Investigation of Rare Earth Element Binding to a Surface-Bound Affinity Peptide Derived from EF-Hand Loop I of Lanmodulin

Geeta Verma[†,1], Jacob Hostert[†,1], Alex A. Summerville[1], Alicia S. Robang[2], Ricardo Garcia Carcamo[3], Anant K. Paravastu[2,4], Rachel B. Getman [3], Christine Duval[1] and Julie Renner*[,1]

[1]Department of Chemical and Biomolecular Engineering, Case Western Reserve University, Cleveland, Ohio 44106

[2]School of Chemical and Biomolecular Engineering, Georgia Institute of Technology, Atlanta, Georgia 30332

[3]Departemnt of Chemical and Biomolecular Engineering, Ohio State University, Columbus, OH 43210

[4]Parker H. Petit Institute for Bioengineering and Biosciences, Georgia Institute of Technology, 315 Ferst Drive, Atlanta, 30332, GA, USA

[†] Co-first author

*Corresponding Author (jxr484@case.edu)

Abstract

Bioinspired strategies have been given extensive attention for the recovery of rare earth elements (REEs) from waste streams because of their high selectivity, regeneration potential, and sustainability, as well as low cost. Lanmodulin protein is an emerging biotechnology that is highly selective for REE binding. Mimicking lanmodulin with shorter peptides is advantageous because they are simpler and potentially easier to manipulate and optimize. Lanmodulin-derived peptides have been found to bind REEs, but their properties have not been explored when immobilized on the solid substrates, which is required for many advanced separation technologies. Here, two peptides, LanM1 and scrambled LanM1 are designed from the EF-hand loop 1 of lanmodulin and investigated for their binding affinity towards different REEs when surface-bound. First, the ability for LanM1 to bind REEs was confirmed and characterized in solution, using circular dichroism (CD), nuclear magnetic resonance (NMR), and molecular dynamics (MD) simulations for Ce (III)

ions. Isothermal titration calorimetry (ITC) was used to further analyze the binding of the LanM1 to Ce (III), Nd (III), Eu (III) and Y(III) ions and in low pH conditions. The performance of the immobilized peptides on a model gold surface was examined using quartz crystal microbalance with dissipation (QCM-D). The studies show LanM1 peptide has a stronger REE binding affinity than scrambled LanM1 when in solution and when immobilized on a gold surface. QCM-D data were fit to the Langmuir adsorption model to estimate the surface-bound dissociation constant (K_d) of LanM1 with Ce (III) and Nd (III). The results indicate LanM1 peptides maintain high affinity for REEs when immobilized, and surface-bound LanM1 has no affinity for potential competitor calcium and copper ions. The utility of surface-bound LanM1 peptides was further demonstrated by immobilizing them to gold nanoparticles (GNPs) and capturing REEs from solution in experiments utilizing an arsenazo-III based colorimetric dye-displacement assay and UV-vis spectrophotometry. The saturated adsorption capacity of GNPs was estimated to be around 3.5 μmol REE/g for Ce (III), Nd (III), Eu (III) and Y(III) ions, with no binding of non-REE Ca (II) ions observed.

Keywords

Rare-earth elements (REEs), biosorption, gold nanoparticles, affinity peptides, lanmodulin, molecular dynamics.

1 Introduction

Rare-earth elements (REEs) are essential in several emerging technologies such as wind turbines, electric vehicles, computer memory, autocatalytic converters, magnetic resonance imaging, and smartphones.[1] Owing to the high cost and limited availability, the recovery of these elements from the industrial waste streams is an attractive option for a green and circular economy.[2] There is an urgent need to identify efficient separation methods that recycle REEs from the waste streams and provide a steady, domestic source of these elements. Various techniques have been applied to recover REEs from the waste streams such as solvent extraction,[3] filtration,[4] ion exchange,[5] chemical precipitation,[6] adsorption,[7] and electrochemical processes.[8] Commercially, solvent

extraction is used to separate REEs from concentrated aqueous waste streams but the solvent requirements are high in this method.[9] Membrane filtration techniques do well under low concentration and high volume throughput conditions but the limiting factor is the selectivity of commercial membranes for trivalent ions over divalent ions.[10] Overall, some of the constraints of these methods include high chemical consumption, high operational cost and the need to treat the generated waste.[11] To overcome these challenges, innovative developments utilizing several emerging technologies such as nanomaterials, bioleaching, biosorption, acidolysis, biomineralization, cryo-milling, and the use of supercritical CO_2[12] are under investigation. Among these, there are several advantages of bio-combined (biosorption) recycling strategies as they show higher selectivity, use fewer toxic chemicals, have high regeneration potential, demonstrate fast kinetics, and are cost-efficient.[13] However, the design of a bio-based approach with selective adsorption of REEs requires deep acquaintance with the support materials and the ligand of choice such as peptides that can be grafted on the desired surface for selective separation of REEs. Peptides are desirable as they are short chains of amino acids (less than 50) and are highly tunable ligands that are selective for ions.[14] Many researchers have attempted to identify or design peptides with the ability to selectively bind to lanthanides.[13, 15, 16] For example, Hatanaka *et al.*[15] studied a linear peptide lanthanide binding tag (LBT3) and by combining experimental and computational techniques provided a deep insight into the mechanism underlying the specificity of the peptide toward lanthanides in aqueous media. Through isothermal titration calorimetry (ITC) experiments, they found that the thermodynamic properties of ion complexation strongly vary with lanthanide ion size and molecular dynamics (MD) simulations revealed that the high binding affinity is achieved through complete ion dehydration. In another investigation, Xu *et al.*[16] derived a peptide sequence from the EF-hand loop I of calmodulin and experimentally showed that the peptide has

the same affinity for cerium (III) ions when tethered to a gold surface (surface-bound) as it does in solution (unbound).[16, 17]

The recent discovery of the lanmodulin protein, which has high selectivity for REEs over non-REEs,[18] opens new possibilities for utilizing lanmodulin-derived peptides for REE recovery. Lanmodulin has four metal-binding EF-hand motifs that undergo a large conformational change in response to REE binding (from a largely disordered state to a more ordered state) and has higher affinity over calmodulin.[19] As a result, several lanmodulin-ion complexation studies have been conducted to understand its structure as well as its REE binding affinity and selectivity.[19-24] In a recent investigation of the four EF-hand loop peptides derived from lanmodulin, Gutenthaler *et al.*[24] examined their affinity for two REEs (Eu(III), Tb(III)) and one non-REE (Ca(II)) in solution and used molecular dynamics simulations to further support their experimental observations. While studies of the shorter peptides are limited, more work has been done to tether the full-length lanmodulin protein to various supports to perform separation. Kwon and co-workers[21] used elastin-like polypeptide (ELP) fused with truncated lanmodulin protein to form REEs-sensitive and thermo-responsive genetically encoded ELP, called "RELP". They studied several REEs ((Tb (III), La (III), Ce (III) and Y(III)) and non-REEs (Zn (II) and Cu (II)) in bulk with the help of calorimetric techniques. Among limited solid surface-bound studies, Dong *et al.*, immobilized lanmodulin protein on agarose microbeads through thiol-maleimide click chemistry and investigated the selectivity between REE pairs (Nd (III)/Dy (III), and Y (III)/Nd (III)) and grouped separation between heavy REEs (Tb(III)-Lu(III)+Y(III) over light REEs (La(III)-Gd (III)) on a resin-packed column.[22] Ye *et al.*[23] immobilized lanmodulin protein on the surface of magnetic nanoparticles (MNPs) through SpyTag-SpyCatcher (Spy) chemistry and studied the binding of several REEs and non-REEs. Xiaoman *et al.* engineered a bio-adsorbent in which lanmodulin was

displayed on the cell surface of the fungus *Yarrowia lipolytica* and the binding capacity for different REEs and non-REEs was characaterized.[20] Although there are a few studies done on surface-bound lanmodulin protein, no such investigation has been done on lanmodulin-derived peptide for REE binding.

In this work, two novel peptides, LanM1, and scrambled LanM1 are derived from the EF-hand loop 1 of lanmodulin and are investigated against four REEs (Ce (III), Nd (III), Eu (III) and Y(III)), and two competing non-REEs (Ca (II) and Cu (II)) in surface-bound and unbound conditions. Cerium is selected as it is an important material in a wide range of applications such as oxygen sensing, industrial catalysis, fuel cells, low-temperature water-gas shift reactions, and electrochromic thin-film application. [25, 26] Neodymium is used mainly in magnets, catalysts, and lasers.[27] Europium has applications in control rods for nuclear reactors, fluorescent bulbs and optoelectronics[1, 28]. The common use of yttrium is in lasers, fluorescent lamps, and lighting. [27, 29] We performed circular dichroism (CD) analysis and nuclear magnetic resonance (NMR) to confirm that the LanM1 peptide sequence modified for surface immobilization binds REEs. Isothermal calorimetry (ITC) experiments were performed to determine the thermodynamic parameters (K_D, ΔH, ΔS, and ΔG) of the interaction between the peptides and the ions in solutions. QCM-D was conducted to show that surface-bound peptdies derived from lanmodulin can bind REEs and characterize the surface-bound affinity using the Langmuir adsoprtion model to estimate equilibrium binding constants. Molecular dynamics simulations were performed to gain molecular insight and to complement the experimental results. Finally, to demonstrate the utility of the surface-bound peptide as a material, the maximum REE adsorption capacity of LanM1 immobilized on gold nanoparticles was determined in a proof-of-concept experiment. Overall, this study characterizes the properties of surface-bound LanM1 peptide for the first time, and

demonstrates its potential utility in REE separation for further optimization and exploration in the future.

Materials and Methods

Materials

The peptide sequences in this study were derived from the EF-hand loop I of lanmodulin and were ordered from GenScript (https://www.genscript.com/) at a purity of >95%. Cerium (III) chloride heptahydrate ($CeCl_3.7H_2O$) 99.9% purity, neodymium nitrate hexahydrate ($Nd(NO_3)_3.6H_2O$ 99.9% purity, europium (III) chloride hexahydrate ($EuCl_3.6H_2O$) 99.9% purity, yttrium (III) chloride hexahydrate ($YCl_3.6H_2O$) 99.9% purity, calcium sulfate dihydrate ($CaSO_2.2H_2O$) 99.0 % purity and copper sulfate pentahydrate ($CuSO_2.5H_2O$) 99.9% purity were purchased from Sigma-Aldrich. Millipore ultrapure water (UPW) was used as a solvent. Nitrogen (N_2) gas (>99%) that was used in circular dichroism experiments was procured from Airgas. Gold nanoparticles with size less than 100 nm (powder), 99.9% trace were obtained from Sigma-Aldrich.

