Supporting Information

Biochemical, mechanistic, and spectroscopic characterization of metallo-β-lactamase VIM-2

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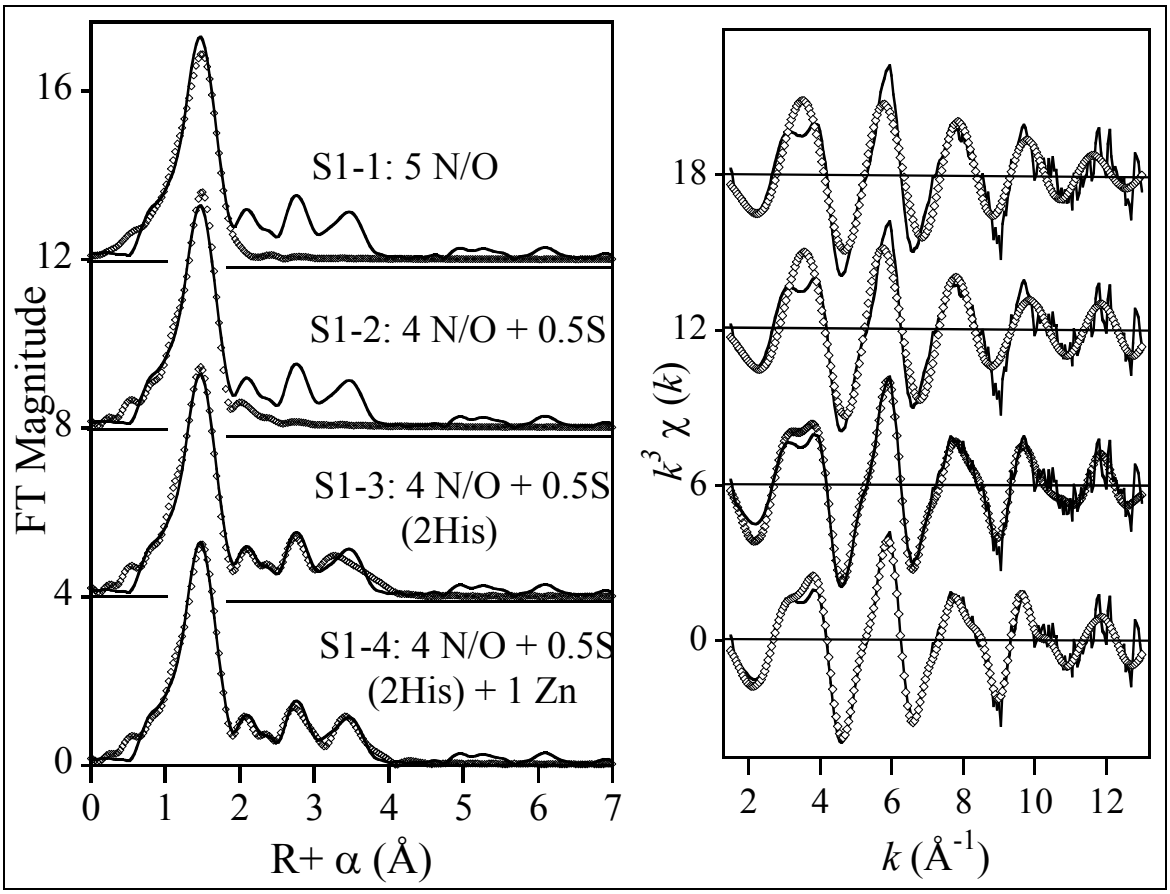

Figure S1. Fourier transforms (A) of Zn *K*-edge EXAFS (B) for as isolated (LB) VIM-2 (0.5 Zn). The solid lines represent the data, the open symbols represent the various fits, corresponding to **Table S1**.

Table S1. Fitting results for Zn *K*-edge EXAFS of as isolated (LB) VIM-2.[a]

Fit	Model	Zn-N/O	Zn-S	Zn-His[b]	Zn-Zn	R_f[c]	R_u[c]
S1-1	5 N/O	2.00 (7.1)				87	186
S1-2	4 N/O + 0.5 S	2.01 (4.7)	2.28 (4.1)			33	165
S1-3	4 N/O (2His) + 0.5S	2.00 (4.8)	2.27 (4.9)	2.91(3.4) 3.15(1.5) 4.13(23) 4.42(13)		39	57
S1-4	4N/O(2His)+ 0.5S+Zn-Zn	2.00 (4.9)	2.28 (6.0)	2.94(5.6) 3.23(8.5) 4.14(9.3) 4.41(18)	3.36(9.2)	18	48

[a] Distances (Å) and disorder parameters (in parentheses, σ^2 (10^{-3} Å^2)) shown derive from integer or half-integer coordination number fits to filtered EXAFS data [Δk = 1.5-13 Å^{-1}; ΔR = 0.5 – 2.2 Å (fits 1-2), 0.3-4.0 Å (fits 3-4)].

