

Lan Huang

List of Publications by Year in descending order

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95
papers

5,109
citations

117625

34
h-index

102487

66
g-index

102
all docs

102
docs citations

102
times ranked

6020
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of a Novel Cross-linking Strategy for Fast and Accurate Identification of Cross-linked Peptides of Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.002170.	3.8	318
2	A Tandem Affinity Tag for Two-step Purification under Fully Denaturing Conditions. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 737-748.	3.8	315
3	Oxidative Stress-Mediated Regulation of Proteasome Complexes. <i>Molecular and Cellular Proteomics</i> , 2011, 10, R110.006924.	3.8	263
4	Cross-Linking Mass Spectrometry: An Emerging Technology for Interactomics and Structural Biology. <i>Analytical Chemistry</i> , 2018, 90, 144-165.	6.5	262
5	An Integrated Mass Spectrometry-based Proteomic Approach. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 366-378.	3.8	246
6	Mass Spectrometric Characterization of the Affinity-Purified Human 26S Proteasome Complex. <i>Biochemistry</i> , 2007, 46, 3553-3565.	2.5	243
7	Regulation of the 26S Proteasome Complex During Oxidative Stress. <i>Science Signaling</i> , 2010, 3, ra88.	3.6	224
8	Identifying Dynamic Interactors of Protein Complexes by Quantitative Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 46-57.	3.8	178
9	Comprehensive Analysis of a Multidimensional Liquid Chromatography Mass Spectrometry Dataset Acquired on a Quadrupole Selecting, Quadrupole Collision Cell, Time-of-flight Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1194-1204.	3.8	171
10	A New in Vivo Cross-linking Mass Spectrometry Platform to Define Protein-Protein Interactions in Living Cells. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3533-3543.	3.8	167
11	TLR8-Mediated Metabolic Control of Human Treg Function: A Mechanistic Target for Cancer Immunotherapy. <i>Cell Metabolism</i> , 2019, 29, 103-123.e5.	16.2	149
12	Site-specific proteasome phosphorylation controls cell proliferation and tumorigenesis. <i>Nature Cell Biology</i> , 2016, 18, 202-212.	10.3	148
13	Characterization of the proteasome interaction network using a QTAX-based tag-team strategy and protein interaction network analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13333-13338.	7.1	129
14	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	6.5	100
15	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
16	Profiling of Protein Interaction Networks of Protein Complexes Using Affinity Purification and Quantitative Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1650-1665.	3.8	89
17	The proteasome-interacting Ecm29 protein disassembles the 26S proteasome in response to oxidative stress. <i>Journal of Biological Chemistry</i> , 2017, 292, 16310-16320.	3.4	82
18	Protein interaction landscapes revealed by advanced in vivo cross-linking mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	77

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19	UBLCP1 is a 26S proteasome phosphatase that regulates nuclear proteasome activity. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18649-18654.	7.1	68
20	RNA Binding and Core Complexes Constitute the U-Insertion/Deletion Editosome. Molecular and Cellular Biology, 2014, 34, 4329-4342.	2.3	67
21	Functional Assignment of the 20 S Proteasome from Trypanosoma brucei Using Mass Spectrometry and New Bioinformatics Approaches. Journal of Biological Chemistry, 2001, 276, 28327-28339.	3.4	64
22	Characterization of the Human COP9 Signalosome Complex Using Affinity Purification and Mass Spectrometry. Journal of Proteome Research, 2008, 7, 4914-4925.	3.7	62
23	Structure of the full-length Clostridium difficile toxin B. Nature Structural and Molecular Biology, 2019, 26, 712-719.	8.2	59
24	Structural dynamics of the human COP9 signalosome revealed by cross-linking mass spectrometry and integrative modeling. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 4088-4098.	7.1	58
25	Developing an Acidic Residue Reactive and Sulfoxide-Containing MS-Cleavable Homobifunctional Cross-Linker for Probing Protein-Protein Interactions. Analytical Chemistry, 2016, 88, 8315-8322.	6.5	56
26	Developing a Multiplexed Quantitative Cross-Linking Mass Spectrometry Platform for Comparative Structural Analysis of Protein Complexes. Analytical Chemistry, 2016, 88, 10301-10308.	6.5	55
27	Mapping the Structural Topology of the Yeast 19S Proteasomal Regulatory Particle Using Chemical Cross-linking and Probabilistic Modeling. Molecular and Cellular Proteomics, 2012, 11, 1566-1577.	3.8	54
28	Characterization of Cell Cycle Specific Protein Interaction Networks of the Yeast 26S Proteasome Complex by the QTAX Strategy. Journal of Proteome Research, 2010, 9, 2016-2029.	3.7	51
29	Global approaches to understanding ubiquitination. Genome Biology, 2005, 6, 233.	9.6	43
30	Synthesis of two new enrichable and MS-cleavable cross-linkers to define protein-protein interactions by mass spectrometry. Organic and Biomolecular Chemistry, 2015, 13, 5030-5037.	2.8	41
31	Ubiquitin orchestrates proteasome dynamics between proliferation and quiescence in yeast. Molecular Biology of the Cell, 2017, 28, 2479-2491.	2.1	41
32	Structural basis for CSPG4 as a receptor for TcdB and a therapeutic target in Clostridioides difficile infection. Nature Communications, 2021, 12, 3748.	12.8	41
33	Mapping the Protein Interaction Network of the Human COP9 Signalosome Complex Using a Label-free QTAX Strategy. Molecular and Cellular Proteomics, 2012, 11, 138-147.	3.8	40
34	Developing New Isotope-Coded Mass Spectrometry-Cleavable Cross-Linkers for Elucidating Protein Structures. Analytical Chemistry, 2014, 86, 2099-2106.	6.5	36
35	Gln40 deamidation blocks structural reconfiguration and activation of SCF ubiquitin ligase complex by Nedd8. Nature Communications, 2015, 6, 10053.	12.8	36
36	Antisense Transcripts Delimit Exonucleolytic Activity of the Mitochondrial Ψ Processome to Generate Guide RNAs. Molecular Cell, 2016, 61, 364-378.	9.7	35

