

Lutz Fischer

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9564394/publications.pdf>

Version: 2024-02-01

20
papers

1,743
citations

471509

17
h-index

713466

21
g-index

28
all docs

28
docs citations

28
times ranked

2066
citing authors

#	ARTICLE	IF	CITATIONS
1	Architecture of the RNA polymerase II-TFIIF complex revealed by cross-linking and mass spectrometry. EMBO Journal, 2010, 29, 717-726.	7.8	355
2	xiNET: Cross-link Network Maps With Residue Resolution. Molecular and Cellular Proteomics, 2015, 14, 1137-1147.	3.8	242
3	Quirks of Error Estimation in Cross-Linking/Mass Spectrometry. Analytical Chemistry, 2017, 89, 3829-3833.	6.5	136
4	Quantitative cross-linking/mass spectrometry using isotope-labelled cross-linkers. Journal of Proteomics, 2013, 88, 120-128.	2.4	121
5	An integrated workflow for crosslinking mass spectrometry. Molecular Systems Biology, 2019, 15, e8994.	7.2	120
6	Defining the <sc>RNA</sc> interactome by total <sc>RNA</sc> associated protein purification. Molecular Systems Biology, 2019, 15, e8689.	7.2	114
7	Serum Albumin Domain Structures in Human Blood Serum by Mass Spectrometry and Computational Biology. Molecular and Cellular Proteomics, 2016, 15, 1105-1116.	3.8	84
8	A Study into the Collision-induced Dissociation (CID) Behavior of Cross-Linked Peptides. Molecular and Cellular Proteomics, 2016, 15, 1094-1104.	3.8	78
9	Reliable identification of protein-protein interactions by crosslinking mass spectrometry. Nature Communications, 2021, 12, 3564.	12.8	69
10	Structure of Complement C3(H2O) Revealed By Quantitative Cross-Linking/Mass Spectrometry And Modeling. Molecular and Cellular Proteomics, 2016, 15, 2730-2743.	3.8	59
11	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. Molecular and Cellular Proteomics, 2017, 16, 1275-1285.	3.8	55
12	In Situ Structural Restraints from Cross-Linking Mass Spectrometry in Human Mitochondria. Journal of Proteome Research, 2020, 19, 327-336.	3.7	52
13	On the Reproducibility of Label-Free Quantitative Cross-Linking/Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2018, 29, 405-412.	2.8	39
14	In-Search Assignment of Monoisotopic Peaks Improves the Identification of Cross-Linked Peptides. Journal of Proteome Research, 2018, 17, 3923-3931.	3.7	36
15	Quantitative cross-linking/mass spectrometry reveals subtle protein conformational changes. Wellcome Open Research, 2016, 1, 5.	1.8	30
16	Quantitative Cross-linking/Mass Spectrometry Using Isotope-labeled Cross-linkers and MaxQuant. Molecular and Cellular Proteomics, 2016, 15, 2769-2778.	3.8	28
17	Noncovalently Associated Peptides Observed during Liquid Chromatography-Mass Spectrometry and Their Effect on Cross-Link Analyses. Analytical Chemistry, 2019, 91, 2678-2685.	6.5	19
18	Improved Peptide Backbone Fragmentation Is the Primary Advantage of MS-Cleavable Crosslinkers. Analytical Chemistry, 2022, 94, 7779-7786.	6.5	15

#	ARTICLE	IF	CITATIONS
19	False discovery rate estimation and heterobifunctional cross-linkers. PLoS ONE, 2018, 13, e0196672.	2.5	14
20	Blind testing cross-linking/mass spectrometry under the auspices of the 11th critical assessment of methods of protein structure prediction (CASP11). Wellcome Open Research, 2016, 1, 24.	1.8	12