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(Article begins on next page)

1 **Title:**

2 The effect of a C298D mutation in CaHydA [FeFe]-hydrogenase: insights into the protein-metal
3 cluster interaction by EPR and FTIR spectroscopic investigation.

4

5 **Authors:**

6 Simone Morra,^a Sara Maurelli,^b Mario Chiesa,^b David W. Mulder,^c Michael W. Ratzloff,^c Elio
7 Giamello,^b Paul W. King,^c Gianfranco Gilardi,^a and Francesca Valetti^{a,*}

8

9 ^a Department of Life Sciences and Systems Biology, University of Torino, Torino 10133, Italy.

10 ^b Department of Chemistry, University of Torino, Torino 10133, Italy.

11 ^c Biosciences Center, National Renewable Energy Laboratory, Golden, Colorado 80401, USA.

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13 *Corresponding Author: francesca.valetti@unito.it

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1 **Abstract**

2 A conserved cysteine located in the signature motif of the catalytic center (H-cluster) of [FeFe]-
3 hydrogenases functions in proton transfer. This residue corresponds to C298 in *Clostridium*
4 *acetobutylicum* CaHydA. Despite the chemical and structural difference, the mutant C298D retains
5 fast catalytic activity, while replacement with any other aminoacid causes significant activity loss.
6 Given the proximity of C298 to the H-cluster, the effect of the C298D mutation on the catalytic
7 center was studied by continuous wave (CW) and pulse electron paramagnetic resonance (EPR) and
8 by Fourier transform infrared (FTIR) spectroscopies.
9 Comparison of the C298D mutant with the *wild type* CaHydA by CW and pulse EPR showed that
10 the electronic structure of the center is not altered. FTIR spectroscopy confirmed that absorption
11 peak values observed in the mutant are virtually identical to those observed in the *wild type*,
12 indicating that the H-cluster is not generally affected by the mutation. Significant differences were
13 observed only in the inhibited state H_{ox}-CO: the vibrational modes assigned to the CO_{exo} and Fe_d-
14 CO in this state are shifted to lower values in C298D, suggesting different interaction of these
15 ligands with the protein moiety when C298 is changed to D298. More relevant to the catalytic
16 cycle, the redox equilibrium between the H_{ox} and H_{red} states is modified by the mutation, causing a
17 prevalence of the oxidized state.
18 This work highlights how the interactions between the protein environment and the H-cluster, a
19 dynamic closely interconnected system, can be engineered and studied in the perspective of
20 designing bio-inspired catalysts and mimics.

21

22 **Keywords**

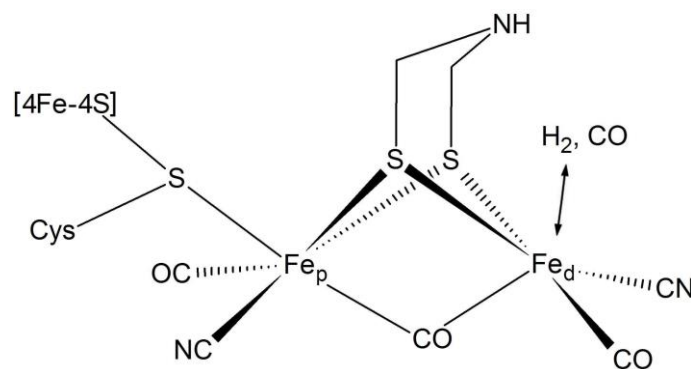
23 [FeFe]-hydrogenase; proton transfer; EPR; HYSCORE; FTIR.

24

1 1. Introduction:

2 [FeFe]-hydrogenases are the redox enzymes that catalyze the reversible reaction $2\text{H}^+ + 2\text{e}^- \rightleftharpoons \text{H}_2$ at
3 high turnover rates. These enzymes are crucial in the biological production of hydrogen gas [1-3], a
4 valuable fuel and an important intermediate in various industrial processes [4,5].
5 The main aim of this work is to investigate the effects of the C298D mutation on the spectroscopic
6 features of *Clostridium acetobutylicum* [FeFe]-hydrogenase I (CaHydA), in order to analyse the
7 consequences on the catalytic site caused by protein modifications in its proximity.
8 The catalytic site of [FeFe]-hydrogenases is an organometallic center named the H-cluster (Fig. 1);
9 it is extremely peculiar for this class of enzymes and its unique chemical makeup requires a
10 complex biosynthetic mechanism by specialized protein maturases [6-10]. The H-cluster is
11 composed of two sub-clusters: a cubane [4Fe-4S] coordinated by four conserved protein cysteines
12 that is bridged to a [2Fe] sub-cluster via one of these residues (Fig. 1) [11,12]. The [2Fe] sub-cluster
13 is composed of two iron atoms, the proximal (Fe_p) and the distal (Fe_d), coordinated by non-protein
14 ligands that are two terminal CO, a bridging CO and two terminal CN [11,13,14]. The two Fe atoms
15 are also bridged by an organic ligand which was identified as a di(thiomethyl)amine [1,15-18].

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18

19 **Figure 1.** Structure of the H-cluster. (Single column fitting image).

20

21 The catalytic mechanism of H_2 evolution is based on the reduction of protons at Fe_d of the H-
22 cluster, involving an hydride intermediate, but the details of the mechanism are still being
23 investigated [19-24].

24 Several redox states of the H-cluster have been identified. The oxidized state (H_{ox}) is characterized
25 by a diamagnetic $[\text{4Fe-4S}]^{2+}$ sub-cluster and a paramagnetic Fe(I)-Fe(II) sub-cluster. A one electron
26 reduction results in the reduced state (H_{red}), characterized by a diamagnetic $[\text{4Fe-4S}]^{2+}$ sub-cluster
27 and a diamagnetic Fe(I)-Fe(I) sub-cluster. A further one electron reduction results in the super-
28 reduced state (H_{sred}), characterized by a paramagnetic $[\text{4Fe-4S}]^{1+}$ sub-cluster and a diamagnetic

1 Fe(I)-Fe(I) sub-cluster. A paramagnetic state $[4\text{Fe-4S}]^{1+}$ Fe(II)-Fe(II) diferrous intermediate has
2 also been recently proposed [21]. Alternatively, binding of exogenous CO to the H_{ox} state at the Fe_d
3 results in the reversibly inhibited form $\text{H}_{\text{ox}}\text{-CO}$, characterized by a diamagnetic $[4\text{Fe-4S}]^{2+}$ sub-
4 cluster and a paramagnetic Fe(I)-Fe(II) sub-cluster [3,20,25-27].

