

Electronic Supporting Information

EPR-derived structures of flavin radical and iron-sulfur cluster from

Methylosinus sporium 5 reductase

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Supplementary Schemes

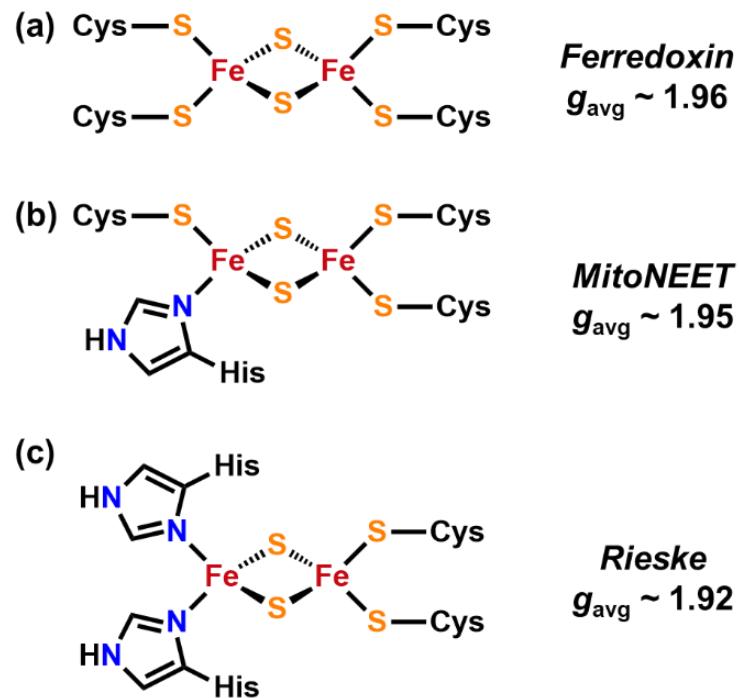
Scheme S1. Alignment of amino acids from ferredoxin domain of sMMO. Gray and red color represent identical and different amino acids, respectively.

Identity / Similarity	
<i>Methylosinus sporium</i> 5	001 MYQIVIETEDGETCSFECGPSEDVISAGLRQSVILLASCRAGGCATCKADCTDGEYEILDVKVQALPPDEEEEDGKVLLCR 080
<i>Methylocystis species</i> M	001 MYQIVIETEDGETCSFECGPSEDVISAGLRQSVILLASCRAGACATCKADCTDGEYEILDVKVQALPPDEEEEDGKVLLCR 080
<i>Methylosinus trichosporium</i> OB3b	001 MYQIVIETEDGETCR-RMRPSEDWISRAEAEARN-LLASCRAG-CATCKADCTDGEYEILDVKVQAVPPDEEEEDGKVLLCR 077
<i>Methylococcus capsulatus</i> Bath	004 VHTITAVTEDGEESLRFECRSDEDVITAALRQNIFLMSSCREGGCATTAKALCSEGDYDLKGCSVQALPPEEEEGLVLLCR 083
<i>Methylovulum miyakonense</i> HT12	005 -HQVITIVTEDHESITFCRSDEDVITAARQDIYLMSSCREGGCATTCKGYCSEGDYVIGKVSQAQALPSQEEEEMVLLCR 083
	081 TFPRLSDLHLIVPYTYD 096
	081 TFPRLSDLHVVPYTYD 096
	078 TFPRLSDLHLVPYTYD 093
	084 TYPKTDLEIELPYTHC 099
	084 CYPPTTDIEVEVPYTYE 099

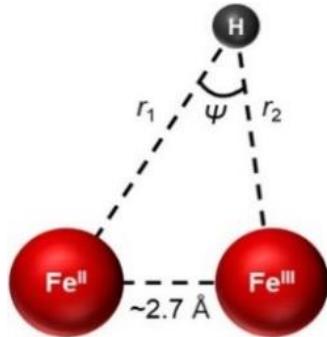
Scheme S2. Alignment of amino acids from FAD binding domain of sMMO. Gray and red color represent identical and different amino acids, respectively.