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37	Development of a Novel Sulfoxide-Containing MS-Cleavable Homobifunctional Cysteine-Reactive Cross-Linker for Studying Protein-Protein Interactions. <i>Analytical Chemistry</i> , 2018, 90, 7600-7607.	6.5	35
38	Reversible phosphorylation of Rpn1 regulates 26S proteasome assembly and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 328-336.	7.1	35
39	Characterization of Dynamic UbR-Proteasome Subcomplexes by In vivo Cross-linking (X) Assisted Bimolecular Tandem Affinity Purification (XBAP) and Label-free Quantitation. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2279-2292.	3.8	33
40	Selective enrichment and identification of azide-tagged cross-linked peptides using chemical ligation and mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1432-1445.	2.8	32
41	SCF ^{FBXO22} targets HDM2 for degradation and modulates breast cancer cell invasion and metastasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11754-11763.	7.1	32
42	Baicalein and Baicalin Promote Melanoma Apoptosis and Senescence via Metabolic Inhibition. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 836.	3.7	29
43	Ribosome-associated pentatricopeptide repeat proteins function as translational activators in mitochondria of trypanosomes. <i>Molecular Microbiology</i> , 2016, 99, 1043-1058.	2.5	28
44	In vivo assembly and trafficking of olfactory Ionotropic Receptors. <i>BMC Biology</i> , 2019, 17, 34.	3.8	28
45	S-nitrosylation of Cofilin-1 Serves as a Novel Pathway for VEGF-Stimulated Endothelial Cell Migration. <i>Journal of Cellular Physiology</i> , 2015, 230, 406-417.	4.1	27
46	Structural Basis for Shelterin Bridge Assembly. <i>Molecular Cell</i> , 2017, 68, 698-714.e5.	9.7	27
47	Nuclear factor-erythroid-2 related transcription factor-1 (Nrf1) is regulated by O-GlcNAc transferase. <i>Free Radical Biology and Medicine</i> , 2017, 110, 196-205.	2.9	26
48	Wor1 establishes opaque cell fate through inhibition of the general co-repressor Tup1 in <i>Candida albicans</i> . <i>PLoS Genetics</i> , 2018, 14, e1007176.	3.5	25
49	Proteomics of proteasome complexes and ubiquitinated proteins. <i>Expert Review of Proteomics</i> , 2007, 4, 649-665.	3.0	24
50	Pivotal role for the ubiquitin Y59-E51 loop in lysine 48 polyubiquitination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8434-8439.	7.1	24
51	Modulation of DRAK2 Autophosphorylation by Antigen Receptor Signaling in Primary Lymphocytes. <i>Journal of Biological Chemistry</i> , 2007, 282, 4573-4584.	3.4	23
52	Ty3 Retrotransposon Hijacks Mating Yeast RNA Processing Bodies to Infect New Genomes. <i>PLoS Genetics</i> , 2015, 11, e1005528.	3.5	23
53	The Hippo pathway kinases LATS1 and LATS2 attenuate cellular responses to heavy metals through phosphorylating MTF1. <i>Nature Cell Biology</i> , 2022, 24, 74-87.	10.3	22
54	Comprehensive Mass Spectrometric Analysis of the 20S Proteasome Complex. <i>Methods in Enzymology</i> , 2005, 405, 187-236.	1.0	21

