

Alexander Leitner

List of Publications by Year in descending order

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Version: 2024-02-01

103
papers

9,097
citations

50276

46
h-index

45317

90
g-index

133
all docs

133
docs citations

133
times ranked

11689
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Chemical derivatization of peptides for quantitative proteomics. , 2022, , 75-94. | | 0 |
| 2 | pH Dependence of Succinimide-Ester-Based Protein Cross-Linking for Structural Mass Spectrometry Applications. ACS Measurement Science Au, 2022, 2, 132-138. | 4.4 | 1 |
| 3 | Sequence-specific RNA recognition by an RGG motif connects U1 and U2 snRNP for spliceosome assembly. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 7.1 | 18 |
| 4 | Cross-linking and mass spectrometry as a tool for studying the structural biology of ribonucleoproteins. Structure, 2022, 30, 441-461. | 3.3 | 9 |
| 5 | Structural architecture of the human NALCN channelosome. Nature, 2022, 603, 180-186. | 27.8 | 18 |
| 6 | Enhancer RNAs stimulate Pol II pause release by harnessing multivalent interactions to NELF. Nature Communications, 2022, 13, 2429. | 12.8 | 19 |
| 7 | Nucleotide-amino acid π -stacking interactions initiate photo cross-linking in RNA-protein complexes. Nature Communications, 2022, 13, 2719. | 12.8 | 15 |
| 8 | Expanding the Cross-Link Coverage of a Carboxyl-Group Specific Chemical Cross-Linking Strategy for Structural Proteomics Applications. Analytical Chemistry, 2021, 93, 1944-1950. | 6.5 | 12 |
| 9 | Structural and functional dissection of reovirus capsid folding and assembly by the prefoldin-TRiC/CCT chaperone network. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 7.1 | 30 |
| 10 | Native mass spectrometry analyses of chaperonin complex TRiC/CCT reveal subunit N-terminal processing and re-association patterns. Scientific Reports, 2021, 11, 13084. | 3.3 | 7 |
| 11 | Puf6 primes 60S pre-ribosome nuclear export at low temperature. Nature Communications, 2021, 12, 4696. | 12.8 | 8 |
| 12 | The human GID complex engages two independent modules for substrate recruitment. EMBO Reports, 2021, 22, e52981. | 4.5 | 21 |
| 13 | Single Nucleotide Resolution RNA-Protein Cross-Linking Mass Spectrometry: A Simple Extension of the CLIR-MS Workflow. Analytical Chemistry, 2021, 93, 14626-14634. | 6.5 | 10 |
| 14 | Molecular architecture of the human tRNA ligase complex. ELife, 2021, 10, . | 6.0 | 22 |
| 15 | The Polyglutamine Expansion at the N-Terminal of Huntingtin Protein Modulates the Dynamic Configuration and Phosphorylation of the C-Terminal HEAT Domain. Structure, 2020, 28, 1035-1050.e8. | 3.3 | 24 |
| 16 | The structure and symmetry of radial spoke protein complex in <i>Chlamydomonas</i> flagella. Journal of Cell Science, 2020, 133, . | 2.0 | 14 |
| 17 | INTS10-INTS13-INTS14 form a functional module of Integrator that binds nucleic acids and the cleavage module. Nature Communications, 2020, 11, 3422. | 12.8 | 44 |
| 18 | Architecture and functional dynamics of the pentafunctional AROM complex. Nature Chemical Biology, 2020, 16, 973-978. | 8.0 | 8 |

