

## Proton Coupling to $[4\text{Fe-4S}]^{2+/+}$ and $[4\text{Fe-4Se}]^{2+/+}$ Oxidation and Reduction in a Designed Protein

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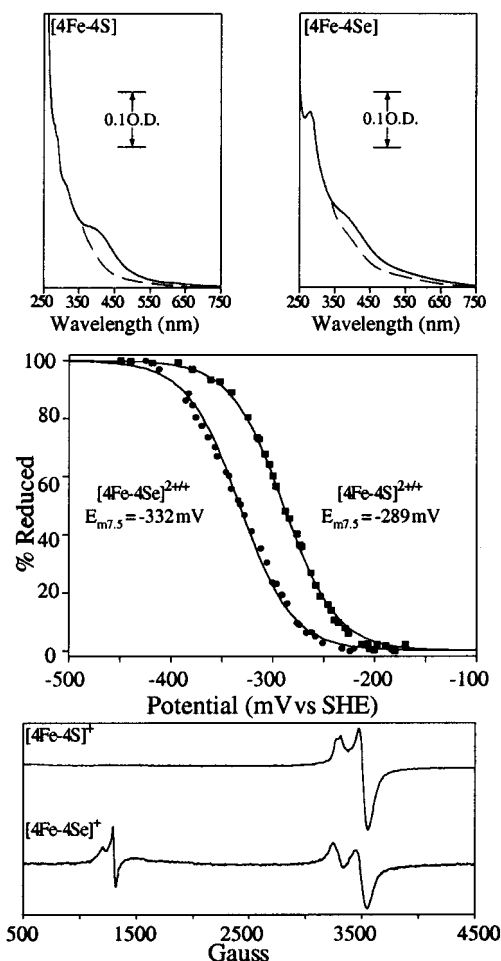
Iron–sulfur (Fe–S) center modules are ubiquitous in biochemistry, serving diverse roles ranging from simple biological electron transfer to chemical catalysis.<sup>1</sup> Metal sites in natural proteins are becoming increasingly recognized as fundamental mechanical units involved in biological proton pumping since metal cofactor oxidation/reduction can be accompanied by proton release/uptake as observed in the natural Fe–S proteins NADH–quinone oxidoreductase at cluster N2, the Reiske iron–sulfur protein, the P-cluster of nitrogenase, and *Azotobacter vinelandii* ferredoxin I, *AvFdI*.<sup>2</sup>

We are utilizing peptide-based  $[4\text{Fe-4S}]^{2+/+}$  coordination complexes, the ferredoxin maquettes, as aqueous soluble and stable synthetic analogues of natural ferredoxins.<sup>3</sup> The minimal size of the prototype ferredoxin maquette and its spectroscopic and electrochemical resemblance to natural  $[4\text{Fe-4S}]$  proteins make it a useful model system to probe the fundamentals of  $[4\text{Fe-4S}]$  protein engineering. To date, the ferredoxin maquettes have provided insight into  $[4\text{Fe-4S}]^{2+/+}$  protein sequence design by delineating the role of ligand<sup>3b</sup> and nonligand<sup>3c</sup> amino acid residues in cluster stability.

We show herein that a novel ferredoxin maquette, **IGA**– $[4\text{Fe-4S}]$ , displays a pH-dependent equilibrium midpoint reduction potential. The data are consistent with a proton-coupled electron-transfer event akin to those observed in natural proteins involved in biochemical proton pumping. The design of **IGA** ( $\text{NH}_2\text{-KLCEGG}\cdot\text{CIGCGAC}\cdot\text{GGW-CONH}_2$ ) is based on the consensus  $[4\text{Fe-4S}]$  binding motif of Clostridial ferredoxins<sup>4</sup>  $\cdot\text{CIGCGAC}\cdot$  and is related to the prototype ferredoxin maquette by a single-residue change at position 9 (Ala→Gly).<sup>5</sup>

The spectroscopic properties of this  $[4\text{Fe-4S}]$  protein maquette are identical to those of the prototype ferredoxin maquette and reminiscent of natural  $[4\text{Fe-4S}]^{2+/+}$  proteins. Optical spectroscopy of the oxidized **IGA**– $[4\text{Fe-4S}]^{2+}$  complex ( $\lambda_{\text{max}}$  at 310 and 385 nm;  $\epsilon$  of 23 200  $\text{M}^{-1} \text{cm}^{-1}$  and 16 100  $\text{M}^{-1} \text{cm}^{-1}$ , respectively) is fully consistent with the  $\text{S}\rightarrow\text{Fe(III)}$  LMCT bands observed in natural<sup>6</sup> and designed<sup>7</sup>  $[4\text{Fe-4S}]^{2+}$  proteins. Reduction by sodium dithionite results in a bleaching of the UV–vis spectrum and an axial EPR spectrum with  $g$ -values (2.05, 1.93, and 1.89) indicative of a low potential  $\text{S} = 1/2 [4\text{Fe-4S}]^+$  cluster. Thus, the oxidized and reduced state spectral properties of this maquette are indistinguishable from the prototype ferredoxin maquette as well as the designed  $\alpha_4\text{-FeS}^{7a}$  of Scott and Biggins.