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55	<scp>PPR</scp> polyadenylation factor defines mitochondrial <scp>mRNA</scp> identity and stability in trypanosomes. <i>EMBO Journal</i> , 2017, 36, 2435-2454.	7.8	20
56	Branched ubiquitin chain binding and deubiquitination by UCH37 facilitate proteasome clearance of stress-induced inclusions. <i>ELife</i> , 2021, 10, .	6.0	20
57	Transcription initiation defines kinetoplast RNA boundaries. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10323-E10332.	7.1	19
58	Enabling Photoactivated Cross-Linking Mass Spectrometric Analysis of Protein Complexes by Novel MS-Cleavable Cross-Linkers. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100084.	3.8	19
59	Dissecting Fission Yeast Shelterin Interactions via MICro-MS Links Disruption of Shelterin Bridge to Tumorigenesis. <i>Cell Reports</i> , 2015, 12, 2169-2180.	6.4	18
60	Mechanisms Underlying Acrolein-Mediated Inhibition of Chromatin Assembly. <i>Molecular and Cellular Biology</i> , 2016, 36, 2995-3008.	2.3	18
61	Microhomology-based CRISPR tagging tools for protein tracking, purification, and depletion. <i>Journal of Biological Chemistry</i> , 2019, 294, 10877-10885.	3.4	16
62	Citrate Promotes Excessive Lipid Biosynthesis and Senescence in Tumor Cells for Tumor Therapy. <i>Advanced Science</i> , 2022, 9, e2101553.	11.2	16
63	Design of CID-cleavable protein cross-linkers: identical mass modifications for simpler sequence analysis. <i>Organic and Biomolecular Chemistry</i> , 2015, 13, 9793-9807.	2.8	14
64	Probing H ₂ O ₂ -mediated Structural Dynamics of the Human 26S Proteasome Using Quantitative Cross-linking Mass Spectrometry (QXL-MS). <i>Molecular and Cellular Proteomics</i> , 2019, 18, 954-967.	3.8	14
65	Pentatricopeptide repeat poly(A) binding protein KPAF4 stabilizes mitochondrial mRNAs in <i>Trypanosoma brucei</i> . <i>Nature Communications</i> , 2019, 10, 146.	12.8	14
66	Quality-Control Mechanism for Telomerase RNA Folding in the Cell. <i>Cell Reports</i> , 2020, 33, 108568.	6.4	14
67	Two-Dimensional Fractionation Method for Proteome-Wide Cross-Linking Mass Spectrometry Analysis. <i>Analytical Chemistry</i> , 2022, 94, 4236-4242.	6.5	13
68	Activation of m1 muscarinic acetylcholine receptor induces surface transport of KCNQ channel via CRMP-2 mediated pathway. <i>Journal of Cell Science</i> , 2015, 128, 4235-45.	2.0	12
69	Akt Phosphorylates Wnt Coactivator and Chromatin Effector Pygo2 at Serine 48 to Antagonize Its Ubiquitin/Proteasome-mediated Degradation. <i>Journal of Biological Chemistry</i> , 2015, 290, 21553-21567.	3.4	10
70	Quantitative Proteomics Analysis of VEGF-Responsive Endothelial Protein S-Nitrosylation Using Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) and LC-MS/MS1. <i>Biology of Reproduction</i> , 2016, 94, 114.	2.7	10
71	Upregulation of GSK3 β Contributes to Brain Disorders in Elderly REG1 β -knockout Mice. <i>Neuropsychopharmacology</i> , 2016, 41, 1340-1349.	5.4	10
72	Spatial Organization and Molecular Interactions of the <i>Schizosaccharomyces pombe</i> Ccq1 β -Tpz1 β -Poz1 Shelterin Complex. <i>Journal of Molecular Biology</i> , 2017, 429, 2863-2872.	4.2	10

