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Observation of Fe-H/D Modes by Nuclear Resonant Vibrational Spectroscopy

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Metal-H bonding is important in chemistry, catalysis, and the mechanisms of hydrogenase (H₂ase)¹ and nitrogenase (N₂ase).² With notable exceptions, 3,4 H atoms are difficult to see in protein crystal structures or by EXAFS. Vibrational spectroscopy can probe M-H bonding, but in IR spectra, peptide bands often obscure M-H stretches, and these enzymes have been "black holes" for resonance Raman work. Another approach is "nuclear resonance vibrational spectroscopy" (NRVS), also known as "nuclear resonant inelastic X-ray scattering" (NRIXS).^{5,6} Here we present NRIXS data on Fe-S₄ and FeH(D)₆ model systems. We interpret the spectra and evaluate prospects for studying more complex samples.

NRIXS combines nuclear excitation and vibrational motion.⁶ The effect was predicted early on,7,8 but ultracentrifuge radioisotope experiments were difficult.9 Later, synchrotron radiation (SR) work demonstrated feasibility. 10,11 Due to the spectral brightness of SR sources, 12 and X-ray optics progress, NRVS can now be done with high-resolution monochromators.¹³ An exciting aspect is that it provides an isotope selective vibrational spectrum—only modes with movement of the resonant nucleus couple to the excitation. With a randomly oriented sample, in the low-temperature limit, the "recoil fraction" ϕ that goes into a $n_{\alpha} \rightarrow n_{\alpha} + 1$ transition is given by: ϕ = $(e^2_{\alpha}/3)(\nu_R/\nu_\alpha)(n_\alpha+1)f^{14}$ The term e^2_{α} is the fraction of kinetic energy associated with nuclear displacement in mode α , ν_R is the nuclear recoil energy, ν_{α} the vibrational energy, f the recoilless fraction, and n_{α} is the mean occupation number of mode α at temperature T.¹⁴

Fe-H stretches have high frequencies¹⁵ and little Fe motionboth factors will reduce NRIXS intensity. To assess whether Fe-H modes could be observed in H₂ase and N₂ase, we studied two simpler systems: tetrahedral FeS₄ in Pyrococcus furiosus (Pf) rubredoxin (Rd), and FeH(D)₆ in [FeH(D)₆][MgBr(THF)₂]₄. The met-Rd NRIXS has bands near 61, 154, and 364 cm⁻¹ (Figure 1). Under T_d symmetry, there are two T_2 normal modes with Fe motion: ν_3 (mostly Fe-S stretch) and ν_4 (mostly Fe-S bend).¹⁶ In Desulfovibrio gigas (Dg) Rd Raman spectra, the degeneracy of v_3 is lifted, and three bands are observed at an average value of $362~cm^{-1}.^{17}$ We assign our $364~cm^{-1}$ NRIXS band to similar modes—partially resolved at 8 cm⁻¹ resolution. In the Raman data, the totally symmetric mode v_1 is very strong; it is essentially invisible in the NRIXS spectrum, as expected for a mode that has no Fe motion in T_d symmetry (Figure 1).

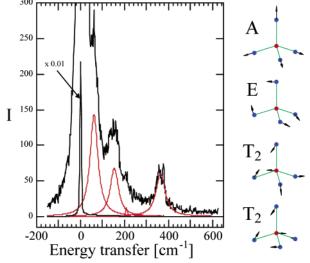


Figure 1. (Left) NRIXS data (black curve) and fits (red curve) for ⁵⁷Fe Pf met-Rd. Ordinate scale is counts/90 s. (Inset) FeS₄ site in Pf Rd. (Right) Diagrams of tetrahedral normal modes.

The lower frequency bands involve mostly bending motion. In T_d symmetry, there is a pure bend, the doubly degenerate E mode (ν_2) , as well as a mixed T₂ ν_4 mode. For Dg Rd, a band at 126 cm⁻¹ was assigned to ν_2 , and a feature at 150 cm⁻¹ to ν_4 . In strict T_d symmetry, there is no Fe motion in ν_2 , hence no intensity for this mode in our experiment. For ν_4 , although it is considered a S-Fe-S bend mode, Fe-S stretch character is not forbidden. A more detailed analysis found that S-Fe-S bending motions mix with Fe-S-C bends, and that the band at 150 cm⁻¹ has about 40% Fe-S-C bend character.¹⁷ This may explain the intensity in this region, but a more detailed analysis requires better statistics and calculations using the Pf Rd coordinates.3

