

# Daniel Jacob

## List of Publications by Year in descending order

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44  
papers

2,702  
citations

236833

25  
h-index

233338

45  
g-index

47  
all docs

47  
docs citations

47  
times ranked

5177  
citing authors

#	ARTICLE	IF	CITATIONS
1	Predictive metabolomics of multiple Atacama plant species unveils a core set of generic metabolites for extreme climate resilience. <i>New Phytologist</i> , 2022, 234, 1614-1628.	3.5	17
2	PeakForest: a multi-platform digital infrastructure for interoperable metabolite spectral data and metadata management. <i>Metabolomics</i> , 2022, 18, .	1.4	4
3	Maize metabolome and proteome responses to controlled cold stress partly mimic early sowing effects in the field and differ from those of Arabidopsis. <i>Plant, Cell and Environment</i> , 2021, 44, 1504-1521.	2.8	32
4	Leaf metabolomic data of eight sunflower lines and their sixteen hybrids under water deficit. <i>OCL - Oilseeds and Fats, Crops and Lipids</i> , 2021, 28, 42.	0.6	2
5	Hyperpolarized NMR Metabolomics at Natural <sup>13</sup> C Abundance. <i>Analytical Chemistry</i> , 2020, 92, 14867-14871.	3.2	44
6	Integrative Metabolomics for Assessing the Effect of Insect ( <i>Hermetia illucens</i> ) Protein Extract on Rainbow Trout Metabolism. <i>Metabolites</i> , 2020, 10, 83.	1.3	27
7	Biomass composition explains fruit relative growth rate and discriminates climacteric from non-climacteric species. <i>Journal of Experimental Botany</i> , 2020, 71, 5823-5836.	2.4	35
8	Comparative Metabolomics and Molecular Phylogenetics of Melon ( <i>Cucumis melo</i> , Cucurbitaceae) Biodiversity. <i>Metabolites</i> , 2020, 10, 121.	1.3	35
9	Making experimental data tables in the life sciences more FAIR: a pragmatic approach. <i>GigaScience</i> , 2020, 9, .	3.3	6
10	FAIRness Literacy: The Achilles™ Heel of Applying FAIR Principles. <i>Data Science Journal</i> , 2020, 19, .	0.6	19
11	NMR-Based Tissular and Developmental Metabolomics of Tomato Fruit. <i>Metabolites</i> , 2019, 9, 93.	1.3	18
12	Optimizing 1D 1H-NMR profiling of plant samples for high throughput analysis: extract preparation, standardization, automation and spectra processing. <i>Metabolomics</i> , 2019, 15, 28.	1.4	37
13	Metabolomic characterization of sunflower leaf allows discriminating genotype groups or stress levels with a minimal set of metabolic markers. <i>Metabolomics</i> , 2019, 15, 56.	1.4	17
14	PhenoMeNal: processing and analysis of metabolomics data in the cloud. <i>GigaScience</i> , 2019, 8, .	3.3	60
15	Characterization of GMO or glyphosate effects on the composition of maize grain and maize-based diet for rat feeding. <i>Metabolomics</i> , 2018, 14, 36.	1.4	9
16	nmrML: A Community Supported Open Data Standard for the Description, Storage, and Exchange of NMR Data. <i>Analytical Chemistry</i> , 2018, 90, 649-656.	3.2	50
17	Metabotyping of 30 maize hybrids under early-sowing conditions reveals potential marker-metabolites for breeding. <i>Metabolomics</i> , 2018, 14, 132.	1.4	15
18	NMRProcFlow: a graphical and interactive tool dedicated to 1D spectra processing for NMR-based metabolomics. <i>Metabolomics</i> , 2017, 13, 36.	1.4	128

