

# Andris Jankevics

## List of Publications by Year in descending order

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Version: 2024-02-01

28  
papers

2,508  
citations

430874

18  
h-index

526287

27  
g-index

35  
all docs

35  
docs citations

35  
times ranked

4167  
citing authors

#	ARTICLE	IF	CITATIONS
1	Serine is a natural ligand and allosteric activator of pyruvate kinase M2. <i>Nature</i> , 2012, 491, 458-462.	27.8	519
2	Toward Global Metabolomics Analysis with Hydrophilic Interaction Liquid Chromatographyâ€“Mass Spectrometry: Improved Metabolite Identification by Retention Time Prediction. <i>Analytical Chemistry</i> , 2011, 83, 8703-8710.	6.5	326
3	IDEOM: an Excel interface for analysis of LCâ€“MS-based metabolomics data. <i>Bioinformatics</i> , 2012, 28, 1048-1049.	4.1	307
4	PeakML/mzMatch: A File Format, Java Library, R Library, and Tool-Chain for Mass Spectrometry Data Analysis. <i>Analytical Chemistry</i> , 2011, 83, 2786-2793.	6.5	305
5	Stable Isotope-Assisted Metabolomics for Network-Wide Metabolic Pathway Elucidation. <i>Analytical Chemistry</i> , 2012, 84, 8442-8447.	6.5	132
6	RankProd 2.0: a refactored bioconductor package for detecting differentially expressed features in molecular profiling datasets. <i>Bioinformatics</i> , 2017, 33, 2774-2775.	4.1	113
7	Metabolomics to Unveil and Understand Phenotypic Diversity between Pathogen Populations. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e904.	3.0	91
8	mzMatchâ€“ISO: an R tool for the annotation and relative quantification of isotope-labelled mass spectrometry data. <i>Bioinformatics</i> , 2013, 29, 281-283.	4.1	91
9	Metabolic engineering against the arginine microenvironment enhances CAR-T cell proliferation and therapeutic activity. <i>Blood</i> , 2020, 136, 1155-1160.	1.4	84
10	Metabolomics methods for the synthetic biology of secondary metabolism. <i>FEBS Letters</i> , 2012, 586, 2177-2183.	2.8	63
11	MetAssign: probabilistic annotation of metabolites from LCâ€“MS data using a Bayesian clustering approach. <i>Bioinformatics</i> , 2014, 30, 2764-2771.	4.1	63
12	Metabolomics for Secondary Metabolite Research. <i>Metabolites</i> , 2013, 3, 1076-1083.	2.9	59
13	Separating the wheat from the chaff: a prioritisation pipeline for the analysis of metabolomics datasets. <i>Metabolomics</i> , 2012, 8, 29-36.	3.0	50
14	Towards an unbiased metabolic profiling of protozoan parasites: optimisation of a <i>Leishmania</i> sampling protocol for HILIC-orbitrap analysis. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 398, 2059-2069.	3.7	48
15	Metabolic adaptations of <i>Leishmania donovani</i> in relation to differentiation, drug resistance, and drug pressure. <i>Molecular Microbiology</i> , 2013, 90, 428-442.	2.5	48
16	LC-MS METABOLOMICS FROM STUDY DESIGN TO DATA-ANALYSIS â€“ USING A VERSATILE PATHOGEN AS A TEST CASE. <i>Computational and Structural Biotechnology Journal</i> , 2013, 4, e201301002.	4.1	39
17	Assessment of human plasma and urine sample preparation for reproducible and high-throughput UHPLC-MS clinical metabolic phenotyping. <i>Analyst</i> , 2020, 145, 6511-6523.	3.5	28
18	Metabolomic analysis of a synthetic metabolic switch in <i>Streptomyces coelicolor</i> A3(2). <i>Proteomics</i> , 2011, 11, 4622-4631.	2.2	20

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19	Characterization of Monophasic Solvent-Based Tissue Extractions for the Detection of Polar Metabolites and Lipids Applying Ultrahigh-Performance Liquid Chromatography–Mass Spectrometry Clinical Metabolic Phenotyping Assays. <i>Journal of Proteome Research</i> , 2021, 20, 831-840.	3.7	20
20	Metabolomic studies of experimental diabetic urine samples by <sup>1</sup> H NMR spectroscopy and LC/MS method. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2009, 97, 11-17.	3.5	19
21	Exploring the metabolic state of microorganisms using metabolomics. <i>Bioanalysis</i> , 2011, 3, 2443-2458.	1.5	19
22	mzMLb: A Future-Proof Raw Mass Spectrometry Data Format Based on Standards-Compliant mzML and Optimized for Speed and Storage Requirements. <i>Journal of Proteome Research</i> , 2021, 20, 172-183.	3.7	12
23	Multi-Omics Analysis of Diabetic Heart Disease in the db/db Model Reveals Potential Targets for Treatment by a Longevity-Associated Gene. <i>Cells</i> , 2020, 9, 1283.	4.1	11
24	An improved strategy for analysis of lipid molecules utilising a reversed phase C30 UHPLC column and scheduled MS/MS acquisition. <i>Talanta</i> , 2021, 229, 122262.	5.5	8
25	Metabolic characterisation of disturbances in the APOC3/triglyceride-rich lipoprotein pathway through sample-based recall by genotype. <i>Metabolomics</i> , 2020, 16, 69.	3.0	3
26	Bioanalysis Young Investigator: Announcing our finalists!. <i>Bioanalysis</i> , 2013, 5, 1963-1964.	1.5	1
27	Bioanalysis Young Investigator Award 2013. <i>Bioanalysis</i> , 2013, 5, 1479-1484.	1.5	0
28	Chapter 7. Algorithms for MS1-Based Quantitation. <i>New Developments in Mass Spectrometry</i> , 2016, , 133-154.	0.2	0