

# Lan Huang

## List of Publications by Year in descending order

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Version: 2024-02-01

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  | Citrate Promotes Excessive Lipid Biosynthesis and Senescence in Tumor Cells for Tumor Therapy. <i>Advanced Science</i> , 2022, 9, e2101553.   | 11.2 | 16        |
| 2  | 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         |
| 3  | 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        |
| 4  | 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         |
| 5  | Structure and conformational dynamics of <i>Clostridioides difficile</i> toxin A. <i>Life Science Alliance</i> , 2022, 5, e202201383.   | 2.8  | 8         |
| 6  | Two-Dimensional Fractionation Method for Proteome-Wide Cross-Linking Mass Spectrometry Analysis. <i>Analytical Chemistry</i> , 2022, 94, 4236-4242.   | 6.5  | 13        |
| 7  | Characterization of <i>In Vivo</i> Protein Complexes via Chemical Cross-Linking and Mass Spectrometry. <i>Analytical Chemistry</i> , 2022, 94, 1537-1542.   | 6.5  | 3         |
| 8  | 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        |
| 9  | Characterization of an A3G-VifHIV-1-CRL5-CBF $\beta$ 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         |
| 10 | 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        |
| 11 | 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         |
| 12 | Proteasome regulation by reversible tyrosine phosphorylation at the membrane. <i>Oncogene</i> , 2021, 40, 1942-1956.  | 5.9  | 7         |
| 13 | Structural basis for CSPG4 as a receptor for TcdB and a therapeutic target in <i>Clostridioides difficile</i> infection. <i>Nature Communications</i> , 2021, 12, 3748.   | 12.8 | 41        |
| 14 | 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        |
| 15 | 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         |
| 16 | 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         |
| 17 | Anterograde regulation of mitochondrial genes and FGF21 signaling by hepatic LSD1. <i>JCI Insight</i> , 2021, 6, .  | 5.0  | 7         |
| 18 | Branched ubiquitin chain binding and deubiquitination by UCH37 facilitate proteasome clearance of stress-induced inclusions. <i>ELife</i> , 2021, 10, .   | 6.0  | 20        |

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|----|--|------|-----------|
| 19 | 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        |
| 20 | 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        |
| 21 | The REG1 <sup>3</sup> inhibitor NIP30 increases sensitivity to chemotherapy in p53-deficient tumor cells. <i>Nature Communications</i> , 2020, 11, 3904.   | 12.8 | 10        |
| 22 | 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         |
| 23 | 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         |
| 24 | 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         |
| 25 | Structural dynamics of the human COP9 signalosome revealed by cross-linking mass spectrometry and integrative modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4088-4098.           | 7.1  | 58        |
| 26 | 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         |
| 27 | Quality-Control Mechanism for Telomerase RNA Folding in the Cell. <i>Cell Reports</i> , 2020, 33, 108568.  | 6.4  | 14        |
| 28 | IKK-Mediated Regulation of the COP9 Signalosome via Phosphorylation of CSN5. <i>Journal of Proteome Research</i> , 2020, 19, 1119-1130.  | 3.7  | 9         |
| 29 | Structure of the full-length <i>Clostridium difficile</i> toxin B. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 712-719.   | 8.2  | 59        |
| 30 | 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         |
| 31 | SCF <sup>FBXO22</sup> 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        |
| 32 | Microhomology-based CRISPR tagging tools for protein tracking, purification, and depletion. <i>Journal of Biological Chemistry</i> , 2019, 294, 10877-10885.   | 3.4  | 16        |
| 33 | In vivo assembly and trafficking of olfactory Ionotropic Receptors. <i>BMC Biology</i> , 2019, 17, 34.   | 3.8  | 28        |
| 34 | First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.  | 6.5  | 100       |
| 35 | 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        |
| 36 | Probing H <sub>2</sub> O <sub>2</sub> -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        |

