



Discovery of cisplatin-binding proteins by competitive cysteinome profiling†

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Cisplatin is a widely used cancer metalloidrug that induces cytotoxicity by targeting DNA and chelating cysteines in proteins. Here we applied a competitive activity-based protein profiling strategy to identify cisplatin-binding cysteines in cancer proteomes. A novel cisplatin target, MetAP1, was identified and functionally validated to contribute to cisplatin's cytotoxicity.

As an anti-cancer drug discovered in 1965, *cis*-dichlorodiamineplatinum(II) (cisplatin) is widely used in the treatment of testicular and ovarian cancer. According to statistics, over 50% of cancer patients have been treated with cisplatin in different treatment stages.¹ When cisplatin enters cells, two chloride ions are removed by hydrolysis and the divalent platinum ions can attack adenines or guanines on DNA.² As the cytotoxicity of cisplatin is generally believed to be mainly caused by the formation of Pt-DNA adducts,³ many research studies have focused on the interaction between cisplatin and DNA in recent years.^{4,5} Nevertheless, it has been estimated that only about 1% of the intracellular platinum can bind to DNA,⁶ and because of the unique structure of the diammonium platinum dihydrate, other intracellular nucleophilic substances can also be attacked extensively, including RNA, reduced cysteine side chains on proteins, thiol-containing ligands (*e.g.* glutathione), *etc.*^{7,8}

Several protein targets of cisplatin have been biochemically characterized that may contribute to its cytotoxicity and drug resistance.⁹ For example, the human copper transport protein (Atox1) was shown to be potentially relevant to cisplatin resistance,¹⁰ and the interaction of cisplatin with human superoxide dismutase (SOD1) could cause cytotoxicity.¹¹ In addition, proteomic techniques such as Multi-dimensional Protein

Identification Technology (MudPIT) and Laser Ablation Inductively Coupled Plasma Mass Spectrometry (LA-ICP-MS) have been implemented for large-scale identification of cisplatin-binding proteins,^{12,13} however, they are limited in detecting targets of low abundance. While clickable cisplatin analogue probes have been developed to label and enrich cisplatin-binding proteins in cells,^{14,15} introduction of the bioorthogonal group may change the physical and chemical properties of cisplatin so that certain *bona fide* targets are missed.

Activity-based protein profiling (ABPP) is a powerful chemoproteomic strategy that can be applied to identify the protein targets of small molecules in complex biological systems.^{16,17} In particular, a site-specific and quantitative version of ABPP, isoTOP-ABPP, has been developed for global profiling of functional cysteines in proteomes.¹⁸ When it is operated in a competitive manner, the strategy can be used not only to identify cysteines that are sensitive to electrophilic metabolites and covalent drugs,^{19–22} but also to profile key metal-binding sites for zinc and iron–sulfur clusters.^{23,24}

In the current study, we were inspired to apply this competitive ABPP strategy to globally profile cisplatin-binding cysteines in proteomes. Firstly, we verified by in-gel fluorescence that cisplatin could compete with the labeling of a cysteine-reactive and alkyne-functionalized iodoacetamide probe (IAyne) in living cells (ESI, † Fig. S1). We then performed a competitive rdTOP-ABPP²⁵ experiment to identify cisplatin-binding sites (Fig. 1a). Briefly, proteomes were obtained from normal and cisplatin-treated MCF-7 cells, labeled by the IAyne probe for 1 h, and then conjugated with an acid-cleavable biotin tag by Cu(I)-catalyzed azide–alkyne cycloaddition (CuAAC).^{26,27} After enrichment by streptavidin and on-bead digestion by trypsin, the probe-adducted peptides from the normal and cisplatin-treated samples were isotopically labeled by light and heavy dimethylation reagents, respectively, prior to combination. The IAyne-adducted peptides were released by acid cleavage and analyzed using LC-MS/MS. After quantitation by CIMAGE2.0,²⁸ we detected and quantified a total of 1947 peptides that belong to 1115 proteins in all three replicates with high confidence (Fig. 1b).

