Supporting Information for

Vibrational Perturbation of the [FeFe] Hydrogenase H-Cluster Revealed by ¹³C²H-ADT Labeling

Vladimir Pelmenschikov,[†] James A. Birrell,^{*,‡} Leland B. Gee,[§] Casseday P. Richers,[∥] Edward J. Reijerse,[‡] Hongxin Wang,[⊥] Simon Arragain,^{#,∇} Nakul Mishra,[∇] Yoshitaka Yoda,[°] Hiroaki Matsuura,[♠] Lei Li,[¶] Kenji Tamasaku,[□] Thomas B. Rauchfuss,^{*,∥} Wolfgang Lubitz,[‡] and Stephen P. Cramer^{*,⊥}

[†]Institut für Chemie, Technische Universität Berlin, 10623 Berlin, Germany

[‡]Max Planck Institute for Chemical Energy Conversion, 45470 Mülheim an der Ruhr, Germany

[§]Department of Chemistry, Stanford University, Stanford, California 94305, United States

[&]quot;School of Chemical Sciences, University of Illinois, Urbana, Illinois 61801, United States

¹SETI Institute, Mountain View, California 94043, United States

[#]IFP Energies nouvelles, 92852 Rueil-Malmaison, France

[▽]Department of Chemistry, University of California, Davis, California 95616, United States

[°]Precision Spectroscopy Division, SPring-8/JASRI, Sayo, Hyogo 679-5198, Japan

[◆]Life Science Research Infrastructure Group, Advanced Photon Technology Division, RIKEN/SPring-8 Center, Sayo, Hyogo 679-5148, Japan

[¶]Hyogo Science and Technology Association, Synchrotron Radiation Research Center, Tatsuno-shi, Hyogo 679-5165, Japan

Research and Utilization Division, SPring-8/JASRI, Sayo, Hyogo 679-5198, Japan

^{*} Corresponding Authors

Materials and Methods

Synthesis of ¹²CH-ADT and ¹³CD-ADT Precursor Complex. We recently reported a new simplified synthesis for a triply labeled [2Fe]_H precursor complex $(Et_4N)_2[^{57}Fe_2[(S^{13}C^2H_2)_2NH](CN)_2(CO)_4] = ^{13}CD-1.^{1} ^{13}CD-1$ and its ⁵⁷Fe-only labeled analogue $(Et_4N)_2[^{57}Fe_2[(S^{12}C^1H_2)_2NH](CN)_2(CO)_4] = 1$ were synthesized as previously described. ¹

Preparation of *Cr*HydA1 **for NRVS and FTIR Spectroscopy.** *Cr*HydA1 was produced recombinantly in *Escherichia coli* and artificially maturated with precursor complexes 1 and ¹³CD-1 as described previously.² NRVS samples (5 mM) were prepared in the H_{hyd} state by reduction with 100 mM sodium dithionite at pH 6 (in 50 mM MES, 50 mM HEPES, 300 mM KCl, pH 6) under an atmosphere of 2% H₂. The *Cr*HydA1 H_{ox} sample was prepared in the same buffer, by incubation under nitrogen in the absence of additional reductants. NRVS cells were filled with 40 μL of sample and frozen in liquid nitrogen, and 10 μL were transferred to an FTIR cell, between two CaF₂ windows (20 mm x 4 mm, Korth Kristalle, Altenholz) separated with a 50 μm Teflon spacer coated with vacuum grease and closed with rubber rings. The temperature of the cell was maintained at 25 °C using a water circulator system (Huber, Offenburg). Spectra were measured on a Bruker IFS 66v/S FTIR spectrometer equipped with a nitrogen cooled Bruker mercury cadmium telluride (MCT) detector. Spectra were collected in the double-sided, forward-backward mode with a resolution of 2 cm⁻¹, an aperture setting of 1.5 mm and a scan velocity of 20 Hz. Spectra are the average of 1000 scans. Data were processed using home-written routines in the MATLABTM environment.

