

# Chaochao Wu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10894928/publications.pdf>

Version: 2024-02-01

14  
papers

1,233  
citations

1040056

9  
h-index

1125743

13  
g-index

14  
all docs

14  
docs citations

14  
times ranked

3055  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Preconditioning in the Rhesus Macaque Induces a Proteomic Signature Following Cerebral Ischemia that Is Associated with Neuroprotection. <i>Translational Stroke Research</i> , 2019, 10, 440-448.       | 4.2  | 11        |
| 2  | Targeted proteomic assays for quantitation of proteins identified by proteogenomic analysis of ovarian cancer. <i>Scientific Data</i> , 2017, 4, 170091.   | 5.3  | 29        |
| 3  | Dysfunction of PLA2G6 and CYP2C44-associated network signals imminent carcinogenesis from chronic inflammation to hepatocellular carcinoma. <i>Journal of Molecular Cell Biology</i> , 2017, 9, 489-503. | 3.3  | 64        |
| 4  | Quantification of mutant SPOP proteins in prostate cancer using mass spectrometry-based targeted proteomics. <i>Journal of Translational Medicine</i> , 2017, 15, 175.                                   | 4.4  | 5         |
| 5  | Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.   | 28.9 | 804       |
| 6  | Recommendations for the Generation, Quantification, Storage, and Handling of Peptides Used for Mass Spectrometry-Based Assays. <i>Clinical Chemistry</i> , 2016, 62, 48-69.                              | 3.2  | 187       |
| 7  | An Optimized Informatics Pipeline for Mass Spectrometry-Based Peptidomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 2002-2008.   | 2.8  | 10        |
| 8  | Sensitive Targeted Quantification of ERK Phosphorylation Dynamics and Stoichiometry in Human Cells without Affinity Enrichment. <i>Analytical Chemistry</i> , 2015, 87, 1103-1110.                       | 6.5  | 32        |
| 9  | Mass Spectrometry for Biomarker Development. <i>Biomarkers in Disease</i> , 2015, , 17-48.   | 0.1  | 1         |
| 10 | Comprehensive Quantitative Analysis of Ovarian and Breast Cancer Tumor Peptidomes. <i>Journal of Proteome Research</i> , 2015, 14, 422-433.  | 3.7  | 26        |
| 11 | Expediting SRM Assay Development for Large-Scale Targeted Proteomics Experiments. <i>Journal of Proteome Research</i> , 2014, 13, 4479-4487.   | 3.7  | 29        |
| 12 | Mass Spectrometry for Biomarker Development. , 2014, , 1-25.   |      | 0         |
| 13 | Delicate Analysis of Post-Translational Modifications on Dishevelled 3. <i>Journal of Proteome Research</i> , 2012, 11, 3829-3837.   | 3.7  | 12        |
| 14 | Proteomic mining in the dysplastic liver of WHV/c-myc mice – insights and indicators for early hepatocarcinogenesis. <i>FEBS Journal</i> , 2010, 277, 4039-4053.   | 4.7  | 23        |