Timothy Ebbels

List of Publications by Year
in descending order

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143 papers	11,538 citations	41627 51 h-index	33145 104 g-index
151 all docs	151 docs citations	151 times ranked	15322 citing authors

#	Article	IF	Citations
1	Metabolic profiling, metabolomic and metabonomic procedures for NMR spectroscopy of urine, plasma, serum and tissue extracts. Nature Protocols, 2007, 2, 2692-2703.	5.5	1,830
2	Human metabolic phenotype diversity and its association with diet and blood pressure. Nature, 2008, 453, 396-400.	13.7	966
3	Contemporary issues in toxicology the role of metabonomics in toxicology and its evaluation by the COMET project. Toxicology and Applied Pharmacology, 2003, 187, 137-146.	1.3	374
4	Proposed minimum reporting standards for data analysis in metabolomics. Metabolomics, 2007, 3, 231-241.	1.4	361
5	Integrated pathway-level analysis of transcriptomics and metabolomics data with IMPaLA. Bioinformatics, 2011, 27, 2917-2918.	1.8	356
6	High-resolution magic-angle-spinning NMR spectroscopy for metabolic profiling of intact tissues. Nature Protocols, 2010, 5, 1019-1032.	5.5	355
7	Recursive Segment-Wise Peak Alignment of Biological ¹H NMR Spectra for Improved Metabolic Biomarker Recovery. Analytical Chemistry, 2009, 81, 56-66.	3.2	303
8	The Consortium for Metabonomic Toxicology (COMET): aims, activities and achievements. Pharmacogenomics, 2005, 6, 691-699.	0.6	277
9	Analytical Reproducibility in1H NMR-Based Metabonomic Urinalysis. Chemical Research in Toxicology, 2002, 15, 1380-1386.	1.7	261
10	Optimized Preprocessing of Ultra-Performance Liquid Chromatography/Mass Spectrometry Urinary Metabolic Profiles for Improved Information Recovery. Analytical Chemistry, 2011, 83, 5864-5872.	3.2	240
11	Correction of mass calibration gaps in liquid chromatographyâ€“mass spectrometry metabolomics data. Bioinformatics, 2010, 26, 2488-2489.	1.8	195
12	Urinary metabolic signatures of human adiposity. Science Translational Medicine, 2015, 7, 285ra62.	5.8	178
13	Bayesian deconvolution and quantification of metabolites in complex 1D NMR spectra using BATMAN. Nature Protocols, 2014, 9, 1416-1427.	5.5	167
14	Improved analysis of multivariate data by variable stability scaling: application to NMR-based metabolic profiling. Analytica Chimica Acta, 2003, 490, 265-276.	2.6	164
15	Prediction and Classification of Drug Toxicity Using Probabilistic Modeling of Temporal Metabolic Data:Â The Consortium on Metabonomic Toxicology Screening Approach. Journal of Proteome Research, 2007, 6, 4407-4422.	1.8	164
16	Optimization and Evaluation of Metabolite Extraction Protocols for Untargeted Metabolic Profiling of Liver Samples by UPLC-MS. Analytical Chemistry, 2010, 82, 7779-7786.	3.2	160
17	Design and Analysis of Metabolomics Studies in Epidemiologic Research: A Primer on -Omic Technologies. American Journal of Epidemiology, 2014, 180, 129-139.	1.6	152
18	Spectral editing and pattern recognition methods applied to high-resolution magic-angle spinning 1H nuclear magnetic resonance spectroscopy of liver tissues. Analytical Biochemistry, 2003, 323, 26-32.	1.1	144

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19	Geometric Trajectory Analysis of Metabolic Responses To Toxicity Can Define Treatment Specific Profiles. Chemical Research in Toxicology, 2004, 17, 579-587.	1.7	143
20	NMR-based metabonomic toxicity classification: hierarchical cluster analysis and k-nearest-neighbour approaches. Analytica Chimica Acta, 2003, 490, 3-15.	2.6	142
21	BATMANâ€"an R package for the automated quantification of metabolites from nuclear magnetic resonance spectra using a Bayesian model. Bioinformatics, 2012, 28, 2088-2090.	1.8	142
22	The evolution of partial least squares models and related chemometric approaches in metabonomics and metabolic phenotyping. Journal of Chemometrics, 2010, 24, 636-649.	0.7	140
