

Alexander Leitner

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9156805/publications.pdf>

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	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007, 25, 887-893.	17.5	694
2	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
3	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
4	The complete structure of the 55 <i>S</i> mammalian mitochondrial ribosome. <i>Science</i> , 2015, 348, 303-308.	12.6	344
5	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
6	Architecture and conformational switch mechanism of the ryanodine receptor. <i>Nature</i> , 2015, 517, 39-43.	27.8	282
7	False discovery rate estimation for cross-linked peptides identified by mass spectrometry. <i>Nature Methods</i> , 2012, 9, 901-903.	19.0	273
8	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
9	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
10	The Molecular Architecture of the Eukaryotic Chaperonin TRiC/CCT. <i>Structure</i> , 2012, 20, 814-825.	3.3	261
11	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
12	The complete structure of the large subunit of the mammalian mitochondrial ribosome. <i>Nature</i> , 2014, 515, 283-286.	27.8	231
13	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
14	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
15	Architecture of the large subunit of the mammalian mitochondrial ribosome. <i>Nature</i> , 2014, 505, 515-519.	27.8	207
16	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
17	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
18	A mass spectrometry-based hybrid method for structural modeling of protein complexes. <i>Nature Methods</i> , 2014, 11, 403-406.	19.0	149

#	ARTICLE	IF	CITATIONS
19	Phosphopeptide enrichment using metal oxide affinity chromatography. <i>TrAC - Trends in Analytical Chemistry</i> , 2010, 29, 177-185.	11.4	147
20	Epoxy-cyclopentenone-Containing Oxidized Phospholipids Restore Endothelial Barrier Function via Cdc42 and Rac. <i>Circulation Research</i> , 2004, 95, 892-901.	4.5	146
21	Cross-Link Guided Molecular Modeling with ROSETTA. <i>PLoS ONE</i> , 2013, 8, e73411.	2.5	144
22	Mass spectrometry supported determination of protein complex structure. <i>Current Opinion in Structural Biology</i> , 2013, 23, 252-260.	5.7	130
23	Molecular Basis of the Rapamycin Insensitivity of Target Of Rapamycin Complex 2. <i>Molecular Cell</i> , 2015, 58, 977-988.	9.7	120
24	Chemistry meets proteomics: The use of chemical tagging reactions for MS-based proteomics. <i>Proteomics</i> , 2006, 6, 5418-5434.	2.2	111
25	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
26	Evolutionary shift toward protein-based architecture in trypanosomal mitochondrial ribosomes. <i>Science</i> , 2018, 362, .	12.6	107
27	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	6.5	100
28	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
29	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
30	Insertion of the Biogenesis Factor Rei1 Probes the Ribosomal Tunnel during 60S Maturation. <i>Cell</i> , 2016, 164, 91-102.	28.9	97
31	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
32	Comparison of methods for the determination of ochratoxin A in wine. <i>Analytica Chimica Acta</i> , 2002, 453, 33-41.	5.4	94
33	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
34	Tools for analyzing the phosphoproteome and other phosphorylated biomolecules: A review. <i>Analytica Chimica Acta</i> , 2011, 703, 19-30.	5.4	86
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	Structure of a human cap-dependent 48S translation pre-initiation complex. <i>Nucleic Acids Research</i> , 2018, 46, 2678-2689.	14.5	76
40	Comparison of toad venoms from different Bufo species by HPLC and LC-DAD-MS/MS. <i>Journal of Ethnopharmacology</i> , 2010, 131, 368-376.	4.1	75
41	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
42	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
43	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
44	Mitoribosomal small subunit biogenesis in trypanosomes involves an extensive assembly machinery. <i>Science</i> , 2019, 365, 1144-1149.	12.6	61
45	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
46	Mechanistic Insights into Autoinhibition of the Oncogenic Chromatin Remodeler ALC1. <i>Molecular Cell</i> , 2017, 68, 847-859.e7.	9.7	53
47	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
48	Huntingtin's spherical solenoid structure enables polyglutamine tract-dependent modulation of its structure and function. <i>ELife</i> , 2016, 5, e11184.	6.0	52
49	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
50	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
51	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
52	Enrichment Strategies in Phosphoproteomics. <i>Methods in Molecular Biology</i> , 2016, 1355, 105-121.	0.9	45
53	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
54	INTS10-INTS13-INTS14 form a functional module of Integrator that binds nucleic acids and the cleavage module. <i>Nature Communications</i> , 2020, 11, 3422.	12.8	44

