

Probing a Homoleptic PbS₃ Coordination Environment in a Designed Peptide Using ²⁰⁷Pb NMR Spectroscopy: Implications for Understanding the Molecular Basis of Lead Toxicity**

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Lead is a ubiquitous environmental contaminant; nearly 5% of American children are affected by lead poisoning (a blood lead level (BLL) of 10 μg dL⁻¹ or higher).^[1] Even lower BLLs have been shown to cause many subtle health effects in children. Lead, which is found in paint and soil, causes toxicity by several possible mechanisms. Pb²⁺ interacts with several zinc enzymes or proteins (such as carbonic anhydrase, acetylcholine esterase, Cys₂His₂ “zinc-finger” proteins, and acid phosphatases)^[2,3] and calcium ion binding proteins (calmodulin, calbindin, and troponin C).^[4] Inhibition of protein function is induced by alternative coordination number and structural preferences.^[5,6] Pb²⁺ is a chemically interesting toxin in that it can replace calcium and sometimes zinc in “hard” active sites that are oxygen/nitrogen rich; it can also attack softer ligands, such as all-sulfur-containing zinc ion coordination sites. Among the sulfur-rich targets for Pb²⁺ are glutathione and metallothioneines, which cause perturbations of essential metal ion homeostasis.

Aminolevulinic acid dehydratase (ALAD), a zinc-dependent enzyme, is inhibited by a femtomolar concentrations of Pb²⁺.^[2] ALAD is found in yeast and mammals and is involved in the second step of heme biosynthesis. Pb²⁺-poisoned ALAD blocks the synthesis of hemoglobin, causing anemia in mammals. Furthermore, toxic levels of aminolevulinic acid can result. The crystal structure of ALAD contains an unusual Zn(Cys)₃H₂O site, where Zn²⁺ is substituted by Pb²⁺ in a trigonal pyramidal geometry.^[7] The high affinity of Pb²⁺ to cysteine thiolates is presumably due to the high enthalpy of Pb–S bond formation and the preferred PbS₃ coordination geometry in thiolate-rich sites of proteins.^[8] A number of peptides^[9–11] and small-molecule synthetic models^[12] have been used to understand the chemistry of the Pb^{II}-poisoned ALAD. UV/Vis and EXAFS studies on the metalloregulatory protein Pb-PbrR691 and Pb²⁺ model compounds reveal that Pb²⁺ binds in a PbS₃ environment.^[13]

Heteronuclear magnetic resonance spectroscopy with nuclei such as ⁴³Ca, ¹¹³Cd, and ¹⁹⁹Hg has been a powerful tool for studying the active site structures of metalloenzymes and their model compounds.^[14–21] Similarly, lead provides an NMR active nucleus (²⁰⁷Pb, nuclear spin *I* = 1/2) with a natural

abundance of 22.6% and a relatively good receptivity (11.7 times higher than that of ¹³C).^[22] However, owing to the wide chemical shift range (over 16000 ppm), the use of ²⁰⁷Pb NMR spectroscopy is non-trivial.^[8,22–24]

Recently, Vogel and co-workers utilized ²⁰⁷Pb NMR spectroscopy (using isotopically enriched ²⁰⁷Pb) to study Pb²⁺ binding to the Ca²⁺ site of calcium-binding proteins, including calmodulin (CaM).^[25] To our knowledge, this is the sole example of ²⁰⁷Pb NMR as a probe in metalloproteins. Of great importance, there are no reported ²⁰⁷Pb spectra for sulfur-rich metalloproteins. A number of small synthetic molecules with or without mixed O, S, and N donor ligands (for example S₂O₂, S₂N₂, N₂O₄, N₃O₃, N₄, N₆) have been characterized using this technique.^[22–24,26–28] The ²⁰⁷Pb NMR signal for the thiol-rich binding sites should be shifted further downfield than that of oxygen- and nitrogen-rich calcium-binding sites. Thus, we can distinguish PbS₃ versus PbS₃O coordination environments very easily by using ²⁰⁷Pb NMR.^[22] The coordination number and geometry of the Pb²⁺ ion can also be examined.^[29] Dean, Payne, Christou, and their co-workers have synthesized [Ph₄As][Pb(SPh)₃] and characterized complexes in non-aqueous media using ²⁰⁷Pb NMR spectroscopy.^[30–32] Despite these studies, no significant advancement of ²⁰⁷Pb NMR has been accomplished to explore the thiolate-rich proteins scaffolds. Herein, we present the ²⁰⁷Pb NMR for a physiologically relevant coordination environment of thiolate-rich metallopeptides in the preferred homoleptic trigonal pyramidal geometry for Pb^{II} ions by utilizing three-strand coiled-coil peptides. To our knowledge, this is the first report of ²⁰⁷Pb NMR spectroscopy used in a Cys₃ motif that can be a direct probe for the thiol-rich metalloenzymes, such as ALAD, which are directly implicated in human lead poisoning.