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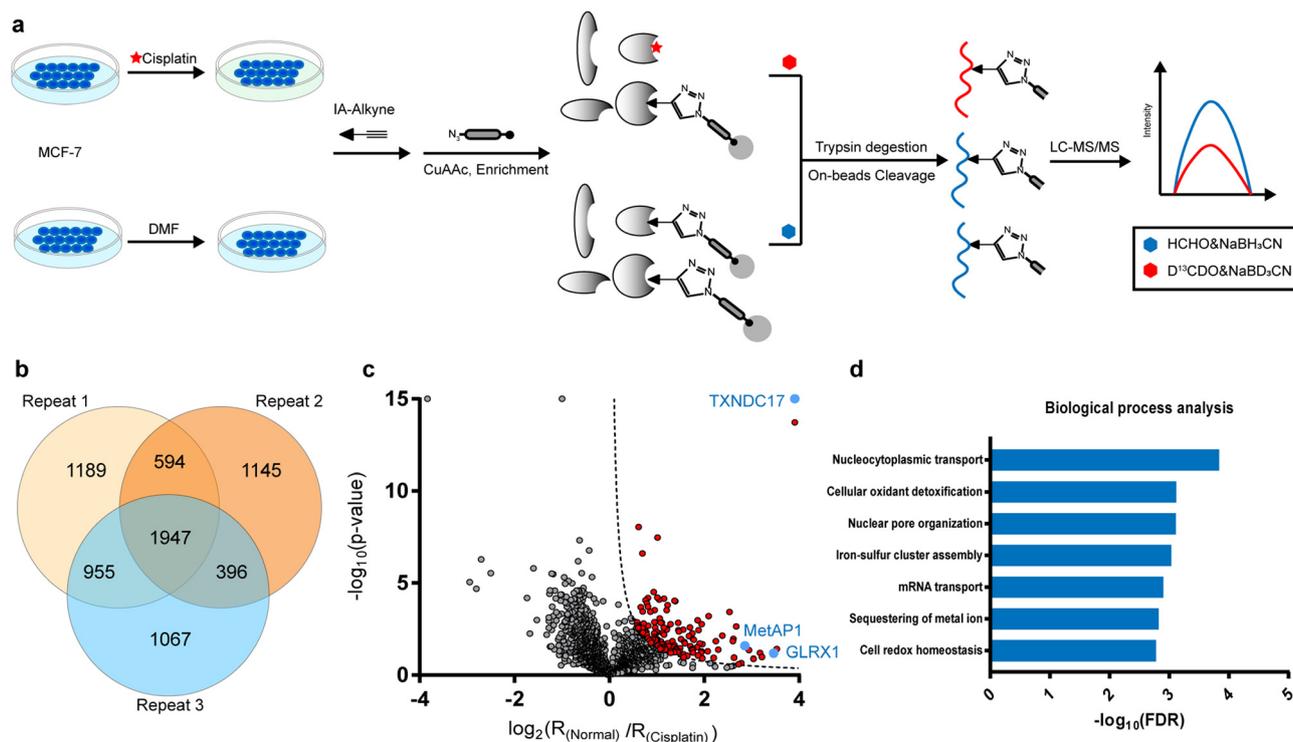


Fig. 1 Quantitative profiling of cisplatin-binding cysteines by rdTOP-ABPP. (a) The scheme of quantitative profiling of cisplatin-binding cysteines by rdTOP-ABPP. Equal numbers of MCF-7 cells were treated with *N,N*-dimethylformamide (DMF) and 300 μ M cisplatin, respectively, for 4 h. The whole proteomes were labeled with the cysteine-reactive IAYne probe and then subjected to the rdTOP-ABPP procedures. (b) Venn diagram showing the number of cisplatin-binding peptides quantified from three biological replicates. (c) Volcano plot of the rdTOP-ABPP ratios for each peptide quantified in the cisplatin-treated group as compared to those in the normal cells. Highlighted in red are cisplatin-targeted cysteines with high confidence in unique peptides. Highlighted in blue are the targets that are biochemically verified in the current study. (d) Gene ontology analysis of the identified cisplatin-binding proteins in terms of biological processes.

In light of the IAYne competition by cisplatin, a credible cisplatin-binding cysteine should yield a light/heavy (“normal/cisplatin”) ratio higher than 1. We analyzed, for every cysteine quantified, the statistical difference (p value) among all three replicates using a Student’s t -test and drew a volcano plot (Fig. 1c). After applying the cutoff of $-\log_{10}(p \text{ value}) \times \log_2(\text{ratio}) > 1.5$, we obtained 125 cysteines from 107 proteins as strong candidates for cisplatin-binding targets (Fig. 1c).

According to the gene ontology (GO) analysis, the 109 cisplatin-binding proteins are enriched in the biological process of cellular oxidant detoxification (Fig. 1d), which are exemplified by glutaredoxin-1 (GLRX1), glutaredoxin-related protein 5 (GLRX5), thioredoxin (TXN) and thioredoxin domain-containing protein 17 (TXNDC17). This is consistent with previous reports that cisplatin induces ROS by disturbing oxidoreductases.²⁹ Interestingly, another enriched pathway is the nucleocytoplasmic transport (Fig. 1d), which is supported by the presence of multiple proteins that are functionally involved in the assembly and maintenance of nuclear pore complexes, including nuclear pore glycoprotein p62 (NUP62), nucleoporin NUP35 (NUP35), nuclear pore complex protein NUP205 (NUP205), nuclear pore complex protein Nup98-Nup96 (NUP98), *etc.* These data suggest that cisplatin may enter a nucleus by interacting with a nuclear pore complex³⁰ and affect its function.