23	COordination of Standards in MetabOlomicS (COSMOS): facilitating integrated metabolomics data access. Metabolomics, 2015, 11, 1587-1597.	1.4	140
24	Use cases, best practice and reporting standards for metabolomics in regulatory toxicology. Nature Communications, 2019, 10, 3041.	5.8	131
25	Optimizing the Use of Quality Control Samples for Signal Drift Correction in Large-Scale Urine Metabolic Profiling Studies. Analytical Chemistry, 2012, 84, 2670-2677.	3.2	127
26	Comparative metabonomics of differential hydrazine toxicity in the rat and mouse. Toxicology and Applied Pharmacology, 2005, 204, 135-151.	1.3	125
27	Opening up the "Black Box": Metabolic phenotyping and metabolome-wide association studies in epidemiology. Journal of Clinical Epidemiology, 2010, 63, 970-979.	2.4	125
28	Metabolic Profiling and the Metabolome-Wide Association Study: Significance Level For Biomarker Identification. Journal of Proteome Research, 2010, 9, 4620-4627.	1.8	123
29	Metabolome-Wide Association Study Identifies Multiple Biomarkers that Discriminate North and South Chinese Populations at Differing Risks of Cardiovascular Disease: INTERMAP Study. Journal of Proteome Research, 2010, 9, 6647-6654.	1.8	116
30	Meeting-in-the-middle using metabolic profiling â€“ a strategy for the identification of intermediate biomarkers in cohort studies. Biomarkers, 2011, 16, 83-88.	0.9	113
31	Serum metabolic signatures of coronary and carotid atherosclerosis and subsequent cardiovascular disease. European Heart Journal, 2019, 40, 2883-2896.	1.0	107
32	Applying 'omics technologies in chemicals risk assessment: Report of an ECETOC workshop. Regulatory Toxicology and Pharmacology, 2017, 91, S3-S13.	1.3	102
33	Data standards can boost metabolomics research, and if there is a will, there is a way. Metabolomics, 2016, 12, 14.	1.4	97
34	Power Analysis and Sample Size Determination in Metabolic Phenotyping. Analytical Chemistry, 2016, 88, 5179-5188.	3.2	95
35	Bioinformatic methods in NMR-based metabolic profiling. Progress in Nuclear Magnetic Resonance Spectroscopy, 2009, 55, 361-374.	3.9	91
36	Consensus-Phenotype Integration of Transcriptomic and Metabolomic Data Implies a Role for Metabolism in the Chemosensitivity of Tumour Cells. PLoS Computational Biology, 2011, 7, e1001113.	1.5	83

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37	Batch statistical processing of1H NMR-derived urinary spectral data. Journal of Chemometrics, 2002, 16, 461-468.	0.7	82
38	Toxicity classification from metabonomic data using a density superposition approach: â€˜CLOUDSâ€™. Analytica Chimica Acta, 2003, 490, 109-122.	2.6	76
39	NMR-Based Metabolic Profiling Identifies Biomarkers of Liver Regeneration Following Partial Hepatectomy in the Rat. Journal of Proteome Research, 2010, 9, 59-69.	1.8	75
40	Subset Optimization by Reference Matching (STORM): An Optimized Statistical Approach for Recovery of Metabolic Biomarker Structural Information from ¹H NMR Spectra of Biofluids. Analytical Chemistry, 2012, 84, 10694-10701.	3.2	75
41	Computational tools and workflows in metabolomics: An international survey highlights the opportunity for harmonisation through Galaxy. Metabolomics, 2017, 13, 12.	1.4	69
42	Statistical experimental design and partial least squares regression analysis of biofluid metabonomic NMR and clinical chemistry data for screening of adverse drug effects. Chemometrics and Intelligent Laboratory Systems, 2004, 73, 139-149.	1.8	64
43	The carcinoGENOMICS project: Critical selection of model compounds for the development of omics-based in vitro carcinogenicity screening assays. Mutation Research - Reviews in Mutation Research, 2008, 659, 202-210.	2.4	60
44	Metabolic response to low-level toxicant exposure in a novel renal tubuleepithelial cell system. Molecular BioSystems, 2011, 7, 247-257.	2.9	60
45	PhenoMeNal: processing and analysis of metabolomics data in the cloud. GigaScience, 2019, 8, .	3.3	60
