7.8	18
51	The future of metabolomics in ELIXIR. <i>F1000Research</i> , 2017 , 6,	3.6	18
50	The association of fish consumption and its urinary metabolites with cardiovascular risk factors: the International Study of Macro-/Micronutrients and Blood Pressure (INTERMAP). <i>American Journal of Clinical Nutrition</i> , 2020 , 111, 280-290	7	18
49	Improving Visualization and Interpretation of Metabolome-Wide Association Studies: An Application in a Population-Based Cohort Using Untargeted H NMR Metabolic Profiling. <i>Journal of Proteome Research</i> , 2017 , 16, 3623-3633	5.6	17
48	MetAssimulo: simulation of realistic NMR metabolic profiles. <i>BMC Bioinformatics</i> , 2010 , 11, 496	3.6	17
47	Metabolomics: The Stethoscope for the Twenty-First Century. <i>Medical Principles and Practice</i> , 2021 , 30, 301-310	2.1	17
46	springScape: visualisation of microarray and contextual bioinformatic data using spring embedding and an 'information landscape'. <i>Bioinformatics</i> , 2006 , 22, e99-107	7.2	16

(2020-1998)

45	Spectroscopic confirmation of redshifts predicted by gravitational lensing. <i>Monthly Notices of the Royal Astronomical Society</i> , 1998 , 295, 75	4.3	16
44	Integrated histopathological and urinary metabonomic investigation of the pathogenesis of microcystin-LR toxicosis. <i>Veterinary Pathology</i> , 2013 , 50, 159-71	2.8	13
43	Metabolic phenotyping for discovery of urinary biomarkers of diet, xenobiotics and blood pressure in the INTERMAP Study: an overview. <i>Hypertension Research</i> , 2017 , 40, 336-345	4.7	12
42	Embedding standards in metabolomics: the Metabolomics Society data standards task group. <i>Metabolomics</i> , 2015 , 11, 782-783	4.7	12
41	Identifying biochemical phenotypic differences between cryptic species. <i>Biology Letters</i> , 2014 , 10,	3.6	12
40	Effect of the histone deacetylase inhibitor trichostatin a on the metabolome of cultured primary hepatocytes. <i>Journal of Proteome Research</i> , 2010 , 9, 413-9	5.6	12
39	A combined metabonomic and transcriptomic approach to investigate metabolism during development in the chick chorioallantoic membrane. <i>Journal of Proteome Research</i> , 2010 , 9, 3126-34	5.6	12
38	Metabonomic investigations into the global biochemical sequelae of exposure to the pancreatic toxin 1-cyano-2-hydroxy-3-butene in the rat. <i>Magnetic Resonance in Chemistry</i> , 2009 , 47 Suppl 1, S26-35	2.1	12
37	Modelling short time series in metabolomics: a functional data analysis approach. <i>Advances in Experimental Medicine and Biology</i> , 2011 , 696, 307-15	3.6	11
36	Proteomic and metabolomic responses to connexin43 silencing in primary hepatocyte cultures. <i>Archives of Toxicology</i> , 2013 , 87, 883-94	5.8	10
35	The future of metabolomics in ELIXIR. <i>F1000Research</i> , 2017 , 6, 1649	3.6	10
34	Construction of confidence regions for isotopic abundance patterns in LC/MS data sets for rigorous determination of molecular formulas. <i>Analytical Chemistry</i> , 2010 , 82, 7319-28	7.8	9
33	Statistical Techniques in Metabolic Profiling 2008 , 347-373		9
32	Predictive modelling using pathway scores: robustness and significance of pathway collections. <i>BMC Bioinformatics</i> , 2019 , 20, 543	3.6	8
31	Statistical analysis in metabolic phenotyping. <i>Nature Protocols</i> , 2021 , 16, 4299-4326	18.8	8
30	Quantitative Investigation of Probabilistic Spectral Processing Methods Using Simulated NMR Data. <i>Applied Spectroscopy</i> , 2001 , 55, 1214-1224	3.1	6
29	Progress towards an OECD reporting framework for transcriptomics and metabolomics in regulatory toxicology. <i>Regulatory Toxicology and Pharmacology</i> , 2021 , 125, 105020	3.4	6
28	Targeted realignment of LC-MS profiles by neighbor-wise compound-specific graphical time warping with misalignment detection. <i>Bioinformatics</i> , 2020 , 36, 2862-2871	7.2	5