Peptide Design

The peptide sequences for binding studies were designed from EF-hand loop I of lanmodulin. The sequence intended for REE binding is called LanM1 (Ac-CGGGDPDKDGTIDLKE-NH_2). It is the same sequence as the EF hand loop I of lanmodulin with additional three glycine amino acids as spacers and one cystine residue for binding to the gold surface. A schematic representation of LanM1 is given in **Figure 1a**. The second sequence, called scrambled LanM1 (Ac-CGGGKGEDDDKTLDIP-NH_2), has the same amino acids as in EF-hand loop I of lanmodulin but are randomly arranged with the same three glycine amino acids as spacers and one cystine for binding to the gold surface (**Figure 1b**). For both peptides, N-terminal acetylation and C-terminal amidation was done to increase the stability by reducing degradation.

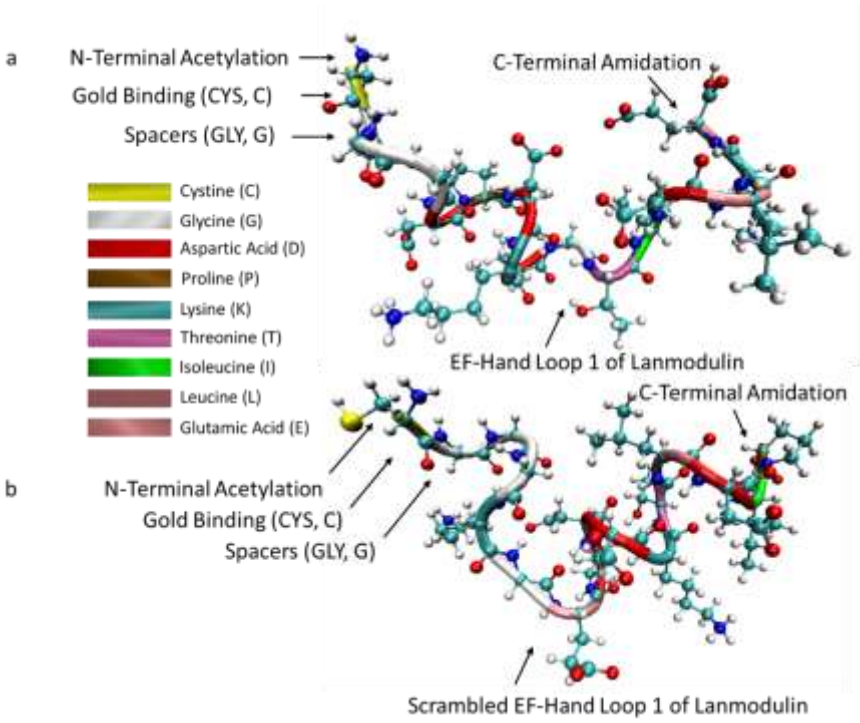

Figure 1. (a) Schematic representations of the energy minimized peptide sequences LanM1 (Ac-CGGGDPDKDGTIDLKE-NH_2) and (b) scrambled LanM1 (Ac-CGGGKGEDDDKTLDIP-NH_2) designed in this study for cerium binding. Different colors in the backbone (tube representation) are used to show different amino acids in the sequence. The energy-minimized molecular images of the peptides were created using the Visual Molecular Dynamics (VMD) package.[30]

Circular Dichroism (CD)

A circular dichroism (CD) spectrometer (Jasco J-815) was used to examine the conformational change of the peptides under the influence of cerium (III) in ultrapure water. The step resolution of 0.1 nm, and the scanning speed of 20 nm/min were selected to scan the samples in a quartz cuvette with a 0.1 cm path length. The absorbance spectra were generated in the range of 190-260 nm wavelength. The post processing of the data including baseline correction and smoothing of

157 the spectra was done using the Spectra Analysis processing tool of the Spectra Manager ver. 2.0
158 program which accompanied the spectrometer.

159 **^{1}H Nuclear Magnetic Resonance (NMR) Measurements**

160 LanM1 and scrambled LanM1 samples were prepared by dissolving 1 mg of peptide in 0.75 mL
161 of deuterated water (D_2O) and then pipetting them into 5 mm Wilmad NMR tubes. Each molar
162 equivalent of cerium (III) was dissolved in 50 µL D_2O before being added into NMR sample tubes.
163 NMR measurements were collected on a 11.75 T magnet (500 MHz, ^{1}H NMR frequency) in a
164 Bruker spectrometer. The Bruker default "zgesgp" pulse sequence for water suppression using
165 excitation sculpting was used to collect ^{1}H spectra. Signals were averaged over 100 scans.

166 **Isothermal Titration Calorimetry (ITC)**

167 Isothermal titration calorimetry (ITC) analysis was performed using MicroCal Auto-ITC_{200}. In the
168 present work, 200 µM REE solutions were titrated in 35 injections of 1 µL each with 300 µL
169 peptide solution (20 mM) at 30^{0}C. The solutions were prepared in ultrapure water and prior to
170 experiments the solutions were degassed. The first injection point was removed due to
171 dilution/mixing effect and the baseline was corrected prior to further analysis. The data analysis
172 was done with Origin 7.0 using the one set of sites fitting model to calculate binding constant (K_d),
173 enthalpy (ΔH) and entropy (ΔS).

174 **Quartz Crystal Microbalance (QCM)**

175 Quartz crystal microbalance with dissipation (QCM-D, Q-Sense Explorer, operated by Q-Soft
176 integrated software from Biolin Scientific was used to investigate the mass adsorption of the ions
177 to surface-bound lanmodulin derived peptides. Frequency shifts and dissipation changes were
178 monitored simultaneously with time, and all experiments were conducted in aqueous solution.

Information about the gold-coated crystal sensors (QSX 301, 5 MHz, Biolin Scientific), module cleaning, and data analysis can be found in our previous work.[31] In general, QCM-D experiments were operated in a flow module at 18°C and at a flow rate of 150 μL/min. Frequency decrease and increase reflects mass accumulation and removal on the surface respectively, and dissipation changes show the viscoelastic characteristics of the adsorbed material. After acquiring a stable baseline with ultrapure water, lanmodulin peptides (**Figure 1**) were introduced at 10 μg/mL in ultrapure water and allowed to adsorb to the gold surface for ten to twenty minutes before rinsing with ultrapure water to remove unbound peptide. Next, ion solutions were introduced to bind to the peptide for at least ten minutes and then rinsed with ultrapure water to remove loosely bound ions. The QCM-D instrument is not sensitive enough to detect the REE loading on the peptide due to extremely small added mass. To improve the sensitivity of detecting REE ion binding, a 1 mM sodium phosphate solution was then introduced for at least ten minutes before a final rinse with ultrapure water. The exact mechanism of phosphate interaction with REEs is still unclear. We speculate co-adsorbed water or precipitation along with the phosphate ions intensifies the frequency change.[17] This technique was validated with a known calmodulin peptide (**Figure S7**). The mass loading during the adsorption was estimated using QSense Dfind software.

MD Simulations

Molecular dynamics (MD) simulations were carried out using the GROMACS package.[32] First, the peptide sequences were drawn in ChimeraX,[33] and the coordinates were saved in pdb format. The coordinate files in pdb format were used to generate the topology and other input files using GROMACS toolkit. By default, termini are ionized (NH_3^+ and COO^-), therefore it is important to cap the N- and C-termini of the peptide to make them uncharged (NH_2 and COOH). Leaving the termini charged leads to artificial charge-charge interactions, particularly in small molecules like

peptides. The CHARMM all-atom force field was selected to model peptides.[34] Cerium (III) was modeled as LJ sphere with $\sigma = 0.306$ nm and $\varepsilon = 0.0676$ kcal/mol [35] with comparable parameters as other previously developed force fields.[36, 37] Water molecules were represented with the TIP3P model as it is widely used for protein ligand simulation.[38] The geometric mixing rule was used to obtain the interaction parameters between unlike atoms. The initial configurations were generated by placing the peptides in the center of a cubic box with side length 5 nm. One cerium ion was inserted at some random position and the boxes were solvated with explicit water molecules. The periodic boundary conditions were used in all directions. Prior to simulation, the geometries of the systems were minimized using the steepest descent algorithm to remove any contact between the atoms. After geometry minimization, the systems were annealed from 600 K to 300 K in NVT ensemble for 5 ns. This was done to facilitate ion binding, overcome slow dynamics and any energy barrier, and possible metastable stages. Finally, three independent 50 ns long simulations were run in NPT ensemble for the analysis. A time step of 2 fs was used with all bonds involving hydrogen atoms constrained by the LINCS algorithm.[39] The electrostatic interactions were treated using the fast particle-mesh Ewald (PME) summation method with a cutoff of 1.5 nm and a grid spacing of 0.1 nm.[40] The temperature was kept constant at 300 K using the velocity-rescale thermostat with a coupling constant of 0.1 ps.[41] In NPT ensemble, 1 bar pressure was maintained used the Parrinello-Rahman pressure coupling with a coupling constant of 2.0 ps.[42] The trajectories obtained from the simulations were visualized in the VMD package and coordination of oxygen atoms in the binding sites were monitored throughout the simulation.[30] A snapshot of the equilibrated configuration of the system comprised of the peptide ion complex after 50 ns is shown in **Figure S1**.