46	Pathway analysis in metabolomics: Recommendations for the use of over-representation analysis. PLoS Computational Biology, 2021, 17, e1009105.	1.5	59
47	Robust Algorithms for Automated Chemical Shift Calibration of 1D 1H NMR Spectra of Blood Serum. Analytical Chemistry, 2008, 80, 7158-7162.	3.2	58
48	Reliability of plasma polar metabolite concentrations in a large-scale cohort study using capillary electrophoresis-mass spectrometry. PLoS ONE, 2018, 13, e0191230.	1.1	58
49	Genetic algorithms for simultaneous variable and sample selection in metabonomics. Bioinformatics, 2009, 25, 112-118.	1.8	56
50	Analytic Properties of Statistical Total Correlation Spectroscopy Based Information Recovery in 1H NMR Metabolic Data Sets. Analytical Chemistry, 2009, 81, 2075-2084.	3.2	56
51	Temporal Metabonomic Modeling of <scp>l</scp>-Arginine-Induced Exocrine Pancreatitis. Journal of Proteome Research, 2008, 7, 4435-4445.	1.8	55
52	Time-Resolved Metabolic Footprinting for Nonlinear Modeling of Bacterial Substrate Utilization. Applied and Environmental Microbiology, 2009, 75, 2453-2463.	1.4	52
53	Correlation Network Analysis reveals a sequential reorganization of metabolic and transcriptional states during germination and gene-metabolite relationships in developing seedlings of Arabidopsis. BMC Systems Biology, 2010, 4, 62.	3.0	52
54	Data-Driven Approach for Metabolite Relationship Recovery in Biological ¹H NMR Data Sets Using Iterative Statistical Total Correlation Spectroscopy. Analytical Chemistry, 2011, 83, 2075-2082.	3.2	52

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55	Intra- and inter-omic fusion of metabolic profiling data in a systems biology framework. Chemometrics and Intelligent Laboratory Systems, 2010, 104, 121-131.	1.8	51
56	nmrML: A Community Supported Open Data Standard for the Description, Storage, and Exchange of NMR Data. Analytical Chemistry, 2018, 90, 649-656.	3.2	50
57	Validation of metabolomics for toxic mechanism of action screening with the earthworm Lumbricus rubellus. Metabolomics, 2009, 5, 72-83.	1.4	48
58	Identification of a gravitationally lensed z = 2.515 star-forming galaxy. Monthly Notices of the Royal Astronomical Society, 1996, 281, L75-L81.	1.6	47
59	Modelling the acid/base 1H NMR chemical shift limits of metabolites in human urine. Metabolomics, 2016, 12, 152.	1.4	47
60	Metabolomics: The Stethoscope for the Twenty-First Century. Medical Principles and Practice, 2021, 30, 301-310.	1.1	46
61	Progress towards an OECD reporting framework for transcriptomics and metabolomics in regulatory toxicology. Regulatory Toxicology and Pharmacology, 2021, 125, 105020.	1.3	46
62	Intra- and Interlaboratory Reproducibility of Ultra Performance Liquid Chromatographyâ€“Time-of-Flight Mass Spectrometry for Urinary Metabolic Profiling. Analytical Chemistry, 2012, 84, 2424-2432.	3.2	44
63	A statistical framework for biomarker discovery in metabolomic time course data. Bioinformatics, 2011, 27, 1979-1985.	1.8	41
64	A Bayesian Model of NMR Spectra for the Deconvolution and Quantification of Metabolites in Complex Biological Mixtures. Journal of the American Statistical Association, 2012, 107, 1259-1271.	1.8	41
65	diXa: a data infrastructure for chemical safety assessment. Bioinformatics, 2015, 31, 1505-1507.	1.8	40
66	Statistical analysis in metabolic phenotyping. Nature Protocols, 2021, 16, 4299-4326.	5.5	40
67	Statistical Total Correlation Spectroscopy Editing of ¹H NMR Spectra of Biofluids: Application to Drug Metabolite Profile Identification and Enhanced Information Recovery. Analytical Chemistry, 2009, 81, 6458-6466.	3.2	38
68	Metabolic Profiling and Population Screening of Analgesic Usage in Nuclear Magnetic Resonance Spectroscopy-Based Large-Scale Epidemiologic Studies. Analytical Chemistry, 2009, 81, 5119-5129.	3.2	37
69	Workflow for Integrated Processing of Multicohort Untargeted ¹H NMR Metabolomics Data in Large-Scale Metabolic Epidemiology. Journal of Proteome Research, 2016, 15, 4188-4194.	1.8	37