The electrochemistry of the **IGA**– $[4\text{Fe-4S}]^{2+/+}$  complex was assayed at 25 °C using redox potentiometry monitored by UV–visible spectroscopy as shown in Figure 1. The observed decrease in the LMCT absorption at 385 nm upon lowering the solution potential is accurately described by a single  $N = 1$  Nernst equation. The equilibrium midpoint reduction potential at pH 7.5,  $E_{\text{m}7.5}$ , of

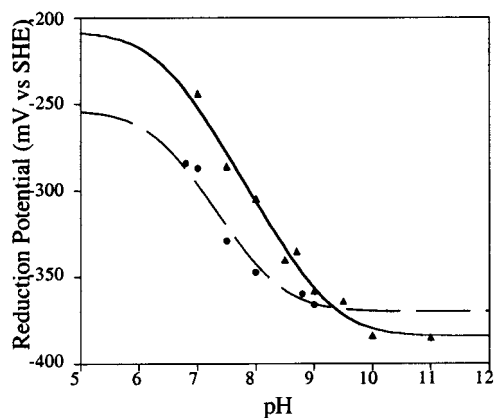


**Figure 1.** Spectroscopic characterization of **IGA**– $[4\text{Fe-4S}]^{2+/+}$  and **IGA**– $[4\text{Fe-4Se}]^{2+/+}$ . (Top) UV–visible spectra of **IGA**– $[4\text{Fe-4S}]$  and **IGA**– $[4\text{Fe-4Se}]$  in the oxidized (solid line) and reduced states (dashed line). (Middle) Potentiometric titration of **IGA**– $[4\text{Fe-4S}]$  and **IGA**– $[4\text{Fe-4Se}]$  at pH 7.5. (Bottom) X-band EPR spectra of reduced state **IGA**– $[4\text{Fe-4S}]^+$  and **IGA**– $[4\text{Fe-4Se}]^+$  recorded at 10 K, 1 mW microwave power, 8 G modulation amplitude.

–289 ± 6 mV vs SHE is consistent with values observed for natural  $[4\text{Fe-4S}]$  ferredoxins. The redox activity of **IGA**– $[4\text{Fe-4S}]^{2+/+}$  is slightly more positive than both the prototype ferredoxin maquette and  $\alpha_4\text{-FeS}$ , –350 ± 15 mV (pH 8) and –422 (pH 8.3) mV, respectively. Thus, the amino acid sequence change Ala→Gly has an effect on the cluster electrochemistry.

The reduction potential of the **IGA**– $[4\text{Fe-4S}]^{2+/+}$  complex displays a pH dependence between pH 7 and 11 as shown in Figure 2. The observed redox-Bohr effect illustrates a 60 mV/pH unit slope between the oxidized and reduced  $\text{pK}_a$  values,  $\text{pK}_a^{\text{ox}}$  and  $\text{pK}_a^{\text{red}}$ ,

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**Figure 2.** pH dependence of the reduction potential of  $\text{IGA-[4Fe-4S]}^{2+/+}$  (triangles, solid line) and  $[4\text{Fe-4Se}]^{2+/+}$  (circles, dashed line)

demonstrating a one proton per electron-coupled event. A  $\text{p}K_{\text{a}}^{\text{red}}$  value of  $9.3 \pm 0.1$  is measured from a fit to the redox data. The redox data alone cannot determine the oxidized  $\text{p}K_{\text{a}}^{\text{ox}}$  precisely, due to  $[4\text{Fe-4S}]^{2+}$  cluster decomposition below pH 7.0, however, an upper limit of  $\text{p}K_{\text{a}}^{\text{ox}} \leq 6.5$  can be placed.

The proton concentration required to dissociate the cluster from the peptide was investigated to place a lower limit on  $\text{p}K_{\text{a}}^{\text{ox}}$ . As the pH is decreased below pH 7.5, the UV-visible spectrum of  $\text{IGA-[4Fe-4S]}^{2+}$  bleaches consistent with cluster decomposition. The data are accurately described by a single protonation event with a  $\text{p}K_{\text{a}}$  value of  $6.35 \pm 0.05$ . Thus, cluster stability places a lower practical limit on  $\text{p}K_{\text{a}}^{\text{ox}}$  at 6.35. Using this  $\text{p}K_{\text{a}}^{\text{ox}}$  value yields a theoretical  $E_{\text{m}5}$  value of  $-209$  mV vs SHE. Thus, proton coupling can perhaps evince a 175 mV (4.1 kcal/mol) effect on the cluster reduction potential (130 mV observed in Figure 2), demonstrating the significant role protons can play in adjusting  $[4\text{Fe-4S}]$  cluster  $E_{\text{m}}$  values.<sup>8</sup>

In an initial attempt to locate the site of proton binding upon reduction of the  $[4\text{Fe-4S}]$  cluster, we have synthesized the  $[4\text{Fe-4Se}]^{2+/+}$  cluster in **IGA** using modified literature procedures.<sup>9</sup> After dialysis to remove excess iron, selenide, and dithiothreitol, the incorporation of a single  $[4\text{Fe-4Se}]^{2+}$  cluster into the **IGA** peptide was confirmed chemically (Fe analysis) and spectroscopically (UV-vis and EPR shown in Figure 1).