Adsorption Experiments on Gold Nanoparticles (GNPs)

A protocol was prepared and used to estimate the adsorption of REEs on LanM1 functionalized GNPs. In all experiments, roughly 8 to 12 mg of GNP power was added to 2.0 ml Eppendorf tube and the exact weight of GNPs was calculated by taking the weight of the tube before and after adding GNPs. Later, 1 mL LanM1 solution at 60.2 μM concentration was added and the tube was incubated on the rocker table for 24 hours to saturate the GNPs with the peptide. Once LanM1 was functionalized on GNPs, the tube was centrifuged, and the supernatant was removed. The LanM1 functionalized GNPs were then rinsed for five times with ultrapure water to assure no unbound LanM1 was left in the tube. The weight of the tube was measured again to estimate leftover water as it was not possible to pipette out all water after centrifugation and rinsing. In the following step, 1.5 mL of REE solution at a specific concentration between 20 to 125 μM was added to the tube and incubated again on a rocker table for another 24 hours. During incubation, the concentration of GNP in the REE solution was 5-8 mg GNP/mL. After centrifuging the tube, the supernatant was titrated against arsenazo III reagent and using colorimetric technique, the concentration of the REE was estimated. Control experiments without GNP were performed to assure that no metal leached from the tube material into the solution and no REE absorbed on the tube surface. A pictorial representation of step-by-step procedure used for REE binding on gold nanoparticles (GNPs) is shown in panel a of Figure 8. The initial and supernatant REE concentrations were used to find the adsorption capacity of LanM1 functionalized GNPs. The pH of the solution remained between 5.0 to 5.5 throughout the experiment.

2 Results and Discussion

Conformational Analysis and Binding Site Investigation

Both the peptides, LanM1 and scrambled LanM1, are newly designed peptides and an initial binding investigation was needed to identify their ability to bind REE ions in solution. Therefore,

the ability to bind to cerium (III) ions was checked using circular dichroism (CD) experiments, as we have done with other EF-hand peptide sequences previously.[16] Several experiments were performed by keeping peptide concentration at 100 μM and varying cerium (III) ion concentration within the range of 100 to 1000 μM. The effect of ion concentration on the secondary structure of the peptides was observed and the spectra for LanM1 and scrambled LanM1 are reported in **Figure 2a and b**, respectively. In case of LanM1, it was observed that at a wavelength around 222 nm, there is a decrease in the ellipticity as cerium ion concentration increases. It has been reported that decreases in the ellipticity at 222 nm are related to an increase in α-helicity caused by metal binding.[16, 24] In case of LanM1, a change in the structure of the peptide is confirmed upon REE binding with shifts at 200 and 222 nm observed. When looking at the spectra of scrambled LanM1, smaller changes in the ellipticity are observed, which indicates negligible shifts in the secondary structure of the peptide in the presence of cerium ions. A slight decrease in ellipticity at 200 nm was observed in the scrambled peptide at 1000 μM, which indicates an increase in random coil content at high cerium ion concentrations. Although, CD results could not quantify binding affinities of the designed peptides, the results indicate that the secondary structure of LanM1 undergoes larger structural changes upon binding than the scrambled peptide. To understand this change, molecular dynamics simulations were performed, and conformational analysis of the peptides was carried out.

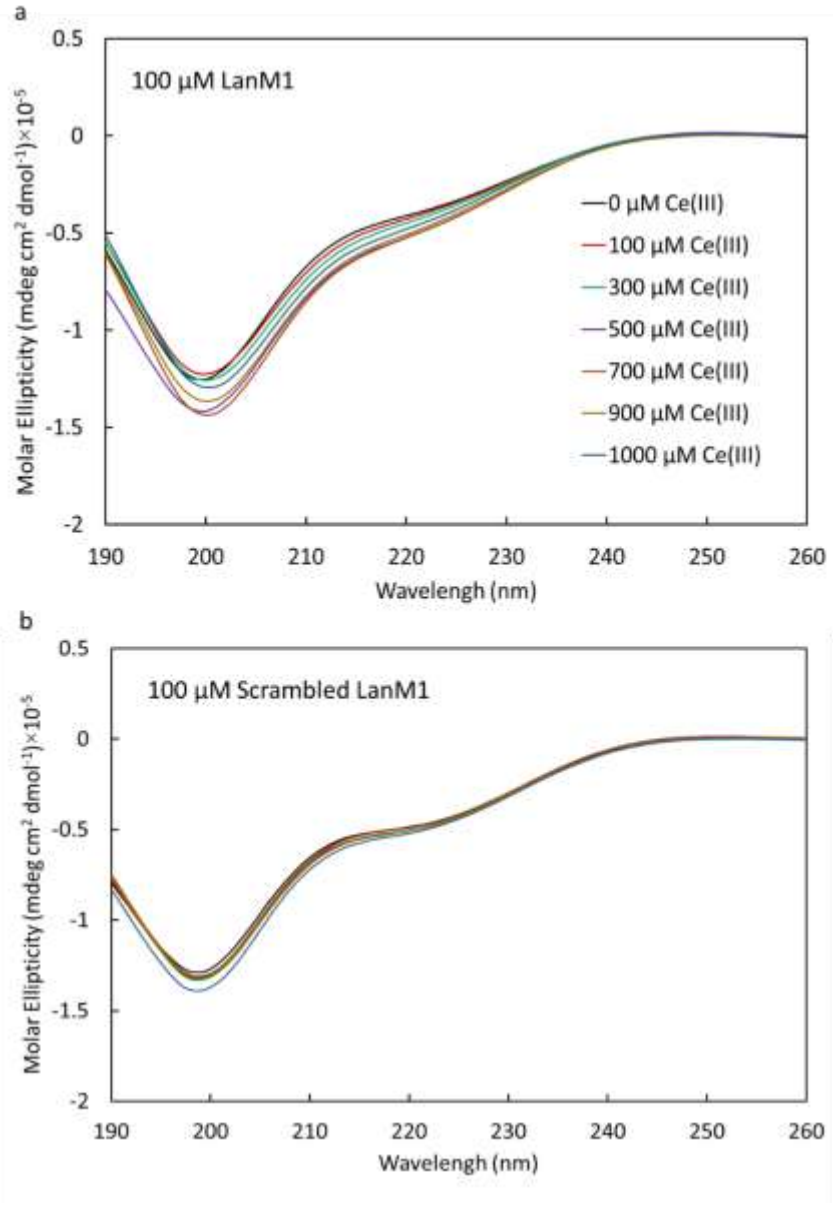

Figure 2. CD spectra of cerium (III) titration experiments with 100 µM of (a) LanM1 peptide and (b) scrambled LanM1 peptide in DI water at different cerium (III) concentrations up to 1000 µM.

Figure 3a shows randomly selected superimposed MD snapshots of free LanM1, and LanM1-cerium (III) complex taken from 50 ns long equilibrated trajectories. The visualization clearly indicates a well-preserved and equilibrated structure of LanM1 before and after binding with the ion. The snapshots illustrate a change in the conformation of the peptide upon binding that is

consistent with the CD results. To better understand the change in molecular conformation, radius of gyration of the peptide in bound and free states were calculated and reported in **Figure 3b**. The results show that the radius of gyration of free peptide is higher than bound peptide. We suspect that this might be due to the peptide being more open in free state and the structure becoming relatively rigid (packed) after complexation with cerium ion. The other possible interpretation could be that the pocket presents more affinity towards the ion than with water; hence the bound state configuration is maximizing the ion-peptide interaction over the ion-solvent interaction. These finding are consistent with Gutenthaler *et al.* who had done a similar binding investigation of europium (III) ions with the EF-hand loops of lanmodulin.[24]

To gain the atomistic details of the binding sites, **Figure 3c** shows the LanM1 binding site and the atoms that are coordinated with the Ce (III) ion. A total of nine oxygen atoms from LanM1 and water were observed to participate in the active binding site throughout the simulation. Out of these, seven were carboxylate oxygen atoms with five having an aspartic acid side chain and two having a glutamic acid side chain. The remaining two atoms were the oxygen atoms of water molecules near the binding site as shown in Figure 3c. Cook *et al*., in their study determined the structure of all four metal-binding sites (EF-hand loops) of lanmodulin protein using NMR spectra when the binding sites were saturated with Y (III).[43] The atomistic investigation of the EF-hand loop I of lanmodulin bound to yttrium ions (the structure is available at protein data bank),[43] reveals that the binding site has nine oxygen atoms. However, in that case, no water molecules were associated in the binding site, defined as 2.3 Å distance from the ion. Gutenthaler *et al.* reported that the binding site for the Eu ion had a total of nine oxygen atoms with four atoms of aspartic acid and one of glutamic acid.[24] The remaining four oxygen atoms belong to the water molecules associated with the binding site. The number of water molecules coordinated in the inner sphere

296 of lanthanide ions decreases from nine to eight across the series (La → Lu) due to the decreasing
297 ionic radii. It has been found that the coordination number from La (III) to Nd (III) is nine, from
298 Nd (III) to Tb (III) it is between nine and eight, and those from Tb (III) to Lu (III) have eight
299 coordinated water molecules in the inner sphere.[44] In addition to coordination number, the average
300 ion-H_2O distance also varies with the atomic radii of REEs. For example, in case of Sm (III), the
301 average ion–H_2O distances is 2.474 Å and the value changes to 2.450 Å for Eu (III).[44] These factors
302 together also impact the coordination chemistry of different ions when bound to the same binding
303 site as found in different studies.[24, 43, 45] For example, in their study of lanthanide-dependent
304 coordination interactions in lanmodulin, Liu *et al*. found that the coordination number of La (III)
305 is 9.99 with the EF-1 hand loop of lanmodulin which changes to 9.00 in case of Lu (III).[45]

306 When a similar analysis on the scrambled LanM1 (**Figure 3d**) was performed, no such
307 multidentate binding was observed. Instead, a weak interaction was found with the two oxygen
308 atoms of the glutamic acid, which is in good agreement with the observation made by CD
309 spectroscopy. To further probe LanM1 structure, an NMR study was conducted.