NRVS Measurements and Processing. Nuclear resonance vibrational spectroscopy measurements of the (13 CD)-1 precursor and (13 CD-1)-CrHydA1 H_{hyd} samples were conducted at SPring-8 BL19LXU.³ A liquid N₂-cooled Si (111) high heat load monochromator was used to produce an incident beam with ~1.0 eV resolution, followed by a high resolution monochromator [Ge (331) x Si (975) crystals] to achieve a ~0.8 meV (6.5 cm⁻¹) energy resolution at 14.4125 keV.⁴ The use of a 25 m undulator at BL19LXU afforded 6.5×10^9 photons s⁻¹.⁵ During NRVS measurements, the samples were maintained at cryogenic temperature using a liquid He cryostat. The real sample temperatures, derived from anti-Stokes / Stokes intensity ratios, were 45-60 K. A 4-channel avalanche photodiode detector (APD) array was used to detect the delayed nuclear fluorescence and the Kα fluorescence following nuclear excitation of ⁵⁷Fe atoms. The spectra were recorded with a step size of 0.27 meV.

The raw NRVS data were analyzed by the PHOENIX software package⁶ executed through spectra.tools,⁷ yielding ⁵⁷Fe partial density of vibrational states (⁵⁷Fe-PVDOS). The resonance peak position for each scan was aligned in the analysis, and the energy was calibrated periodically with a standard sample of NEt₄⁵⁷FeCl₄ with a prominent peak at 380 cm⁻¹. The ADT-labeled ¹³CD-1-*Cr*HydA1 H_{hyd} samples were measured in 4 beamtimes with 90 total scans in 5 datasets while the regular 1-*Cr*HydA1 H_{hyd} samples were measured in 5 beamtimes with 125 total scans in 6 datasets. There were two pairs of (¹³CD-)1-*Cr*HydA1 datasets where an *in-situ* energy calibration was performed with a ⁵⁷Fe powder sample measured at a room temperature stage outside the sample chamber. Those scans were individually calibrated before using the analysis software PHOENIX. However, we did not find any obvious difference between the *in-situ* calibrated and regular periodically calibrated datasets.

The scans were divided into segments with very different collection times with respect to energy regions. In this study, the acquisition time for every data point in the region of interest (*i.e.* from 640 to 830 cm⁻¹, X–Fe–H related bending region) was 30 seconds/point (s/p), in the middle region of 400 to 640 cm⁻¹ (Fe–CO and Fe–CN) was 6 s/p, and that for the front region of -240 cm⁻¹ to 400 cm⁻¹ was 1 s/p. For the two pairs of *in-situ* calibrated datasets, the acquisition time for the X–Fe–H bending region (*from* 640 to 830 cm⁻¹) was still 30 s/p. However, as the ⁵⁷Fe powder peaks and the nuclear resonant regions need to be well captured, the -90 to 90 cm⁻¹ region used 2 s/p while the 215 to 355 cm⁻¹ region used 10 s/p.

The *Cr*HydA1 H_{ox} sample was measured at P01, PETRA-III, Hamburg.⁸ The experimental setup established at the beamline including a two-step monochromatization (energy resolution of ~1 meV) and detection by avalanche photo diodes was used. Sample, in home-built copper sample holder, was positioned in the beam on the top of a closed cycle helium cryostat with a copper cold finger, using a home-built copper adapter. The sample was then covered with a mylar cylinder and a metal cover. The temperature at the base of the sample was maintained at 10 K and the Stokes/anti-Stokes imbalance derived real sample temperatures were 10–20 K. NRVS spectral analysis was performed using routines written in Python. The experimentally determined ⁵⁷Fe-PVDOS was calculated with a binning of 0.5 meV.

DFT Calculations. Initial coordinates for the density functional theory (DFT) modeling of the precursor complex $(Et_4N)_2[Fe_2[(SCH_2)_2NH](CN)_2(CO)_4] = 1$ were based on its crystallographic characterization. The Et_4N^+ counterions were omitted in the calculations, leading to the anionic $[Fe_2[(SCH_2)_2NH](CN)_2(CO)_4]^{2-}$ monomolecular species. The protein H_{hyd} and H_{ox} models were based on the 1.73 Å resolution 5BYQ X-ray data for the semisynthetic *Clostridium pasteurianum* [FeFe] hydrogenase (CpI) maturated with the ODT variant of the $[2Fe]_H$ subcluster (CpI^{ODT}) . To account for the presently relevant CrHydA1 species, only a single side chain S232 (CpI) had to be modified to A94 (CrHydA1). This approach is equivalent to the H-cluster DFT model construction applied by some of us earlier $^{11-13}$ for studying states H_{hyd} , $H_{sred}H^+$, and $H_{red}H^+$. Denoted as L' (*Large prime*), this molecular system includes the (i) $[2Fe]_H$ subcluster, (ii) its immediate protein environment, and (iii) the $[4Fe-4S]_H$ subcluster. All the $13\times C_\alpha$ carbon nuclei of the L' model were locked to their original X-ray crystallographically defined positions during structure optimizations.