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73	Human red and green cone opsins are O-glycosylated at an N-terminal Ser/Thr-rich domain conserved in vertebrates. <i>Journal of Biological Chemistry</i> , 2019, 294, 8123-8133.	3.4	10
74	The REG1 ³ inhibitor NIP30 increases sensitivity to chemotherapy in p53-deficient tumor cells. <i>Nature Communications</i> , 2020, 11, 3904.	12.8	10
75	Effects of fucoidans and alginates from <i>Sargassum graminifolium</i> on allergic symptoms and intestinal microbiota in mice with OVA-induced food allergy. <i>Food and Function</i> , 2022, 13, 6702-6715.	4.6	10
76	Proteomic profiling of the monothiol glutaredoxin Grx3 reveals its global role in the regulation of iron dependent processes. <i>PLoS Genetics</i> , 2020, 16, e1008881.	3.5	9
77	Inhibitors of cullin-RING E3 ubiquitin ligase 4 with antitumor potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	9
78	IKK-Mediated Regulation of the COP9 Signalosome via Phosphorylation of CSN5. <i>Journal of Proteome Research</i> , 2020, 19, 1119-1130.	3.7	9
79	Characterizing the Dynamics of Proteasome Complexes by Proteomics Approaches. <i>Antioxidants and Redox Signaling</i> , 2014, 21, 2444-2456.	5.4	8
80	Characterization and distribution of drug resistance associated β -lactamase, membrane porin and efflux pump genes in MDR <i>A. baumannii</i> isolated from Zhenjiang, China. <i>International Journal of Clinical and Experimental Medicine</i> , 2015, 8, 15393-402.	1.3	8
81	Structure and conformational dynamics of <i>Clostridioides difficile</i> toxin A. <i>Life Science Alliance</i> , 2022, 5, e202201383.	2.8	8
82	Downregulated Rac1 promotes apoptosis and inhibits the clearance of apoptotic cells in airway epithelial cells, which may be associated with airway hyperresponsiveness in asthma. <i>Scandinavian Journal of Immunology</i> , 2019, 89, e12752.	2.7	7
83	Poly(A) binding KPAF4/5 complex stabilizes kinetoplast mRNAs in <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 2020, 48, 8645-8662.	14.5	7
84	Proteasome regulation by reversible tyrosine phosphorylation at the membrane. <i>Oncogene</i> , 2021, 40, 1942-1956.	5.9	7
85	Anterograde regulation of mitochondrial genes and FGF21 signaling by hepatic LSD1. <i>JCI Insight</i> , 2021, 6, .	5.0	7
86	Exploring Spacer Arm Structures for Designs of Asymmetric Sulfoxide-Containing MS-Cleavable Cross-Linkers. <i>Analytical Chemistry</i> , 2020, 92, 6026-6033.	6.5	6
87	Global Phosphoproteomic Analysis Reveals Significant Metabolic Reprogramming in the Termination of Liver Regeneration in Mice. <i>Journal of Proteome Research</i> , 2020, 19, 1788-1799.	3.7	6
88	Developing a Bimolecular Affinity Purification Strategy to Isolate 26S Proteasome Holocomplexes for Complex-Centric Proteomic Analysis. <i>Analytical Chemistry</i> , 2021, 93, 13407-13413.	6.5	5
89	Characterization of an A3G-VifHIV-1-CRL5-CBF β Structure Using a Cross-linking Mass Spectrometry Pipeline for Integrative Modeling of Host-Pathogen Complexes. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100132.	3.8	4
90	Purification of MAP kinase protein complexes and identification of candidate components by XL-TAP-MS. <i>Plant Physiology</i> , 2021, 187, 2381-2392.	4.8	4

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91	Dissecting Dynamic and Heterogeneous Proteasome Complexes Using In Vivo Cross-Linking-Assisted Affinity Purification and Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2018, 1844, 401-410.	0.9	3
92	Developing a Targeted Quantitative Strategy for Sulfoxide-Containing MS-Cleavable Cross-Linked Peptides to Probe Conformational Dynamics of Protein Complexes. <i>Analytical Chemistry</i> , 2022, 94, 4390-4398.	6.5	3
93	Characterization of <i>In Vivo</i> Protein Complexes <i>via</i> Chemical Cross-Linking and Mass Spectrometry. <i>Analytical Chemistry</i> , 2022, 94, 1537-1542.	6.5	3
94	Spatial Organization of the Ccq1-Tpz1-Poz1 Telomere Complex. <i>Microscopy and Microanalysis</i> , 2017, 23, 1242-1243.	0.4	0
95	The Ubiquitin Interacting Motif-Like Domain of Met4 Selectively Binds K48 Polyubiquitin Chains. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100175.	3.8	0