5 Electron paramagnetic resonance (EPR) and Fourier transform infrared (FTIR) spectroscopies have
6 been used for the characterisation of such intermediates because of their complementarity in the
7 investigation of the electronic structure and the chemical environment of the different redox states
8 of the H-cluster. Also, these spectroscopies have been used on [FeFe]-hydrogenases from different
9 microorganisms, allowing the study of the similarities and the differences between different
10 enzymes [3,25].

11 EPR and the related hyperfine techniques of ENDOR (electron nuclear double resonance) and
12 HYSCORE (Hyperfine Sublevel Correlation) have proven to be powerful tools to elucidate the
13 structure-function relationships of [FeFe]-hydrogenases. The EPR investigation has been focused
14 on the paramagnetic states of the catalytic cycle namely the H_{ox} state and the H_{sred} state of algal
15 enzymes (*Chlamydomonas reinhardtii*). The H_{sred} state, which has been proposed to be part of the
16 catalytic cycle, displays a $[4\text{Fe-4S}]^{1+}$ Fe(I)Fe(I) configuration, with an EPR spectrum typical for a
17 reduced $[4\text{Fe-4S}]^{1+}$ cluster [19]. By studying the hyperfine interactions of the ^{57}Fe nuclei of the
18 cluster-core as well as the ^{14}N and ^{13}C nuclei belonging to the ligands, important insights were
19 obtained on the spin density distribution and electronic structure of the H-cluster [3,17,28,29].

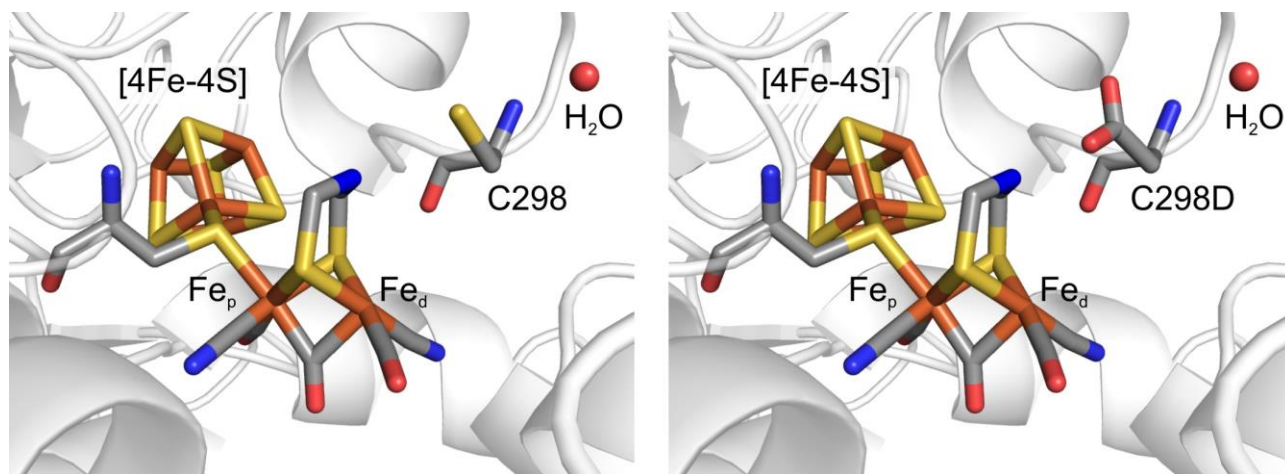
20 Moreover, the CO inhibited state of the enzyme, $\text{H}_{\text{ox}}\text{-CO}$, which is paramagnetic, yielded additional
21 information on the redistribution of spin density in the H-cluster upon binding a π -accepting ligand
22 in the exchangeable site at the distal iron [30].

23 FTIR spectroscopy was crucial in the identification of the non-protein CO and CN ligands in the H-
24 cluster [31,32]. Subsequently, it has become a powerful specific tool to study how the redox state
25 influences such ligands [19,20,23,33-35], their source during the assembly process [36] and the
26 effect of mutagenesis [21,37].

27 The protein environment around the H-cluster was shown to be highly conserved in the entire
28 enzyme class [1,26]. One of these strictly conserved residues is a cysteine that is adjacent to the Fe_d ,
29 namely C298 in *Clostridium acetobutylicum* HydA, C299 in *Clostridium pasteurianum* CpI and
30 C169 in *Chlamydomonas reinhardtii* HydA1; its role in [FeFe]-hydrogenases has been investigated
31 by means of X-ray crystallography [11], mutagenesis [21,37-40] and computational simulations
32 [21,41,42].

33 In particular, we have previously shown [40] by site saturation mutagenesis that replacement of
34 C298 in *Clostridium acetobutylicum* [FeFe]-hydrogenase (CaHydA) with any other aminoacid

1 causes severe impairment or loss of activity, with the only exception being aspartic acid. The
2 mutant C298D, where the –SH group of cysteine was replaced by the –COOH group of aspartic
3 acid in the proximity of the di(thiomethyl)amine bridge of H-cluster (Fig. 2), displays an enzymatic
4 activity in the same order of magnitude of the *wild type* (WT), with only a 2-fold decrease in both
5 H₂ evolution and H₂ uptake kinetics. Also, the activity pH profile was shifted towards acidic values.
6 These data demonstrated a direct involvement of C298 in the proton transfer to the H-cluster.
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10 **Figure 2.** The H-cluster in a model of the protein environment of *Clostridium acetobutylicum*
11 CaHydA [FeFe]-hydrogenase [40]. The structural position of the *wild type* cysteine 298 (C298) is
12 depicted on the left, and the effect of the C298D mutation is modeled on the right. **(2 columns**
13 **fitting image).**

14
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16 In this work, we report a combination of continuous wave (CW) EPR, pulse EPR and FTIR
17 spectroscopies that was used to compare CaHydA *wild type* (WT) to the C298D mutant to
18 investigate, in detail, the effect of the mutation on the H-cluster structure under steady-state
19 conditions of various redox states and its implications for catalysis.

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1 **2. Materials and methods:**

2
3 **2.1 Recombinant expression and purification**

4 CaHydA WT and C298D were recombinantly expressed in *E. coli* by adapting previously described
5 protocols [40,43-45]. The plasmids pCaE2 (harbouring the genes *hydA* and *hydE*) and pCaFG
6 (harbouring the genes *hydF* and *hydG*) were co-transformed in *E. coli* Rosetta2(DE3). Cultures
7 were aerobically grown in Terrific Broth medium supplemented with 2 mM ferric ammonium
8 citrate, 200 µg/mL carbenicillin, 50 µg/uL streptomycin and 34 µg/mL chloramphenicol. When the
9 OD₆₀₀ reached ~0.4, the culture was supplemented with 2 mM cysteine, 25 mM fumarate, 0.5 %
10 w/v glucose and induced with 1.5 mM IPTG. The expression was performed overnight at 30 °C
11 under argon sparging.