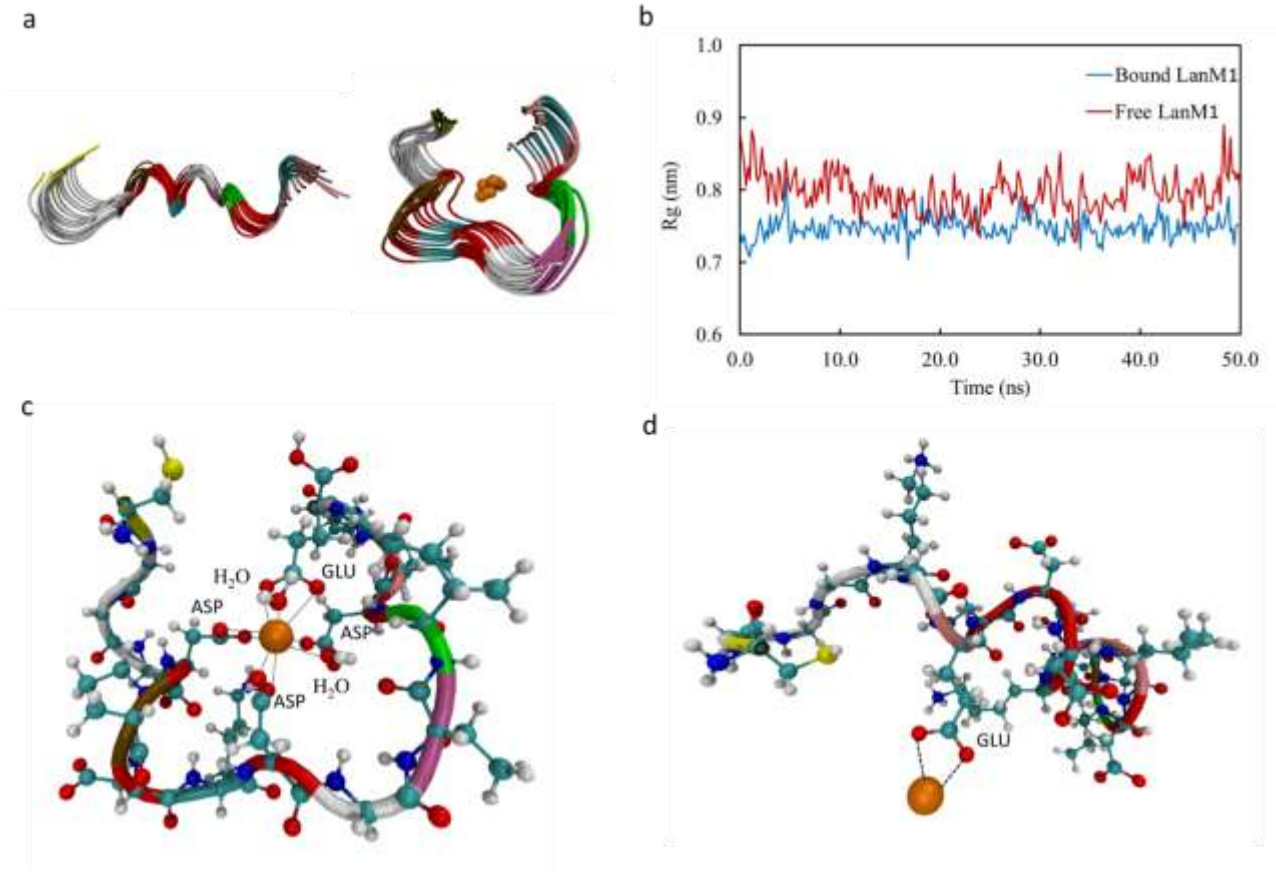

Figure 3. (a) Fifteen randomly selected superimposed MD snapshots of free LanM1 and cerium-bound LanM1 from the trajectory upon equilibration. Rod representation with different colors (same color scheme as in Figure 1) for amino acids is used for LanM1 and the cerium ion is presented in orange color. The water molecules are not displayed for clarity. (b) Radius of gyration (Rg) of the free (red) and ion-bound (blue) LanM1 in a 50 ns long simulation. (c) Coordination of the cerium (III) ion with the LanM1 peptide after equilibration of molecular dynamics simulation. A total of nine oxygen atoms are associated with the site. The cavity is formed with five oxygens from aspartic acid side chains, two from a glutamic acid side chain and two water molecule oxygen atoms. (d) Cerium ion binding site in scrambled LanM1 peptide after equilibration. Only two oxygen atoms of glutamic acid are involved, resulting in a weak binding and no "pocket" in comparison to LanM1.

^{1}H solution NMR spectra of LanM1 and scrambled LanM1 at different NMR frequency ranges are shown side by side for comparison in **Figure 4**. We detect a greater effect to the spectra of LanM1 compared to scrambled LanM1 as cerium (III) is added to the peptide solutions. We suggest that the sidechains within scrambled LanM1 may have transient interactions with the cerium (III) ions but not a cooperative binding effect that would result in distinct bound and unbound states. An additional control experiment conducted on polyproline, which does not bind to cerium (III), shows little to no change in ^{1}H NMR peaks and chemical shifts as cerium (III) is added (**Figure S2**).

As cerium (III) is added to LanM1, we observe broadening of peaks in the ranges of 0.75 to 1 ppm, 2.95 to 3.05 ppm, and 3.75 to 3.85 ppm (gray highlighted regions in **Figures 4a, 4c, and 4e**). We observe less to the scrambled LanM1 sample as cerium (III) is added to the peptide solution (**Figures 4b, 4d, and 4f)**. ^{1}H NMR peaks at the 0.75 to 1 ppm range can be assigned to the leucine and isoleucine methyl groups. We also note peak splitting for LanM1 at 1.05 ppm to 1.25 ppm in **Figure 4a**, which is within the ^{1}H NMR frequency range of the threonine methyl group.[46] Another difference in the NMR spectra is shown with the emergence of a new peak at ~ 3.7 ppm in the LanM1 sample that does not appear in the scrambled LanM1 sample (**Figure 4e and Figure 4f**). The linewidth of an NMR peak can be affected by the following factors when paramagnetic ions such as cerium (III) are involved: 1) distribution of conformations, 2) distance of the ^{1}H atom to the paramagnetic ion, and 3) dynamics, e.g., binding/unbinding of the ion, flipping between distinct conformations, and lifetimes of bound and unbound states.[47] When a ^{1}H atom is within spatial proximity consistent with peptide binding to the unpaired electron in cerium (III), electron-nuclear interaction is likely to be the dominant factor in peak broadening and shifting. Furthermore, we expect peak broadening to increase as ^{1}H atoms get closer to the unpaired

345 electron. For the ^{1}H atoms closest to the electron, peak broaden may make the NMR signal difficult
346 to detect; for example: in **Figure 4c**, we see a "baseline roll" between 3.0 to 3.2 ppm, suggesting
347 the presence very broad NMR signals. Hence, the changes to the ^{1}H chemical shifts of the residues
348 that are closer to the cerium (III) ion and directly participate in ion binding may be difficult to
349 detect, creating what is known as "dark-states" in NMR spectroscopy.[47] The peak broadening and
350 shifting we highlight in **Figures 4a, 4c, and 4e** is more detectable because they correspond to
351 weaker electron-nuclear interactions, providing information about the residues that may not
352 directly participate in cerium (III) binding and are farther from the binding site. We interpret the
353 peak broadening in **Figures 4a, 4c and 4e** to be a result of multi-site occupancy between structural
354 conformations that produce multiple peaks per atomic site (though they may overlap). In **Figure**
355 **4a**, we observe peak splitting rather than peak broadening at 1.2 ppm because the peptide adopts
356 two different conformations with a larger chemical shift difference and no spectral overlap. The
357 phenomenon of "pseudocontact shifts" induced by lanthanides is likely to be relevant here.[48-50]
358 The emergence of a new peak in **Figure 4e** indicates a new conformation that only occurs in the
359 presence of the cerium (III) ion. Further NMR experiments can provide more information about
360 the precise interactions involved between the peptide residues and cerium (III) ions. Overall, our
361 data support the conclusion that LanM1 binds to cerium (III), confirming CD and MD simulation
362 results. In contrast, scrambled LanM1 has the same sidechains as LanM1, but does not bind cerium
363 (III), indicating the importance of the amino acid sequence.