[b] Imidazole multiple scattering paths represent combined paths, as described previously (see Materials and Methods).

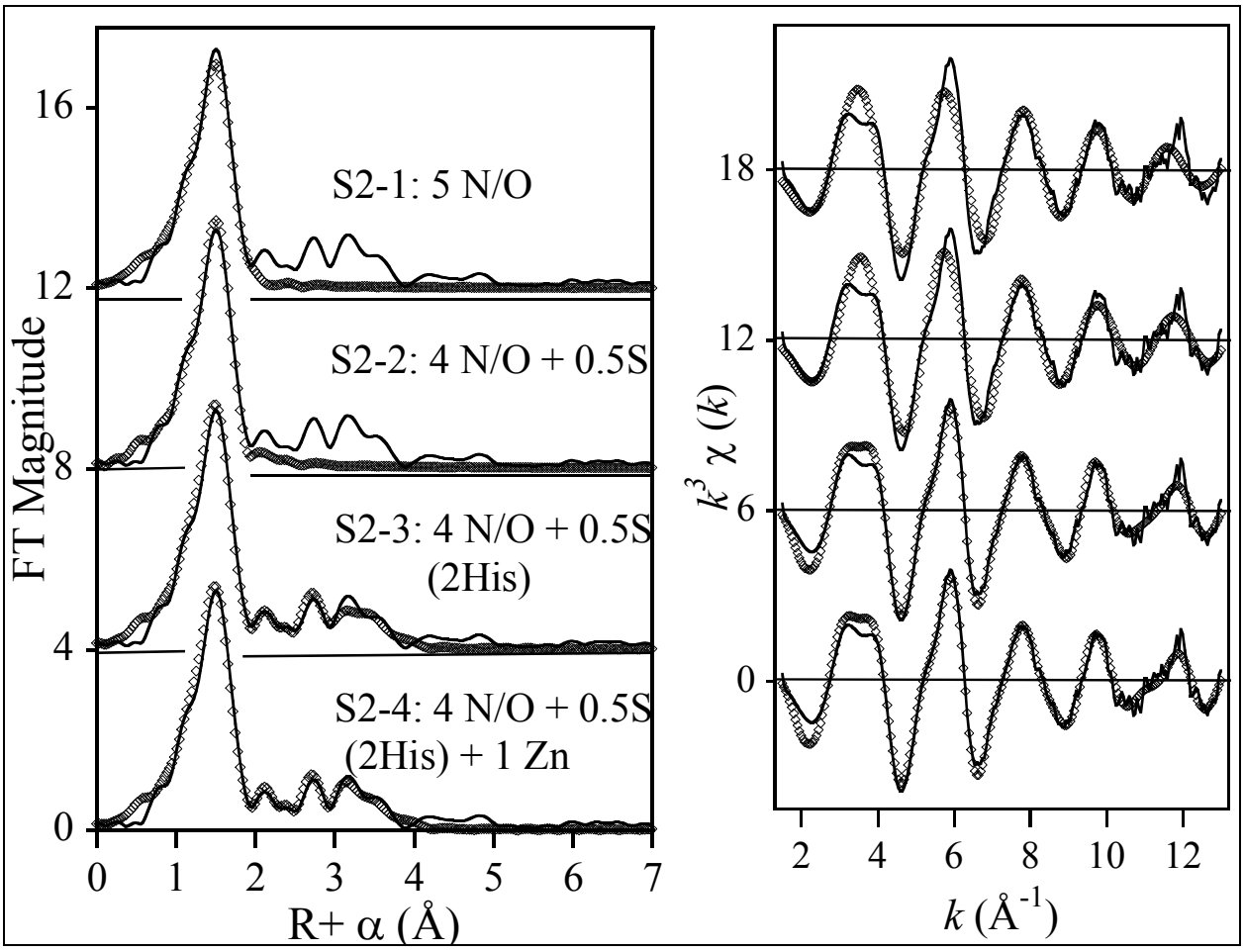

Figure S2. Fourier transforms (A) of Zn K-edge EXAFS (B) for 1Zn-VIM-2. The solid lines represent the data, the open symbols represent the various fits, corresponding to **Table S2.**

Table S2. Fitting results for Zn *K*-edge EXAFS of 1Zn-VIM-2.[a]

