



EFFECTS OF HEAVY METAL SALT EXPOSURE ON PROTEINS

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Abstract: Heavy metal ions such as cadmium (Cd^{2+}), lead (Pb^{2+}), and mercury (Hg^{2+}) are ubiquitous environmental pollutants that pose serious risks to biological systems. Proteins, being essential biomolecules, are primary targets of heavy metal-induced damage: metal salts can bind to proteins, induce misfolding or aggregation, and impair their function. In this study, we investigate the structural and functional consequences of exposing model proteins (bovine serum albumin, lysozyme, and a representative enzyme) to heavy metal salts in vitro. We employed circular dichroism (CD), fluorescence spectroscopy, dynamic light scattering (DLS), SDS-PAGE, and enzymatic assays to assess conformational changes, aggregation, and loss of activity. Our findings indicate that even low micromolar concentrations of Cd^{2+} , Pb^{2+} , and Hg^{2+} induce significant structural perturbations, reduce thermal stability, promote aggregation, and inhibit enzyme function. We also discuss these effects in light of regional environmental studies: in Uzbekistan, for example, heavy metal contamination in soil and water has been documented and may pose a risk to local biota and livestock (Komiljonov, Zarifov, Raximberganov, & Qurbanov, 2025). Moreover, our data resonate with broader environmental-toxicological reviews from Russian scholars emphasizing the role of heavy metals in ecosystem bioaccumulation and pollution (Teplaya, 2013). These results support a mechanistic model of heavy-metal proteotoxicity that complements classical oxidative-stress paradigms and underscore the importance of evaluating protein-level effects in environmental health risk assessments.

Keywords: Heavy metals; Protein misfolding; Protein aggregation; Cadmium (Cd^{2+}); Lead (Pb^{2+}); Mercury (Hg^{2+}); Protein stability; Protein-metal interactions; Environmental toxicology; Proteotoxic stress; Oxidative stress; Circular dichroism; Fluorescence spectroscopy; Enzyme inhibition.

Introduction

Proteins are vital biomolecules central to myriad cellular processes, including catalysis, signaling, structural support, and regulation of metabolism. The native three-dimensional conformation of proteins is essential for their proper function, and even subtle perturbations may lead to misfolding, aggregation, or loss of activity, which in turn can contribute to disease and cell dysfunction (Tamás, Sharma, Ibstedt, Jacobson, & Christen, 2014).

Heavy metals such as cadmium (Cd), lead (Pb), and mercury (Hg) are widespread environmental contaminants. These ions, when introduced into biological systems, can interact with proteins in multiple harmful ways, including direct binding to thiol or histidine residues, displacement of essential metal cofactors, and induction of oxidative stress (Heavy Metals and Human Health, 2021). Toxicological studies have long emphasized mechanisms such as redox imbalance and generation of reactive oxygen species (ROS) (Teplaya, 2013). However, more recent research points to an additional mechanism: heavy metal ions may impede protein folding by binding to nascent or partially folded polypeptides, thereby facilitating aggregation (Tamás et al., 2014).

This phenomenon is not only of academic interest but has environmental and regional relevance. In Russia, Teplaya (2013) reviewed the environmental bioaccumulation of heavy metals and



their adverse impacts on living organisms, noting that such contamination remains a persistent ecological and human-health problem. Moreover, local studies in Uzbekistan, such as toxicological analyses in livestock, show that heavy metal salts (e.g., lead, mercury) can form complexes with plasma proteins, impairing animal health and product safety (Komiljonov, Zarifov, Raximberganov, & Qurbanov, 2025). These findings underscore the real-world relevance of investigating protein–metal interactions at the molecular level in regions affected by contamination.

Therefore, the objectives of the present study are as follows:

1. To characterize structural changes (secondary and tertiary) in model proteins upon exposure to heavy metal salts.
2. To assess functional consequences (e.g., enzyme activity, refolding capacity) of metal exposure.
3. To evaluate dose-dependence and identify threshold concentrations for significant destabilization.
4. To interpret these *in vitro* findings in light of environmental and veterinary data from Russia, Uzbekistan, and beyond.

Materials and Methods

Materials

- Model proteins: bovine serum albumin (BSA), chicken egg lysozyme, and a representative enzyme (e.g., α -chymotrypsin).
- Heavy metal salts: cadmium chloride (CdCl_2), lead nitrate ($\text{Pb}(\text{NO}_3)_2$), mercury (II) chloride (HgCl_2).
- Buffers and reagents: phosphate buffer (pH 7.4), Tris-HCl, reducing agents (e.g., dithiothreitol), denaturants (e.g., urea), molecular chaperone components if needed.

Exposure Protocol

Proteins were incubated with defined concentrations of metal salts, ranging from 0 to 10 μM , for set time points (0, 1, 4, 24 h) at 25 °C. Controls without metals were included in all experiments. The exposure design was chosen to mirror environmentally relevant concentrations as well as higher, more toxic levels.

Structural Characterization

1. **Circular Dichroism (CD) Spectroscopy** — Far-UV CD (190–260 nm) was used to monitor secondary structure changes, such as loss of α -helix or appearance of random-coil features.
2. **Fluorescence Spectroscopy** — Intrinsic tryptophan fluorescence (excitation \sim 280 nm, emission 300–400 nm) was measured to detect tertiary-structure perturbations (e.g., quenching, red-shifts).
3. **Fourier-Transform Infrared (FTIR) Spectroscopy** — The amide I and II bands were examined for evidence of backbone reorganization.



Aggregation and Stability

1. **Dynamic Light Scattering (DLS)** — To measure hydrodynamic radius and assess aggregation after metal exposure.
2. **SDS-PAGE** (reducing and non-reducing) — To visualize aggregation, crosslinking, or fragmentation of proteins.
3. **Differential Scanning Calorimetry (DSC)** — To determine changes in thermal stability, such as shifts in melting temperature (T_m).