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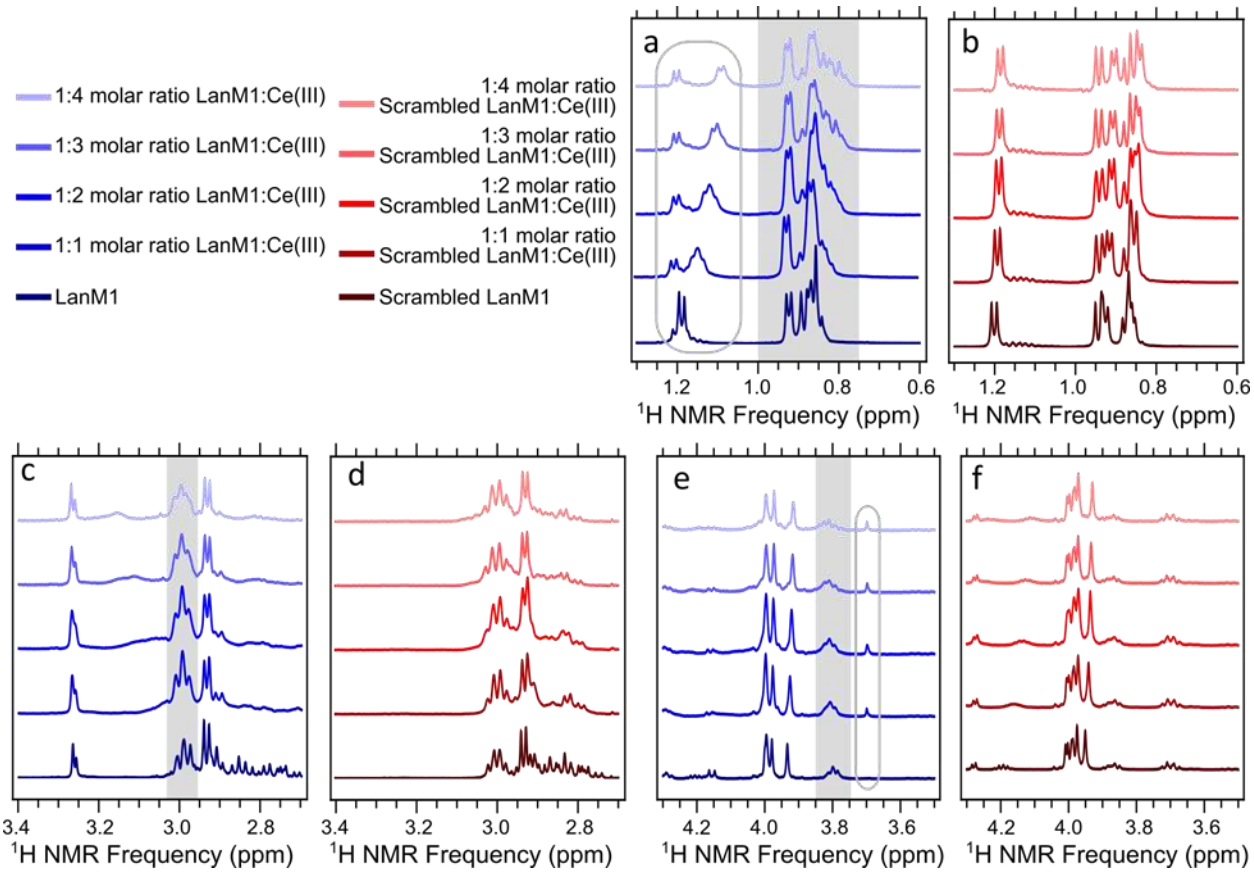
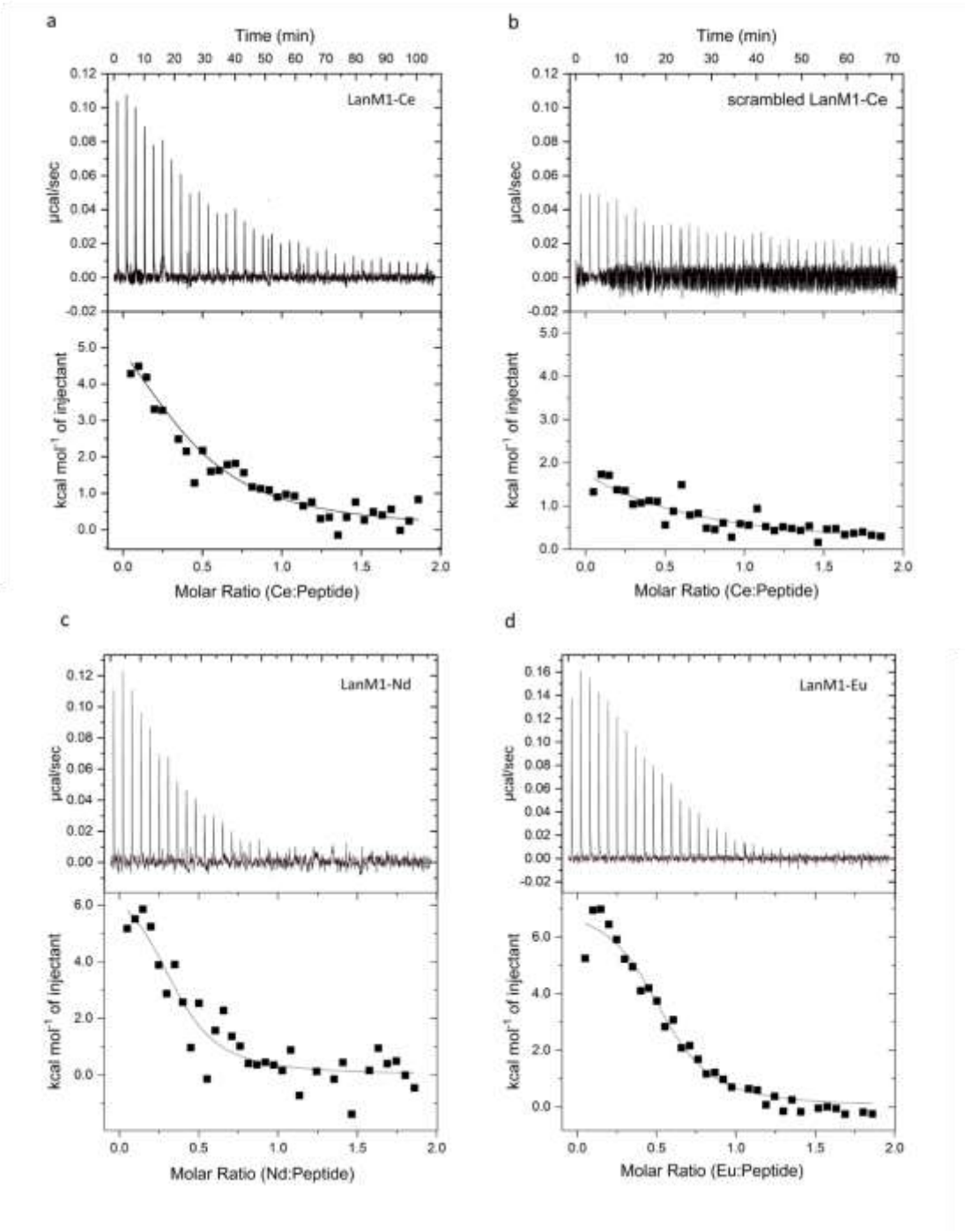


Figure 4. ^{1}H NMR measurements of LanM1 peptide and scrambled LanM1 peptide at different molar ratios of peptide to cerium (III). Panel a, c, and e show the NMR spectra of of LanM1 in blue (the shade gets lighter with increasing cerium concentration from zero to 1:4 molar ratio). The NMR spectra for scrambled LanM1 is shown in red (the shade gets lighter with increasing cerium concentration from zero to 1:4 molar ratio) Panels b, d, and f. Gray highlighted regions in Panels a, c, and e identify peaks which experience line broadening as more cerium is added to the LanM1 peptide. Gray encircled regions identify peak splitting or the emergence of new peaks.

Thermodynamic Properties of Binding in Solution

To better understand and elucidate the binding affinity, isothermal titration calorimetry was conducted to estimate thermodynamic properties of binding for various REEs (Ce (III), Nd (III),

376 Eu (III), and Y(III)) at 303.15 K. In addition, experiments on scrambled LanM1 with cerium (III)
377 ions were conducted to serve as comparison. **Figure 5a and b** show the cerium titration curves
378 (raw data), isotherm and one site-binding model fit for LanM1 and scrambled LanM1,
379 respectively. The titration results for neodymium and europium ions with LanM1 are provided in
380 **Figure 5c and d,** respectively. LanM1 had low affinity for Y(III) ions making thermodynamic
381 properties difficult to estimate. ITC raw data, Wiseman plot, and one-site binding model fit for
382 yttrium with LanM1 is provided in **Figure S3**.



383

384 **Figure 5.** ITC raw data, Wiseman plot and one-site binding model fit for (a) LanM1 with cerium
385 (III) ions (b) scrambled LanM1 with cerium (III) ions (c) LanM1 with neodymium (III) ions (d)
386 LanM1 with europium (III) ions. In all experiments, the peptides were in the cell at 20.0 µM and

the ions were in the syringe at a concentration 200.0 μM. The experiments were performed at 30 ^{0}C using ultrapure water.

At a given temperature, the change in enthalpy (ΔH), and change in entropy (ΔS) determine the sign and magnitude of the binding free energy using the expression ΔG = ΔH-TΔS. The estimated thermodynamic properties of binding for Ce (III), Nd (III), and Eu (III) with LanM1 and Ce (III) with the scrambled LanM1 are reported in **Table 1**. In the case of cerium (III) binding with LanM1, the change in enthalpy (ΔH) and entropy (ΔS) were measured to be 6.66 ± 1.32 kcal/mol and 46.85 ± 3.54 cal/mol K, respectively, and used to obtain the binding free energy (ΔG) of -7.50 ± 0.31 kcal/mol. The dissociation constant K_d was estimated to be 3.84 ± 1.47 μM which is comparable to similar investigations of cerium (III) via ITC using a different peptide sequence that was derived from calmodulin.[16, 24, 51] A negative ΔG is an indication of spontaneous binding. The process is enthalpically disfavored with the increase in entropy driving the process. For scrambled LanM1, K_d was estimated to be 20.59±5.84 μM, nearly and order of magnitude higher.

The obtained K_d values for neodymium and europium ions with LanM1 were 1.44 ± 0.07 μM and 0.80 ± 0.48 μM, respectively. The dissociation constants were correlated to the ionic radius of REEs as shown in **Figure S4** where K_d increases as the ionic radius increases. Nitz *et al.*[52] studied the binding affinity of REEs with lanthanide-binding tags (LBTs) and found a non-monotonic change in K_d with the ionic radius. The minimum K_d of 57±3 nM was observed for Tb (III) that has an atomic radius of ~1.04 A. In light REE range, the K_d increased with the ionic radius consistent with our results. Similar results were found in the calmodulin protein.[53]

The ITC results for potential competitor ions calcium (Ca (II)) and copper (Cu (II)) with LanM1 are reported in **Figure S5**. It was found that LanM1 does not bind with copper and calcium ions, consistent with the similar investigation in which lanmodulin protein was immobilized onto

agarose microbeads and was studied for its affinity towards several REEs and non-REEs by Dong *et al.*[22] In an investigation of the four EF-hand loop peptides of the lanmodulin protein by Gutenthaler et *al.*[24] the peptide showed no affinity towards calcium ion. In a study by Hussain *et al.*[21] of a thermo-responsive genetically encoded elastin-like polypeptide that has an REE-binding domain (lanmodulin) it was found that the polypeptide did not bind to copper and zinc ions, further supporting our findings. The results are also in agreement with Wei and co-workers[23] who found lanmodulin protein immobilized to magnetic nanoparticles (MNP-LanM) did not adsorb non-REEs.

Table 1. Estimated thermodynamic properties for LanM1 binding with cerium (III), neodymium (III) and europium (III) ions using isothermal titration calorimetry (ITC). Results for the scrambled LanM1 with cerium (III) are also reported. The experiments were conducted at 30°C and pH was between 5.0 to 5.5. Data are represented by the average ± the standard deviation for n=3 repeats.

Peptide	REE Ion	Association Constant K_a (μM^{-1})	Dissociation Constant K_d (μM)	ΔH (kcal/mol)	ΔS (cal/mol K)	ΔG (kcal/mol)
LanM1	Ce	0.30 ± 0.13	3.84 ± 1.47	6.66 ± 1.32	46.85 ± 3.54	-7.50 ± 0.31
LanM1	Nd	0.70 ± 0.03	1.44 ± 0.07	6.10 ± 1.51	48.15 ± 3.04	-8.09 ± 0.03
LanM1	Eu	1.47 ± 0.80	0.80 ± 0.48	6.84 ± 5.09	50.60 ± 0.57	-8.49 ± 0.34
Scrambled LanM1	Ce	0.05 ± 0.01	20.59 ± 5.84	13.11 ± 4.74	64.63 ± 15.61	-6.47 ± 0.25

We also tested LanM1 binding affinity with cerium (III) at low pH conditions. The studies at low pH conditions are relevant to coal mine drainages where the discharges are at low pH (<5).[54] ITC experiments at three pH conditions 2.0, 3.0 and 3.5 were performed (**Figure S6**). It was found that there was no binding at pH 2.0. However, the titration curves at pH 3.0 and 3.5 show increasingly distinct changes in energy during the first few injections, indicating increasing binding affinity. This suggests free peptide could be regenerated by lowering the pH to release the ions. In recent work by Dong *et al.*[22] desorption studies were performed on agarose beads with grafted lanmodulin

430 protein in which the effect of pH was investigated. It was found that immobilized lanmodulin can
431 effectively bind Nd (III) ions down to pH 2.4. However, further lowering the pH to 2.2 resulted in
432 a 50% drop in binding and it became insignificant below pH 1.7. Our results also agree with
433 Gauthier *et al.*,[19] who showed that solubilized lanmodulin protein retains REE binding affinity
434 down to around pH 2.5. The pKa of aspartic acid and glutamic acid are ~3.9 and ~4.3, respectively
435 so below this pH range, the peptide loses its negatively charged groups and might contribute to
436 low affinity for REEs below pH 2.5.