Fit	Model	Zn-N/O	Zn-S	Zn-His[b]	Zn-Zn	R_f[c]	R_u[c]
S2-1	5 N/O	2.01 (6.9)				46	119
S2-2	4 N/O + 0.5 S	2.00 (4.9)	2.27 (5.4)			14	103
S2-3	4 N/O (2His)+ 0.5S	2.00 (5.1)	2.27 (6.5)	2.89(6.0) 3.11(3.7) 4.10(19) 4.40(16)		22	34
S2-4	4N/O(2His)+ 0.5S+Zn-Zn	2.00 (5.2)	2.27 (6.6)	2.88(6.1) 3.10(2.8) 4.05(28) 4.40(15)	3.37(15)	17	30

[a] Distances (Å) and disorder parameters (in parentheses, σ^2 (10^{-3} Å^2)) shown derive from integer or half-integer coordination number fits to filtered EXAFS data [Δk = 1.5-13 Å^{-1}; ΔR = 0.5 – 2.2 Å (fits 1-2), 0.3-4.0 Å (fits 3-4)].

[b] Imidazole multiple scattering paths represent combined paths, as described previously (see Materials and Methods).

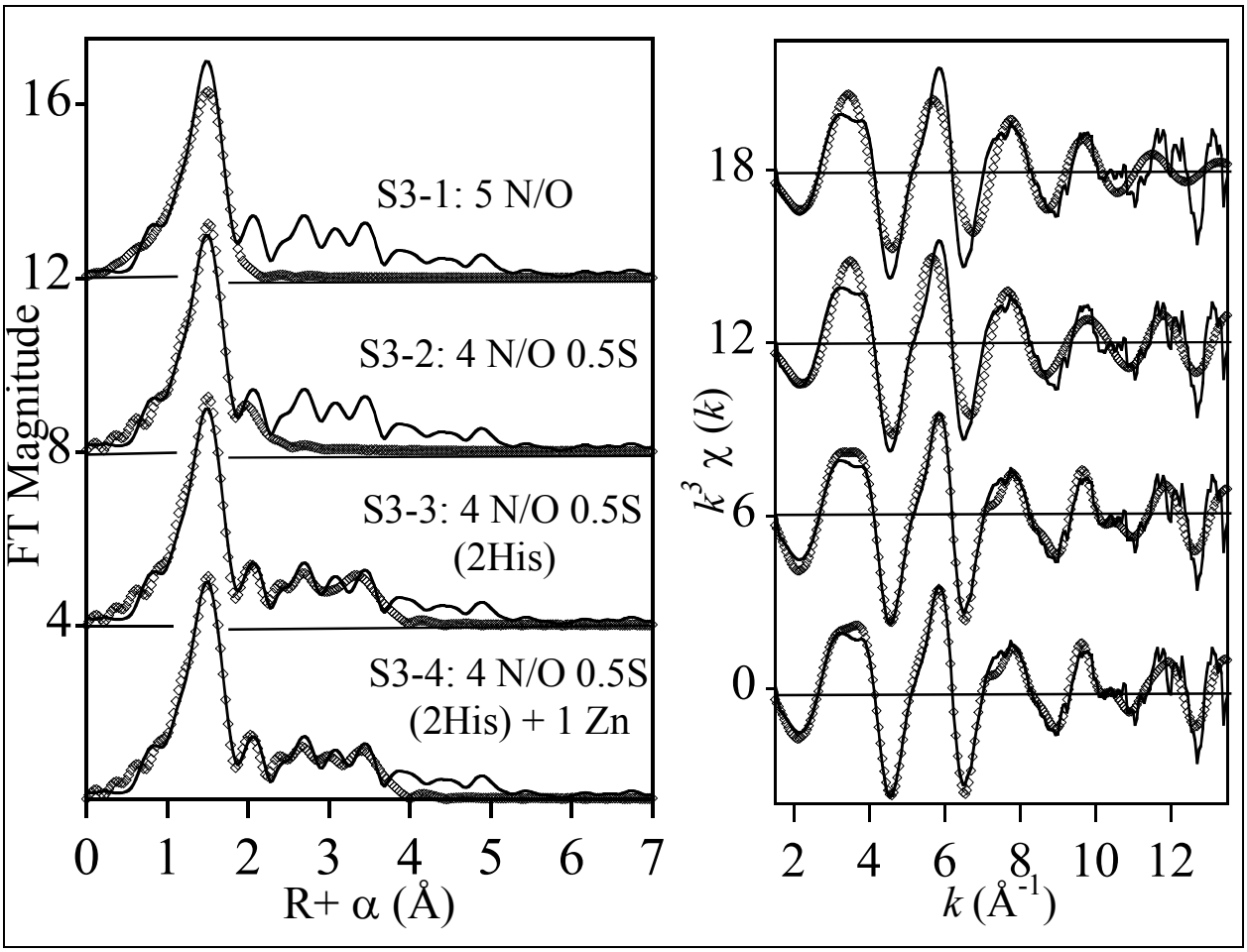

Figure S3. Fourier transforms (A) of Zn K-edge EXAFS (B) for 2Zn-VIM-2. The solid lines represent the data, the open symbols represent the various fits, corresponding to **Table S3.**