27	A combination of transcriptomics and metabolomics uncovers enhanced bile acid biosynthesis in HepG2 cells expressing CCAAT/enhancer-binding protein [[C/EBP]] hepatocyte nuclear factor 4[] (HNF4)], and constitutive androstane receptor (CAR). <i>Journal of Proteome Research</i> , 2013 , 12, 2732-41	5.6	5
26	Integrative analysis of time course metabolic data and biomarker discovery. <i>BMC Bioinformatics</i> , 2020 , 21, 11	3.6	4
25	Orders of magnitude extension of the effective dynamic range of TDC-based TOFMS data through maximum likelihood estimation. <i>Journal of the American Society for Mass Spectrometry</i> , 2014 , 25, 1824-7	3.5	4
24	Variance and covariance heterogeneity analysis for detection of metabolites associated with cadmium exposure. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014 , 13, 191-201	1.2	4
23	Pathway analysis in metabolomics: Recommendations for the use of over-representation analysis. <i>PLoS Computational Biology</i> , 2021 , 17, e1009105	5	4
22	Characterization of data analysis methods for information recovery from metabolic 1H NMR spectra using artificial complex mixtures. <i>Metabolomics</i> , 2012 , 8, 1170-1180	4.7	3
21	Prospects for a statistical theory of LC/TOFMS data. <i>Journal of the American Society for Mass Spectrometry</i> , 2012 , 23, 779-91	3.5	3
20	Non-linear Methods for the Analysis of Metabolic Profiles 2007 , 201-226		3
19	Comparison of Bi- and Tri-Linear PLS Models for Variable Selection in Metabolomic Time-Series Experiments. <i>Metabolites</i> , 2019 , 9,	5.6	2
18	Over-representation of correlation analysis (ORCA): a method for identifying associations between variable sets. <i>Bioinformatics</i> , 2015 , 31, 102-8	7.2	2
17	Extraction and Integration of Genetic Networks from Short-Profile Omic Data Sets. <i>Metabolites</i> , 2020 , 10,	5.6	2
16	Bayesian estimation of the number of protonation sites for urinary metabolites from NMR spectroscopic data. <i>Metabolomics</i> , 2018 , 14, 56	4.7	2
15	Data mining and visualisation: general discussion. <i>Faraday Discussions</i> , 2019 , 218, 354-371	3.6	2
14	Statistical Data Analysis in Metabolomics 2011 , 163-180		2
13	Response to Comment on Optimized Preprocessing of Ultra-Performance Liquid Chromatography/Mass Spectrometry Urinary Metabolic Profiles for Improved Information Recovery (Information Analytical Chemistry, 2011, 83, 9721-9722	7.8	2
12	Semiempirical Molecular-Orbital Properties of Some Polycyclic Aromatic Hydrocarbons and Correlation with Environmental Toxic Equivalency Factors. <i>Polycyclic Aromatic Compounds</i> , 2003 , 23, 23-47	1.3	2
11	Processing and Analysis of Untargeted Multicohort NMR Data. <i>Methods in Molecular Biology</i> , 2019 , 2037, 453-470	1.4	2
10	Big Data and Databases for Metabolic Phenotyping 2019 , 329-367		2

LIST OF PUBLICATIONS

9	PhenoMeNal: Processing and analysis of Metabolomics data in the Cloud		1	
8	Statistical Methods in Metabolomics 2019 , 949-976		1	
7	CHAPTER 12:Advances in Computational Analysis of Metabolomic NMR Data. <i>New Developments in NMR</i> , 2018 , 310-323	0.9	1	
6	Estimation of permutation-based metabolome-wide significance thresholds		1	
5	Bayesian Deconvolution and Quantification of Metabolites from J-Resolved NMR Spectroscopy. <i>Bayesian Analysis</i> , 2021 , 16,	2.3	1	
4	Urinary hippurate and proline betaine relative to fruit intake, blood pressure, and body mass index. <i>Proceedings of the Nutrition Society</i> , 2016 , 75,	2.9	1	
3	Multiple-testing correction in metabolome-wide association studies. <i>BMC Bioinformatics</i> , 2021 , 22, 67	3.6	1	
2	Blood pressure interactions with the DASH dietary pattern, sodium, and potassium: The International Study of Macro-/Micronutrients and Blood Pressure (INTERMAP) <i>American Journal of Clinical Nutrition</i> , 2022 ,	7	1	
1	Report on the 9th Annual International Conference of the Metabolomics Society. <i>Metabolomics</i> , 2013 , 9, 935-937	4.7		