Satisfyingly, several proteins identified in our work have been previously reported as cisplatin-binding proteins (Table 1). Our rdTOP-ABPP experiments additionally revealed the detailed cisplatin-binding sites in them. For example, rdTOP-ABPP identified C23/C26 and C43/C46 as cisplatin-sensitive cysteines in GLRX1 and TXNDC17, respectively, and we therefore set out to validate them biochemically. For each target, we first recombinantly expressed and purified the protein and showed by in-gel fluorescence that cisplatin could dose-dependently inhibit IAYne’s labeling (Fig. 2a and d). We then constructed the corresponding cysteine mutants (C23A and C26A for GLRX1, C43A and C46A for TXNDC17) and validated by Inductively Coupled

Table 1 rdTOP-ABPP-revealed cisplatin-binding sites in previously reported targets

Protein name	Log ₂ (ratio)	−Log ₁₀ (p value)	Sites identified by rdTOP-ABPP	Ref.
CTSD	3.9	13.7	C117	32
TXNDC17	3.9	15.0	C43	33
GLRX	3.5	1.2	C23, C26	34
TXN	3.4	1.1	C32	32
EEF1A1	1.6	1.8	C363, C370	14
COX17	1.0	1.9	C24	35
CPS1	0.9	1.7	C1327, C1337	14



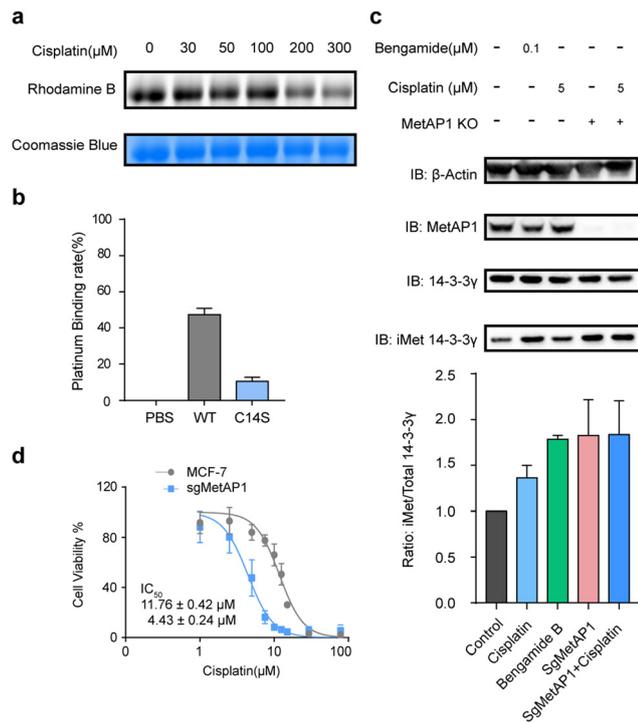


Fig. 3 Cisplatin binds and inhibits human MetAP1. (a) Cisplatin competes with IAYne on MetAP1 dose dependently. (b) MetAP1 is a cisplatin-binding protein as measured by ICP-MS, whose binding site contains Cys14. (c) Inhibition of iMet processing of 14-3-3 γ by cisplatin in human cell lines. The levels of iMet 14-3-3 γ and the total 14-3-3 γ were immunoblotted (top) and quantified by ImageJ (bottom). (d) Knockout of MetAP1 sensitized cells to cisplatin. Dose-dependent cell death induced by cisplatin was measured by MTT. Results are from three independent experiments. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Statistical differences were determined by a two-sided Student's t -test.

Finally, the cell viability assays demonstrated that knocking out MetAP1 significantly increased the sensitivity of cells toward cisplatin treatment (Fig. 3d), suggesting that MetAP1 partially contributes to protect cells from cisplatin-induced death.

In summary, we report the application of competitive cysteine profiling to identify cisplatin-binding cysteines in MCF-7 proteomes. Among the targets of cisplatin, we not only verified its binding sites in GLRX1 and TXNDC17, but also functionally characterized a novel target, MetAP1, in terms of cisplatin binding on the enzyme activity and cellular toxicity. While the former provided strong evidence that the thioredoxin and glutathione systems would be disturbed by cisplatin to impact the intracellular ROS level, the latter suggests that MetAP1 could serve as a potential target for improving cytotoxicity of cisplatin to avoid tumor resistance. Considering that the competitive labeling was performed in cell lysates and changes in cysteine ratios are not all directly caused by cisplatin, the resulting proteomic data by ABPP should be carefully interpreted. Further biochemical experiments are advised to confirm the targets as cisplatin-binding proteins before functional assay are applied. In addition, whether these targets are functionally impactful *in vivo* remain to be explored. Nevertheless, the ABPP-based chemoproteomic technology proves to be an

enabling tool to systemically study protein-metal/metallo drug interactions.

Conflicts of interest

There are no conflicts to declare.

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