Table S3. Fitting results for Zn *K*-edge EXAFS of 2Zn-VIM-2.[a]

Fit	Model	Zn-N/O	Zn-S	Zn-His[b]	Zn-Zn	R_f[c]	R_u[c]
S3-1	5 N/O	2.02 (7.4)				127	222
S3-2	4 N/O + 0.5 S	2.01 (5.1)	2.31 (2.9)			22	172
S3-3	4 N/O (2His)+ 0.5S	2.01 (5.0)	2.31 (3.2)	2.93(4.0) 3.15(4.0) 4.11(9.3) 4.41(19)		23	61
S3-4	5N/O(2His)+ 0.5S+Zn-Zn	2.01 (5.1)	2.31 (3.2)	2.94(4.4) 3.20(8.3) 4.12(8.2) 4.40(22)	3.36(15)	17	60

[a] Distances (Å) and disorder parameters (in parentheses, σ^2 (10^{-3} Å^2)) shown derive from integer or half-integer coordination number fits to filtered EXAFS data [Δk = 1.5-13 Å^{-1}; ΔR = 0.5 – 2.2 Å (fits 1-2), 0.3-4.0 Å (fits 3-4)].

[b] Imidazole multiple scattering paths represent combined paths, as described previously (see Materials and Methods).

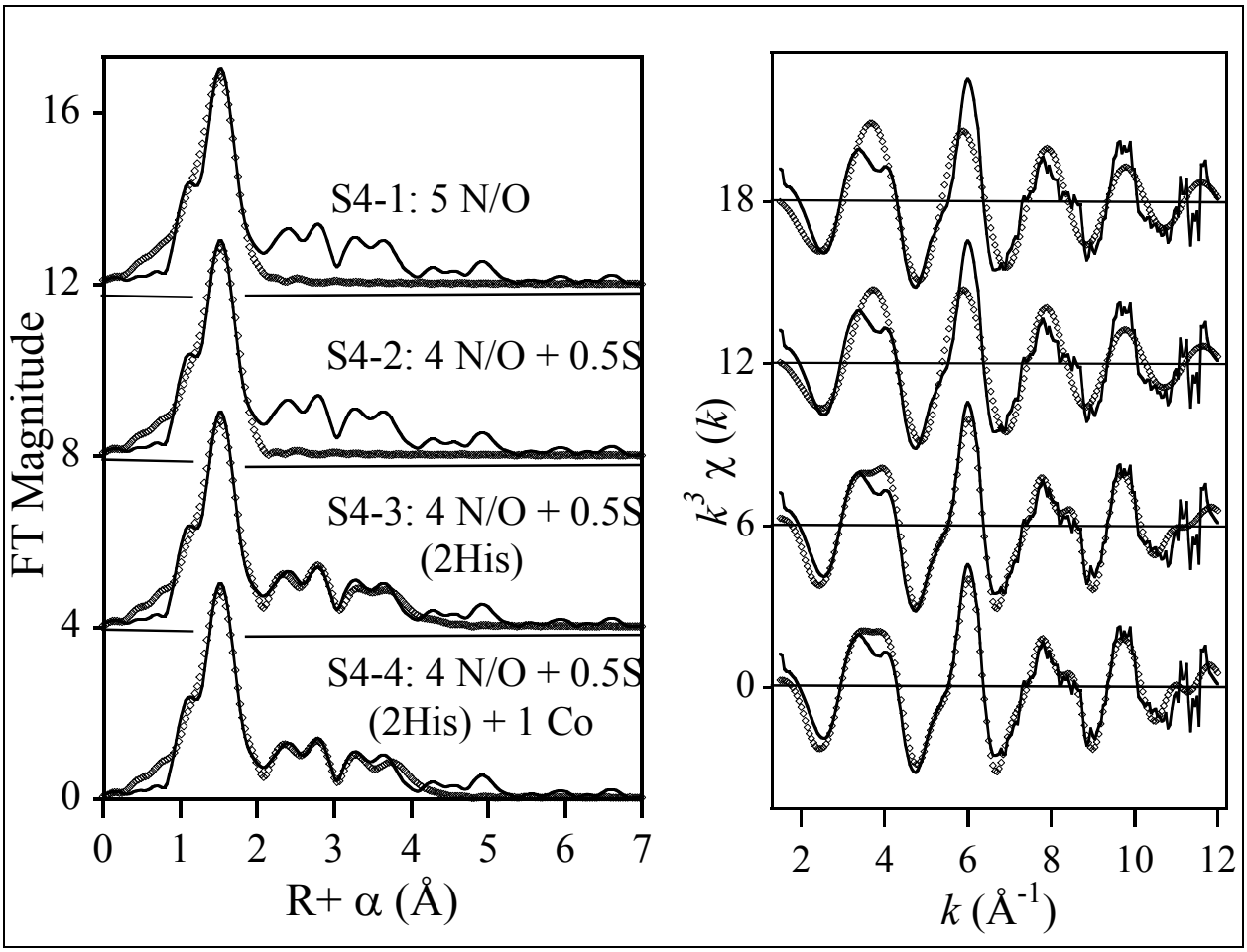