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|----|--|------|-----------|
| 19 | A precisely positioned MED12 activation helix stimulates CDK8 kinase activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2894-2905. | 7.1 | 47 |
| 20 | Combining Mass Spectrometry (MS) and Nuclear Magnetic Resonance (NMR) Spectroscopy for Integrative Structural Biology of Protein-RNA Complexes. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032359. | 5.5 | 11 |
| 21 | Assessment of chemical-crosslink-assisted protein structure modeling in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1283-1297. | 2.6 | 27 |
| 22 | CryoEM structures of Arabidopsis DDR complexes involved in RNA-directed DNA methylation. <i>Nature Communications</i> , 2019, 10, 3916. | 12.8 | 31 |
| 23 | Mitoribosomal small subunit biogenesis in trypanosomes involves an extensive assembly machinery. <i>Science</i> , 2019, 365, 1144-1149. | 12.6 | 61 |
| 24 | First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961. | 6.5 | 100 |
| 25 | The Chaperonin TRiC/CCT Associates with Prefoldin through a Conserved Electrostatic Interface Essential for Cellular Proteostasis. <i>Cell</i> , 2019, 177, 751-765.e15. | 28.9 | 98 |
| 26 | Proteomic identification of a marker signature for MAPK resistance in melanoma. <i>EMBO Journal</i> , 2019, 38, e95874. | 7.8 | 26 |
| 27 | Structure of a human cap-dependent 48S translation pre-initiation complex. <i>Nucleic Acids Research</i> , 2018, 46, 2678-2689. | 14.5 | 76 |
| 28 | Integrative Structural Investigation on the Architecture of Human Importin4_Histone H3/H4_Asf1a Complex and Its Histone H3 Tail Binding. <i>Journal of Molecular Biology</i> , 2018, 430, 822-841. | 4.2 | 17 |
| 29 | A review of the role of chemical modification methods in contemporary mass spectrometry-based proteomics research. <i>Analytica Chimica Acta</i> , 2018, 1000, 2-19. | 5.4 | 26 |
| 30 | Insights into autophagosome biogenesis from structural and biochemical analyses of the ATG2A-WIPI4 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9792-E9801. | 7.1 | 159 |
| 31 | Molecular basis for disassembly of an importin:ribosomal protein complex by the escortin Tsr2. <i>Nature Communications</i> , 2018, 9, 3669. | 12.8 | 17 |
| 32 | Evolutionary shift toward protein-based architecture in trypanosomal mitochondrial ribosomes. <i>Science</i> , 2018, 362, . | 12.6 | 107 |
| 33 | An Unbiased Screen for Human Cytomegalovirus Identifies Neuropilin-2 as a Central Viral Receptor. <i>Cell</i> , 2018, 174, 1158-1171.e19. | 28.9 | 171 |
| 34 | Conformational control and DNA-binding mechanism of the metazoan origin recognition complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5906-E5915. | 7.1 | 34 |
| 35 | Contribution of Mass Spectrometry-Based Proteomics to the Understanding of TNF Signaling. <i>Journal of Proteome Research</i> , 2017, 16, 14-33. | 3.7 | 11 |
| 36 | Insights into chemoselectivity principles in metal oxide affinity chromatography using tailored nanocast metal oxide microspheres and mass spectrometry-based phosphoproteomics. <i>Analyst</i> , The, 2017, 142, 1993-2003. | 3.5 | 13 |

