# Lutz Fischer

## List of Publications by Year
## in descending order

| 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 | Improved Peptide Backbone Fragmentation Is the Primary Advantage of MS-Cleavable Crosslinkers. Analytical Chemistry, 2022, 94, 7779-7786. | 6.5 | 15 |
| 2 | Reliable identification of protein-protein interactions by crosslinking mass spectrometry. Nature Communications, 2021, 12, 3564. | 12.8 | 69 |
| 3 | In Situ Structural Restraints from Cross-Linking Mass Spectrometry in Human Mitochondria. Journal of Proteome Research, 2020, 19, 327-336. | 3.7 | 52 |
| 4 | An integrated workflow for crosslinking mass spectrometry. Molecular Systems Biology, 2019, 15, e8994. | 7.2 | 120 |
| 5 | Defining the <scp>RNA</scp> interactome by total <scp>RNA</scp> â€‹associated protein purification. Molecular Systems Biology, 2019, 15, e8689. | 7.2 | 114 |
| 6 | 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 |
| 7 | 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 |
| 8 | False discovery rate estimation and heterobifunctional cross-linkers. PLoS ONE, 2018, 13, e0196672. | 2.5 | 14 |
| 9 | In-Search Assignment of Monoisotopic Peaks Improves the Identification of Cross-Linked Peptides. Journal of Proteome Research, 2018, 17, 3923-3931. | 3.7 | 36 |
| 10 | Quirks of Error Estimation in Cross-Linking/Mass Spectrometry. Analytical Chemistry, 2017, 89, 3829-3833. | 6.5 | 136 |
| 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 | A Study into the Collision-induced Dissociation (CID) Behavior of Cross-Linked Peptides. Molecular and Cellular Proteomics, 2016, 15, 1094-1104. | 3.8 | 78 |
| 13 | Quantitative Cross-linking/Mass Spectrometry Using Isotope-labeled Cross-linkers and MaxQuant. Molecular and Cellular Proteomics, 2016, 15, 2769-2778. | 3.8 | 28 |
| 14 | 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 |
| 15 | 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 |
| 16 | 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 |
| 17 | Quantitative cross-linking/mass spectrometry reveals subtle protein conformational changes. Wellcome Open Research, 2016, 1, 5. | 1.8 | 30 |
| 18 | xiNET: Cross-link Network Maps With Residue Resolution. Molecular and Cellular Proteomics, 2015, 14, 1137-1147. | 3.8 | 242 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Quantitative cross-linking/mass spectrometry using isotope-labelled cross-linkers. Journal of Proteomics, 2013, 88, 120-128. | 2.4 | 121 |
| 20 | Architecture of the RNA polymerase II–TFIIF complex revealed by cross-linking and mass spectrometry. EMBO Journal, 2010, 29, 717-726. | 7.8 | 355 |