Figure S4. Fourier transforms (A) of Co K-edge EXAFS (B) for as isolated (MM) VIM-2 containing 0.5 eq of Co. The solid lines represent the data, the open symbols represent the various fits, corresponding to **Table S4.**

Table S4. Fitting results for Co *K*-edge EXAFS of as isolated (MM) VIM-2.[a]

Fit	Model	Co-N/O	Co-S	Co-His[b]	Co-Co	R_f[c]	R_u[c]
S4-1	5 N/O	2.04 (7.0)				41	247
S4-2	4 N/O + 0.5 S	2.03 (5.1)	2.27 (4.0)			28	230
S4-3	4 N/O (2His)+ 0.5S	2.04 (6.1)	2.26 (12)	2.98(4.5) 3.20(1.1) 4.20(7.5) 4.56(12)		30	86
S4-4	5N/O(2His)+ 0.5S+Co-Co	2.04 (6.0)	2.26 (11)	2.98(4.8) 3.19(1.0) 4.15(18) 4.55(11)	3.51(15)	24	78

[a] Distances (Å) and disorder parameters (in parentheses, σ^2 (10^{-3} Å^2)) shown derive from integer or half-integer coordination number fits to filtered EXAFS data [Δk = 1.5-12 Å^{-1}; ΔR = 0.5 – 2.2 Å (fits 1-2), 0.3-4.0 Å (fits 3-4)].

[b] Imidazole multiple scattering paths represent combined paths, as described previously (see Materials and Methods).