We have utilized new three-strand coiled-coil (3-SCC) peptides (CoilSer and TRI family) to obtain insight into how toxic metals, such as Hg²⁺, As³⁺, Cd²⁺, and Pb²⁺, bind in thiol-rich sites of metalloenzymes.^[19–21,33–38] These α-helical peptide families have heptad repeats of seven amino acid residues that contain hydrophobic leucine residues in the **a** (first) and **d** (fourth) positions (Table 1).^[39] The resultant 3-SCC has all of the hydrophobic leucine residues packed on the interior of the 3-SCC and hydrophilic residues (*e* and *g*) on the exterior, forming salt bridges that stabilize the coiled coil. A metal binding site can be created by the substitution of a leucine by cysteine in the **a** or **d** positions of the heptad repeat unit to give a metal binding site within the hydrophobic core of the peptide trimer.^[35,39] The sulfur atoms in an **a** site are oriented towards the interior of the coiled coil and preorganized for

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Table 1: Sequence and name of the peptides used in this study.

Peptides	Sequence
	abcdefg abcdefg abcdefg abcdefg
CSL12C	Ac-E WEALEKK LAACESK LQALEKK LEALEHG-NH ₂
CSL16C	Ac-E WEALEKK LAALESK CQALEKK LEALEHG-NH ₂
CSL12AL16C	Ac-E WEALEKK LAAAESK CQALEKK LEALEHG-NH ₂
BabyL12C	Ac-G LKALEEK LKACEEK LKALEEK G-NH ₂
GrandL12AL16CL26C	Ac-G LKALEEK LKAAEEK CKALEEK LKACEEK LKALEEK G-NH ₂

metal binding, whereas the sulfur atoms in a **d** site point away from the interior towards the helical interface, creating a relatively larger cavity (Figure 1). Metal ions such as Cd²⁺, Hg²⁺, and As³⁺ are preferentially bound to the **a** site, whereas larger metal ions such as Pb²⁺ prefer the **d** site.^[40]

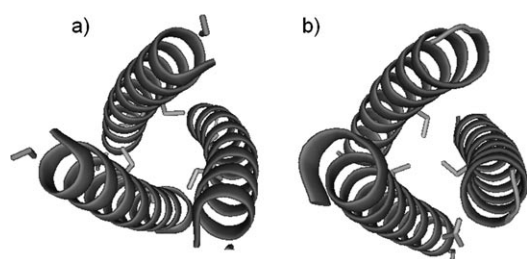


Figure 1. Pymol representation showing the orientation of cysteine residues. a) CoilSerL12C, **d** site; b) CoilSerL16C, **a** site. Cysteine side chains are shown as sticks and peptide α helices are shown as coils. PDB code: 3H5F.^[45]

The use of these well-defined peptides provides several advantages for detecting the ²⁰⁷Pb signal in an all-thiolate (homoleptic) environment that mimics ALAD. In contrast to small organic lead thiolate complexes, the designed peptides are highly soluble and stable in water. Therefore, ²⁰⁷Pb NMR studies at relatively high concentrations (10–12 mM) and physiological pH is successful without peptide aggregation or Pb(OH)₂ precipitation. Similar preparations were unsuccessful for cysteine, which was due to the precipitation of a PbCys₃ complex that can only be dissolved at high pH (> 12). Thus, a solely PbS₃ coordination environment cannot be attained by cysteine at physiological pH.