70	The association of fish consumption and its urinary metabolites with cardiovascular risk factors: the International Study of Macro-/Micronutrients and Blood Pressure (INTERMAP). American Journal of Clinical Nutrition, 2020, 111, 280-290.	2.2	37
71	Cluster Analysis Statistical Spectroscopy Using Nuclear Magnetic Resonance Generated Metabolic Data Sets from Perturbed Biological Systems. Analytical Chemistry, 2009, 81, 6581-6589.	3.2	36
72	Evaluation of metabolic variation in normal rat strains from a statistical analysis of 1H NMR spectra of urine. Journal of Pharmaceutical and Biomedical Analysis, 2004, 36, 823-833.	1.4	33

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73	A Differential Network Approach to Exploring Differences between Biological States: An Application to Prediabetes. PLoS ONE, 2011, 6, e24702.	1.1	33
74	Framework for the quality assurance of â€™omics technologies considering GLP requirements. Regulatory Toxicology and Pharmacology, 2017, 91, S27-S35.	1.3	32
75	A comparison of human serum and plasma metabolites using untargeted 1H NMR spectroscopy and UPLC-MS. Metabolomics, 2018, 14, 32.	1.4	31
76	Optimized Phenotypic Biomarker Discovery and Confounder Elimination via Covariate-Adjusted Projection to Latent Structures from Metabolic Spectroscopy Data. Journal of Proteome Research, 2018, 17, 1586-1595.	1.8	29
77	Bidirectional Correlation of NMR and Capillary Electrophoresis Fingerprints: A New Approach to Investigating Schistosoma mansoni Infection in a Mouse Model. Analytical Chemistry, 2010, 82, 203-210.	3.2	28
78	A Statistically Rigorous Test for the Identification of Parentâ^'Fragment Pairs in LC-MS Datasets. Analytical Chemistry, 2010, 82, 1766-1778.	3.2	26
79	Improving Visualization and Interpretation of Metabolome-Wide Association Studies: An Application in a Population-Based Cohort Using Untargeted ¹H NMR Metabolic Profiling. Journal of Proteome Research, 2017, 16, 3623-3633.	1.8	26
80	Untargeted Metabolome Quantitative Trait Locus Mapping Associates Variation in Urine Glycerate to Mutant Glycerate Kinase. Journal of Proteome Research, 2012, 11, 631-642.	1.8	25
81	Statistical Correlations between NMR Spectroscopy and Direct Infusion FT-ICR Mass Spectrometry Aid Annotation of Unknowns in Metabolomics. Analytical Chemistry, 2016, 88, 2583-2589.	3.2	25
82	Processing and Modeling of Nuclear Magnetic Resonance (NMR) Metabolic Profiles. Methods in Molecular Biology, 2011, 708, 365-388.	0.4	25
83	1H NMR-Based Profiling Reveals Differential Immune-Metabolic Networks during Influenza Virus Infection in Obese Mice. PLoS ONE, 2014, 9, e97238.	1.1	25
84	Piecewise multivariate modelling of sequential metabolic profiling data. BMC Bioinformatics, 2008, 9, 105.	1.2	24
85	Dietary and Urinary Metabonomic Factors Possibly Accounting for Higher Blood Pressure of Black Compared With White Americans. Hypertension, 2013, 62, 1074-1080.	1.3	24
86	Bayesian inference for multiple Gaussian graphical models with application to metabolic association networks. Annals of Applied Statistics, 2017, 11, .	0.5	23
87	springScape: visualisation of microarray and contextual bioinformatic data using spring embedding and an 'information landscape'. Bioinformatics, 2006, 22, e99-e107.	1.8	22
88	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. Environmental Health Perspectives, 2016, 124, 88-96.	2.8	21
89	Genome metabolome integrated network analysis to uncover connections between genetic variants and complex traits: an application to obesity. Journal of the Royal Society Interface, 2014, 11, 20130908.	1.5	20
90	Combining Spectral Ordering with Peak Fitting for One-Dimensional NMR Quantitative Metabolomics. Analytical Chemistry, 2013, 85, 4605-4612.	3.2	19

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91	Spectroscopic confirmation of redshifts predicted by gravitational lensing. Monthly Notices of the Royal Astronomical Society, 1998, 295, 75.	1.6	19
92	The future of metabolomics in ELIXIR. F1000Research, 2017, 6, 1649.	0.8	19