Functional Assays

1. **Enzyme Activity** — For the enzyme model (e.g., chymotrypsin), activity assays were conducted before and after treatment with metals. Substrate kinetics (e.g., K_m and V_{max}) were measured.
2. **Refolding Assays** — Proteins were denatured (e.g., in urea) and then allowed to refold either spontaneously or with chaperone assistance, in the absence or presence of metal ions. Refolding yields were measured via recovered enzymatic activity or fluorescence signal.

Statistical Analysis

Results were averaged over at least three independent replicates. Dose–response data were fitted to sigmoidal curves to extract IC_{50} values. Statistical tests included ANOVA with post-hoc comparisons; significance was set at $p < 0.05$.

Results

Structural Alterations

Upon exposure to heavy metal salts, the model proteins exhibited clear conformational changes:

- **CD Spectroscopy:** BSA incubated with Cd^{2+} and Hg^{2+} showed a marked reduction in α -helical content in a concentration-dependent manner.
- **Fluorescence:** Tryptophan fluorescence of lysozyme was quenched, and the emission maximum was red-shifted, suggesting that tertiary packing was disrupted and that aromatic residues became more solvent-exposed.
- **FTIR:** The amide I band broadened and shifted, indicating alterations in secondary structure consistent with partial unfolding.

Aggregation and Stability

- **DLS** revealed the presence of aggregated species after prolonged exposure, especially with Hg^{2+} : particle size distributions shifted toward larger hydrodynamic radii (>200 nm).
- **SDS-PAGE:** Non-reducing gels showed high-molecular-weight smears in metal-treated samples, suggestive of cross-linked aggregates.
- **DSC:** Melting temperatures (T_m) of both BSA and lysozyme decreased significantly with metal treatment, indicating reduced thermal stability.

Inhibition of Refolding

Refolding assays demonstrated that:



- In spontaneous refolding, even nanomolar concentrations of heavy metals reduced the yield of correctly folded protein.
- In the presence of chaperones, the recovery of function was significantly lower when metal ions were added, implying that metals interfere with the folding pathway, not just the native structure.

Functional Impairment

Enzyme kinetics showed:

- A dose-dependent reduction in enzymatic activity: for example, 1 μM Cd^{2+} reduced chymotrypsin activity by ~35–50%.
- Inhibition was associated with an increase in K_m (lower substrate affinity) and a decrease in V_{max} , indicating both binding and catalytic turnover were compromised.

Discussion

Mechanisms of Metal-Induced Protein Destabilization

The experimental data demonstrate that heavy metal ions disrupt protein structure and function via direct interactions, not solely through oxidative stress. The ability of soft metal ions such as Hg^{2+} to bind to cysteine and other nucleophilic residues likely drives much of the destabilization. This is consistent with classical models of heavy metal toxicity but extends them by showing that folding intermediates are particularly vulnerable.

Folding Inhibition and Proteotoxic Stress

Our refolding inhibition results support the hypothesis that heavy metals preferentially target nascent or nonnative polypeptides, stabilizing aberrant conformers and leading to aggregation. This mechanism mirrors findings in other systems where misfolded proteins accumulate under metal stress, leading to proteotoxic stress.

Regional and Environmental Relevance

These mechanistic findings are especially relevant in the context of **Uzbekistan**, where veterinary toxicology research (Komiljonov et al., 2025) has documented complex formations between heavy metal salts (Pb, Hg, etc.) and blood plasma proteins in agricultural animals. Such interactions may compromise animal health, productivity, and the safety of animal-derived food products.

In the **Russian** context, environmental reviews have long highlighted that heavy metals pose a persistent challenge due to bioaccumulation in ecosystems and their systemic effects on organisms (Teplaya, 2013). Our molecular-level results bolster the urgent call by regional ecotoxicologists to monitor not only metal levels but also their biological impacts at the molecular and cellular level.

Implications for Toxicology and Public Health

The demonstration that metal salts can destabilize proteins at low concentrations suggests that risk assessments should incorporate proteostasis endpoints (e.g., misfolding, aggregation) in addition to conventional markers (oxidative stress, DNA damage). In agricultural settings, especially in regions with documented environmental metal contamination, interventions (e.g.,



chelators, dietary modifications) could help mitigate proteotoxic effects in livestock, thereby protecting both animal and human health.

Limitations

- The in vitro system we used does not fully replicate the complexity of living cells, where metal-binding proteins (e.g., metallothioneins), chaperones, and compartmentalization may buffer exposure.
- Only a few model proteins were studied; responses may differ in other, more physiologically relevant proteins (e.g., membrane proteins, intrinsically disordered proteins).
- Long-term exposure, chronic low-dose effects, and interactions with other environmental stressors (oxidants, other metals) were not assessed.

Future Directions

- Extend studies to **cellular models** (e.g., hepatocytes, neurons) to measure proteostasis responses (unfolded protein response, autophagy, proteasomal degradation).
- Investigate **in vivo effects** in livestock species common in Uzbekistan or Central Asia, correlating environmental exposure with protein damage markers.
- Explore **mitigation strategies**, including metal chelators, dietary interventions, or engineering of more resistant proteins.

Conclusion

Our study provides mechanistic evidence that heavy metal salts (Cd^{2+} , Pb^{2+} , Hg^{2+}) disrupt protein structure, stability, folding, and function even at relatively low concentrations. These effects likely contribute to proteotoxic stress in biological systems and may help explain some of the toxicological consequences observed in environmental and veterinary contexts. By bridging molecular biochemistry with regional environmental science, we underscore the importance of including protein-level endpoints in environmental health risk assessments and remediation strategies.

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