The molecular geometry optimizations, as well as subsequent normal mode analyses, were performed using GAUSSIAN 09 Revision D.01¹⁵ based on the densities exported from single point calculations performed by JAGUAR 9.4¹⁶ that provided a high-quality initial guess for the starting (non-optimized) structures. The PBE0¹⁷⁻¹⁸ hybrid functional and the LACV3P** basis set (as implemented in JAGUAR) were employed. For the first- and second-row elements, LACV3P** implies 6-311G** triple- ζ basis sets including polarization functions. For the Fe atoms, LACV3P** consists of a triple- ζ basis set for the outermost core and valence orbitals, and the quasi-relativistic Los Alamos effective core potential (ECP) for the innermost electrons. The molecular systems environment was considered using a self-consistent reaction field (SCRF) polarizable continuum model and integral equation formalism (IEF-PCM)¹⁹ as implemented in GAUSSIAN 09, with the static dielectric constant set to ε = 4.0 as often used for proteins, and the remaining IEF-PCM parameters at their default values for water. The computational scheme for the protein models furthermore included two-body D3 empirical dispersion correction by Grimme *et al.* in its original formulation.²⁰ The H-cluster redox states [4Fe-4S]_H⁺-Fe_p(II)Fe_d(II) and [4Fe-4S]_H²⁺-Fe_p(II)Fe_d(I), correspondingly, were confirmed for the electronic configurations of the present H_{hyd} and H_{ox} models.

The 57 Fe-PVDOS intensities and internuclear displacements were extracted from normal mode outputs using an in-house Q-SPECTOR program tool, successfully applied by us to simulate the [FeFe] hydrogenase^{11-13, 21} and other molecular systems' NRVS spectra. To empirically account for experimental NRVS lineshapes of the (13 CD-)1 / (13 CD-)1- C PHydA1 samples, the DFT-computed 57 Fe-PVDOS intensities were correspondingly broadened by convolution with a full width at half maximum (FWHM) = 12 / 14 cm⁻¹ Lorentzian; homogeneous empirical scaling by 96% / 94% was applied to the calculated frequencies > 350 / 400 cm⁻¹.

Supplementary Figures

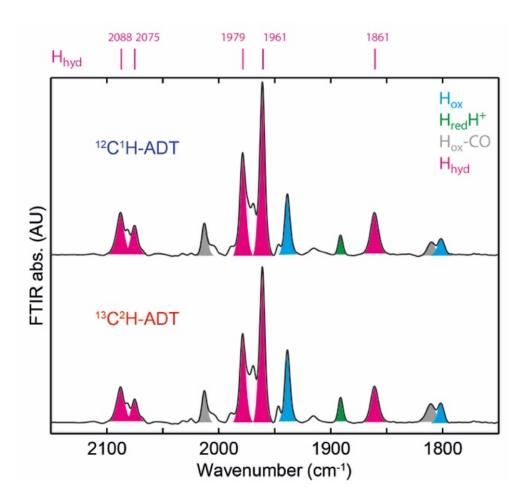


Figure S1. FTIR spectra of the (12CH-)1-CrHydA1 (top) and 13CD-1-CrHydA1 (bottom) samples poised in the H_{hyd} state. Bands from the H_{hyd} state are colored purple. Bands of smaller intensity from the additional states H_{ox}, H_{red}H⁺ and H_{ox}-CO are colored blue, green, and gray, respectively. From the relative intensity of the CO stretch at 1961 cm⁻¹ in the H_{hyd} state vs. the equivalent H_{ox} band at 1940 cm⁻¹, we estimate that $\sim 80\%$ of the samples were in the H_{hyd} state for 1-CrHydA1 and $\sim 70\%$ in ¹³CD-1-CrHydA1. Obtaining pure H_{hyd} spectra is challenging as H_{hyd} is a rather unstable intermediate that decays with time and can only be captured under specific conditions (low pH and high amounts of reductant). There is always a contribution from a few additional states due to reoxidation of H_{hvd} (giving H_{ox}) or degradation of the H-cluster (producing H_{ox}-CO through "cannibalization"). Note that NRVS samples were frozen at the same time as IR samples were prepared, but there is a small delay 5-10 min before the IR samples are measured. Thus, the true proportion of H_{hyd} is likely to be higher in the NRVS samples. The contribution from other states to the NRVS spectrum will be small and certainly not responsible for the large isotope dependent changes we report in the current manuscript. In particular, H_{hyd} is the only state so far identified with peaks in the 650 - 750 cm⁻¹ region of the NRVS spectrum and so changes in this region are entirely from H_{hyd}.