93	Automated Annotation of Untargeted All-Ion Fragmentation LCâ€“MS Metabolomics Data with MetaboAnnotatoR. Analytical Chemistry, 2022, 94, 3446-3455.	3.2	18
94	MetAssimulo:Simulation of Realistic NMR Metabolic Profiles. BMC Bioinformatics, 2010, 11, 496.	1.2	17
95	Predictive modelling using pathway scores: robustness and significance of pathway collections. BMC Bioinformatics, 2019, 20, 543.	1.2	17
96	Integrated Histopathological and Urinary Metabonomic Investigation of the Pathogenesis of Microcystin-LR Toxicosis. Veterinary Pathology, 2013, 50, 159-171.	0.8	16
97	A Combined Metabonomic and Transcriptomic Approach to Investigate Metabolism during Development in the Chick Chorioallantoic Membrane. Journal of Proteome Research, 2010, 9, 3126-3134.	1.8	15
98	Metabonomic investigations into the global biochemical sequelae of exposure to the pancreatic toxin 1â€cyanoâ€2â€hydroxyâ€3â€butene in the rat. Magnetic Resonance in Chemistry, 2009, 47, S26-35.	1.1	14
99	Metabolic phenotyping for discovery of urinary biomarkers of diet, xenobiotics and blood pressure in the INTERMAP Study: an overview. Hypertension Research, 2017, 40, 336-345.	1.5	14
100	Targeted realignment of LC-MS profiles by neighbor-wise compound-specific graphical time warping with misalignment detection. Bioinformatics, 2020, 36, 2862-2871.	1.8	14
101	Statistical Techniques in Metabolic Profiling. , 2008, , 347-373.		13
102	Identifying biochemical phenotypic differences between cryptic species. Biology Letters, 2014, 10, 20140615.	1.0	13
103	Embedding standards in metabolomics: the Metabolomics Society data standards task group. Metabolomics, 2015, 11, 782-783.	1.4	13
104	Bayesian estimation of the number of protonation sites for urinary metabolites from NMR spectroscopic data. Metabolomics, 2018, 14, 56.	1.4	13
105	Multiple-testing correction in metabolome-wide association studies. BMC Bioinformatics, 2021, 22, 67.	1.2	13
106	Blood pressure interactions with the DASH dietary pattern, sodium, and potassium: The International Study of Macro-/Micronutrients and Blood Pressure (INTERMAP). American Journal of Clinical Nutrition, 2022, 116, 216-229.	2.2	13
107	Effect of the Histone Deacetylase Inhibitor Trichostatin A on the Metabolome of Cultured Primary Hepatocytes. Journal of Proteome Research, 2010, 9, 413-419.	1.8	12
108	Modelling Short Time Series in Metabolomics: A Functional Data Analysis Approach. Advances in Experimental Medicine and Biology, 2011, 696, 307-315.	0.8	12

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109	Proteomic and metabolomic responses to connexin43 silencing in primary hepatocyte cultures. Archives of Toxicology, 2013, 87, 883-894.	1.9	12
110	Integrative analysis of time course metabolic data and biomarker discovery. BMC Bioinformatics, 2020, 21, 11.	1.2	11
111	The future of metabolomics in ELIXIR. F1000Research, 2017, 6, 1649.	0.8	11
112	Construction of Confidence Regions for Isotopic Abundance Patterns in LC/MS Data Sets for Rigorous Determination of Molecular Formulas. Analytical Chemistry, 2010, 82, 7319-7328.	3.2	10
113	Over-representation of correlation analysis (ORCA): a method for identifying associations between variable sets. Bioinformatics, 2015, 31, 102-108.	1.8	9
114	Finding Correspondence between Metabolomic Features in Untargeted Liquid Chromatographyâ€“Mass Spectrometry Metabolomics Datasets. Analytical Chemistry, 2022, 94, 5493-5503.	3.2	9
115	Prospects for a Statistical Theory of LC/TOFMS Data. Journal of the American Society for Mass Spectrometry, 2012, 23, 779-791.	1.2	8
116	Non-linear Methods for the Analysis of Metabolic Profiles. , 2007, , 201-226.		7
117	The international Metabolomics Society in 2015: the path forward to success. Metabolomics, 2015, 11, 1-2.	1.4	7
118	Quantitative Investigation of Probabilistic Spectral Processing Methods Using Simulated NMR Data. Applied Spectroscopy, 2001, 55, 1214-1224.	1.2	6