12 All the following manipulations were performed under strict anaerobic conditions in a glove box
13 (Plas Labs) under a 5% hydrogen - 95% nitrogen atmosphere. All solutions were supplemented with
14 2-20 mM sodium dithionite and equilibrated with the glove box atmosphere before use.

15 Purification was obtained by affinity chromatography using Strep-Tactin Superflow high capacity
16 cartridges (IBA) following the manufacturer's instructions. Protein concentration was assayed with
17 the Bradford assay using bovine serum albumin as standard. The typical yield for both CaHydA WT
18 and C298D was 1.7 mg pure protein/L culture. Hydrogenase activity assay was performed as
19 previously described [40]; CaHydA WT samples had typically a specific activity of approximately
20 1356 µmol min⁻¹ (mg protein)⁻¹; CaHydA C298D sample had typically a specific activity of
21 approximately 660 µmol min⁻¹ (mg protein)⁻¹. The specific activities were consistent with those of
22 other recombinant [FeFe]-hydrogenases [2,40,43-45].

23 An homology model of the enzyme structure was built as previously described [40].
24

25 **2.2 EPR spectroscopy**

26 Purified enzymes were anaerobically concentrated and the buffer was exchanged to remove trace
27 dithionite. 5% v/v glycerol was added to the solution. The oxidized sample was obtained by the
28 addition of 3.1 mM thionine and the final protein concentration was 0.4 mM. The CO-treated
29 sample was obtained by sparging the oxidized sample with CO twice for 30 seconds on ice. A
30 sample of 60 µL was sealed into a quartz tube (Wilmad LabGlass) with internal diameter 2 mm.
31 Continuous wave (CW) EPR spectra were recorded with a Bruker EMX spectrometer operating at
32 X-band (9.47 GHz) equipped with a cylindrical cavity. All the spectra were recorded with 100 kHz
33 field modulation, microwave power 10 mW, modulation amplitude 0.2 mT and temperature 77 K.
34 No attempts were made to obtain absolute spin concentrations.

1 Pulse EPR experiments were performed at X-band (9.76 GHz) on an ELEXYS 580 Bruker
2 spectrometer equipped with a liquid-helium cryostat from Oxford Inc. The magnetic field was
3 measured by means of a Bruker ER035 M NMR gauss meter. The spectra were recorded at T = 15
4 K.

5 Electron-spin-echo (ESE) detected EPR experiments were carried out with the pulse sequence: $\pi/2-$
6 $\tau-\pi-\tau-echo$. The mw pulse lengths $t_{\pi/2} = 16$ ns and $t_{\pi} = 32$ ns and a τ value of 200 ns was used.

7 Hyperfine Sublevel Correlation (HYSCORE) experiments were carried out with the pulse sequence
8 $\pi/2-\tau-\pi/2-t_1-\pi-t_2-\pi/2-\tau-echo$. The mw pulse lengths $t_{\pi/2} = t_{\pi} = 16$ ns were used, with
9 starting time 96 ns for t_1 and t_2 , and time increment $\Delta t = 16$ ns (data matrix 250×250). The spectra
10 were recorded with different τ values, specified in the figures caption. A four-step phase cycle was
11 used to remove unwanted echoes. The time traces of the HYSCORE spectra were baseline corrected
12 with a third-order polynomial, apodized with a Hamming window and zero filled. After two-
13 dimensional Fourier transformation, the absolute value spectra were calculated. For all the pulse
14 experiments a shot repetition rate of 0.5 kHz was used.

15 Field swept EPR and HYSCORE spectra were simulated using the Easyspin package [46].

16

17 **2.3 FTIR spectroscopy**

18 All the manipulations and the assembly of the transmission cell were performed under strict
19 anaerobic conditions using a glove box (Belle Technology) under a pure nitrogen atmosphere.

20 Purified samples were concentrated by ultrafiltration up to 0.9-1 mM using Amicon Ultra 0.5 mL
21 30K MWCO (Millipore). The various samples were obtained as follows: the “as purified” sample
22 was acquired just after concentration without any other treatment (the buffer contains approximately
23 2 mM sodium dithionite as a purification residual); the thionine oxidized sample was obtained by
24 the addition of 6.7 mM thionine; the hydrogen reduced sample was obtained by sparging the sample
25 with H₂ twice for 1 minute on ice; the dithionite reduced sample was obtained by the addition of
26 16.7 mM fresh sodium dithionite for 1 minute; the CO inhibited sample was obtained by sparging
27 the sample with carbon monoxide twice for 30 seconds on ice.

28 The spectra were acquired at room temperature using a Bruker Tensor 27 FT-IR spectrometer
29 (Bruker Instruments). A transmission cell equipped with CaF₂ window and 50 μ m pathlength
30 (Specac) was used; the sample chamber was purged with pure nitrogen gas. Spectra were acquired
31 with a resolution of 2 cm⁻¹ accumulating 256 scans. The baseline correction was obtained using the
32 Opus 6.0 software (Bruker Instruments) by the concave rubberband algorithm and manual
33 refinement of the baseline.