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|----|---|------|-----------|
| 37 | Structural modeling of protein-RNA complexes using crosslinking of segmentally isotope-labeled RNA and MS/MS. <i>Nature Methods</i> , 2017, 14, 487-490. | 19.0 | 44 |
| 38 | Molecular Details Underlying Dynamic Structures and Regulation of the Human 26S Proteasome. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 840-854. | 3.8 | 93 |
| 39 | Mechanistic Insights into Autoinhibition of the Oncogenic Chromatin Remodeler ALC1. <i>Molecular Cell</i> , 2017, 68, 847-859.e7. | 9.7 | 53 |
| 40 | The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1275-1285. | 3.8 | 55 |
| 41 | Molecular Architecture of Yeast Chromatin Assembly Factor 1. <i>Scientific Reports</i> , 2016, 6, 26702. | 3.3 | 26 |
| 42 | Mass Spectrometry Applied to Bottom-Up Proteomics: Entering the High-Throughput Era for Hypothesis Testing. <i>Annual Review of Analytical Chemistry</i> , 2016, 9, 449-472. | 5.4 | 266 |
| 43 | Cross-linking and other structural proteomics techniques: how chemistry is enabling mass spectrometry applications in structural biology. <i>Chemical Science</i> , 2016, 7, 4792-4803. | 7.4 | 38 |
| 44 | Crosslinking and Mass Spectrometry: An Integrated Technology to Understand the Structure and Function of Molecular Machines. <i>Trends in Biochemical Sciences</i> , 2016, 41, 20-32. | 7.5 | 330 |
| 45 | Insertion of the Biogenesis Factor Rei1 Probes the Ribosomal Tunnel during 60S Maturation. <i>Cell</i> , 2016, 164, 91-102. | 28.9 | 97 |
| 46 | Enrichment Strategies in Phosphoproteomics. <i>Methods in Molecular Biology</i> , 2016, 1355, 105-121. | 0.9 | 45 |
| 47 | Huntingtin's spherical solenoid structure enables polyglutamine tract-dependent modulation of its structure and function. <i>ELife</i> , 2016, 5, e11184. | 6.0 | 52 |
| 48 | Structural and kinetic analysis of the COP9-Signalosome activation and the cullin-RING ubiquitin ligase deneddylation cycle. <i>ELife</i> , 2016, 5, . | 6.0 | 82 |
| 49 | Antigenic Characterization of the HCMV gH/gL/gO and Pentamer Cell Entry Complexes Reveals Binding Sites for Potently Neutralizing Human Antibodies. <i>PLoS Pathogens</i> , 2015, 11, e1005230. | 4.7 | 65 |
| 50 | Molecular Basis of the Rapamycin Insensitivity of Target Of Rapamycin Complex 2. <i>Molecular Cell</i> , 2015, 58, 977-988. | 9.7 | 120 |
| 51 | The complete structure of the 55 S mammalian mitochondrial ribosome. <i>Science</i> , 2015, 348, 303-308. | 12.6 | 344 |
| 52 | xTract: software for characterizing conformational changes of protein complexes by quantitative cross-linking mass spectrometry. <i>Nature Methods</i> , 2015, 12, 1185-1190. | 19.0 | 83 |
| 53 | Architecture and conformational switch mechanism of the ryanodine receptor. <i>Nature</i> , 2015, 517, 39-43. | 27.8 | 282 |
| 54 | Lysine-specific chemical cross-linking of protein complexes and identification of cross-linking sites using LC-MS/MS and the xQuest/xProphet software pipeline. <i>Nature Protocols</i> , 2014, 9, 120-137. | 12.0 | 244 |

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|----|---|------|-----------|
| 55 | Conserved Peptide Fragmentation as a Benchmarking Tool for Mass Spectrometers and a Discriminating Feature for Targeted Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2056-2071. | 3.8 | 96 |
| 56 | A mass spectrometry-based hybrid method for structural modeling of protein complexes. <i>Nature Methods</i> , 2014, 11, 403-406. | 19.0 | 149 |
| 57 | Architecture of the large subunit of the mammalian mitochondrial ribosome. <i>Nature</i> , 2014, 505, 515-519. | 27.8 | 207 |
| 58 | The complete structure of the large subunit of the mammalian mitochondrial ribosome. <i>Nature</i> , 2014, 515, 283-286. | 27.8 | 231 |
| 59 | Chemical cross-linking/mass spectrometry targeting acidic residues in proteins and protein complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9455-9460. | 7.1 | 213 |
| 60 | Interaction of 2-oxoglutarate dehydrogenase OdhA with its inhibitor OdhI in <i>Corynebacterium glutamicum</i> : Mutants and a model. <i>Journal of Biotechnology</i> , 2014, 191, 99-105. | 3.8 | 26 |
| 61 | Mass spectrometry supported determination of protein complex structure. <i>Current Opinion in Structural Biology</i> , 2013, 23, 252-260. | 5.7 | 130 |
| 62 | SnapShot: Mass Spectrometry for Protein and Proteome Analyses. <i>Cell</i> , 2013, 154, 252-252.e1. | 28.9 | 24 |
| 63 | Cross-Link Guided Molecular Modeling with ROSETTA. <i>PLoS ONE</i> , 2013, 8, e73411. | 2.5 | 144 |
| 64 | Expanding the Chemical Cross-Linking Toolbox by the Use of Multiple Proteases and Enrichment by Size Exclusion Chromatography. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014126. | 3.8 | 264 |
| 65 | Structural Probing of a Protein Phosphatase 2A Network by Chemical Cross-Linking and Mass Spectrometry. <i>Science</i> , 2012, 337, 1348-1352. | 12.6 | 357 |
| 66 | False discovery rate estimation for cross-linked peptides identified by mass spectrometry. <i>Nature Methods</i> , 2012, 9, 901-903. | 19.0 | 273 |
| 67 | Quantitative high-performance liquid chromatography-tandem mass spectrometry impurity profiling methods for the analysis of parenteral infusion solutions for amino acid supplementation containing l-alanyl-l-glutamine. <i>Journal of Chromatography A</i> , 2012, 1259, 111-120. | 3.7 | 9 |
| 68 | The Molecular Architecture of the Eukaryotic Chaperonin TRiC/CCT. <i>Structure</i> , 2012, 20, 814-825. | 3.3 | 261 |
| 69 | Development of an Indole-Based Chemically Cleavable Linker Concept for Immobilizing Bait Compounds for Protein Pull-Down Experiments. <i>Bioconjugate Chemistry</i> , 2011, 22, 211-217. | 3.6 | 6 |
| 70 | Tools for analyzing the phosphoproteome and other phosphorylated biomolecules: A review. <i>Analytica Chimica Acta</i> , 2011, 703, 19-30. | 5.4 | 86 |
| 71 | Probing the Phosphoproteome of HeLa Cells Using Nanocast Metal Oxide Microspheres for Phosphopeptide Enrichment. <i>Analytical Chemistry</i> , 2010, 82, 2726-2733. | 6.5 | 63 |
| 72 | Phosphopeptide enrichment using metal oxide affinity chromatography. <i>TrAC - Trends in Analytical Chemistry</i> , 2010, 29, 177-185. | 11.4 | 147 |