119	Extraction and Integration of Genetic Networks from Short-Profile Omic Data Sets. Metabolites, 2020, 10, 435.	1.3	6
120	A Combination of Transcriptomics and Metabolomics Uncovers Enhanced Bile Acid Biosynthesis in HepG2 Cells Expressing CCAAT/Enhancer-Binding Protein Î² (C/EBPÎ²), Hepatocyte Nuclear Factor 4Î± (HNF4Î±), and Constitutive Androstane Receptor (CAR). Journal of Proteome Research, 2013, 12, 2732-2741.	1.8	5
121	Metabolic Signatures of Gestational Weight Gain and Postpartum Weight Loss in a Lifestyle Intervention Study of Overweight and Obese Women. Metabolites, 2020, 10, 498.	1.3	5
122	Orders of Magnitude Extension of the Effective Dynamic Range of TDC-Based TOFMS Data Through Maximum Likelihood Estimation. Journal of the American Society for Mass Spectrometry, 2014, 25, 1824-1827.	1.2	4
123	Variance and covariance heterogeneity analysis for detection of metabolites associated with cadmium exposure. Statistical Applications in Genetics and Molecular Biology, 2014, 13, 191-201.	0.2	4
124	Characterization of data analysis methods for information recovery from metabolic 1H NMR spectra using artificial complex mixtures. Metabolomics, 2012, 8, 1170-1180.	1.4	3
125	Comparison of Bi- and Tri-Linear PLS Models for Variable Selection in Metabolomic Time-Series Experiments. Metabolites, 2019, 9, 92.	1.3	3
126	Bayesian Deconvolution and Quantification of Metabolites from J-Resolved NMR Spectroscopy. Bayesian Analysis, 2021, 16, .	1.6	3

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127	Semiempirical Molecular-Orbital Properties of Some Polycyclic Aromatic Hydrocarbons and Correlation with Environmental Toxic Equivalency Factors. Polycyclic Aromatic Compounds, 2003, 23, 23-47.	1.4	2
128	Response to Comment on â€œOptimized Preprocessing of Ultra-Performance Liquid Chromatography/Mass Spectrometry Urinary Metabolic Profiles for Improved Information Recoveryâ€• Analytical Chemistry, 2011, 83, 9721-9722.	3.2	2
129	MEtabolomics standaRds Initiative in Toxicology (MERIT). Toxicology Letters, 2018, 295, S214.	0.4	2
130	Data mining and visualisation: general discussion. Faraday Discussions, 2019, 218, 354-371.	1.6	2
131	Big Data and Databases for Metabolic Phenotyping. , 2019, , 329-367.		2
132	Processing and Analysis of Untargeted Multicohort NMR Data. Methods in Molecular Biology, 2019, 2037, 453-470.	0.4	2
133	Urinary hippurate and proline betaine relative to fruit intake, blood pressure, and body mass index. Proceedings of the Nutrition Society, 2016, 75, .	0.4	1
134	Advances in Computational Analysis of Metabolomic NMR Data. New Developments in NMR, 2018, , 310-323.	0.1	1
135	We-P14:381 Metabonomics to assess self-reported data: The international study on macronutrients and blood pressure (INTERMAP). Atherosclerosis Supplements, 2006, 7, 430-431.	1.2	0
136	The continuing growth and development of YOUR metabolomics society. Metabolomics, 2013, 9, 529-531.	1.4	0
137	Report on the 9th Annual International Conference of the Metabolomics Society. Metabolomics, 2013, 9, 935-937.	1.4	0
138	One minute with the Metabolomics Societyâ€™s Honorary Fellows 2015. Metabolomics, 2015, 11, 779-781.	1.4	0
139	Ask not what your Society can do for you, ask what you can do for your Society!. Metabolomics, 2015, 11, 499-500.	1.4	0
140	Results of the 2015 elections to the board of directors. Metabolomics, 2015, 11, 1473-1474.	1.4	0
141	Abstract P228: Relationships of Dietary and Supplement Magnesium Intake and Its Urinary Metabolomic Biomarkers With Blood Pressure: The INTERMAP Study. Circulation, 2019, 139, .	1.6	0
142	Abstract P229: Cross-Sectional Investigation of the Relationship Between Fish Consumption and Its Urinary Biomarkers With Blood Pressure Across Asian and Western Populations: Results From the INTERMAP Study. Circulation, 2019, 139, .	1.6	0
143	Abstract MP45: A Metabolome-wide Association Study of Plant Food Consumption With Blood Pressure. Circulation, 2020, 141, .	1.6	0