The last Rd feature we consider is the band near 60 cm⁻¹. In heme proteins and models, bands between 40 and 80 cm⁻¹ are ascribed to heme doming modes.¹⁹ The Pf Rd crystal structure reveals an Fe site enclosed in a loop at the far end of the protein (Figure 1).³ The NMR structure of Zn-substituted Dg Rd suggests that Fe can oscillate with an amplitude of $\sim 0.2 \text{ Å};^{20}$ and we interpret the 60 cm⁻¹ mode as a collective motion of Fe and some or all cysteine ligands.

The FeH(D)₆ samples have very different spectra (Figure 2). In O_h symmetry, only T_{1u} modes, ν_3 and ν_4 , have central atom motion. ¹⁶ The ν_4 mode is mostly bending and hence occurs at lower energy than the primarily stretching v_3 ; we thus assign the FeD₆

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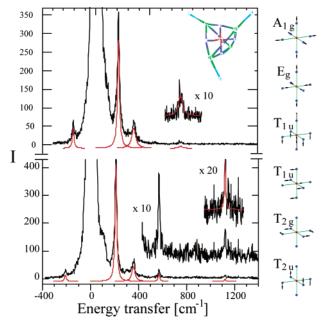


Figure 2. (Left) NRIXS for (top) FeH₆ and (bottom) FeD₆ complexes. Ordinate scales: counts/40 s. (Inset) [FeH₆][MgBr(THF)₂]₄ structure (THF removed for clarity). (Right) Octahedral normal modes.

resonance at 571 cm $^{-1}$ to ν_{4D} . A \sim 787 cm $^{-1}$ FeH $_6$ band is at 1.38 $\nu_{\rm 4D}$, the isotope shift is close to the $\sim \sqrt{2}$ limit for H/D substitution; we assign this as ν_{4H} . For FeD₆, there is a feature at 1122 cm⁻¹ that we ascribe to ν_{3D} : the Fe-H(D) stretch; IR bands are seen at 1138 and 1107 cm⁻¹.²¹ There could also be some contribution from an overtone of $\nu_{4\mathrm{D}}$. Better statistics are needed to observe $\nu_{3\mathrm{H}}$ (seen at 1514 and 1569 cm⁻¹ in the IR).²¹

The FeH(D)₆ complexes also exhibit bands at \sim 357 \pm 2 cm⁻¹ and \sim 212 cm⁻¹. These bands show virtually no isotope effect. A plausible assignment is thus to a collective motion of the [FeH(D)₆]⁴⁻ anion. In the solid state, the [FeH(D)₆]⁴⁻ octahedron is surrounded by four [MgBr(THF)₂]⁺ ions on alternate faces (Figure 2).^{22,23} If both complex ions are considered as point masses, then the structure has T_d symmetry. In this picture, the central $[FeH(D)_6]^{4-}$ anion will behave akin to Fe in Rd. As before, the T₂ vibrations will be NRIXS allowed, and we assign the 212 and 357 cm⁻¹ bands to ν_4 and ν_3 respectively.

We now return to the original question—can this technique be extended to Fe in H₂ase and N₂ase? The Rd results show that Fe-S vibrations in more complex enzymes will be readily observed but will not interfere in the Fe-H(D) bend regions. Given the difficulty in observing Fe-H stretches in [FeH₆][MgBr(THF)₂]₄, prospects for seeing Fe-H stretches in proteins are not at first encouraging. However, the Br in this sample (K-edge at 13.5 keV) reduced the penetration length for 14.4 keV photons ~200-fold vs a protein sample. We observed a count rate in the Fe-D bend region of \sim 1 $\rm s^{-1}$, and comparable rates would be seen for proteins with ~ 1750

ppm or ~35 mM Fe. Observation of Fe-D bonds at the mM level would require several days. Better insertion devices, optics, and detectors are needed to make this a routine experiment. The continuing evolution of SR sources and optics could yield orders of magnitude better sensitivity soon.^{24,25}

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Supporting Information Available: Procedures for ⁵⁷Fe-met-Rd and [57FeH(D)₆][MgBr(THF)₂]₄ preps and NRIXS measurements (PDF). This material is available free of charge via the Internet at http:// pubs.acs.org.

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