Identity / Similarity	
<i>Methylosinus sporium</i> 5	057 RISFEAIQTNWLAIEIVECDRVSSNNVRLQLTADGAAPISLNFPAGQFVDIEIPGHTRRSYSMASVAE-DGRLEFFI 175
<i>Methylocystis species</i> M	057 RISFQAQTNWLAIEITECDRVSSNNVRLVILQPLTADGAAPISLNFLPGQFVDIEIPGHTTRRSYSMASVAE-DGRLEFFI 175
<i>Methylosinus trichosporium</i> OB3b	054 RISFEAIQTNWLAIEILACDRVSSNNVRLVQ-RSRPMAARISLNFPAGQFVDIEIPGHTTRRSYSMASVAE-DGQLEFFI 171
<i>Methylococcus capsulatus</i> Bath	100 RISFGEVGS-FEAEVVGLNWVSSNTVQFLLQK-RPDECGRNGVKFEPGQFMDLTIPGTDVSRSYSPANLPNPEGRLEFFI 177
<i>Methylovulum miyakonense</i> HT12	100 RISFSPEGMDFEAEVVGLQEIQISINVVKFQLRRTGDDK---TIKFEAGQFFDIEIPGTETTRSYSPANISNSQGDLEFFI 175
	176 RLLPDGAFSNYLRLTQASVGQRVALRGPAGSFFLH-KSE-RPRFFVAGGTGLSPVLSMIRQLKEADPQPATLFFGVNTYE 253
	176 RLLPDGAFSNYLRLTQARVGQRVALRGPAGSFSLH-KSE-RPRFFVAGGTGLSPVLSMIRQLKEADPQPATLFFGVNTYE 253
	172 RLLPDGAFSKFLQTEAKVGMRVDLRGPGASFFLHDHGG-RSRVFAAGGTGLSPVLSMIRQLKAADPSPATILLFGVNTRE 250
	178 RVLPAGEGRFSNDLARVGQVLSVKPLGVFGLKERGM-APRYFAAGGTGLAPVVSMVRQMQEWTAPETRIYFGVNTEP 256
	176 RIVDGGKFSEFLKEAKVQORLAKAKPGSGVFGLK-ENGFTPRYFAAGGTGLAPILSMVRHMKEWGPQKCVTFGVNTREA 254
	254 ELYFVEELRALQKAMPSLDVQAVVNATEANGVAKGTVIDLMLRAELEKLRGAPDIYLCGPPGMIEAAAFDAATAGVPKEQ 333
	254 ELYFVDELKALQHAMPSLDVQIAVNVSSEGNGVAKGTVIDLQDELGRRAEKPDYILCGPPGMIDAAFAAASSAGVPKEQ 333
	251 ELYFVDELKTLAQSMPTLGVRIAVNNDGGNGVDKGTVIDLRAELEKSDAKPDYILCGPPGMIEAAFAAAATAGVPKEQ 330
	257 ELYFIIDELKSLERSMRNLTVKACVWHPSGDWEGEQGSPIDADREDLESSDANPDYILCGPPGMIDAACELVRSRGTPGEQ 336
	255 EIFHLDLEQIQAQMPTELRCNCVWKCSDDWHCEKGSVVDIIRRDLVETGAKPDLYLCGPPGMVDATFAVCADLGIPKER 334
	334 VYLEKFLASG 343
	334 VYLEKFLASG 343
	331 VYLEKFLASG 340
	337 VFEEKFLPSG 346
	335 IYLEKFLPSG 344

Scheme S3. The schematic drawing of three types of [2Fe-2S]⁺ clusters. (a) Ferredoxin, (b) MitoNEET, and (c) Rieske-type.



Scheme S4. Schematic representation of a proton positioned nearly from the Fe^{II} and Fe^{III} ions of the [2Fe-2S]⁺ cluster.