437 **Binding Analysis of Immobilized Peptides**

438 To understand binding affinity of the immobilized peptide with some REEs and competing non-
439 REEs, quartz crystal microbalance with dissipation (QCM-D) analysis was performed. In a typical
440 QCM-D experiment, ultrapure water is introduced on the gold sensor to generate a baseline. Once
441 a stable baseline is established, peptide solution of known concentration is introduced and a
442 negative shift in frequency observed which is proportional to the hydrated mass loading of the
443 peptide on the surface. Rinses are often employed to remove weakly bound molecules. In addition
444 to frequency, dissipation is measured – which provides information about the energy loss and gives
445 an indication of the viscoelastic properties. If there is no significant shift in dissipation, the layer
446 is rigid, otherwise, the layer is viscoelastic.[55] After the desired peptide is immobilized on the gold
447 surface, and an ultrapure water rinse is performed, REE binding on the immobilized peptide is
448 done by allowing an REE solution of known concentration to flow over the surface. Then, another
449 round of ultrapure water rinsing is performed to remove weakly bound REE. In this study, the
450 amount of REE that binds to the peptide isn't enough to illicit a significant shift in frequency.
451 Therefore, after ultrapure water rinsing, 1 mM sodium phosphate solution is allowed to flow over
452 the surface and bind to surface-bound REEs as a way to quantify the amount of REE bound. This

technique using phosphate was confirmed by using it to estimate the K_d of a peptide derived from calmodulin, and was found to be similar to our previous work (**Figure S7**[16]). During LanM1 peptide loading, there was no significant changes in dissipation observed, resulting in a rigid layer formation and thus Sauerbrey model was sufficient to estimate the mass loading. However, a viscoelastic layer was formed upon phosphate loading and the Voigt model[56] was used to estimate the mass loading.

All surface binding studies were conducted assuming the peptide binding to REE was a reversible process as shown by **Equation 1**:

$$\text{Peptide} + \text{REE} \underset{k_r}{\overset{k_f}{\rightleftharpoons}} \text{Peptide-REE} \quad (1)$$

Where k_f represents the forward rate constant and k_r is the reverse rate constant. The binding affinity, K_d is then defined as the ratio k_r/k_f. K_d is a dissociation constant and is the reciprocal of the association constant K_a which is often reported for ligand-ion complexation. The linearized slope of binding for a peptide-REE-phosphate system as shown in **Note S1** is found to be identical to that of a peptide-REE system. When tested with calmodulin peptides, we see that the K_d estimated from phosphate addition was 1.6 μM as shown in **Figure S7** which is around what was previously reported (1.3 μM[16]). We assume that the amount of phosphate bound is proportional to the amount of cerium bound on the surface of the QCM sensor. To ensure phosphate does not interact with the lanmodulin peptides, control experiments were conducted where no binding was observed, shown in **Figure S8.** Our previous study shows that when no peptide was present on the QCM sensor, no irreversible binding was observed for phosphate[17] – indicating all phosphate binding seen is due to interactions with peptide-cerium films. We also observed that higher LanM1 loading on gold senor (frequency change ~15 Hz or greater) will result in minimal REE binding as

shown in **Figure S9**. Thus, it is critical to control the loading of the peptide on the surface to maintain peptide affinity. This observation suggests that the density of the peptides on a surface plays a role in ion binding. In solution, the peptides are freely suspended at low concentrations. Whereas peptides tethered to a surface or particle are more crowded and we speculate the crowding of peptides on a surface may cause changes in the peptide secondary structure thereby altering the binding pocket, changes to water organization around the peptide, steric hinderance, or interaction of peptides with each other. Therefore, depending on the peptide density on the surface, the trends in peptide-ion affinity may be different for a surface immobilized peptide than a peptide in solution. Any changes to trends in affinity will manifest in the peptide selectivity for REEs over non-REEs or one REE over another.

Figure 6a-d show QCM-D results for gold-immobilized LanM1 exposed to Ce (III), Nd (III), Eu (III) and Y(III) ion, respectively. **Figure 6** displays experiments performed at the lowest REE concentrations where binding was observed where the blue line corresponds to the frequency shift, while the red line corresponds to the dissipation shift. Ultrapure water served as the baseline for the experiment, which was immediately followed by a 6.0 μM peptide solution. An experiment exposing gold-immobilized scrambled LanM1 to Ce (III) is shown in **Figure S10**. In the case of LanM1 and scrambled LanM1, frequency shift upon addition of phosphate ions was observed down to 0.45 μM Ce (III), with much less binding occurring in the case of the scrambled LanM1. These results are consistent with bulk investigations using CD, NMR, ITC and molecular dynamics results showing scrambled LanM1 having lower affinity for cerium (III) than LanM1. In the case of Nd (III), Eu (III) and Y (III), the lowest concentrations binding was observed at was 0.14 μM, 2.24 μM and 16.48 μM, respectively.

Non-REE ions are also known to complex with phosphate and when using solubility product constant as an rough indication of the affinity of the ions for phosphate, Ca (II), and Cu (II) will have at least as high of an affinity when compared to cerium (III).[57] Therefore, similar QCM-D experiments were performed with two non-REE Ca (II) and Cu (II) competitor ions. The results of surface-bound LanM1 peptide with these ions are provided in **Figure S11**. Like the bulk, LanM1 peptide does not show affinity for either calcium or copper ions. Even at a higher competitor ion concentration of 29.0 μM, no change in the frequency was observed.

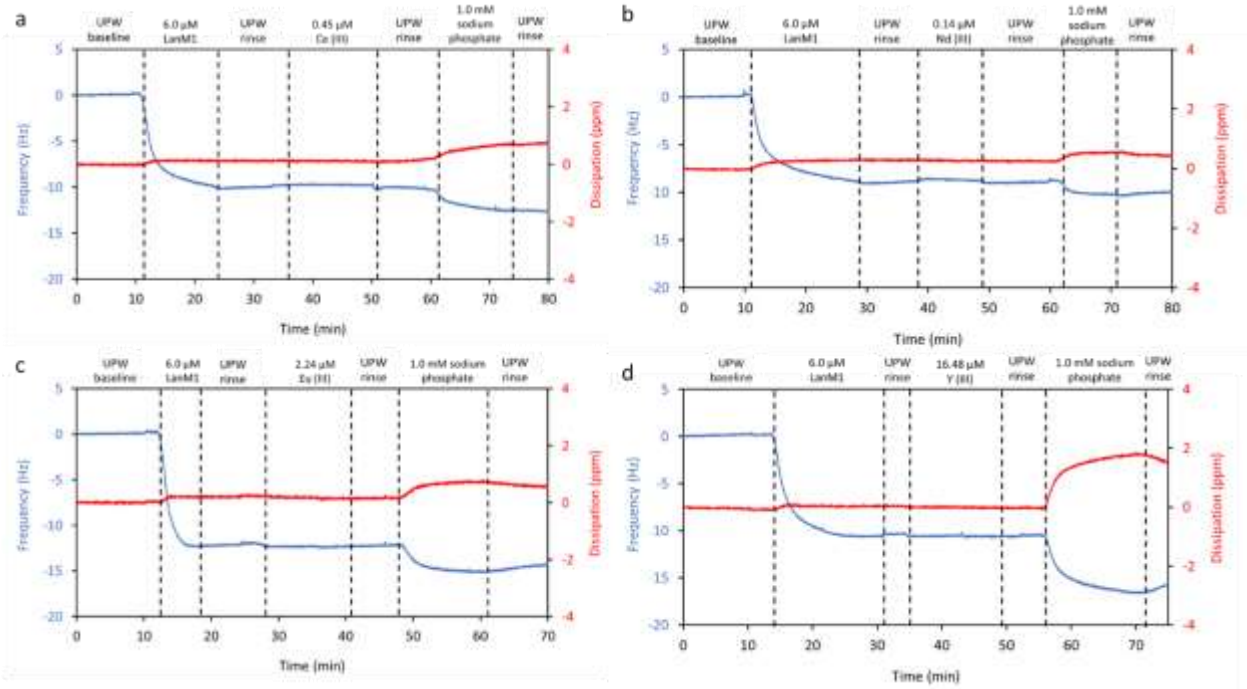


Figure 6. Frequency and dissipation shifts measured using a quartz crystal microbalance (QCM-D) for (a) cerium (III), (b) neodymium (III), (c) europium (III), and (d) yttrium (III) adsorption on LanM1. The dashed lines show when the solution was changed, and the labels within the lines show the solution being during that time. The blue line corresponds to the frequency shift, and the red line corresponds to the dissipation shift. The 9th overtones are shown.

QCM-D experiments were performed at various REE ion concentrations to estimate surface-bound LanM1 dissociation constants for Ce (III) and Nd (III). In acid mine drainage, the concentration of Ce (III) and Nd (III) is the highest among other REEs[58] which makes this pair of particular interest for that application. The Langmuir adsorption isotherm model was fit to phosphate loading data at different REE concentration in QCM-D experiments to describe the adsorption process.[59, 60] Although, it is an ideal model that may not fully capture the complexity of adsorption, it can still provide valuable insights into adsorption behavior. The model is given as:

$$q_e = \frac{R_T C_e}{C_e + K_d} \quad (2)$$

where q_e is phosphate loading (mol/cm^2), R_T (mol/cm^2) is the Langmuir constant related to maximum phosphate loading, K_d (mol/ml) is the dissociation constant, and C_e (mol/ml) is the equilibrium bulk concentration of the ions. In this work, non-linear regression was performed using OriginLab software to fit the data. The removal of one outlier was allowed for each ion data set.