Binding studies of Pb²⁺ to TRIL12C and TRIL16C were previously monitored by UV/Vis, EXAFS, and CD spectroscopy^[35] and shown to have high affinity (> 10⁸ M⁻¹) with the peptides studied herein. The presence of a characteristic ligand-to-metal charge-transfer (LMCT) band at about 345 nm ($\epsilon \approx 3500 \text{ L mol}^{-1} \text{ cm}^{-1}$) is indicative of PbS₃ in a trigonal pyramidal geometry. Recent EXAFS studies by Matzapetakis et al. identified a three-coordinate Pb²⁺ site in Pb(TRIL16C)₃⁻ with Pb–S scatters at 2.63 Å. Similar results have been reported by Giedroc and co-workers for the preference of Pb²⁺ for a PbS₃ coordination environment in the metalloregulatory protein CadC.^[41,42] This data compares well with Pb–S scatters found for the lead-inhibited active site of ALAD. Therefore, the metalloptides described herein are

in close approximation to the Pb²⁺-inhibited active site of ALAD and related lead-binding proteins.

The natural-abundance ²⁰⁷Pb NMR spectra of all of the metalloptides with a single binding site had a single lead signal at 5500–5800 ppm with broad linewidths (15–25 ppm) (Figure 2). Similar

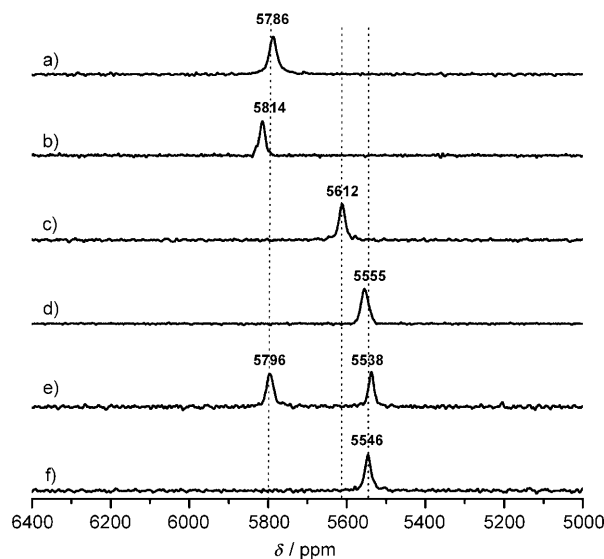


Figure 2. Natural-abundance ²⁰⁷Pb NMR spectra (104.435 MHz) of Pb^{II}-bound three-strand coiled-coil peptides (10–12 mM): a) Pb-(BabyL12C)₃⁻, b) Pb(CSL12C)₃⁻, c) Pb(CSL16C)₃⁻, d) Pb(CSL12AL16C)₃⁻, e) Pb₂(GrandL12AL16L26C)₃²⁻, f) Pb(GrandL12AL16L26C)₃⁻. All spectra were recorded for 10–12 h using natural-abundance Pb(NO₃)₂, (²⁰⁷Pb = 22.6%), pH 7.35 ± 0.05, at 25 °C.

broad signals have been reported in protein NMR studies with ¹⁹⁹Hg and ²⁰⁵Tl, which may be due to nuclear relaxation by chemical shift anisotropy (CSA).^[43,44] The peptides with a **d** metal binding site have downfield chemical shifts relative to those of the **a** site peptides. Several interesting trends can be extracted from these data: similar chemical shifts for the peptides having a **d** site are seen independent of the length of the peptide or the intrinsic stability of the aggregate, Pb-(BabyL12C)₃⁻ ($\delta = 5786 \text{ ppm}$, $w_{1/2} = 20 \text{ ppm}$) and Pb-(CSL12C)₃⁻ ($\delta = 5814 \text{ ppm}$, $w_{1/2} = 18 \text{ ppm}$). These chemical shifts are similar to the previously reported trigonal pyramidal PbS₃ structure of a small synthetic organic compound [Ph₄As][Pb(SPh)₃] ($\delta = 5828 \text{ ppm}$).^[31] The possibility of formation of nitrogen- or oxygen-bound species can be ruled out as a distinct upfield chemical shift has been observed for mixed-donor ligand types (PbN₂S, $\delta = 5318 \text{ ppm}$; PbS₂O₂, $\delta = 4100\text{--}4500 \text{ ppm}$).^[8,24,26] Therefore, the observed ²⁰⁷Pb signal can be confidently assigned to the formation of a PbS₃ coordination environment.