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|----|--|------|-----------|
| 37 | 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        |
| 38 | 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       |
| 39 | Cross-Linking Mass Spectrometry: An Emerging Technology for Interactomics and Structural Biology. <i>Analytical Chemistry</i> , 2018, 90, 144-165.   | 6.5  | 262       |
| 40 | 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         |
| 41 | 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        |
| 42 | 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        |
| 43 | 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        |
| 44 | 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        |
| 45 | 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        |
| 46 | 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        |
| 47 | Spatial Organization and Molecular Interactions of the <i>Schizosaccharomyces pombe</i> Ccq1-Tpz1-Poz1 Shelterin Complex. <i>Journal of Molecular Biology</i> , 2017, 429, 2863-2872.  | 4.2  | 10        |
| 48 | Ubiquitin orchestrates proteasome dynamics between proliferation and quiescence in yeast. <i>Molecular Biology of the Cell</i> , 2017, 28, 2479-2491.  | 2.1  | 41        |
| 49 | Structural Basis for Shelterin Bridge Assembly. <i>Molecular Cell</i> , 2017, 68, 698-714.e5.  | 9.7  | 27        |
| 50 | <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        |
| 51 | Spatial Organization of the Ccq1-Tpz1-Poz1 Telomere Complex. <i>Microscopy and Microanalysis</i> , 2017, 23, 1242-1243.  | 0.4  | 0         |
| 52 | Ribosome-associated pentatricopeptide repeat proteins function as translational activators in mitochondria of trypanosomes. <i>Molecular Microbiology</i> , 2016, 99, 1043-1058.   | 2.5  | 28        |
| 53 | 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        |
| 54 | 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        |

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|----|--|------|-----------|
| 55 | Mechanisms Underlying Acrolein-Mediated Inhibition of Chromatin Assembly. <i>Molecular and Cellular Biology</i> , 2016, 36, 2995-3008.   | 2.3  | 18        |
| 56 | Developing a Multiplexed Quantitative Cross-Linking Mass Spectrometry Platform for Comparative Structural Analysis of Protein Complexes. <i>Analytical Chemistry</i> , 2016, 88, 10301-10308.  | 6.5  | 55        |
| 57 | Developing an Acidic Residue Reactive and Sulfoxide-Containing MS-Cleavable Homobifunctional Cross-Linker for Probing Protein-Protein Interactions. <i>Analytical Chemistry</i> , 2016, 88, 8315-8322.   | 6.5  | 56        |
| 58 | Site-specific proteasome phosphorylation controls cell proliferation and tumorigenesis. <i>Nature Cell Biology</i> , 2016, 18, 202-212.  | 10.3 | 148       |
| 59 | Antisense Transcripts Delimit Exonucleolytic Activity of the Mitochondrial 3' Processome to Generate Guide RNAs. <i>Molecular Cell</i> , 2016, 61, 364-378.  | 9.7  | 35        |
| 60 | Upregulation of GSK3 $\beta$ Contributes to Brain Disorders in Elderly REG1 $\beta$ -knockout Mice. <i>Neuropsychopharmacology</i> , 2016, 41, 1340-1349.  | 5.4  | 10        |
| 61 | 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        |
| 62 | Ty3 Retrotransposon Hijacks Mating Yeast RNA Processing Bodies to Infect New Genomes. <i>PLoS Genetics</i> , 2015, 11, e1005528.   | 3.5  | 23        |
| 63 | Gln40 deamidation blocks structural reconfiguration and activation of SCF ubiquitin ligase complex by Nedd8. <i>Nature Communications</i> , 2015, 6, 10053.  | 12.8 | 36        |
| 64 | 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        |
| 65 | Synthesis of two new enrichable and MS-cleavable cross-linkers to define protein-protein interactions by mass spectrometry. <i>Organic and Biomolecular Chemistry</i> , 2015, 13, 5030-5037.   | 2.8  | 41        |
| 66 | 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        |
| 67 | 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        |
| 68 | 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        |
| 69 | Characterization and distribution of drug resistance associated $\beta$ -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         |
| 70 | 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       |
| 71 | 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        |
| 72 | Characterizing the Dynamics of Proteasome Complexes by Proteomics Approaches. <i>Antioxidants and Redox Signaling</i> , 2014, 21, 2444-2456.   | 5.4  | 8         |