34

1 **3. Results:**

3 **3.1 CW and Pulse EPR spectroscopy**

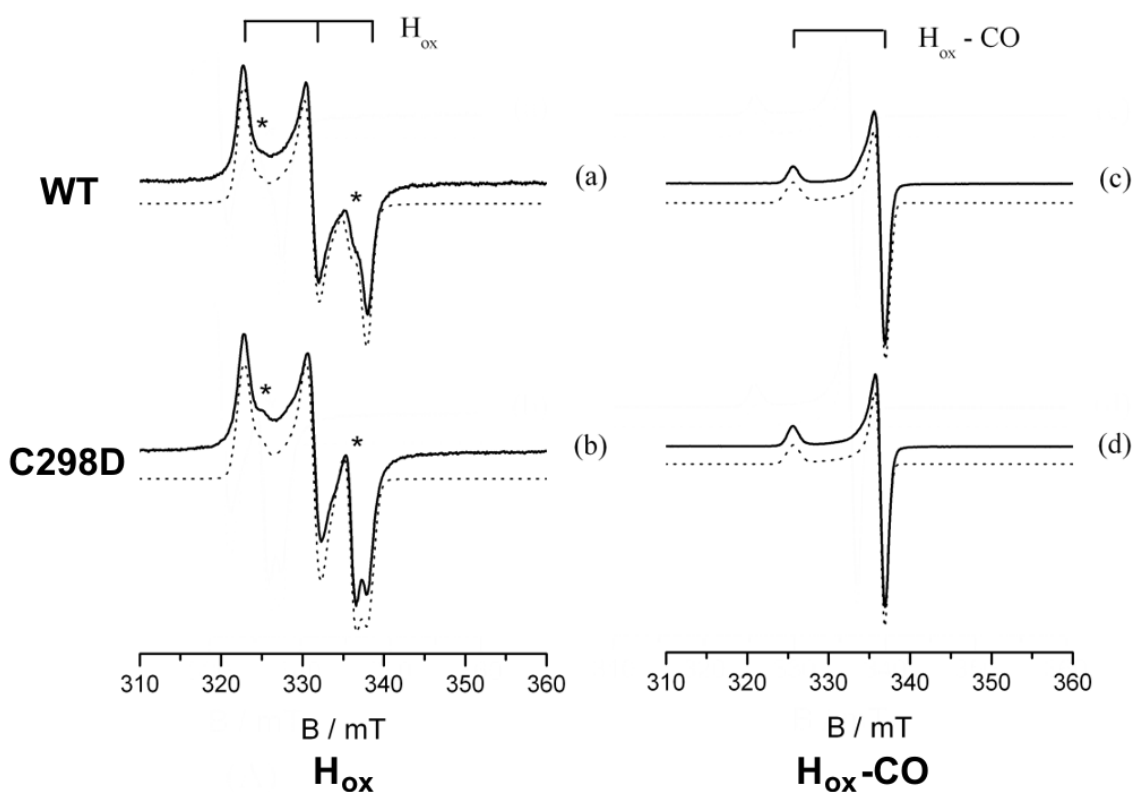
4 X-band EPR experiments were performed on the paramagnetic H_{ox} and H_{ox}-CO states of CaHydA
5 *wild type* (WT) and C298D mutant in order to examine possible structural changes in the local
6 geometry of the EPR active site upon mutagenesis.

7 Prior to EPR analysis, the CaHydA samples were oxidized with an excess of thionine in order to
8 enrich for the H_{ox} state of the H-cluster. The oxidation treatment was necessary to remove
9 overlapping signals typical of reduced [2Fe-2S]⁺ centers [47-50], presumably arising from the [2Fe-
10 2S] redox center of CaHydA (Fig. S1 in Supplementary Material).

11 It has to be noted that the oxidation by “auto-oxidation”, as described for *Chlamydomonas*
12 *reinhardtii* HydA1 [20], was not sufficient for CaHydA, because the presence of the accessory iron
13 sulphur centers in the so-called F-domain are not completely oxidized by this process resulting in a
14 background of paramagnetic signals that do not originate from the H-cluster.

15 The CW EPR spectra recorded for the oxidized WT protein and C298D mutant are reported in
16 Figure 3. The EPR spectrum of the WT sample (Fig. 3a) is dominated by a rhombic signal with
17 principal g values $g_1 = 2.0892$, $g_2 = 2.0363$, $g_3 = 1.9954$. These values are in agreement with those
18 reported for the oxidized form of the H-cluster (H_{ox} state) of other hydrogenases
19 [3,17,19,20,28,37,51-54]. In Figure 3c the CW EPR spectrum of the oxidized sample after flushing
20 with CO shows the presence of the axial signal ascribable to the inhibited state of the H-cluster
21 (H_{ox}-CO), characterized by g values $g_1 = 2.0755$ and $g_2 = g_3 = 2.0080$, as already reported for other
22 systems [30,34,52].

23 The CW EPR spectra related to the H_{ox} and H_{ox}-CO states of the thionine oxidized C298D mutant
24 are reported in Figure 3b and 3d, respectively. For both states a clear analogy with the spectra of the
25 WT protein can be observed, namely a rhombic pattern for the H_{ox} state and an axial signal for the
26 H_{ox}-CO state, with g values matching those found for the WT protein (Table 1). The comparison of
27 the CW EPR spectra shown in Figure 3 thus suggests that the local geometry of the paramagnetic
28 [2Fe] sub-cluster is essentially unaltered upon the mutagenesis process for the C298D mutant.



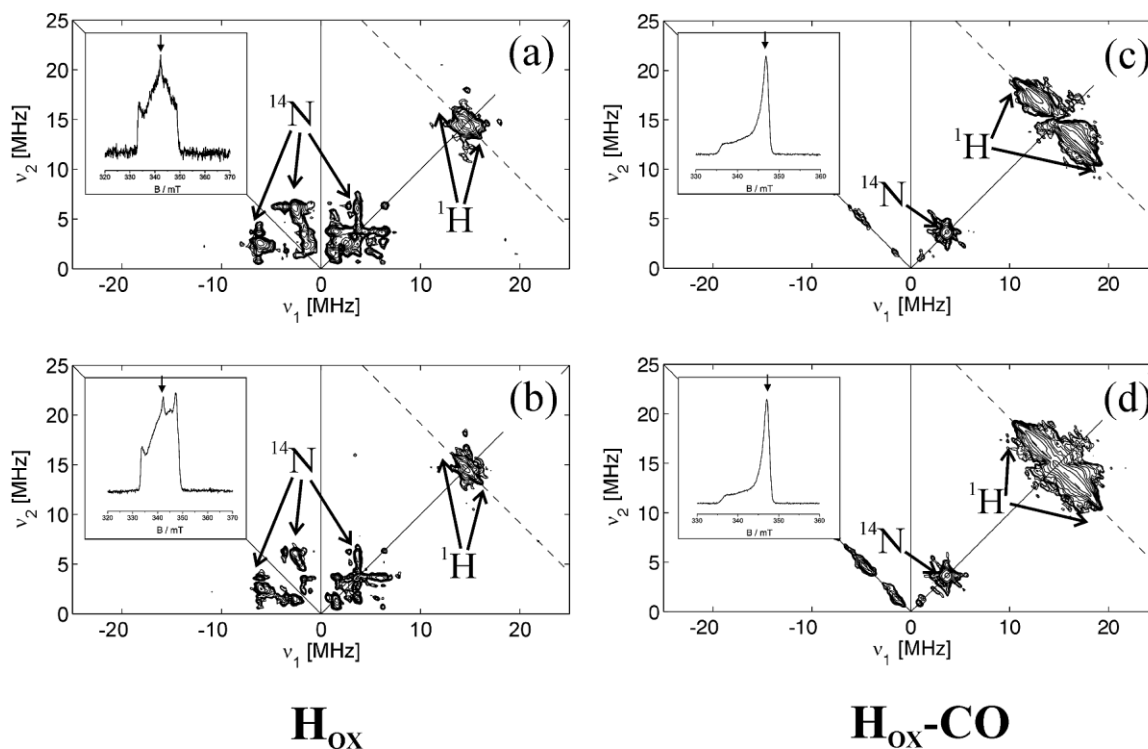
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Figure 3. Experimental (solid lines) and computer simulated (dotted lines) X-band CW EPR spectra of the thionine oxidized CaHydA samples in the H_{ox} (left) and H_{ox-CO} (right) states of the H-cluster. Spectra (a), (c) refer to the WT protein and (b), (d) to the C298D mutant. The spin Hamiltonian parameters extracted from the computer simulations are reported in Table 1. The experimental spectra were recorded at $T = 77$ K. The stick diagrams on top of the spectra indicate the spectral features of the H_{ox} and H_{ox-CO} states. Asterisks in spectra (a) and (b) indicate the EPR pattern of the H_{ox-CO} state present as an impurity. **(2 columns fitting image).**