An upfield chemical shift of approximately 200 ppm was observed when a lead-binding site was created in the **a** site peptide (Pb(CSL16C)₃⁻; $\delta = 5612 \text{ ppm}$, $w_{1/2} = 18 \text{ ppm}$). Fur-

thermore, substitution of a sterically less-demanding amino acid residue above the **a** metal binding site leads to a 55–60 ppm further upfield shift (Pb(CSL12AL16C)₃⁻; $\delta = 5555$ ppm, $w_{1/2} = 25$ ppm). We conclude that ²⁰⁷Pb NMR spectroscopy is sufficiently sensitive to distinguish between two similar trigonal pyramidal PbS₃ centers based on the **a** versus **d** substitution pattern of the peptide. Furthermore, the upfield shift in the Pb(CSL12AL16C)₃⁻ suggests that the additional space provided above the PbS₃ plane by the alanine accommodates the bulky Pb²⁺ lone pair within the helical assembly better. A similar rationale can be applied to the longer Pb₂(GrandL12AL16L26C)₃²⁻, in which the leucine layer above the **a** site is substituted by alanine and leucines at the 16th (**a**) and 26th (**d**) sites are replaced with cysteines, creating two Pb²⁺ binding sites. The **d** site has a ²⁰⁷Pb NMR signal at $\delta = 5796$ ppm (Figure 2e; $w_{1/2} = 17$ ppm); this value is between the signal obtained for Pb(BabyL12C)₃⁻ and Pb(CSL12C)₃⁻, but clearly in the region of **d** cysteine ligands. A ²⁰⁷Pb peak at 5538 ppm ($w_{1/2} = 18$ ppm) is assigned to the **a** site with a hole oriented towards the N terminus, which compares well with the value obtained for Pb(CSL12AL16C)₃⁻. These data illustrate that ²⁰⁷Pb NMR is sufficiently sensitive to discriminate complexation of Pb²⁺ in these similar yet non-identical sites. Furthermore, the simultaneous observation of both peaks and the relatively narrow linewidths suggest that the Pb²⁺ ions are in slow exchange on the NMR timescale.

Interestingly, the addition of one equivalent of Pb(NO₃)₂ into GrandL12AL16L26C gives a ²⁰⁷Pb signal at the **a** site region only ($\delta = 5546$ ppm, $w_{1/2} = 19$ ppm), indicating a selective binding of Pb²⁺ to the **a** site with a hole above (Figure 2f). This observation is in contrast to the previously reported **a** versus **d** preference for Pb²⁺ complexation. The inversion of selectivity is a consequence of the added space made available by substituting alanine for leucine. The stereochemically active lone pair of Pb²⁺ no longer clashes with the alkyl side chain of leucine and can now be accommodated within the generated cavity, leading to a higher thermodynamic stability of lead binding. It has been shown that Cd²⁺, which forms a mixture of three- (CdS₃) and four-coordinate (CdS₃(H₂O)) structures with TRIL16C, becomes fully four-coordinate, using an exogenous water ligand, when space is made available above the metal by the same leucine to alanine substitution in TRIL12AL16C.^[46]

These results provide experimental confirmation of the importance of the lone pair on the selectivity of Pb²⁺ for sulfur sites in proteins such as PbrR691 and ALAD (in which Pb²⁺ displaces Zn²⁺ from three cysteines and one exogenous water rather than the five-coordinate zinc binding site with nitrogen and oxygen atoms as ligands). These data suggest that there will be a significant preference for Pb²⁺ to be sequestered into an environment that provides sufficient space to accommodate the large lone pair of this ion. Such a situation exists when Pb²⁺ displaces Zn²⁺ in ALAD.

