# Chen Shao

## List of Publications by Year
## in descending order

Source: https://exaly.com/author-pdf/5697705/publications.pdf

Version: 2024-02-01

| | | 623734 | 610901 |
|---|---|---|---|
| 29<br>papers | 736<br>citations | 14<br>h-index | 24<br>g-index |
| 31<br>all docs | 31<br>docs citations | 31<br>times ranked | 1303<br>citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Urinary Proteomic Characteristics of Hyperuricemia and Their Possible Links with the Occurrence of Its Concomitant Diseases. ACS Omega, 2021, 6, 9500-9508. | 3.5 | 6 |
| 2 | A qualitative and quantitative analysis of the human gingival crevicular fluid proteome and metaproteome. Proteomics, 2021, 21, e2000321. | 2.2 | 5 |
| 3 | A dynamic mouse peptidome landscape reveals probiotic modulation of the gut-brain axis. Science Signaling, 2020, 13, . | 3.6 | 17 |
| 4 | Differential urinary proteomics analysis of myocardial infarction using iTRAQ quantification. Molecular Medicine Reports, 2019, 19, 3972-3988. | 2.4 | 5 |
| 5 | Comprehensive Analysis of Individual Variation in the Urinary Proteome Revealed Significant Gender Differences. Molecular and Cellular Proteomics, 2019, 18, 1110-1122. | 3.8 | 50 |
| 6 | A Comparative Proteomics Analysis of Five Body Fluids: Plasma, Urine, Cerebrospinal Fluid, Amniotic Fluid, and Saliva. Proteomics - Clinical Applications, 2018, 12, e1800008. | 1.6 | 53 |
| 7 | A comprehensive analysis and annotation of human normal urinary proteome. Scientific Reports, 2017, 7, 3024. | 3.3 | 127 |
| 8 | Differential urinary glycoproteome analysis of type 2 diabetic nephropathy using 2D-LCâ€“MS/MS and iTRAQ quantification. Journal of Translational Medicine, 2015, 13, 371. | 4.4 | 29 |
| 9 | A Proteomic Analysis of Individual and Gender Variations in Normal Human Urine and Cerebrospinal Fluid Using iTRAQ Quantification. PLoS ONE, 2015, 10, e0133270. | 2.5 | 52 |
| 10 | A comprehensive map and functional annotation of the normal human cerebrospinal fluid proteome. Journal of Proteomics, 2015, 119, 90-99. | 2.4 | 57 |
| 11 | Data for a comprehensive map and functional annotation of the human cerebrospinal fluid proteome. Data in Brief, 2015, 3, 103-107. | 1.0 | 11 |
| 12 | Urinary Protein Biomarker Database: A Useful Tool for Biomarker Discovery. Advances in Experimental Medicine and Biology, 2015, 845, 195-203. | 1.6 | 12 |
| 13 | Applications of Peptide Retention Time in Proteomic Data Analysis. Advances in Experimental Medicine and Biology, 2015, 845, 67-75. | 1.6 | 2 |
| 14 | Dynamic changes of urinary proteins in a focal segmental glomerulosclerosis rat model. Proteome Science, 2014, 12, 42. | 1.7 | 39 |
| 15 | Statistical characterization of HCD fragmentation patterns of tryptic peptides on an LTQ Orbitrap Velos mass spectrometer. Journal of Proteomics, 2014, 109, 26-37. | 2.4 | 15 |
| 16 | Comparison at the peptide level with postâ€translational modification consideration reveals more differences between two unenriched samples (778.1). FASEB Journal, 2014, 28, 778.1. | 0.5 | 0 |
| 17 | An individual urinary proteome analysis in normal human beings to define the minimal sample number to represent the normal urinary proteome. Proteome Science, 2012, 10, 70. | 1.7 | 27 |
| 18 | Applications of urinary proteomics in biomarker discovery. Science China Life Sciences, 2011, 54, 409-417. | 4.9 | 33 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 19 | A Tool for Biomarker Discovery in the Urinary Proteome: A Manually Curated Human and Animal Urine Protein Biomarker Database. Molecular and Cellular Proteomics, 2011, 10, M111.010975. | 3.8 | 85 |
| 20 | The urinary biomarker database. FASEB Journal, 2011, 25, . | 0.5 | 0 |
| 21 | Oscore: a combined score to reduce false negative rates for peptide identification in tandem mass spectrometry analysis. Journal of Mass Spectrometry, 2009, 44, 25-31. | 1.6 | 11 |
| 22 | Improving peptide identification using an empirical peptide retention time database. Rapid Communications in Mass Spectrometry, 2009, 23, 109-118. | 1.5 | 7 |
| 23 | An Attempt to Understand Kidney's Protein Handling Function by Comparing Plasma and Urine Proteomes. PLoS ONE, 2009, 4, e5146. | 2.5 | 60 |
| 24 | systematic analysis of a simple adaptor protein PDZK1: ligand identification, interaction and functional prediction of complex. FASEB Journal, 2009, 23, 516.1. | 0.5 | 1 |
| 25 | An Efficiency machine learning system prediction coupled with yeast two hybrid confirmations to identify HPV 16 E6 interacting PDZ proteins. FASEB Journal, 2009, 23, 858.9. | 0.5 | 1 |
| 26 | Differential ConA-enriched urinary proteome in rat experimental glomerular diseases. Biochemical and Biophysical Research Communications, 2008, 371, 385-390. | 2.1 | 31 |
| 27 | Understanding kidney function by comparing serum and urine proteomes. FASEB Journal, 2007, 21, A1004. | 0.5 | 0 |
| 28 | Improve the tandem mass spectra identification and reduce false negative rate using peptide LC retention time.. FASEB Journal, 2007, 21, A265. | 0.5 | 0 |
| 29 | An integrated machine learning system to computationally screen protein databases for Protein binding peptide ligands.. FASEB Journal, 2006, 20, A528. | 0.5 | 0 |