To estimate the position of the proton from the [2Fe-2S]⁺ cluster, the dipolar hyperfine coupling value of A_{dip} is used by considering the spin projection factor of the respective nucleus. The spin projection factors of two metal atoms, p_A and p_B , are given as follows:

$$p_A = \frac{S(S+1) + S_A(S_A+1) - S_B(S_B+1)}{2S(S+1)}$$

$$p_B = \frac{S(S+1) - S_A(S_A+1) + S_B(S_B+1)}{2S(S+1)}$$

where S is total spin of the cluster, and S_A and S_B are the local spin of each metal atom.^{S1,S2} The spin projection factors of Fe(II) ($S_A = 2$) and Fe(III) ($S_B = 5/2$) of the [2Fe-2S]⁺ cluster are $-4/3$ (p_A) and $+7/3$ (p_B), respectively. Thus, A_{dip} can be calculated by equations as follows:

$$A_{\text{dip}} = c \left(-\delta, -\Gamma + \frac{\delta}{2}, \Gamma + \frac{\delta}{2} \right)$$

$$\delta = p_A r_1^{-3} + p_B r_2^{-3}$$

$$\Gamma = \frac{3}{2} \sqrt{p_A^2 r_1^{-6} + p_A p_B r_1^{-3} r_2^{-3} \cos 2\psi + p_B^2 r_2^{-6}}$$

where c is $g_{\text{eff}} \mu_{\text{e}} g_{\text{N}} \mu_{\text{e}}$ and equals 79 MHz Å³ for a proton, and geometrical parameters r and ψ are defined in **Scheme S3**.^{S3,S4} From the equation, the distances between the iron ions and the exchangeable proton are estimated to be $r_1 = 4.1\text{-}4.4$ and $r_2 = 3.50\text{-}3.60$ Å with $\psi \sim 40^\circ$. The distance between the Fe^{II} and Fe^{III} centers can also be calculated in accordance with the law of cosines and was estimated to be ~2.7 Å.^{S5}

Supplementary Tables

Table S1. The simulation parameters for ^1H Davies ENDOR spectra of the [2Fe-2S] $^+$ cluster.

	$A(^1\text{H})$ (MHz)	$[\alpha, \beta, \lambda]$ ($^\circ$)
Exchangeable proton	$[6.15 \pm 0.35, -3.50 \pm 0.15, -2.90 \pm 0.15]$	$[30, 90, 50]$
Non-exchangeable proton	$[2.32 \pm 0.12, 11.70 \pm 0.20, 1.58 \pm 0.08]$	$[80, 30, 90]$

Table S2. Simulation parameters for ^{14}N three-pulse ESEEM and HYSCORE spectra of the [2Fe-2S] $^+$ cluster.

	N ₁	N ₂
$A(^{14}\text{N})$ (MHz)	[1.2, 1.2, 1.2]	[0.9, 0.6, 0.6]
$A_{\text{iso}}(^{14}\text{N})$ (MHz)	1.2	0.7
$e^2 q Q / h$ (MHz)	3.4	3.0
η	0.4	0.9
$[Q_\alpha, Q_\beta, Q_\gamma]$ ($^\circ$)	[-75, 100, 60]	[0, 90, 0]

Table S3. The reported hyperfine and quadrupole coupling parameters of ^{14}N s coupled to the $[2\text{Fe}-2\text{S}]^+$ cluster.

	A_{iso} (MHz)	e^2qQ/h (MHz)	Refs.
Rieske or Rieske-type			
bc1 (bovine)	3.55	2.25	S6
	5.20	2.93	
bc1 (bovine) + UHDBT	3.40	2.30-2.65	
	5.30	2.60-3.00	
<i>Cytochrome b6f</i> (spinach)	4.58	2.70	S7
	3.75	2.70	
<i>Burkholderia cepacia</i>	3.70	2.15	S8
	4.70	3.85	
<i>B. cepacia</i> AC 1100	3.87	2.40	S9
	4.90	2.32	
<i>Pseudomonas putida</i>	3.56	2.43	S10
	4.78	2.31	
<i>Pseudomonas cepacia</i>	4.28	2.60	S9
	5.49	2.30	
2,4,5-Trichlorophenoxyacetate Monooxygenase	3.40	2.36	S11
	5.10	2.52	
Ferredoxin or ferredoxin-type			
<i>P. putida</i>	1.11	3.27	S10
<i>Clostridum pasteurianum</i>	0.61	3.29	S12
<i>Arum maculatum</i>	1.10	3.32	S6
<i>Spirulina platensis</i>	1.01	3.52	S6
<i>E. coli</i> (reduced)	1.06	3.41	S6
<i>E. coli</i> (oxidized)	1.10	3.30	S13
<i>Porphyra umbilicalis</i>	1.16	3.24	S14
	0.40	3.04	
<i>Yarrowia lipolytica</i>	0.90	3.10	S15
<i>Adrenodoxin</i>	1.05	3.10	S16
	0.65	2.90	
<i>Arthrosphaera plantensis</i> ferredoxin	1.16	3.10	
	0.72	2.90	