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19	Plant metabolism as studied by NMR spectroscopy. Progress in Nuclear Magnetic Resonance Spectroscopy, 2017, 102-103, 61-97.	3.9	85
20	Highly Repeatable Dissolution Dynamic Nuclear Polarization for Heteronuclear NMR Metabolomics. Analytical Chemistry, 2016, 88, 6179-6183.	3.2	57
21	COordination of Standards in MetabOlogicS (COSMOS): facilitating integrated metabolomics data access. Metabolomics, 2015, 11, 1587-1597.	1.4	140
22	Workflow4Metabolomics: a collaborative research infrastructure for computational metabolomics. Bioinformatics, 2015, 31, 1493-1495.	1.8	333
23	Metabolomic profiling in tomato reveals diel compositional changes in fruit affected by source–sink relationships. Journal of Experimental Botany, 2015, 66, 3391-3404.	2.4	62
24	MeRy-B, a Metabolomic Database and Knowledge Base for Exploring Plant Primary Metabolism. Methods in Molecular Biology, 2014, 1083, 3-16.	0.4	22
25	High-Resolution 1H-NMR Spectroscopy and Beyond to Explore Plant Metabolome. Advances in Botanical Research, 2013, , 1-66.	0.5	14
26	Deciphering genetic diversity and inheritance of tomato fruit weight and composition through a systems biology approach. Journal of Experimental Botany, 2013, 64, 5737-5752.	2.4	20
27	An efficient spectra processing method for metabolite identification from 1H-NMR metabolomics data. Analytical and Bioanalytical Chemistry, 2013, 405, 5049-5061.	1.9	24
28	Draft Genome Sequences of Mycoplasma alkalescens, Mycoplasma arginini, and Mycoplasma bovigenitalium, Three Species with Equivocal Pathogenic Status for Cattle. Genome Announcements, 2013, 1, .	0.8	8
29	Complete Genome Sequence of Mycoplasma putrefaciens Strain 9231, One of the Agents of Contagious Agalactia in Goats. Genome Announcements, 2013, 1, .	0.8	1
30	Draft Genome Sequences of Mycoplasma auris and Mycoplasma yeatsii, Two Species of the Ear Canal of <i>Caprinae</i> . Genome Announcements, 2013, 1, .	0.8	3
31	Management and dissemination of MS proteomic data with PROTiCdb: Example of a quantitative comparison between methods of protein extraction. Proteomics, 2013, 13, 1457-1466.	1.3	25
32	MetaBase--the wiki-database of biological databases. Nucleic Acids Research, 2012, 40, D1250-D1254.	6.5	40
33	Toward interoperable bioscience data. Nature Genetics, 2012, 44, 121-126.	9.4	362
34	MeRy-B: a web knowledgebase for the storage, visualization, analysis and annotation of plant NMR metabolomic profiles. BMC Plant Biology, 2011, 11, 104.	1.6	54
35	Mycoplasma mycoides, from "mycoides Small Colony" to "capri". A microevolutionary perspective. BMC Genomics, 2011, 12, 114.	1.2	64
36	Comparative genomic and proteomic analyses of two Mycoplasma agalactiae strains: clues to the macro- and micro-events that are shaping mycoplasma diversity. BMC Genomics, 2010, 11, 86.	1.2	83

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37	Life on Arginine for <i>Mycoplasma hominis</i> : Clues from Its Minimal Genome and Comparison with Other Human Urogenital Mycoplasmas. <i>PLoS Genetics</i> , 2009, 5, e1000677.	1.5	172
38	Proton NMR quantitative profiling for quality assessment of greenhouse-grown tomato fruit. <i>Metabolomics</i> , 2009, 5, 183-198.	1.4	51
39	An integrative genomics approach for deciphering the complex interactions between ascorbate metabolism and fruit growth and composition in tomato. <i>Comptes Rendus - Biologies</i> , 2009, 332, 1007-1021.	0.1	30
40	<sup>1</sup> H NMR, GC-MS, and Data Set Correlation for Fruit Metabolomics: Application to Spatial Metabolite Analysis in Melon. <i>Analytical Chemistry</i> , 2009, 81, 2884-2894.	3.2	147
41	Being Pathogenic, Plastic, and Sexual while Living with a Nearly Minimal Bacterial Genome. <i>PLoS Genetics</i> , 2007, 3, e75.	1.5	176
42	Mapping the proteome of poplar and application to the discovery of drought-stress responsive proteins. <i>Proteomics</i> , 2006, 6, 6509-6527.	1.3	155
43	In silico exploration of the fructose-6-phosphate phosphorylation step in glycolysis: genomic evidence of the coexistence of an atypical ATP-dependent along with a PPI-dependent phosphofructokinase in <i>Propionibacterium freudenreichii</i> subsp. <i>shermanii</i> . <i>In Silico Biology</i> , 2004, 4, 517-28.	0.4	8
44	Whey drainage during soft cheese manufacture and properties of drained curd as modified by casein concentration, whey protein to casein ratio, and pasteurisation of milk. <i>Dairy Science and Technology</i> , 2000, 80, 573-587.	0.9	6