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|----|---|------|-----------|
| 73 | Synthesis, in vitro progesterone receptors affinity of gadolinium containing mifepristone conjugates and estimation of binding sites in human breast cancer cells. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 1891-1898. | 3.0 | 10 |
| 74 | Probing Native Protein Structures by Chemical Cross-linking, Mass Spectrometry, and Bioinformatics. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1634-1649. | 3.8 | 407 |
| 75 | Comparison of toad venoms from different <i>Bufo</i> species by HPLC and LC-DAD-MS/MS. <i>Journal of Ethnopharmacology</i> , 2010, 131, 368-376. | 4.1 | 75 |
| 76 | Optimizing the performance of tin dioxide microspheres for phosphopeptide enrichment. <i>Analytica Chimica Acta</i> , 2009, 638, 51-57. | 5.4 | 22 |
| 77 | Applications of Chemical Tagging Approaches in Combination with 2DE and Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2009, 519, 83-101. | 0.9 | 3 |
| 78 | Chemical Tagging Strategies for Mass Spectrometry-Based Phospho-proteomics. <i>Methods in Molecular Biology</i> , 2009, 527, 229-243. | 0.9 | 32 |
| 79 | Malondialdehyde tagging improves the analysis of arginine oligomers and arginine-containing dendrimers by HPLC-MS. <i>Journal of Separation Science</i> , 2008, 31, 499-506. | 2.5 | 10 |
| 80 | Tin Dioxide Microspheres as a Promising Material for Phosphopeptide Enrichment Prior to Liquid Chromatography-Tandem Mass Spectrometry Analysis. <i>Advanced Functional Materials</i> , 2008, 18, 2381-2389. | 14.9 | 68 |
| 81 | ATF4-dependent transcription is a key mechanism in VEGF up-regulation by oxidized phospholipids: critical role of oxidized sn-2 residues in activation of unfolded protein response. <i>Blood</i> , 2008, 112, 330-339. | 1.4 | 97 |
| 82 | Photooxidation Generates Biologically Active Phospholipids That Induce Heme Oxygenase-1 in Skin Cells. <i>Journal of Biological Chemistry</i> , 2007, 282, 16934-16941. | 3.4 | 52 |
| 83 | Reaction of the Indole Group with Malondialdehyde: Application for the Derivatization of Tryptophan Residues in Peptides. <i>Bioconjugate Chemistry</i> , 2007, 18, 1678-1683. | 3.6 | 34 |
| 84 | Selective Enrichment of Tryptophan-Containing Peptides from Protein Digests Employing a Reversible Derivatization with Malondialdehyde and Solid-Phase Capture on Hydrazide Beads. <i>Journal of Proteome Research</i> , 2007, 6, 3827-3834. | 3.7 | 29 |
| 85 | Improving fragmentation of poorly fragmenting peptides and phosphopeptides during collision-induced dissociation by malondialdehyde modification of arginine residues. <i>Journal of Mass Spectrometry</i> , 2007, 42, 950-959. | 1.6 | 31 |
| 86 | Use of the arginine-specific butanedione/phenylboronic acid tag for analysis of peptides and protein digests using matrix-assisted laser desorption/ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 1321-1330. | 1.5 | 16 |
| 87 | The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007, 25, 887-893. | 17.5 | 694 |
| 88 | Influence of Solvent Additive Composition on Chromatographic Separation and Sodium Adduct Formation of Peptides in HPLC-ESI MS. <i>Chromatographia</i> , 2007, 65, 649-653. | 1.3 | 29 |
| 89 | Identification of Marker Proteins for the Adulteration of Meat Products with Soybean Proteins by Multidimensional Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2006, 5, 2424-2430. | 3.7 | 76 |
| 90 | Chemistry meets proteomics: The use of chemical tagging reactions for MS-based proteomics. <i>Proteomics</i> , 2006, 6, 5418-5434. | 2.2 | 111 |