12 Further insights into the electronic structure of the active site and its chemical environment upon
 13 mutagenesis were obtained by extending the EPR investigation to pulse methods. For the present
 14 study HYSCORE experiments were performed at X-band in order to characterize both the H_{ox} and
 15 H_{ox-CO} states of the H-cluster of the oxidized WT and C298D mutant. The comparison between the
 16 HYSCORE spectra recorded for the two samples is reported in Figure 4 (see also Fig. S2 of the
 17 Supplementary Material). The spectra corresponding to the H_{ox} state (Fig. 4a and 4b) of the H-
 18 cluster show cross peaks stemming from the hyperfine interaction of the unpaired electron of the
 19 $[2Fe]$ sub-cluster with nitrogen nuclei in both $(+,+)$ and $(-,+)$ quadrants. The computer simulation
 20 analysis of such nitrogen signals carried out on the spectra recorded at three magnetic field
 21 positions (Fig. S3 in Supplementary Material) allowed extracting the spin-Hamiltonian parameters

1 of the ^{14}N hyperfine and quadrupole couplings, which are listed in Table 2. In the simulation, one
2 nitrogen nucleus was considered, whose hyperfine and quadrupole tensors are in line with those
3 attributed to the CN ligand at the distal iron (Fe_d) site of the $[\text{2Fe}]$ sub-cluster in DdH and CpI on
4 the basis of the observed nuclear quadrupole interaction and comparison with DFT calculations
5 [17,29,57]. The same ^{14}N signals have been observed for the C298D mutant, (Fig. 4b), clearly
6 indicating a structural analogy in the CN ligand at the Fe_d site for the two systems in their H_{ox} state.
7 HYSCORE spectra recorded for the $\text{H}_{\text{ox}}\text{-CO}$ state both CaHydA WT and C298D mutant (Fig. 4c
8 and 4d), show cross peaks in the (+,+) quadrant due to the hyperfine interaction of the unpaired
9 electron of the $[\text{2Fe}]$ sub-cluster with nitrogen, carbon and proton nuclei. The spectra are similar to
10 those reported by different authors for similar systems [28,30,58,59]. As in the case of the H_{ox} state,
11 also for the $\text{H}_{\text{ox}}\text{-CO}$ case the HYSCORE spectra of both WT and C298D mutant display nearly
12 identical signals. A first set of cross peaks is centered along the (+,+) diagonal at about 3.7 MHz.
13 The simulation analysis (Table 2) allowed ascribing this signal to double quantum transitions of a
14 ^{14}N nuclear spin, as already reported for analogous HYSCORE spectra recorded for DdH [30]. The
15 measured hyperfine interaction points to a weakly coupled ^{14}N nucleus with a large quadrupole
16 interaction of 3.3 MHz, compatible with the nitrogen belonging to the CN ligand at the distal Fe of
17 the $[\text{2Fe}]$ sub-cluster in the $\text{H}_{\text{ox}}\text{-CO}$ state [30].
18 Finally, an extended ridge centered at the proton Larmor frequency ($\nu_{\text{1H}} = 14.766$ MHz at $B_0 =$
19 346.8 mT) is observed in the HYSCORE spectra of both the WT and the C298D mutant. The signal
20 has a maximum extension of about 9 MHz consistent with previous observations for the $\text{H}_{\text{ox}}\text{-CO}$
21 state of DdH [30] and of CpI [60]. Inspection of the ridge of the CaHydA samples reveals the
22 presence of at least two proton signals, characterized by a different maximum extension (Fig. 4c
23 and 4d). The computer simulation analysis performed at three field positions (Fig. S4 in
24 Supplementary Material) allowed extracting the full hyperfine tensor for the two couplings, both
25 dominated by the dipolar contribution (Table 2). Since several protons are present at distances
26 compatible with the observed hyperfine couplings, a structural assignment is not possible at this
27 stage.
28 To summarize, the comparison between the EPR and HYSCORE spectra recorded for CaHydA WT
29 and C298D mutant indicates the absence of any significant structural and electronic modification of
30 the H-cluster upon mutagenesis, suggesting that both the local geometry and the chemical
31 environment of the active site are preserved.

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Figure 4. Experimental X-band HYSCORE spectra of the H_{ox} (left) and H_{ox-CO} (right) states of the thionine oxidized CaHydA. Spectra (a), (c) refer to the WT protein and (b), (d) to the C298D mutant. The spectra were recorded at field positions corresponding to (a) 341.6 mT, (b) 346.8 mT, (c) 342.2 mT and (d) 347.1 mT, as indicated by the arrow in the echo detected spectra in the insets. The τ values adopted for the experiments are: (a), (b) $\tau = 112$ ns; for spectra (c), (d) two spectra recorded at $\tau = 136$ and $\tau = 160$ ns were summed together after Fourier transformation. All spectra were recorded at $T = 15$ K. The simulation analysis of the spectra is reported in the Supplementary Material (Fig. S3 and S4) and the corresponding spin Hamiltonian parameters are listed in Table 2. **(2 columns fitting image).**

1 **3.2 FTIR spectroscopy**

2 FTIR spectroscopy was used to investigate the structure of the H-cluster through the vibrational
3 features of the CO and CN ligands under steady-state conditions (Fig. 5).

4 The spectrum of CaHydA WT without any treatment (“as purified”) is complex and composed of a
5 mixture of different redox states of the H-cluster. In order to dissect the various components,
6 various oxidative and reductive treatments were applied.

7 When the WT enzyme was oxidized by thionine treatment, a much more homogeneous spectrum
8 was obtained. The five major components of this spectrum (2082, 2070, 1969, 1946, 1801 cm^{-1}) can
9 be associated with the spectra of previously studied [FeFe]-hydrogenases in their H_{ox} state and have
10 been assigned to the five CO and CN ligands of the H-cluster (Table 3).