Figure 7 shows the change in phosphate loading (proportional to REE loading) with ion concentration for cerium (III) and neodymium (III) along with Langmuir fitting. Surface bound LanM1 dissociation constants (K_d) of ~ 0.9 μM and ~ 1.8 μM were obtained for cerium (III) and neodymium (III), respectively. Details of the non-linear fitting are provided in **Table S1**. When compared with the bulk results, it is found that the affinity for cerium (III) ions increases upon immobilization. Because of the high error, it is difficult to determine if there is a shift for Nd (III) upon peptide immobilization. However, these results show for the first time that surface-bound LanM1 peptides bind REEs, and motivates future studies to explore how immobilization impacts the trends in K_d.

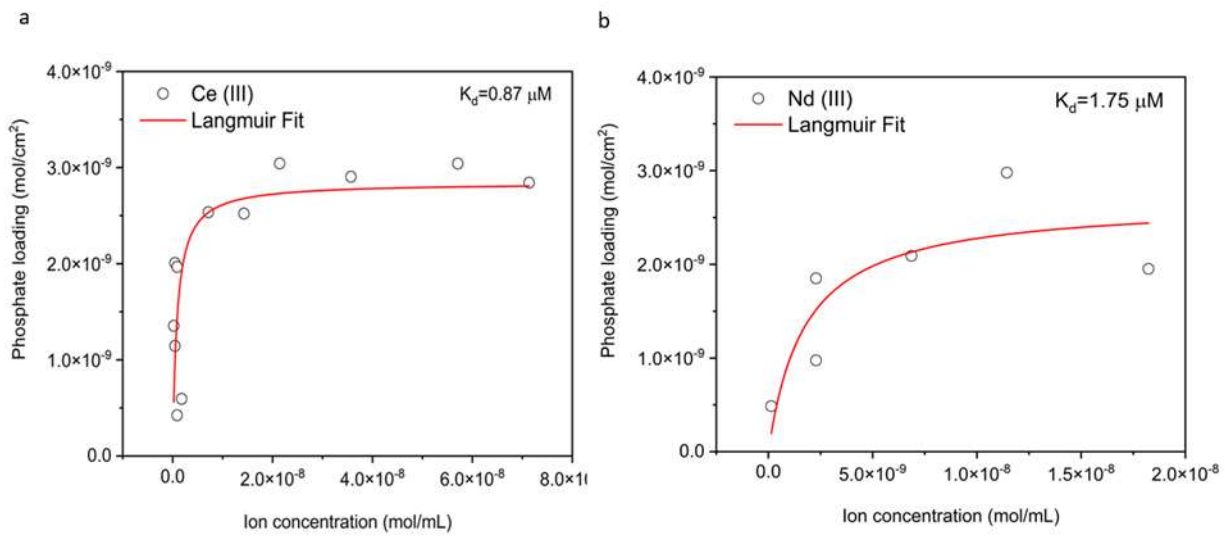


Figure 7. Binding of (a) Ce (III) and (b) Nd (III) ions to gold-immobilized LanM1 peptides where phosphate is proportional to REE binding. In both cases, a simple Langmuir adsorption model was fit to estimate the K_d. Open circles represent experimental data points whereas the red lines show the Langmuir fit. Estimated K_d values are shown in the respective panels.

Selectivity Analysis of Immobilized Peptides

In a practical separation scheme, immobilized peptides are exposed to a mixture of REEs. Separation occurs if the peptide has a higher affinity (lower K_d) for one REE over another due to the preferential partitioning of the REE ion on to the solid peptide-containing phase. For dilute solutions, selectivity can be approximated using a ratio of association constants ($K_a=1/K_d$) where the ideal selectivity is represented as $\alpha_{1/2} = K_{a1}/K_{a2}$, and 1 and 2 represent different metal species.[61] Since $\alpha_{1/2}$ is based on the association reaction, $\alpha_{1/2} > 1$ indicates a higher affinity for species 1. Higher values of $\alpha_{1/2}$ indicate higher degrees of separation between the two ions. The selectivity of the LBT peptide, LanM protein, and LanM1 peptide for Nd over Ce are summarized in **Table 2.** Typically, selectivity for neighboring lanthanides is compared; however, the Nd/Ce ion pair was selected to enable the comparison with this work. Two non-biological ligands are included as these

549 are the leading commercial extractive resins for REE separations: DGA-linear and DGA-branched
550 (Eichrom Technologies, Ltd.). A key distinguishing factor between the bio-derived ligands and the
551 DGAs are the solution conditions under which selectivity is achieved. DGA-linear and DGA-
552 branched resin exhibit selectivity for one REE over another REE at high acid concentrations < pH
553 1 whereas the bio-derived ligands exhibit selectivity in more moderate pH solutions, i.e. > pH 3.
554 The K_a, k' and K_d values used to construct **Table 2** are in **Tables S2** and **S3** of the **SI**.

555 **Table 2.** Calculated ideal selectivity for DGA resins, LBT peptide, LanM protein, and LanM1
556 peptide for selected REE pairs.

Ligand, Support	Matrix	Ion Pair	Selectivity (K_{a1}/K_{a2}) or (k'_1/k'_2)	K_a or k' Reference
DGA-branched, resin	1 M HNO_3	Nd/Ce	1.8	Horwitz 2005[62]
DGA-linear, resin	0.05 M HNO_3	Nd/Ce	4.1	Horwitz 2005[62]
LanM protein, unsupported	pH 5, 100 mM KCl	Nd/Pr	0.5	DeBlonde 2020*[19]
LBT, unsupported	pH 7.0, 10 mM HEPES, 100 mM NaCl	Nd/Ce	3.5	Nitz 2004[52]
LanM1, unsupported	pH 5.4, ultrapure water	Nd/Ce	2.0	This Work
LanM1, on gold	pH 5.4, ultrapure water	Nd/Ce	0.5	This Work

557 *Ce data was not available therefore Pr selectivity is reported instead.
558 **k' is proportional to the Ka
559
560 A common challenge when comparing association and dissociation constants (K_a and K_d) across
561 the literature is the wide variation of matrices used for binding (pH, ionic strength, buffer, or acid
562 type) and the ions tested. For this reason, the discussion herein will refer to general trends and
563 order of magnitude differences. Recognizing the caveat that the lanmodulin protein data in **Table**
564 **2** represents a more challenging separation of neighbors Pr/Nd than Nd/Ce—both LBT and LanM1
565 peptides in solution exhibit selectivity that is on par with the LanM protein: 3.5, 2.3, and 2.0,
566 respectively. This is interesting because the K_d of LanM protein is 6 orders of magnitude lower
567 than the LBT and LanM1 peptides. Recall, the K_d for LanM protein across the lanthanide series

ranges from 0.4 to 10 pM;[19] the K_d for the LBT peptide ranges from 0.057 to 3.5 μM;[52] and the K_d for solution phase LanM1 in this work ranges from 0.8 to 3.8 μM. Thus, high affinity does not necessarily correlate to high selectivity between the tested REEs.

Common ligands for lanthanide separations such as EDTA, DOTA, and DTPA exhibit a monotonic increase in affinity as the atomic number and charge density increase across the lanthanide series[63] known as the size selectivity trend. Specialty macrocyclic ligands like macropa exhibit a reverse size selectivity trend where the affinity decreases monotonically as the atomic number and charge density increase across the lanthanide series.[64] The lanmodulin protein exhibits a dual selectivity in which an inflection point in dissociation constant occurs at Sm. The selectivity trend of the LBT peptide is more consistent with the traditional ligands as the affinity increases with increasing atomic number for the light lanthanides, La → Eu. The LBT peptide shows negligible selectivity between the heavier lanthanides, Eu → Lu. Based on the first three lanthanides tested in this series, the LanM1 peptide exhibits the traditional size selectivity trend in solution, **Table 1**. Further investigation of dissociation constants with heavier lanthanides will be necessary to discern the full extent of the selectivity trend for LanM1 in solution. Based on the first two tested lanthanides (Nd and Ce) for immobilized LanM1, the selectivity trend may reverse or exhibit non-traditional behavior when LanM1 is bound to particular surfaces, as observed in this study.

Binding Investigation on Gold Nanoparticles (GNPs)

The potential to use surface-bound LanM1 in REE separation is demonstrated by immobilizing LanM1 peptide on gold nanoparticles (diameter <100 nm) and subsequently estimating the adsorption capacity of peptide-immobilized GNPs as shown in **Figure 8a**.