Table S4. Cartesian coordinates for the optimized geometries.

(a) Neutral flavin radical

N	-2.414300	-0.002840	-0.350910
C	-3.462390	-0.897250	-0.246360
O	-4.627580	-0.565660	-0.307690
N	-3.138700	-2.262240	-0.051520
C	-1.874220	-2.791590	0.086793
O	-1.632360	-3.978330	0.277746
C	-0.837230	-1.785230	-0.022260
N	0.456424	-2.186840	0.095316
C	1.504528	-1.294860	0.027977
C	2.828325	-1.711820	0.191791
C	3.887589	-0.817000	0.124517
C	5.303507	-1.301680	0.305671
C	3.605500	0.547178	-0.111610
C	4.717485	1.562933	-0.185910
C	2.283268	0.960011	-0.273760
C	1.208267	0.066410	-0.215640
N	-0.127170	0.473334	-0.397930
C	-1.171850	-0.432620	-0.255420
C	-0.439600	1.848180	-0.819620
C	-0.571960	2.888741	0.313996
O	-0.743920	4.156021	-0.303730
C	-1.747170	2.618377	1.259150
O	-2.972070	2.721223	0.552885
H	-1.750510	3.397190	2.026123
H	-1.641730	1.648105	1.758025
H	-1.694010	4.220592	-0.481240
H	0.356189	2.936861	0.893044
H	-1.381320	1.807795	-1.363370
H	0.331908	2.182590	-1.512290
H	4.326743	2.563902	-0.372580
H	5.424233	1.324163	-0.987180
H	5.292986	1.596094	0.744891
H	5.331793	-2.378230	0.479685
H	5.916107	-1.088840	-0.576160
H	5.789284	-0.812210	1.155769
H	2.093608	2.010381	-0.442460
H	3.018837	-2.764480	0.374478
H	0.599304	-3.178510	0.258702
H	-3.923420	-2.896660	0.021065
H	-3.120640	1.856585	0.129258

(b) Anionic flavin radical

N	-2.393210	0.005143	-0.330220
C	-3.448690	-0.864050	-0.246410
O	-4.622990	-0.512970	-0.312350
N	-3.136460	-2.216060	-0.069330
C	-1.870250	-2.794930	0.079038
O	-1.761710	-4.001410	0.255585
C	-0.783340	-1.820840	-0.010800
N	0.493493	-2.261470	0.116041
C	1.470644	-1.329430	0.038786
C	2.819761	-1.727500	0.190895
C	3.885654	-0.841370	0.122710
C	5.300808	-1.342940	0.294573
C	3.623364	0.525053	-0.105480
C	4.742748	1.535137	-0.182030
C	2.294739	0.946729	-0.259690
C	1.221315	0.057218	-0.199190
N	-0.113000	0.461644	-0.372360
C	-1.147640	-0.470040	-0.234840
C	-0.425130	1.816773	-0.823720
C	-0.560970	2.884238	0.281675
O	-0.825780	4.136787	-0.353690
C	-1.690840	2.586511	1.271689
O	-2.940450	2.625999	0.602347
H	-1.700620	3.376591	2.029453
H	-1.529180	1.625828	1.773354
H	-1.782440	4.114978	-0.507490
H	0.383766	2.994508	0.823344
H	-1.369170	1.768735	-1.363740
H	0.347130	2.142130	-1.523370
H	4.351766	2.538702	-0.364540
H	5.450330	1.305212	-0.988450
H	5.328536	1.573263	0.744996
H	5.310111	-2.421890	0.461970
H	5.918142	-1.136970	-0.588030
H	5.802444	-0.868950	1.146720
H	2.112575	2.001270	-0.423490
H	2.984989	-2.785440	0.364386
H	-3.921760	-2.848300	-0.004520
H	-3.028010	1.744914	0.171956