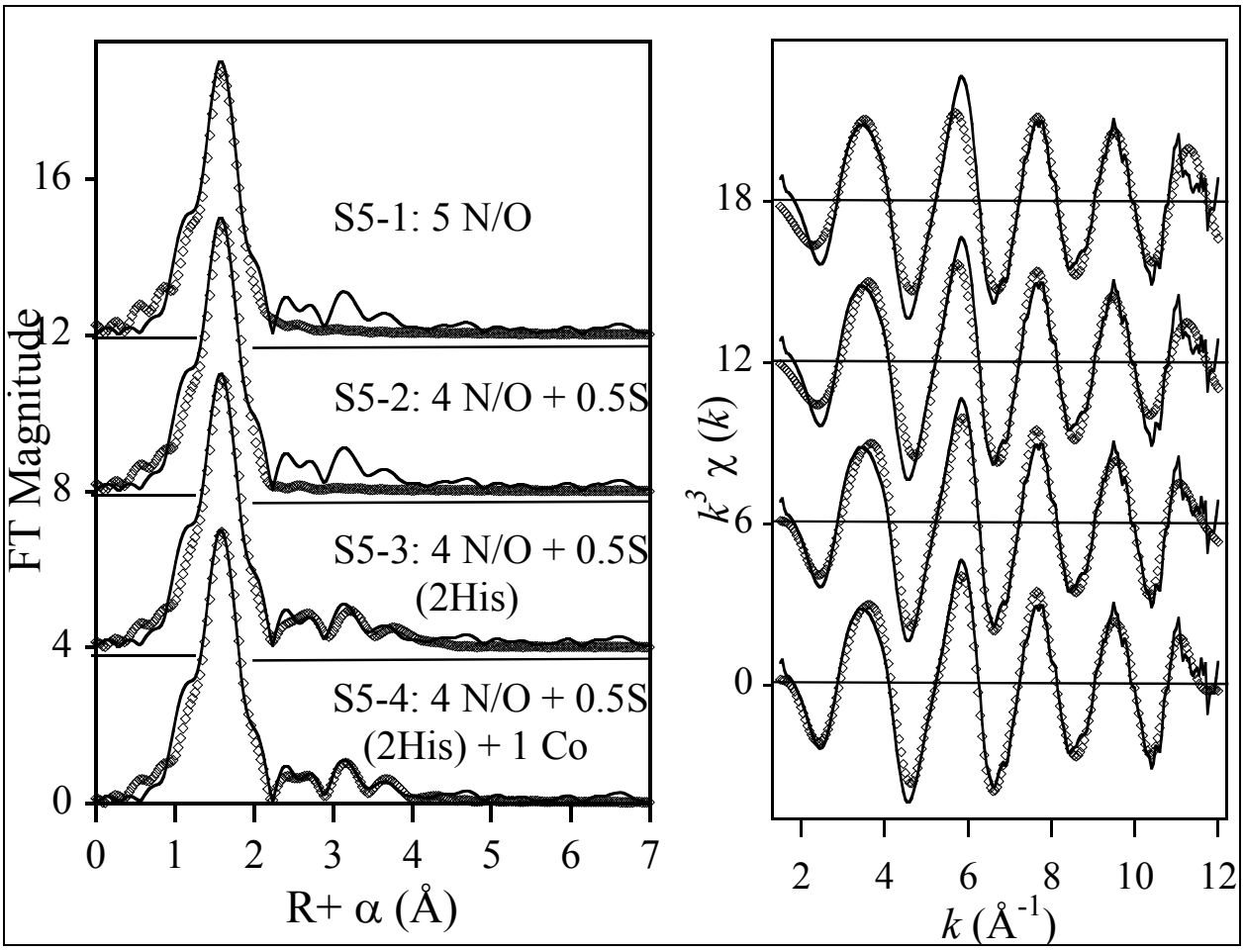

Figure S5. Fourier transforms (A) of Co K-edge EXAFS (B) for 1Co-VIM-2. The solid lines represent the data, the open symbols represent the various fits, corresponding to **Table S5.**

Table S5. Fitting results for Co *K*-edge EXAFS of 1Co-VIM-2.[a]

Fit	Model	Co-N/O	Co-S	Co-His[b]	Co-Co	R_f[c]	R_u[c]
S5-1	5 N/O	2.08 (3.5)				37	90
S5-2	4 N/O + 0.5 S	2.07 (2.1)	2.29 (2.4)			23	79
S5-3	4 N/O (2His) + 0.5S	2.07 (3.3)	2.28 (1.8)	3.00(5.6) 3.14(2.5) 4.10(6.4) 4.59(14)		34	45
S5-4	5N/O(2His)+ 0.5S+Co-Co	2.07 (3.0)	2.29 (2.1)	3.01(5.6) 3.15(0.5) 4.10(6.9) 4.59(17)	3.52(7.3)	16	39

[a] Distances (Å) and disorder parameters (in parentheses, σ^2 (10^{-3} Å^2)) shown derive from integer or half-integer coordination number fits to filtered EXAFS data [Δk = 1.5-12 Å^{-1}; ΔR = 0.5 – 2.2 Å (fits 1-2), 0.3-4.0 Å (fits 3-4)].

[b] Imidazole multiple scattering paths represent combined paths, as described previously (see Materials and Methods).