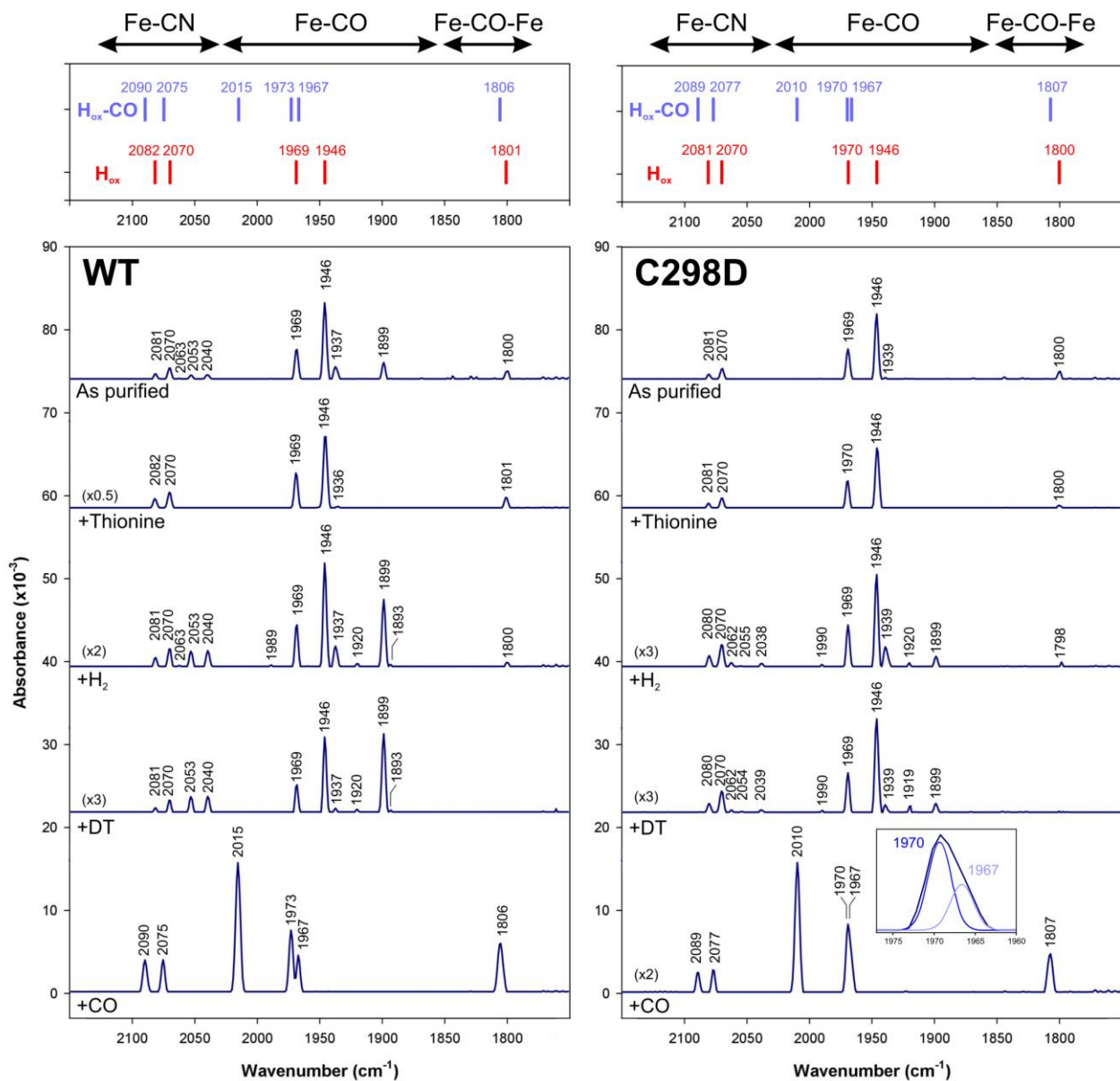
11 Reduction of the WT enzyme by H_2 resulted in the decrease of the H_{ox} signals and the increase of
12 several other components (2063, 2053, 2040, 1989, 1937, 1920, 1899, 1893 cm^{-1}), that are also
13 present in the “as purified” sample.

14 Reduction with dithionite gave a similar result, with few differences. In this case, the 1800 cm^{-1}
15 peak was not detectable and the increase of the 1899 cm^{-1} was larger, while there was no
16 proportionality in the increase of the 1937, 1920 and 1893 cm^{-1} signals; also, the signals at 2063 and
17 1989 cm^{-1} were absent.

18 The assignment of the signals observed in the reduced samples to a specific redox state and ligand
19 is more complicated, because multiple bands were observed indicating a population of multiple
20 states. Nevertheless, by differential spectroscopy (Fig. S5a and S5b in Supplementary Material) and
21 a comparison with other [FeFe]-hydrogenases (Table 3) it is clear that the most intense signal at
22 1899 cm^{-1} can be assigned to the H_{red} state. This vibrational mode has been assigned to a shift of the
23 bridging CO to a terminal position in H_{red} of DdH [33] and has also been observed in other [FeFe]-
24 hydrogenases having a F-domain (such as CpI) [25]. However, this shift has not been observed in
25 enzymes lacking these accessory redox centers (such as CrHydA1) [35]. Also the signals at 2053
26 and 2040 cm^{-1} can be assigned to the H_{red} state and to the cyanide ligands, while the assignment of
27 the other signals remains ambiguous. Importantly, no signal was observed in the region around
28 1882-1883 cm^{-1} , which has been assigned to the H_{sred} state in DdH and CrHydA1 [34,35].

29 Treatment with CO generated an intense and homogeneous spectrum with six signals (2090, 2075,
30 2015, 1973, 1967, 1806 cm^{-1}) that are coherent with the expected peak shifts induced by the binding
31 of exogenous CO at the Fe_d in the H_{ox} -CO state. All the signals can be assigned by comparison with
32 the literature (Table 3) to the five endogenous ligands and the exogenous CO.

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Figure 5. FTIR spectra under steady-state conditions acquired at room temperature. Left) CaHydA WT. Right) CaHydA C298D. The same conditions were used for the two enzymes: “as purified” was only concentrated without further treatment; thionine oxidation; H₂ reduced; dithionite reduced; CO inhibited. Note that some spectra have been scaled by the coefficient indicated in parentheses. For the assignments of the wavenumber to the H_{ox} and H_{ox}-CO states compare with the data in table 3. **(2 columns fitting image).**

1 The spectrum of the “as purified” CaHydA C298D is more homogeneous than the WT (Fig. 5).
2 Also, the spectrum is almost identical after thionine oxidation, showing that the enzyme
3 spontaneously equilibrates into the H_{ox} state even in the presence of 2 mM dithionite. Concerning
4 the wavenumber of the signals, they are the same as the WT: the apparent small differences are not
5 of significant relevance, considering the experimental spectral resolution.