Despite the fact that lead-substituted ALAD is strongly implicated in lead toxicity, to date there have been no examples of biomolecules or model compounds that have exhibited a ²⁰⁷Pb NMR spectrum for a PbS₃ center in aqueous solution at physiological pH. Our ability to detect such a

chromophore using natural-abundance isotope levels, to illustrate the sensitivity of the chemical shift range and to demonstrate how slight amino acid sequence changes affect lead binding to a protein are significant advances for understanding the biochemistry of human lead poisoning. Our data also indicate that Pb²⁺ exchange between homoleptic thiolate sites is slow on the NMR timescale. Most importantly, we have demonstrated that high-quality spectra do not require expensive enriched ²⁰⁷Pb, but can be obtained using natural-abundance lead salts. We hope that ²⁰⁷Pb NMR spectroscopy may now be useful to identify and characterize proteins associated with lead toxicity directly from human samples if a sufficiently concentrated sample can be obtained.

Experimental Section

Peptide synthesis and purification: All of the peptides were synthesized on an Applied Biosystems 433A peptide synthesizer by using standard Fmoc/tBu-based protection strategies on Rink Amide MBHA resin (0.25 mmol scale) with HBTU/HOBt/DIEPA coupling methods.^[47] The peptides were then cleaved from the resin either using a mixture of 95% trifluoroacetic acid (TFA), 2.5% ethanedithiol, and 2.5% triisopropyl silane or a mixture of 90% TFA, 5% thioanisole, 3% ethanedithiol, and 2% anisole. The cleaved peptide solutions were filtered and then evaporated under a dry N₂ flow to give a glassy film. The white film was washed with ice-cold diethyl ether (peroxide free) to obtain a crude peptide powder. The peptides were dissolved in 10% acetic acid, lyophilized, and subsequently purified by reverse-phase HPLC (Waters 600 with Vydac protein and peptide C-18 column; solvent A: 0.1% TFA in H₂O; solvent B: 0.1% TFA in acetonitrile/H₂O (9:1); linear gradient 20–80% of solvent B over 30 min; flow rate: 10 mL min⁻¹). The identity and purity of the purified peptides was confirmed by electrospray mass spectrometry (Waters) in positive-ion mode and by analytical HPLC. The purity of peptides was more than 95%. All of the peptides studied herein were N-terminally acetylated and C-terminally amidated. A list of the peptides synthesized with their sequences is given in Table 1.

Natural abundance ²⁰⁷Pb NMR spectroscopy: NMR samples (10–12 mm) were prepared under a nitrogen atmosphere by dissolving of pure and dried peptide (70–80 mg) in D₂O/H₂O (15%, 400–500 μ L; degassed). The peptide concentration was determined by Ellman's test.^[48] Calculated amounts of 250 mM Pb(NO₃)₂ (natural abundance) stock solution was added to the peptide solution and the pH was adjusted by the slow addition of a small aliquot of KOH/15% D₂O until the pH reached 7.35 ± 0.05 . All of the ²⁰⁷Pb NMR spectra were recorded at a frequency of 104.435 MHz on a Varian 500 MHz NMR spectrometer at room temperature (25 °C) using 60° pulses, a 20 ms relaxation delay, and a 20 ms acquisition time. Initially, a large spectral width of 300 KHz was used to find the position of the peak. Once the peak position was found, the spectral window was reduced to about 166 KHz. However, the chemical shift difference was not observed when the spectral window was about 300 KHz (3000 ppm), 166 KHz (1500 ppm), or 50 KHz (500 ppm). A linear prediction was performed to remove the noise, and the real FID was determined before the data processing. After zero-filling, the data (128 K data points) were processed with an exponential line broadening of 200–250 Hz using the software MestRe-C.^[49] The ²⁰⁷Pb NMR chemical shifts are reported downfield from tetramethyllead ($\delta = 0$ ppm; toluene) using 1.0 M Pb(NO₃)₂ salt (natural) as an external standard ($\delta = -2990$ ppm, D₂O, 25 °C; relative to PbMe₄).

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