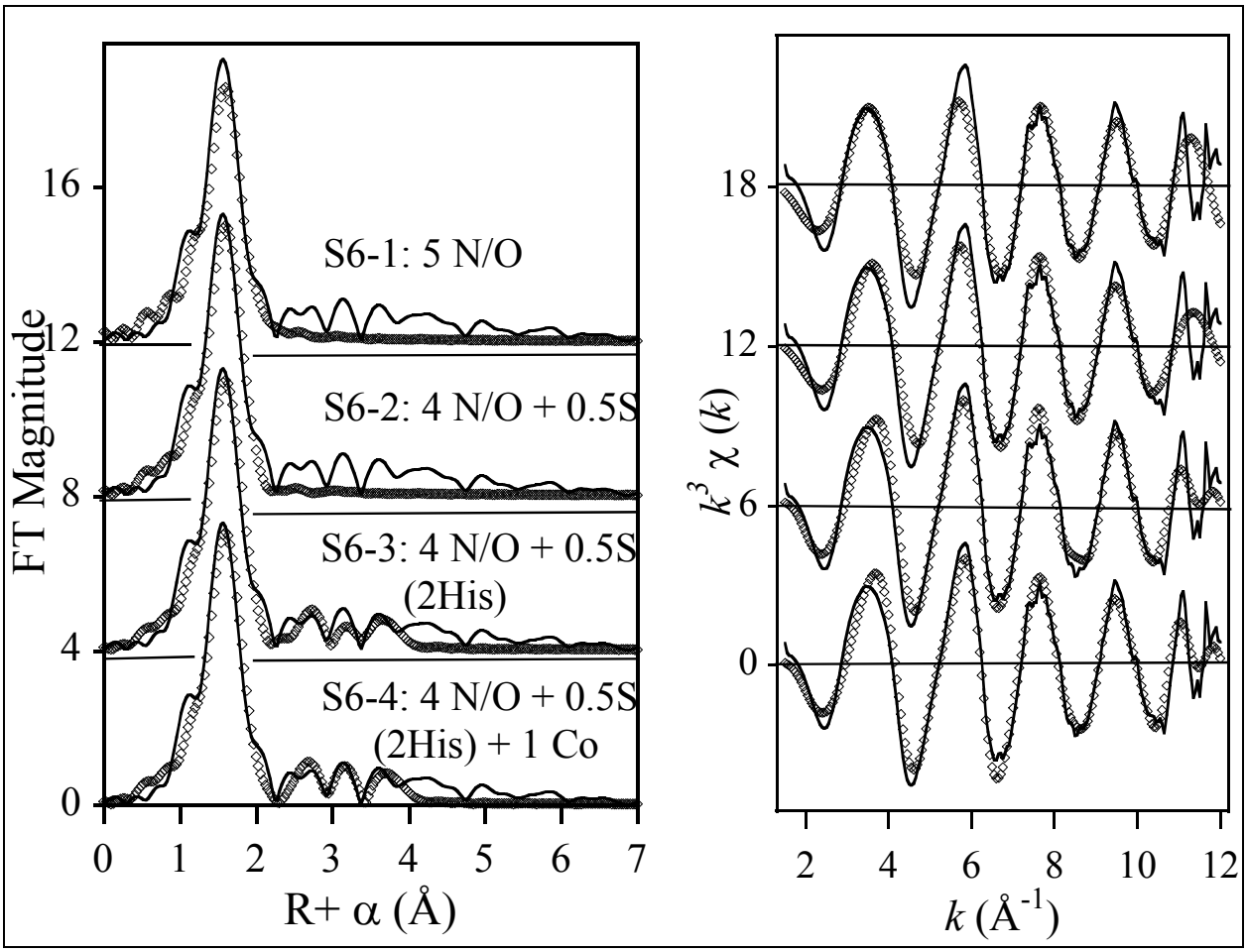

Figure S6. Fourier transforms (A) of Zn K-edge EXAFS (B) for 2Co-VIM-2. The solid lines represent the data, the open symbols represent the various fits, corresponding to **Table S6**.

Table S6. Fitting results for Zn *K*-edge EXAFS of 2Co-VIM-2.[a]

Fit	Model	Co-N/O	Co-S	Co-His[b]	Co-Co	R_f[c]	R_u[c]
S6-1	5 N/O	2.09 (2.1)				43	118
S6-2	4 N/O + 0.5 S	2.07 (2.2)	2.31 (1.3)			26	99
S6-3	4 N/O (2His) + 0.5S	2.07 (2.4)	2.31 (0.9)	3.00(3.9) 3.14(1.6) 4.29(2.9) 4.58(26)		72	62
S6-4	5N/O(2His)+ 0.5S+Co-Co	2.07 (2.3)	2.31 (0.8)	3.01(4.0) 3.15(0.8) 4.28(2.2) 4.58(33)	3.51(9.1)	45	54

[a] Distances (Å) and disorder parameters (in parentheses, σ^2 (10^{-3} Å^2)) shown derive from integer or half-integer coordination number fits to filtered EXAFS data [Δk = 1.5-12 Å^{-1}; ΔR = 0.5 – 2.2 Å (fits 1-2), 0.3-4.0 Å (fits 3-4)].

[b] Imidazole multiple scattering paths represent combined paths, as described previously (see Materials and Methods).