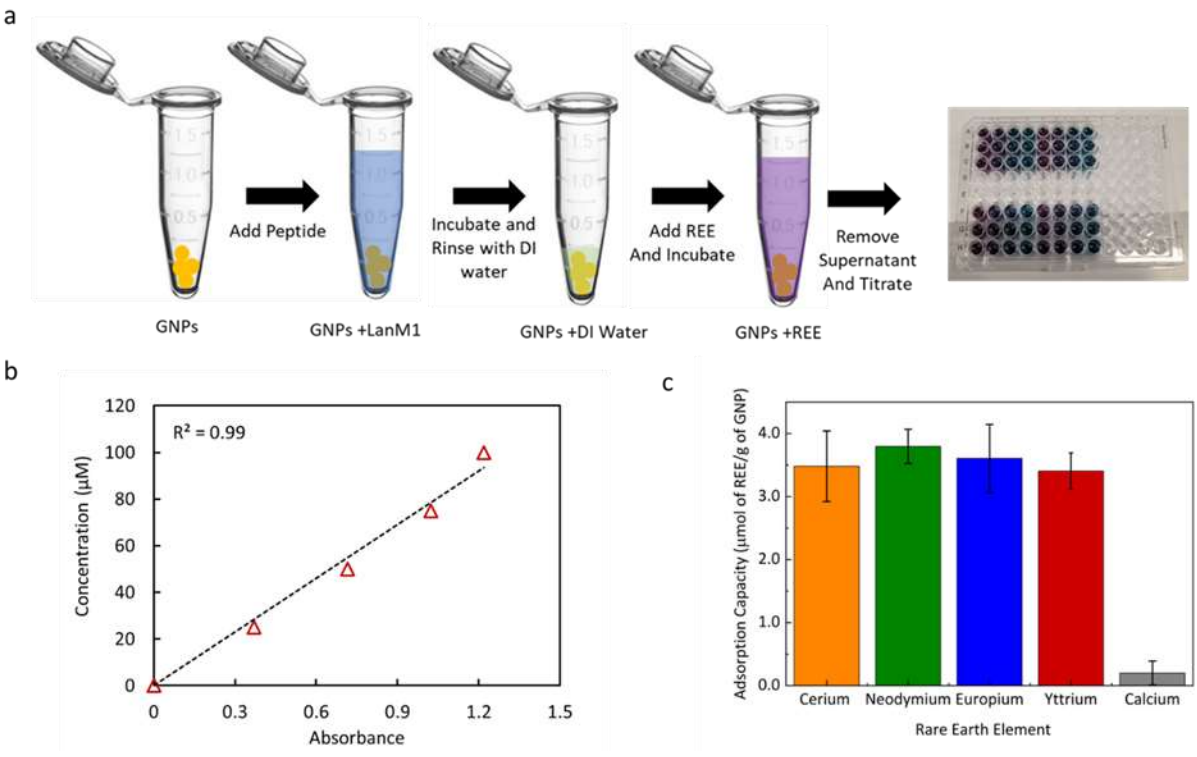


Figure 8. (a) Pictorial representation of the step-by-step procedure used make peptide-bound gold nanoparticles (GNPs) and analyze REE binding capacity. (b) The calibration curve for Ce (III) ions based on the UV-visible absorption spectra. (c) A comparison of the adsorption capacities (μmol REE/ g GNP-LanM1) for different REEs and negligible adsorption of calcium (II) ions.

After peptide functionalization GNPs were incubated with REE containing solution, then the GNPs were separated from the supernatant and titrated with arsenazo III reagent. The absorption at 655 nm wavelength was measured and used to generate a calibration curve like that shown in **Figure 8b**, from which the concentration of sample supernatant was estimated. **Figure 8b** shows an example calibration curve for Ce (III) ions and calibration curves for Nd (III), Eu (III), and Y (III) and Ca (II) ions can be found in **Figure S12**. UV-visible absorption spectra of known cerium concentration solutions titrated against arsenazo III reagent used to generate the calibration curve is provided in **Figure S13**.

603 The adsorption capacity (μmol-REE/g-GNP-LanM1) was calculated using **Equation 3**:

604 $$Q_e = \frac{(C_0 - C_e) \times V}{m} \quad (3)$$

605 where C_0 is the initial REE concentration (μM); C_e is the REE concentration of the supernatant; V
606 is the volume in the vial (L), and m is the mass of the GNP-LanM1 (g).

607 Several equilibrium adsorption experiments of LanM1-GNPs at different concentrations were
608 performed for REEs Ce (III), Nd (III), Eu (III), and Y (III) and non-REEs Ca (II) and the estimated
609 the adsorption capacity for the ions at different concentrations are reported in **Table S4**. A
610 comparison of average equilibrium adsorption capacities of REEs and competing non-REE
611 calcium (II) ion is shown in **Figure 8c**. These values for REEs are assumed to be the saturated
612 adsorption capacity since saturation appears to occur at concentrations tested (see **Table S4**). The
613 results show LanM1 grafted GNPs do not adsorb calcium ions. These findings align well with ITC
614 and QCM-D results in this study and are consistent with similar investigations.[22, 24] The REE
615 saturated adsorption capacities of GNP-grafted LanM1 for Ce (III), Nd (III), Eu (III), and Y (III)
616 are similar, ~3.5 μmol of REE per g of GNP-LanM1, further supporting that concentration range
617 is above the saturation point for these REE ions.
618 In a recent study of lanmodulin-functionalized magnetic nanoparticles for REE recovery, the
619 saturated adsorption capacity of 5.46 ± 0.46 μmol-Tb/g-MNP was reported. The experiment was
620 performed using 20 mM 2-(N-Morpholino)-ethanesulfonic acid (MES) buffer at pH 5.0 with 2.5
621 mg/ml of MNP-LanM and ~62.93 μM Tb (III),[23] which has some similarities to our experiment
622 in DI water at pH 5.0-5.5 with 5-8 mg GNP/mL and 20 to 125 μM REE, serving as a useful
623 comparison. In their study, loading on MNPs was 2.67 ± 0.15 μmol LanM SpyCatcher/g-MNP.
624 We roughly estimated the molar loading of LanM1 to be ~3.74 μmol LanM1/g-GNP based on our

QCM-D mass estimates, noting that our estimate is likely and overestimate because we did not account for water. The results in QCM-D experiment show a minimum dissipation during peptide loading which indicates a rigid layer formation and low water content, however the degree of hydration of the layer is unknown. Nonetheless, the molar peptide loading on GNPs is of similar order of magnitude to that of the SpyCatcher MNPs. When adsorbing in a monolayer, the molar surface density of peptides is expected to be higher than the bulkier proteins due to the smaller size.[65] However, in this case, the comparison is made between monolayer of LanM1 peptide and lanmodulin protein immobilized on the branched polymer (SpyCatcher) functionalized on MNPs. The branched polymer provides a three-dimensional scaffold onto which the proteins can be conjugated whereas the peptides were directly conjugated to the gold nanoparticle surface in a monolayer. The three-dimensional structure of the brushes provides additional capacity per unit surface area of the underlying MNP. In addition, the lanmodulin protein has more available REE binding sites per mole than the LanM1 peptide, thus resulting in an appropriately lower saturated binding capacity for the material in this study. One study had shown that immobilized lanmodulin protein had two sites available for REE binding in comparison to three in the solution.[22] The study suggested inaccessibility of one site upon immobilization. We note that our estimated molar loading of peptide is close the saturated adsorption capacity measured of ~3.5 μmol of REE per g of GNP-LanM1, indicating high site accessibility. Lanmodulin protein has a molecular weight that is ~7 times higher than the LanM1 peptide, indicating that the maximum adsorption capacity achieved with the peptide is relatively high when considering the mass of peptide used compared to the lanmodulin-MNP material. While this comparison is useful, we note it is difficult to compare the two studies because adsorption capacity can depend on several factors.[66]

3 Conclusion

In summary, LanM1 peptide derived from the EF-hand loop 1 of lanmodulin was tested for its binding affinity for different REEs, Ce (III), Nd (III), Eu (III) and Y (III), both in bulk and when bound to a gold surface using both experimental and computational techniques. The ability of Ce (III) ions to bind with LanM1 and scrambled LanM1 was confirmed using circular dichroism (CD) and corroborated using molecular dynamics and nuclear magnetic resonance spectroscopy (NMR) analysis. Isothermal titration calorimetry (ITC) results showed spontaneous binding for all REEs to the LanM1 peptide. The binding was enthalpically disfavored but driven by a positive change in entropy. The dissociation constants from ITC were correlated to the ionic radius of REEs with a K_d of 3.84 ± 1.47, 1.44 ±0 .07 and 0.80 ± 0.48 μM for Ce (III), Nd (III) and Eu (III), respectively. In the case of non-REE ions, calcium Ca (II) and Cu (II), no affinity with LanM1 was observed. At pH below 2, Ce (III) was not observed to bind with LanM1, suggesting pH swing as a possible regeneration mechanism. Quartz crystal microbalance with dissipation (QCM-D) analysis was performed to characterize the binding of REEs and non-REEs to surface-immobilized LanM1. The dissociation constants obtained from Langmuir model fitting suggested that the binding affinities for Ce (III) and Nd (III) with surface bound LanM1 were estimated to be roughly ~0.9 and 1.8 μM, respectively. The saturated adsorption capacity of LanM1 immobilized on gold nanoparticles were estimated using arsenazo-III based colorimetric dye-displacement assay and UV-vis spectrophotometry to be around 3.5 μmol of REE/mg of GNP-LanM1, with negligible binding to Ca (II) ions. Overall, this study demonstrates the potential for surface-bound LanM1 peptides to have high affinity for REEs and be used in advanced separation technologies. The work also motivates future studies to investigate how immobilizing this peptide might impact trends in REE

affinity and how the LanM1 peptide sequence might be manipulated to optimize the separation of REE mixtures.

Acknowledgements

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Supporting Information

Additional experimental results and data, including a snapshot of molecular dynamics system; NMR results, ITC results; QCM-D results; Scatchard plot; Langmuir model regression data, Summary of adsorption metrics used in the selectivity analysis; Estimated adsorption capacities for REEs using GNPs; Derivation for a two-step Scatchard analysis. A repository of the GROMCAS input files is created on GitHub: https://github.com/gev28/Gromacs_input_file.

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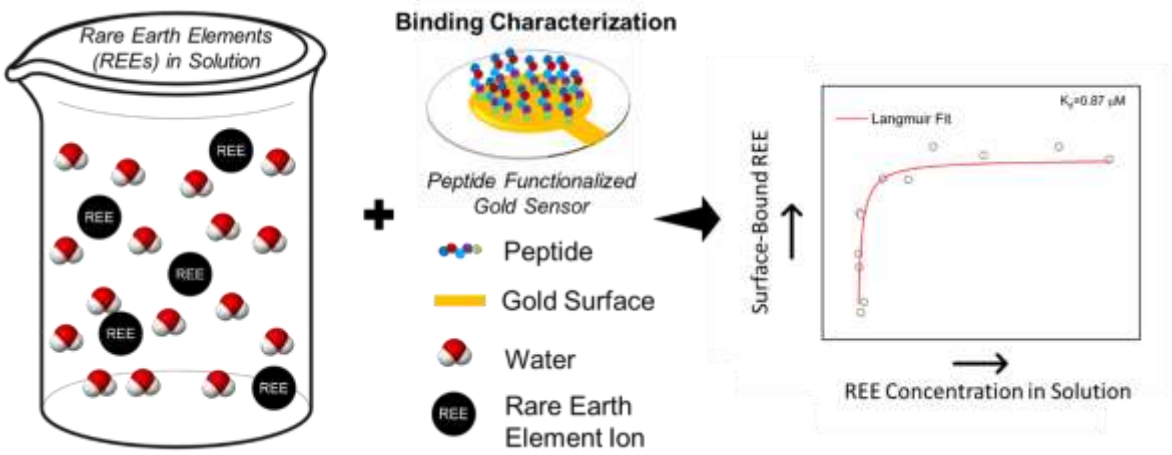

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694 **References**

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