Supplementary Figures

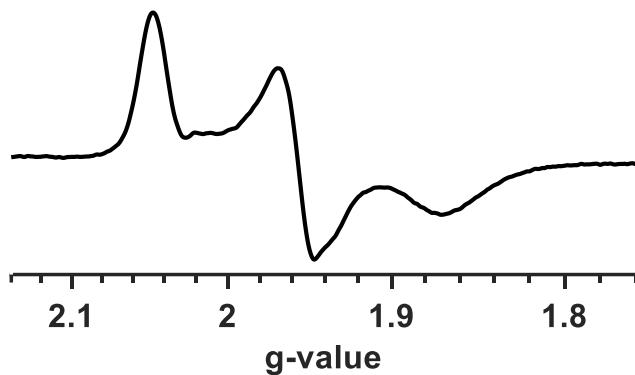


Fig. S1 X-band CW-EPR spectrum of the reduced MMOR after addition of $\text{Na}_2\text{S}_2\text{O}_4$ measured at 35 K. The experimental conditions: microwave frequency = 9.64 GHz, microwave power = 1 mW, modulation amplitude = 10 G, modulation frequency = 100 kHz, time constant = 40.96 ms.

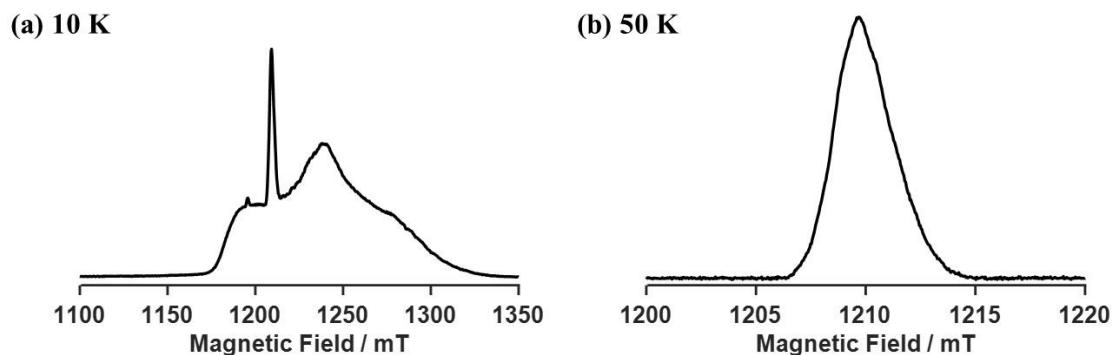


Fig. S2 Q-band ESE spectra of reduced MMOR at different temperatures. The experimental conditions: microwave frequency = 33.9 GHz, microwave power = 10 dB, pulse sequence = $\pi/2(32 \text{ ns}) - \tau - \pi(64 \text{ ns})$, $\tau = 300 \text{ ns}$, temperature = (a) 10 K, (b) 50 K.

