Andris Jankevics

List of Publications by Year
in descending order

28	2,508	430754 18	526166 27
papers	citations	h-index	g-index

35	35	35	4167
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Characterization of Monophasic Solvent-Based Tissue Extractions for the Detection of Polar Metabolites and Lipids Applying Ultrahigh-Performance Liquid Chromatographyâ€“Mass Spectrometry Clinical Metabolic Phenotyping Assays. Journal of Proteome Research, 2021, 20, 831-840.	1.8	20
2	mzMLb: A Future-Proof Raw Mass Spectrometry Data Format Based on Standards-Compliant mzML and Optimized for Speed and Storage Requirements. Journal of Proteome Research, 2021, 20, 172-183.	1.8	12
3	An improved strategy for analysis of lipid molecules utilising a reversed phase C30 UHPLC column and scheduled MS/MS acquisition. Talanta, 2021, 229, 122262.	2.9	8
4	Assessment of human plasma and urine sample preparation for reproducible and high-throughput UHPLC-MS clinical metabolic phenotyping. Analyst, The, 2020, 145, 6511-6523.	1.7	28
5	Multi-Omics Analysis of Diabetic Heart Disease in the db/db Model Reveals Potential Targets for Treatment by a Longevity-Associated Gene. Cells, 2020, 9, 1283.	1.8	11
6	Metabolic engineering against the arginine microenvironment enhances CAR-T cell proliferation and therapeutic activity. Blood, 2020, 136, 1155-1160.	0.6	84
7	Metabolic characterisation of disturbances in the APOC3/triglyceride-rich lipoprotein pathway through sample-based recall by genotype. Metabolomics, 2020, 16, 69.	1.4	3
8	RankProd 2.0: a refactored bioconductor package for detecting differentially expressed features in molecular profiling datasets. Bioinformatics, 2017, 33, 2774-2775.	1.8	113
9	Chapter 7. Algorithms for MS1-Based Quantitation. New Developments in Mass Spectrometry, 2016, , 133-154.	0.2	0
10	MetAssign: probabilistic annotation of metabolites from LCâ€“MS data using a Bayesian clustering approach. Bioinformatics, 2014, 30, 2764-2771.	1.8	63
11	Metabolic adaptations of <scp>L</scp>eishmania donovani in relation to differentiation, drug resistance, and drug pressure. Molecular Microbiology, 2013, 90, 428-442.	1.2	48
12	LC-MS METABOLOMICS FROM STUDY DESIGN TO DATA-ANALYSIS â€“ USING A VERSATILE PATHOGEN AS A TEST CASE. Computational and Structural Biotechnology Journal, 2013, 4, e201301002.	1.9	39
13	Bioanalysis Young Investigator Award 2013. Bioanalysis, 2013, 5, 1479-1484.	0.6	0
14	mzMatchâ€“ISO: an R tool for the annotation and relative quantification of isotope-labelled mass spectrometry data. Bioinformatics, 2013, 29, 281-283.	1.8	91
15	Bioanalysis Young Investigator: Announcing our finalists!. Bioanalysis, 2013, 5, 1963-1964.	0.6	1
16	Metabolomics for Secondary Metabolite Research. Metabolites, 2013, 3, 1076-1083.	1.3	59
17	IDEOM: an Excel interface for analysis of LCâ€“MS-based metabolomics data. Bioinformatics, 2012, 28, 1048-1049.	1.8	307
18	Serine is a natural ligand and allosteric activator of pyruvate kinase M2. Nature, 2012, 491, 458-462.	13.7	519

#	Article	IF	Citations
19	Stable Isotope-Assisted Metabolomics for Network-Wide Metabolic Pathway Elucidation. Analytical Chemistry, 2012, 84, 8442-8447.	3.2	132
20	Separating the wheat from the chaff: a prioritisation pipeline for the analysis of metabolomics datasets. Metabolomics, 2012, 8, 29-36.	1.4	50
21	Metabolomics methods for the synthetic biology of secondary metabolism. FEBS Letters, 2012, 586, 2177-2183.	1.3	63
22	PeakML/mzMatch: A File Format, Java Library, R Library, and Tool-Chain for Mass Spectrometry Data Analysis. Analytical Chemistry, 2011, 83, 2786-2793.	3.2	305
23	Exploring the metabolic state of microorganisms using metabolomics. Bioanalysis, 2011, 3, 2443-2458.	0.6	19
24	Toward Global Metabolomics Analysis with Hydrophilic Interaction Liquid Chromatographyâ€“Mass Spectrometry: Improved Metabolite Identification by Retention Time Prediction. Analytical Chemistry, 2011, 83, 8703-8710.	3.2	326
25	Metabolomic analysis of a synthetic metabolic switch inStreptomyces coelicolorA3(2). Proteomics, 2011, 11, 4622-4631.	1.3	20
26	Towards an unbiased metabolic profiling of protozoan parasites: optimisation of a Leishmania sampling protocol for HILIC-orbitrap analysis. Analytical and Bioanalytical Chemistry, 2010, 398, 2059-2069.	1.9	48
27	Metabolomics to Unveil and Understand Phenotypic Diversity between Pathogen Populations. PLoS Neglected Tropical Diseases, 2010, 4, e904.	1.3	91
28	Metabolomic studies of experimental diabetic urine samples by 1H NMR spectroscopy and LC/MS method. Chemometrics and Intelligent Laboratory Systems, 2009, 97, 11-17.	1.8	19