The spectroscopic properties of this  $[4\text{Fe-4Se}]^{2+/+}$  protein maquette are strikingly similar to those of  $[4\text{Fe-4Se}]^{2+/+}$  substituted *Clostridium pasteurianum* ferredoxin, *CpFd*.<sup>10</sup> Figure 1 shows the UV-vis spectrum of the oxidized  $\text{IGA-[4Fe-4Se]}^{2+}$  complex,  $\lambda_{\text{max}}$  at 290 and 386 nm;  $\epsilon$  of  $42\,600\text{ M}^{-1}\text{ cm}^{-1}$  and  $22\,600\text{ M}^{-1}\text{ cm}^{-1}$ , respectively. One electron reduction of  $\text{IGA-[4Fe-4Se]}^{2+}$  by sodium dithionite yields a complex EPR spectrum with  $g$ -values indicative of a mixture of  $S = 1/2$  ( $g = 1.90, 1.96, \text{ and } 2.07$ ),  $3/2$  ( $g \approx 4.5$ ) and  $7/2$  ( $g = 5.17 \text{ and } 5.63$ ) spin-states. The EPR spectrum of  $\text{IGA-[4Fe-4Se]}^{+}$  is nearly identical to that observed for *CpFd*<sup>10</sup> and distinct from small-molecule complexes such as  $[4\text{Fe-4Se}]$ (SR)<sub>4</sub>.<sup>11</sup>

The equilibrium midpoint reduction potential of  $\text{IGA-[4Fe-4Se]}^{2+/+}$  is  $-332 \pm 6$  mV at pH 7.5, a value slightly lower than the corresponding  $[4\text{Fe-4S}]$  cluster. Figure 2 shows that the reduction potential of the  $\text{IGA-[4Fe-4Se]}^{2+}$  complex is pH dependent over the range of pH 6.8 to 9.<sup>12</sup> The Pourbaix diagram shows a 60 mV per pH unit slope with the  $\text{p}K_{\text{a}}^{\text{red}}$  value of  $8.3 \pm 0.2$ , suggesting that the bridging sulfides of the cluster are involved in modulating proton uptake. This indicates a  $\mu_3$ -sulfide or Cys ligand protonation site. The pH titration of  $\text{IGA-[4Fe-4Se]}^{2+}$  indicates a  $\text{p}K_{\text{a}}^{\text{ox}}$  value of  $\leq 6.29$ . These results are consistent with

the conclusions from studies of both small molecule  $[4\text{Fe-4X}](\text{YR})_4$  ( $X, Y = \text{S or Se}$ ) complexes in aqueous and micellar solutions<sup>13</sup> and the recent detailed study of *AzFdI*, a  $[3\text{Fe-4S}]$  protein.<sup>2f</sup> Thus, the more negative reduction potential of  $\text{IGA-[4Fe-4Se]}^{2+/+}$  as compared to  $\text{IGA-[4Fe-4S]}^{2+/+}$  at pH 7.5 is a consequence of the alteration in the reduced state  $\text{p}K_{\text{a}}^{\text{red}}$  value; their values are coincidentally identical at pH 9.2.

In the present work, we have demonstrated a proton-coupled electron-transfer event in a peptide-based  $[4\text{Fe-4S}]$  synthetic analogue. Furthermore, we have illustrated the significant effect protons can have on cofactor equilibrium midpoint reduction potentials in simple peptide-cofactor coordination complexes. Our results indicate protonation of iron ligands must be considered in  $[4\text{Fe-4S}]$  redox-Bohr effects. Our efforts are now focused on precise determination of the site of proton coupling in this and related  $[4\text{Fe-4S}]$  maquettes as well as delineating the factors influencing the relevant  $\text{p}K_{\text{a}}$  values.

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- (5) The **IGA** ferredoxin maquette peptide ligand was synthesized using standard Fmoc/Bu solid-phase peptide synthesis methodologies using HBTU/HOBT amino acid activation. The crude peptide was purified to homogeneity by C<sub>18</sub> RP-HPLC and evaluated for purity and identity by analytical HPLC and mass spectrometry, respectively. The  $[4\text{Fe-4S}]^{2+/+}$  cluster was incorporated into the **IGA** peptide ligand using standard literature protocols under strictly anaerobic conditions in pH 7.5 buffer (20 mM HEPES, 100 mM KCl).<sup>6a</sup> Following dialysis against aqueous buffers to remove excess iron and sulfide salts and  $\beta$ -mercaptoethanol, microanalysis for iron<sup>6b</sup> and sulfide<sup>6c</sup> demonstrate a 1:1  $[4\text{Fe-4S}]$  cluster to peptide stoichiometry, as designed. Sedimentation equilibrium analytical ultracentrifugation demonstrated that the peptide exists as monomer species prior to and after  $[4\text{Fe-4S}]^{2+}$  incorporation.
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