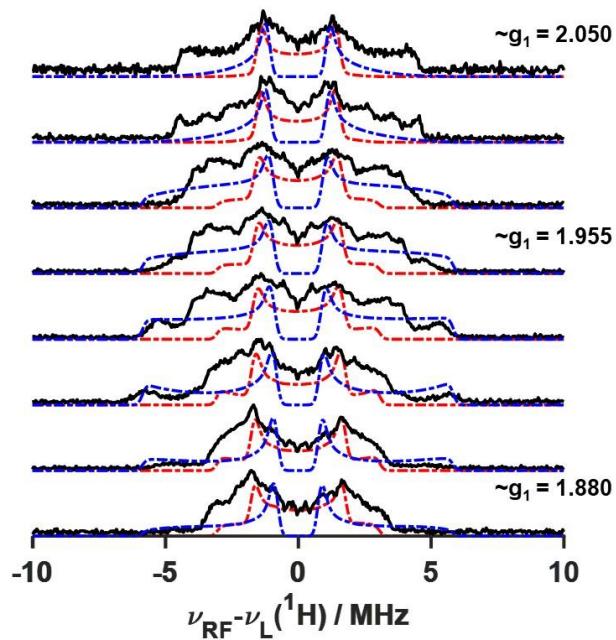
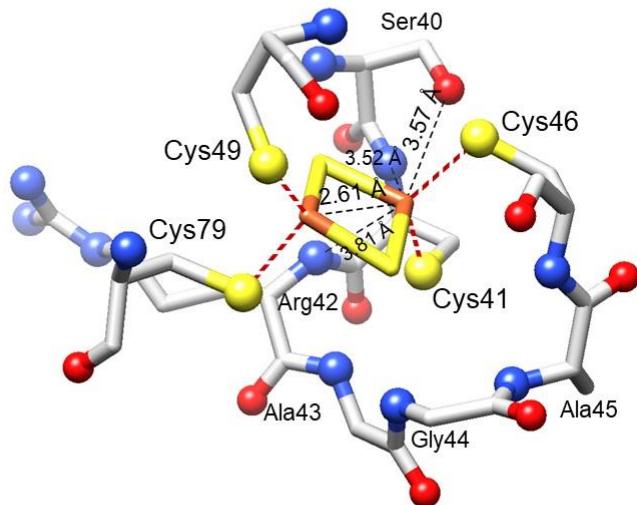


Figure S3. Q-band ^1H Davies ENDOR of $[2\text{Fe}-2\text{S}]^+$ cluster in MMOR (black line) and simulated spectra (dashed red line: exchangeable proton, dashed blue line: non-exchangeable proton). The simulation parameters are shown in table S1. The experimental conditions: microwave frequency = 33.9 GHz, $\pi/2$ = 32 ns, τ = 300 ns, RF length = 20 μs , temperature = 10 K.

(a)

<i>Methylosinus sporium</i> 5	³⁹ SCRAGGCATC...L ⁸⁰ CR
<i>Anthrospira platensis</i>	⁴⁰ SCRAGACSTC...T ⁷⁹ CV

(b)



Anthrospira platensis

PDB ID: 4FXC

Figure S4. (a) Amino acid sequences of residues located around the [2Fe-2S]⁺ cluster of *Methylosinus sporium* 5 and *Anthrospira platensis*, and the immediate environment of the [2Fe-2S]⁺ cluster of the ferredoxin of (b) *Anthrospira platensis* with selected bond distances of Fe-Fe and proximal H...Fe. Note that the positions of protons in the ferredoxin domain of *Anthrospira platensis* were not well resolved by X-ray crystallography. Color code: orange, Fe; yellow, S; red, O; blue, N; gray, C; white, H.

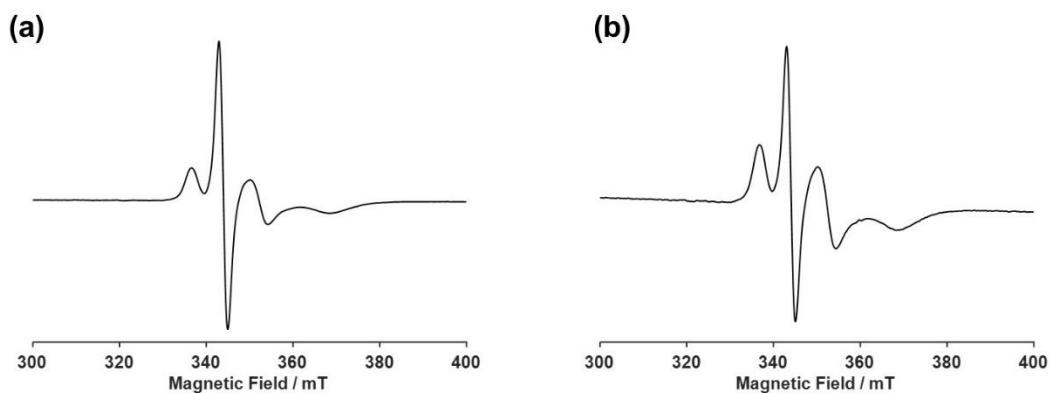


Figure S5. CW-EPR spectra of MMOR (a) and MMOR+MMOB (b). The experimental conditions: microwave frequency = 9.64 GHz, microwave power = 1 mW, modulation amplitude = 10 G, modulation frequency = 100 kHz, time constant = 40.96 ms, temperature = 35 K.