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|-----|---|-----|-----------|
| 91 | Silica-based monolithic columns with mixed-mode reversed-phase/weak anion-exchange selectivity principle for high-performance liquid chromatography. <i>Journal of Separation Science</i> , 2006, 29, 966-978. | 2.5 | 51 |
| 92 | Derivatisation of arginine residues with malondialdehyde for the analysis of peptides and protein digests by LC-ESI-MS/MS. <i>Journal of Mass Spectrometry</i> , 2006, 41, 623-632. | 1.6 | 47 |
| 93 | Effects of an arginine-selective tagging procedure on the fragmentation behavior of peptides studied by electrospray ionization tandem mass spectrometry (ESI-MS/MS). <i>Analytica Chimica Acta</i> , 2005, 528, 165-173. | 5.4 | 13 |
| 94 | Solid-phase capture and release of arginine peptides by selective tagging and boronate affinity chromatography. <i>Journal of Chromatography A</i> , 2005, 1079, 187-196. | 3.7 | 25 |
| 95 | Comparative study on the use of ortho-phthalaldehyde, naphthalene-2,3-dicarboxaldehyde and anthracene-2,3-dicarboxaldehyde reagents for α -amino acids followed by the enantiomer separation of the formed isoindolin-1-one derivatives using quinine-type chiral stationary phases. <i>Journal of Chromatography A</i> , 2005, 1083, 80-88. | 3.7 | 21 |
| 96 | Functional Probing of Arginine Residues in Proteins Using Mass Spectrometry and an Arginine-Specific Covalent Tagging Concept. <i>Analytical Chemistry</i> , 2005, 77, 4481-4488. | 6.5 | 24 |
| 97 | Epoxycyclopentenone-Containing Oxidized Phospholipids Restore Endothelial Barrier Function via Cdc42 and Rac. <i>Circulation Research</i> , 2004, 95, 892-901. | 4.5 | 146 |
| 98 | Current chemical tagging strategies for proteome analysis by mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2004, 813, 1-26. | 2.3 | 109 |
| 99 | Probing of arginine residues in peptides and proteins using selective tagging and electrospray ionization mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2003, 38, 891-899. | 1.6 | 31 |
| 100 | Comparison of methods for the determination of ochratoxin A in wine. <i>Analytica Chimica Acta</i> , 2002, 453, 33-41. | 5.4 | 94 |
| 101 | Determination of the metabolites of nitrofurantoin antibiotics in animal tissue by high-performance liquid chromatography-tandem mass spectrometry. <i>Journal of Chromatography A</i> , 2001, 939, 49-58. | 3.7 | 210 |
| 102 | Application of a chromolith speedROD RP-18e HPLC column: Determination of ochratoxin A in different wines by high-performance liquid chromatography-tandem mass spectrometry. <i>Chromatographia</i> , 2000, 52, 818-820. | 1.3 | 83 |
| 103 | Mapping protein-RNA interactions with single residue resolution by CLIR-MS/MS. <i>Protocol Exchange</i> , 0, , . | 0.3 | 2 |