

Daniel Jaschob

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/4973398/daniel-jaschob-publications-by-year.pdf>

Version: 2024-04-25

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.

9
papers

133
citations

5
h-index

10
g-index

10
ext. papers

175
ext. citations

6.1
avg. IF

2.19
L-index

#	Paper	IF	Citations
9	Proxl (Protein Cross-Linking Database): A Public Server, QC Tools, and Other Major Updates. <i>Journal of Proteome Research</i> , 2019 , 18, 759-764	5.6	0
8	MetaGOmics: A Web-Based Tool for Peptide-Centric Functional and Taxonomic Analysis of Metaproteomics Data. <i>Proteomes</i> , 2017 , 6,	4.6	29
7	ProXL (Protein Cross-Linking Database): A Platform for Analysis, Visualization, and Sharing of Protein Cross-Linking Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2016 , 15, 2863-70	5.6	33
6	Visualization and dissemination of multidimensional proteomics data comparing protein abundance during <i>Caenorhabditis elegans</i> development. <i>Journal of the American Society for Mass Spectrometry</i> , 2015 , 26, 1827-36	3.5	5
5	Mason: a JavaScript web site widget for visualizing and comparing annotated features in nucleotide or protein sequences. <i>BMC Research Notes</i> , 2015 , 8, 70	2.3	4
4	The molecular architecture of the Dam1 kinetochore complex is defined by cross-linking based structural modelling. <i>Nature Communications</i> , 2015 , 6, 8673	17.4	36
3	Determining protein complex structures based on a Bayesian model of in vivo Förster resonance energy transfer (FRET) data. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2812-23	7.6	22
2	JobCenter: an open source, cross-platform, and distributed job queue management system optimized for scalability and versatility. <i>Source Code for Biology and Medicine</i> , 2012 , 7, 8	1.9	3
1	Discovery and visualization of uncharacterized drug-protein adducts using mass spectrometry		1