6 Reduction with H₂ caused a decrease of the H_{ox} signals and the increase of various other peaks
7 (2062, 2055, 2038, 1990, 1939, 1920, 1899 cm⁻¹). Reduction with dithionite caused a similar
8 behaviour and the complete disappearance of the 1800 cm⁻¹ peak. Under reducing conditions,
9 excluding the H_{ox} signals, the most intense peaks were 1939 and 1899 cm⁻¹, in the region of the
10 terminal COs, 2062 and 2038 cm⁻¹ in the CNs region. The wavenumbers of these signals are the
11 same as the WT, but the relative intensity is different especially in the CN region. Given the low
12 intensity of the signals, the assignment of the peaks to a specific redox state and ligand is
13 particularly difficult. Nevertheless, one interpretation is that the 1899 cm⁻¹ signal correlates to the
14 H_{red} state of the “semibridging” CO; by differential spectroscopy (Fig. S5c and S5d in
15 Supplementary Material) and similar to the WT, signals at 2055 and 2038 cm⁻¹ are assigned to CNs
16 (Table 3).

17 Also, it is remarkable that the intensity of the H_{red} peaks in comparison to the H_{ox} was much weaker
18 than in the WT; for example, the ratio between the 1899 cm⁻¹ (H_{red}) and the 1946 cm⁻¹ (H_{ox}) peaks
19 is 0.65 for the H₂-reduced WT and only 0.11 for the C298D. Considering also that the signals of the
20 H_{red} state are not present in the “as purified” state, these data suggest that the C298D mutant
21 displays a difference in the equilibrium between the H_{ox} and the H_{red} states, that might be caused by
22 a different mid-point redox potential of the transition and/or a difference in the balance between the
23 oxidation/reduction kinetics of the H-cluster.

24 Treatment with CO caused the typical peak shifts, but apparently only five signals could be
25 observed in the spectrum. However, a detailed analysis showed that the peak in the region 1960-
26 1970 cm⁻¹ was composed of two signals at 1970 cm⁻¹ and 1967 cm⁻¹. In comparison to the WT, the
27 cyanide and the bridging CO signals did not show a significant difference, while the region of the
28 terminal COs was influenced. The peaks assigned to Fe_d shifted significantly, from 2015 and 1973
29 (WT) to 2010 and 1970 (C298D) cm⁻¹, while the peak assigned to Fe_p-CO was unaffected: 1967 cm⁻¹.
30

31 On the basis of the FTIR results, it is clear that the C298D mutation does not cause changes in the
32 H-cluster geometry and environment when the enzyme is under its functional condition (*e.g.* the H_{ox}
33 and H_{red} states); however, when the enzyme is inhibited by CO and the free coordination of Fe_d is
34 occupied, slight modifications occur. These differences arise probably by the steric interaction of

- 1 the exogenous CO (a diatomic ligand) with the side chain of aspartic acid that is slightly bulkier
- 2 than that of cysteine and that has a different charge distribution.
- 3

1 **4. Discussion**

2 In this work, the *wild type* [FeFe]-hydrogenase CaHydA was characterized for the first time by
3 FTIR, CW and pulse EPR spectroscopies. Subsequently, the spectroscopic features of the WT
4 enzyme were compared to the C298D mutant, in order to investigate in details the effect of such
5 mutation on the H-cluster.

6 The characterisation of the WT enzyme showed features consistent with other [FeFe]-hydrogenases,
7 both in the case of EPR and FTIR spectroscopies. A clear assignment of the H_{ox} and H_{ox}-CO signals
8 was done, while given the presence of the accessory iron sulphur centers in the F-domain, the study
9 of the reduced states was more complicated and no EPR experiments have been performed on these
10 states.

11 The results presented here show that the electronic structure of the H-cluster is unaltered in the
12 C298D mutant, as observed in CW and pulse EPR experiments, and that the vibrational modes of
13 the CO and CN ligands are substantially unaffected, as observed in FTIR experiments. Remarkably,
14 the signal positions were the same in the WT and C298D mutant in most redox states. The only
15 significant difference in terms of signal position could be observed in the H_{ox}-CO state in FTIR
16 spectra: the peaks assigned to the terminal COs are shifted to lower wavenumbers in C298D. This
17 shift is probably caused by hindrance between the CO_{exo} and the side chain of aspartic acid, also
18 affecting the adjacent Fe_d-CO and its interactions with the surrounding protein framework. This
19 spectroscopic difference was only observed when the sixth coordination of Fe_d was occupied by
20 exogenous CO; in this situation the difference in size and charge distribution between the side
21 chains of cysteine (WT) and aspartic acid (C298D) becomes evident. This suggests that, even upon
22 exogenous CO treatment, there is no structural change in the C298D mutant, but only fine
23 modifications in the vibrational properties of the CO ligands occur.

24 The effects of mutations in the close proximity of the H-cluster have been spectroscopically studied
25 only in few other cases [21,37]. In both cases the homologue of cysteine 298 was studied in
26 CrHydA1: the mutation C169S, where cysteine was replaced by serine, a non-ionisable residue,
27 caused either complete loss of activity [37] or an important activity decrease (30-40 fold) [21]. In
28 both works the impairment of the proton transfer pathway to the H-cluster caused several
29 spectroscopic differences in comparison to the WT, including the shift of the spectroscopic signals
30 to other positions and the alteration of the steady-state equilibrium of the H-cluster.

31 In contrast, given the high catalytic activity of our C298D mutant (cysteine replacement with
32 aspartic acid, an ionisable residue where the activity decrease was only 2 fold), the spectral
33 differences in comparison with the WT enzyme were very small.

1 The replacement of cysteine with non-ionisable residues, such as serine, leads to impairment in the
2 proton transfer and severely alters the catalysis by affecting the H-cluster reactivity [21], while the
3 replacement with an ionisable residue, such as aspartic acid, can sustain catalytic activity at high
4 rates because the proton transfer kinetics are influenced very little [40]. In fact, we did not observe
5 the accumulation of a reduced intermediate with terminally bound H-species that slows down and
6 prevents CO binding at the H-cluster; such an intermediate was suggested for the homologous
7 serine mutant where the proton exchange between the H-cluster and the protein was severely altered
8 [21].

9 A small impairment of optimal proton transfer kinetics is also expected in our experimental
10 condition due to aspartic acid replacement and accounting for the decreased rates of enzyme
11 activity. Although less pronounced than in the serine mutant the signature of this altered proton
12 transfer is observed as an imbalance between the H_{ox}/H_{red} states, as the H_{red} signals in the FTIR
13 spectra of the C298D mutant were proportionally lower than in the WT even when reductive
14 treatments were applied. In the future, the determination of the mid-point potential of the two
15 proteins might contribute to interpret this difference.