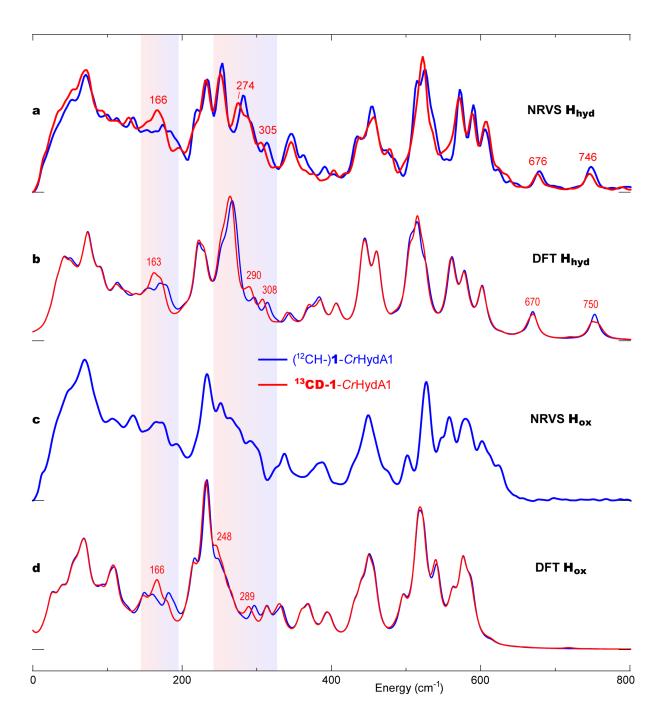


Figure S2. ⁵⁷Fe-PVDOS for the [FeFe] hydrogenase H_{hyd} / H_{ox} state isotopologues (¹²CH-)**1**-*Cr*HydA1 (blue) vs. ¹³C**D**-**1**-*Cr*HydA1 (red) from (**a**) / (**c**) NRVS experiment and (**b**) / (**d**) DFT calculations, correspondingly; the ¹³C**D**-**1**-*Cr*HydA1 NRVS data availability is limited to the H_{hyd} sample. Notable isotope-dependent spectral features unique to the ¹³C**D**-**1**-*Cr*HydA1 species are marked with their vibrational energies (numbers shown in red). Regions displaying consistent ¹²CH-vs-¹³CD ADT spectral shifts (in **a**, **b**, and **d**) are highlighted using vertical semitransparent bars.

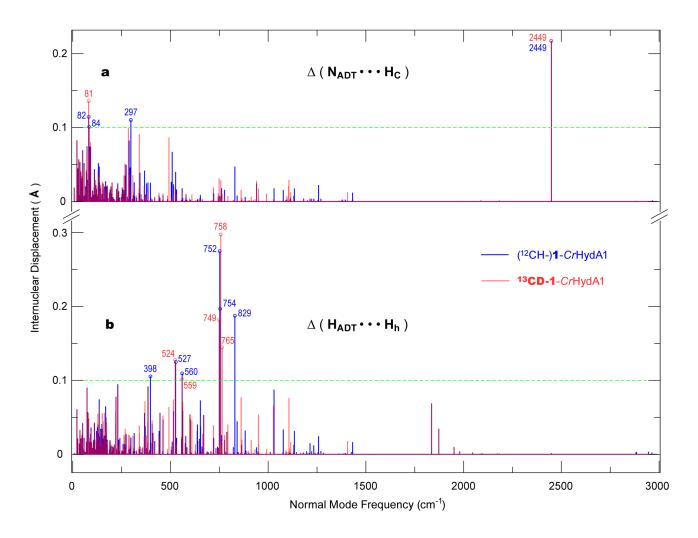


Figure S3. Relative displacement amplitudes in the nuclei pairs (a) N_{ADT}····H_C and (b) H_{ADT}····H_h (as designated in **Figure 1b**) from the **1**-*Cr*HydA1 (blue) and ¹³CD-1-*Cr*HydA1 (red) H_{hyd} state DFT models across the entire vibrational spectra. Normal modes with significant internuclear displacements (>0.1 Å cut-off shown as green broken line) of the types (a) and (b) are labeled with their frequencies, listed in **Table S1**, and provided as animations as part of the **Supporting Information**.

