**Supplementary materials** 

## Dissection of Targeting Molecular Mechanisms of Aristolochic Acid-induced

## Nephrotoxicity via a Combined Deconvolution Strategy of

## **Chemoproteomics and Metabolomics**

Qian Zhang<sup>a, b, c, #</sup>, Piao Luo<sup>a, c, #</sup>, Jiayun Chen<sup>a, #</sup>, Chuanbin Yang<sup>d, #</sup>, Fei Xia<sup>a</sup>, Junzhe Zhang<sup>a</sup>, Huan Tang<sup>a</sup>, Dandan Liu<sup>a</sup>, Liwei Gu<sup>a</sup>, Qiaoli Shi<sup>a</sup>, Xueling He<sup>a</sup>, Tong Yang<sup>a</sup>, Jigang Wang<sup>a, b,</sup> c, d, e, f, g, \*



**Figure S1.** Fluorescence labeling and cellular imaging of AA-probe. (A) The inhibition effects of aristolochic acid I (AAI) and two analogues (AAIVa, AAIIIa) on HK-2 cell. (**B-C**) fluorescence labelling protein of cellular imaging location of the AP2 (40  $\mu$ M) in HK-2 cells (scale bar = 75  $\mu$ m). (**D**) *Ex vivo* labelling protein in an AP2 dose-dependent manner in the lysate of the kidney. (**E**) The competition of labelling protein with AP2 by excess AAI in the lysate of the kidney. (**F**) *In vivo* fluorescence labelling protein of AP2.



**Figure S2**. Aristolochic acid target proteins in the lysate of the kidney. Volcano plot depicting the differential enrichment of proteins in AP2 vs DMSO groups.



**Figure S3**. Validation of aristolochic acid other targets (A) Pull-down Western blotting study to verify AA directly targeting to ACACA, ATP synthase, FASN and HK2 proteins. (B) CETSA-Western blotting experiment to validate the AA binding to HK2, VDAC1 and PC proteins. (C) Immunofluorescence staining of target proteins (green) and AA-probe (a red fluorescence dye), scale bar = 9  $\mu$ m.



**Figure S4.** Binding model of AAI with HK2 (**A**), PKM (**B**), LDHA (**C**), ATP synthase (**D**), IDH2 (**E**), MDH2 (F), FASN (**G**) and VDAC1 (**H**) by docking analysis. Yellow dotted lines represent hydrogen bonds.



**Figure S5**. Relative parameters of AAI-treated mice. (A) Representation of the appearance of mice and kidneys. (**B**) The kidney/body weight ratio and the score of the pathology changes of kidney from AA-treated and control mice. (C) The parameters of routine blood tests. All data represent means  $\pm$  SEM, n $\geq$ 3, \*p<0.05, \*\*p<0.01, \*\*\*p<0.001 model (AA treatment) vs control.



**Figure S6**. Metabolomic analysis of AA-induced nephrotoxicity. (**A-B**) The correlation analysis of samples QC in kidney sample. (**C-D**) The correlation analysis of samples QC in the serum sample. (**E**) The PCA plots of the DMSO and treatment groups in the serum sample. (**F**) Ortho PLS-DA analysis of the DMSO and treatment groups in the serum sample. (**G**) The volcano map displays the different metabolites in serum. Up-regulated metabolites were represented by red dots, down-regulated metabolites were represented by blue dots. (**H**) Classification information of HMDB database annotations in serum. (**I**) KEGG biochemical metabolic pathway and signal transduction pathway in serum.



**Figure S7**. The effect of AAI on cellular respiration and metabolism. (A-C) The indicators of oxygen consumption rate (OCR) include basal respiration, spare respiratory capacity (%) and non-mitochondrial oxygen consumption. n = 3, \*P < 0.05, \*\*P < 0.01 compared with control.



## <sup>1</sup>H NMR, <sup>13</sup>C NMR and HRMS of aristolochic acids probes (AP1 and AP2)





HRMS of AP1



<sup>13</sup>C NMR of **AP2** 