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	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
58	Chemical Tagging Strategies for Mass Spectrometry-Based Phospho-proteomics. <i>Methods in Molecular Biology</i> , 2009, 527, 229-243.	0.9	32
59	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
60	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
61	CryoEM structures of Arabidopsis DDR complexes involved in RNA-directed DNA methylation. <i>Nature Communications</i> , 2019, 10, 3916.	12.8	31
62	Structural and functional dissection of reovirus capsid folding and assembly by the prefoldin-TRiC/CCT chaperone network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	30
63	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
64	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
65	Assessment of chemical crosslink-assisted protein structure modeling in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1283-1297.	2.6	27
66	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
67	Molecular Architecture of Yeast Chromatin Assembly Factor 1. <i>Scientific Reports</i> , 2016, 6, 26702.	3.3	26
68	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
69	Proteomic identification of a marker signature for MAPK i resistance in melanoma. <i>EMBO Journal</i> , 2019, 38, e95874.	7.8	26
70	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
71	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
72	SnapShot: Mass Spectrometry for Protein and Proteome Analyses. <i>Cell</i> , 2013, 154, 252-252.e1.	28.9	24

#	ARTICLE	IF	CITATIONS
73	The Polyglutamine Expansion at the N-Terminal of Huntingtin Protein Modulates the Dynamic Configuration and Phosphorylation of the C-Terminal HEAT Domain. <i>Structure</i> , 2020, 28, 1035-1050.e8.	3.3	24
74	Optimizing the performance of tin dioxide microspheres for phosphopeptide enrichment. <i>Analytica Chimica Acta</i> , 2009, 638, 51-57.	5.4	22
75	Molecular architecture of the human tRNA ligase complex. <i>ELife</i> , 2021, 10, .	6.0	22
76	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
77	The human GID complex engages two independent modules for substrate recruitment. <i>EMBO Reports</i> , 2021, 22, e52981.	4.5	21
78	Enhancer RNAs stimulate Pol II pause release by harnessing multivalent interactions to NELF. <i>Nature Communications</i> , 2022, 13, 2429.	12.8	19
79	Sequence-specific RNA recognition by an RGG motif connects U1 and U2 snRNP for spliceosome assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	18
80	Structural architecture of the human NALCN channelosome. <i>Nature</i> , 2022, 603, 180-186.	27.8	18
81	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
82	Molecular basis for disassembly of an importin:ribosomal protein complex by the escortin Tsr2. <i>Nature Communications</i> , 2018, 9, 3669.	12.8	17
83	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
84	Nucleotide-amino acid π -stacking interactions initiate photo cross-linking in RNA-protein complexes. <i>Nature Communications</i> , 2022, 13, 2719.	12.8	15
85	The structure and symmetry of radial spoke protein complex in <i>Chlamydomonas</i> flagella. <i>Journal of Cell Science</i> , 2020, 133, .	2.0	14
86	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
87	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
88	Expanding the Cross-Link Coverage of a Carboxyl-Group Specific Chemical Cross-Linking Strategy for Structural Proteomics Applications. <i>Analytical Chemistry</i> , 2021, 93, 1944-1950.	6.5	12
89	Contribution of Mass Spectrometry-Based Proteomics to the Understanding of TNF- α Signaling. <i>Journal of Proteome Research</i> , 2017, 16, 14-33.	3.7	11
90	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

#	ARTICLE	IF	CITATIONS
91	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
92	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
93	Single Nucleotide Resolution RNA-Protein Cross-Linking Mass Spectrometry: A Simple Extension of the CLIR-MS Workflow. <i>Analytical Chemistry</i> , 2021, 93, 14626-14634.	6.5	10
94	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
95	Cross-linking and mass spectrometry as a tool for studying the structural biology of ribonucleoproteins. <i>Structure</i> , 2022, 30, 441-461.	3.3	9
96	Architecture and functional dynamics of the pentafunctional AROM complex. <i>Nature Chemical Biology</i> , 2020, 16, 973-978.	8.0	8
97	Puf6 primes 60S pre-ribosome nuclear export at low temperature. <i>Nature Communications</i> , 2021, 12, 4696.	12.8	8
98	Native mass spectrometry analyses of chaperonin complex TRiC/CCT reveal subunit N-terminal processing and re-association patterns. <i>Scientific Reports</i> , 2021, 11, 13084.	3.3	7
99	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
100	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
101	Mapping protein-RNA interactions with single residue resolution by CLIR-MS/MS. <i>Protocol Exchange</i> , 0, , ,	0.3	2
102	pH Dependence of Succinimide-Ester-Based Protein Cross-Linking for Structural Mass Spectrometry Applications. <i>ACS Measurement Science Au</i> , 2022, 2, 132-138.	4.4	1
103	Chemical derivatization of peptides for quantitative proteomics. , 2022, , 75-94.		0