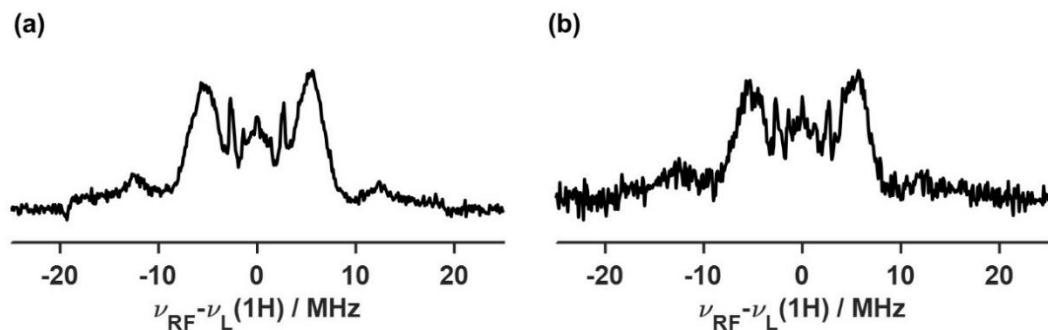


Figure S6. 34 GHz ¹H Davies ENDOR of neutral flavin radical species in (a) MMOR and (b) MMOR+MMOB. The experimental conditions: microwave frequency = 33.9 GHz, Pulse sequence = 64 ns-32 ns-64 ns ($\pi-\pi/2-\pi$), τ = 300 ns, RF length = 20 μ s, temperature = 50 K.

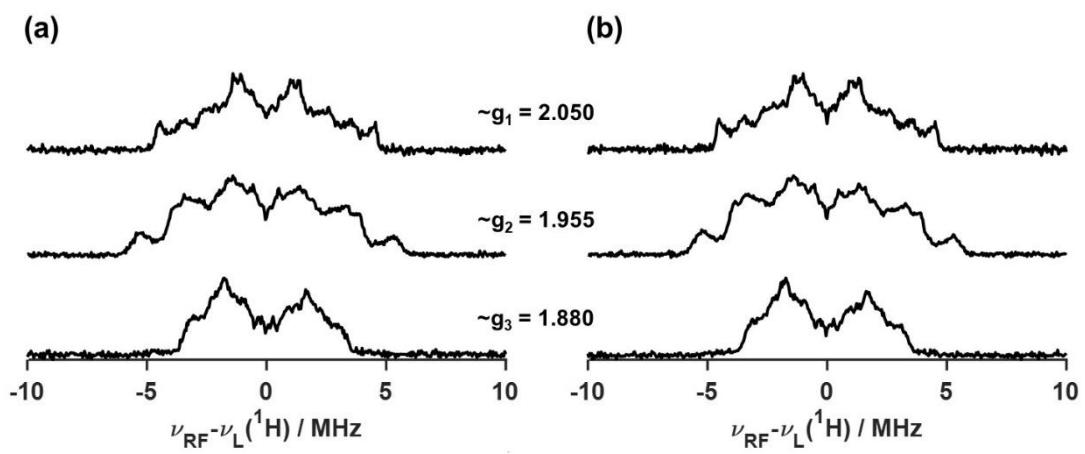


Figure S7. 34 GHz ^1H Davies-ENDOR of $[2\text{Fe}-2\text{S}]^+$ cluster in (a) MMOR and (b) MMOR+MMOB. The experimental conditions: microwave frequency = 33.9 GHz, $\pi = 64$ ns, $\pi/2 = 32$ ns, $\tau = 300$ ns, RF length = 20 μs , temperature = 10 K.

References

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