16 The very precise and fine tuning of the redox and kinetic equilibria in the hydrogenase catalytic
17 cycle are clearly matching the stringent requirement selected by evolution of cysteine at position
18 298 (or homologous): although aspartate was demonstrated here to be a good substitute both in
19 terms of structural integrity and of activity of the cluster, there is no evidence to date of any natural
20 [FeFe]-hydrogenase [1,26] displaying such aminoacid at the key position for proton transfer
21 between the H-cluster and the protein moiety.

22 23 **5. Conclusions**

24 In conjunction with previous works [21,37,39,40], our data enhance the importance of considering
25 the H-cluster and its protein environment as a dynamic inseparable system that synergistically
26 cooperates for an efficient and fast catalytic mechanism. The results presented here are required for
27 the understanding of the [FeFe]-hydrogenases function in the perspective of an improvement for the
28 exploitation in biotechnological applications [62,63], but also they must be considered when
29 designing bio-inspired catalysts and mimics [26,63-67].

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6

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1 **Tables and captions:**

2

3 **Table 1.** Spin-Hamiltonian parameters of the H_{ox} and H_{ox-CO} states of H-cluster extracted by the
 4 computer simulations of the CW EPR spectra reported in Figure 3 in comparison with selected data
 5 from the literature.

6

Enzyme	H_{ox} state			H_{ox-CO} state			Ref.
	g^1	g^2	g^3	g^1	g^2	g^3	
CaHydA WT	2.0892 ± 0.0005	2.0360 ± 0.0005	1.9954 ± 0.0005	2.0750 ± 0.0005	2.007 ± 0.005	2.007 ± 0.005	This work
CaHydA C298D	2.0892 ± 0.0005	2.0360 ± 0.0005	1.9954 ± 0.0005	2.0750 ± 0.0005	2.007 ± 0.005	2.007 ± 0.005	This work
CaHydA	nd	nd	nd	2.075	2.009	2.009	53
CpI	2.098	2.040	2.001	2.074	2.011	2.011	55
CpHydA	2.0892	2.0363	1.9954	2.0755	2.008	2.008	56
	2.10	2.04	2.00	2.06	2.00	2.00	52
DdH	2.100	2.040	1.998	2.065	2.007	2.001	51
	2.100	2.040	1.997	2.065	2.007	2.001	17
	2.102	2.040	1.998	2.052	2.007	2.007	54
CrHydA1	2.10	2.037	1.996	2.052	2.007	2.007	19
	2.100	2.039	1.997	2.045	2.007	2.007	20
CsHydA	2.100	2.040	1.998	2.056	2.008	2.008	54
CmHydA1	2.103	2.038	1.998	2.050	2.008	2.008	54

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1 **Table 2.** ^{14}N and ^1H hyperfine and quadrupole couplings deduced from the simulation analysis of
2 the HYSCORE spectra of the H_{ox} and $\text{H}_{\text{ox}}\text{-CO}$ states of H-cluster for both the thionine oxidized WT
3 CaHydA protein and the C298D mutant of Figure 4. The computer simulations are reported in
4 Figures S3 and S4 of the Supplementary Material section. The coupling constants are given in
5 MHz, the Euler angles are in degree. Comparison is made with the signals reported in the literature
6 for other hydrogenases.

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	Species	H-cluster state	A_x	A_y	A_z	α, β, γ	e^2qQ/h	η	α', β', γ'	Ref.
^{14}N	CaHydA	H_{ox}	1.5 ± 0.1	3.9 ± 0.1	-0.4 ± 0.1	$30 \pm 10, 30 \pm 10, 0 \pm 10$	3.7 ± 0.1	0.3 ± 0.05	$0 \pm 10, 40 \pm 10, 0 \pm 10$	This work
^{14}N (CN at Fe _d)		H_{ox}	1.5	3.8	-0.4	41, 34, 0	3.84	0.34	-26, 24, 0	
^{14}N (DTMA)	DdH	H_{ox}	1.0	1.9	1.4	40, 25, 0	4.92	0.13	10, 0, 0	17
^{14}N (Lys)		H_{ox}	-2.4	1.4	-0.7	0, 4, 20	1.44	0.80	147, 56, 0	
^{14}N (CN at Fe _d)	CpI	H_{ox}	0.6	4.5	-0.8	45, -20, 0				29
^{14}N	CaHydA	$\text{H}_{\text{ox}}\text{-CO}$	0.4 ± 0.1	-0.2 ± 0.1	0.6 ± 0.1	$20 \pm 10, -10 \pm 10, 0 \pm 10$	3.3 ± 0.1	0.6 ± 0.1	$50 \pm 20, 50 \pm 20, 0 \pm 10$	This work
^{14}N (CN at Fe _d)	DdH	$\text{H}_{\text{ox}}\text{-CO}$	0.4	-0.2	0.56	0, -10, 0	3.04	0.64	0, 30, 0	30
^1H	CaHydA	$\text{H}_{\text{ox}}\text{-CO}$	-2.5 ± 0.2	-2.5 ± 0.2	9.5 ± 0.5	$0 \pm 10, 80 \pm 10, 0 \pm 10$	-	-	-	This work
			-2.0 ± 0.2	-2.0 ± 0.2	5.0 ± 0.2	$0 \pm 10, 80 \pm 10, 0 \pm 10$	-	-	-	

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1 **Table 3.** Summary of FTIR wavenumbers of CaHydA WT and C298D in comparison with other
 2 [FeFe]-hydrogenases from the literature in various redox states.

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Enzyme	H_{ox} state				Ref.	
	CNs	Fe _p -CO	Fe _d -CO	μ -CO		
CaHydA WT	2082, 2070	1969	1946	1801	This work	
CaHydA C298D	2081, 2070	1970	1946	1800	This work	
CpI	2086, 2072	1971	1948	1802	61	
CpHydA	2087, 2080	1968	1944	1800	56	
DdH	2093, 2079	1965	1940	1802	34	
CrHydA1 WT	2088, 2072	1964	1940	1800	35	
Enzyme	H_{ox} -CO state					Ref.
	CNs	Fe _p -CO	Fe _d -CO	CO _{exo}	μ -CO	
CaHydA WT	2090, 2075	1967	1973	2015	1806	This work
CaHydA C298D	2089, 2077	1967	1970	2010	1807	This work
CpI	2095, 2077	1971	1974	2017	1810	61
CpHydA	2091, 2088	1967	1971	2013	1806	56
DdH	2096, 2088	1963	1971	2016	1810	34
CrHydA1 WT	2092, 2084	1964	1970	2013	1810	35
Enzyme	H_{red} state		COs	Ref.		
	CNs					
CaHydA WT	2053, 2040		1899	This work		
CaHydA C298D	2055, 2038		1899	This work		
CpHydA	2066, 2039		1897	56		
DdH	2079, 2041		1965, 1916, 1894	34		
CrHydA1 WT	2083, 2070		1935, 1891, 1793	35		

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