Supplementary Tables

Table S1. Normal modes with significant (>0.1 Å) relative displacement amplitudes in the nuclei pairs $H_{ADT} \cdots H_h$ and $N_{ADT} \cdots H_C$ (as designated in **Figure 1b**) from the **1**-*Cr*HydA1 and ¹³CD-1-*Cr*HydA1 H_{hyd} state DFT models. Animated representations of these vibrational modes are provided as a separate part of the **Supporting Information**.

$\mathbf{H}_{ADT}\cdots\mathbf{H}_{\mathbf{h}} (= 2.06 \text{ Å})^a$				$N_{ADT}\cdots H_{C} (= 2.26 \text{ Å})^a$				
1 -CrHydA1		¹³ CD-1 - <i>Cr</i> HydA1		1- CrHydA1		¹³ CD-1 - <i>Cr</i> HydA1		
Frequency (cm ⁻¹)	Displacement ^b (Å)	Frequency (cm ⁻¹)	Displacement ^b (Å)	Frequency (cm ⁻¹)	Displacement ^b (Å)	Frequency (cm ⁻¹)	Displacement ^b (Å)	
398	0.106	524	0.128	82	0.115	81	0.136	
527	0.125	559	0.102	84	0.101	2449	0.217	
560	0.110	749	0.182	297	0.110			
752	0.275	758	0.297	2449	0.217			
754	0.197	765	0.145					
829	0.187							

^a Optimized internuclear distance.

^b The corresponding internuclear distance contraction is approximately 50% of the displacement amplitude.

Table S2. [2Fe]_H precursor vibrational modes summary from the (¹²CH-)1 and ¹³CD-1 DFT models. Animated representations of selected vibrational modes are provided as a separate part of the **Supporting Information**.

	ı	T	1	
Mode atomic	Frequency	Frequency	Difference	Characterization
motions	1	¹³ CD-1	1 - ¹³ CD-1	
	(cm ⁻¹)	(cm ⁻¹)	(cm ⁻¹)	
	1058/902	769/734	289/168	In-phase bending/rotation of the –CH ₂ – groups, admixed with ADT amine proton motion parallel to the mirror symmetry plane of 1 .
	848	674	174	Out-of-phase bending/rotation of the -CH ₂ - groups, admixed with ADT amine proton motion perpendicular to the mirror symmetry plane of 1.
	534	530	4	ADT motion coupled to the CO bending/stretching.
	518	518	0	Similar to 534/ 530 but negligible ADT motion, hence no isotope shift.
	508	492	16	Similar to 534/ 530 but with a different phase of CO/ADT motions, and different CN motion.
	506	489	17	Similar to 508 but with larger contribution of the Fe _p -bound CO bending, and smaller contribution of the Fe _d -bound CO bending.

(Table continued on the next page)

	T	T	T	
~~	326	329/314	-3/12	Fe–S motion coupled to CO and CN movement and ADT
				"flapping". 329 has much less
				CO/CN motion and does not show
				the "flapping". 314 is like 329 but
				with less CO/CN/FeS motion.
_ (292	287	5	ADT fragment wagging/rotation
				between 2xFe. Similar for
				(¹² CH-) 1 and ¹³ CD-1.
•				
121	286	285	1	ADT fragment bending/rocking
				between 2xFe. Similar for
				(¹² CH-) 1 and ¹³ CD-1.
1	272	264	8	Independent S movement with Fe
				side-to-side motion. Again, very
				similar for (¹² CH-)1 and ¹³ CD-1.
<i>*</i>				
4 %	225	224	1	Fe ₂ S ₂ unit flattening, out of phase
	223	224	1	with the ADT movement.
				With the Fib Fine venient
4				
, Lil	203	201	2	Fe ₂ S ₂ unit flattening but in phase
				with ADT movement.
XI				
	173	168	5	Rocking of the -H ₂ C-NH-CH ₂ -
				assembly / Seesaw motion of the Fe_2S_2 unit.
A second				1 0202 time.
•				

(Table continued on the next page)

160	143	17	Out-of-phase rotation of the two ADT -µSCH ₂ - groups around their S-C axes.
129	127	2	In-phase rotation of the two ADT $-\mu$ SCH ₂ $-$ groups / Fe ₂ S ₂ swivel motion.
105	104	1	ADT fragment wagging/rotation between 2xFe, as well involving CO/CN ligands.

Supplementary References

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