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|----|--|-----|-----------|
| 73 | RNA Binding and Core Complexes Constitute the U-Insertion/Deletion Editosome. <i>Molecular and Cellular Biology</i> , 2014, 34, 4329-4342.   | 2.3 | 67        |
| 74 | Developing New Isotope-Coded Mass Spectrometry-Cleavable Cross-Linkers for Elucidating Protein Structures. <i>Analytical Chemistry</i> , 2014, 86, 2099-2106.  | 6.5 | 36        |
| 75 | Mapping the Structural Topology of the Yeast 19S Proteasomal Regulatory Particle Using Chemical Cross-linking and Probabilistic Modeling. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1566-1577.  | 3.8 | 54        |
| 76 | Mapping the Protein Interaction Network of the Human COP9 Signalosome Complex Using a Label-free QTAX Strategy. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 138-147.  | 3.8 | 40        |
| 77 | 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       |
| 78 | UBLCP1 is a 26S proteasome phosphatase that regulates nuclear proteasome activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18649-18654.  | 7.1 | 68        |
| 79 | Oxidative Stress-Mediated Regulation of Proteasome Complexes. <i>Molecular and Cellular Proteomics</i> , 2011, 10, R110.006924.  | 3.8 | 263       |
| 80 | Regulation of the 26S Proteasome Complex During Oxidative Stress. <i>Science Signaling</i> , 2010, 3, ra88.  | 3.6 | 224       |
| 81 | 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        |
| 82 | 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        |
| 83 | Characterization of Cell Cycle Specific Protein Interaction Networks of the Yeast 26S Proteasome Complex by the QTAX Strategy. <i>Journal of Proteome Research</i> , 2010, 9, 2016-2029.   | 3.7 | 51        |
| 84 | Identifying Dynamic Interactors of Protein Complexes by Quantitative Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 46-57.   | 3.8 | 178       |
| 85 | Characterization of the Human COP9 Signalosome Complex Using Affinity Purification and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2008, 7, 4914-4925.  | 3.7 | 62        |
| 86 | 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       |
| 87 | Proteomics of proteasome complexes and ubiquitinated proteins. <i>Expert Review of Proteomics</i> , 2007, 4, 649-665.  | 3.0 | 24        |
| 88 | Modulation of DRAK2 Autophosphorylation by Antigen Receptor Signaling in Primary Lymphocytes. <i>Journal of Biological Chemistry</i> , 2007, 282, 4573-4584.   | 3.4 | 23        |
| 89 | Mass Spectrometric Characterization of the Affinity-Purified Human 26S Proteasome Complex. <i>Biochemistry</i> , 2007, 46, 3553-3565.  | 2.5 | 243       |
| 90 | An Integrated Mass Spectrometry-based Proteomic Approach. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 366-378.   | 3.8 | 246       |

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|----|--|-----|-----------|
| 91 | 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       |
| 92 | 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       |
| 93 | Comprehensive Mass Spectrometric Analysis of the 20S Proteasome Complex. <i>Methods in Enzymology</i> , 2005, 405, 187-236.  | 1.0 | 21        |
| 94 | Global approaches to understanding ubiquitination. <i>Genome Biology</i> , 2005, 6, 233.   | 9.6 | 43        |
| 95 | Functional Assignment of the 20 S Proteasome from <i>Trypanosoma brucei</i> Using Mass Spectrometry and New Bioinformatics Approaches. <i>Journal of Biological Chemistry</i> , 2001, 276, 28327-28339.  | 3.4 | 64        |