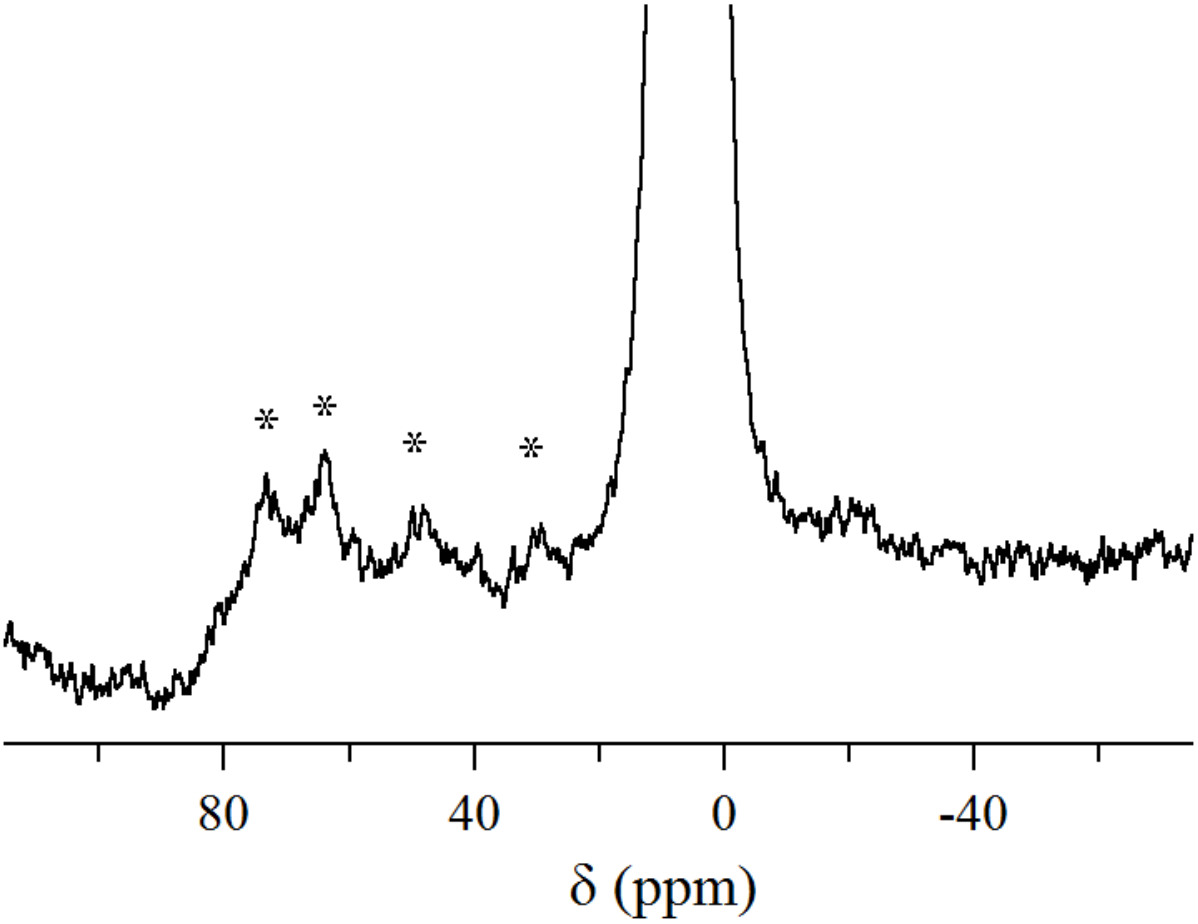

Figure S7. 200 MHz ^{1}H NMR spectrum of 2Co-VIM-2 in 90 % H_2O. Solvent exchangeable protons are indicated by an asterisk.

Table S7. X-ray data collection and structure refinement.

Psuedomonas aeruginosa VIM-2	
Data Collection	
Beam Line	ALS 4.2.2
Wavelength (Å)	1.0000
Space group	*I*222
Cell dimensions	
a, *b*, *c* (Å)	68.3, 78.3, 79.8
α, β, γ (°)	90, 90, 90
Resolution (Å)[a]	55.87-1.55 (1.63-1.55)
R_{merge}[b]	0.070 (0.447)
$\langle I/\sigma I \rangle$	16.9 (4.0)
Wilson *B* factor (Å^2)	15.17
Completeness (%)	99.8 (99.2)
Redundancy	7.2 (7.2)
No. of reflections	228,457
No. of unique reflections	32,317
Refinement	
Resolution (Å)	55.87-1.55
No. reflections for refinement	31,217
R_{work}/R_{free}	0.176 / 0.209
No. atoms	1,992
Protein	1,714
Water	267
Zinc	3
Acetate	8
Average *B* factors	
Protein	22.4
Water	33.8
Zinc	20.2
Acetate	20.4
R.m.s deviations	
Bond lengths (Å)	0.007
Bond angles (°)	1.049
Ramachandran plot statistics	
Favored regions % (#)	97.4 (224/230)
Allowed regions % (#)	100.0 (230/230)
Disallowed regions	0.0
MolProbity validation statistics	
Cβ deviations >0.25Å	0
MolProbity clash score	2.96 (99th percentile, N=730, 1.550Å ± 0.25Å)
MolProbity score	1.21 (98th percentile, N=6,779, 1.550Å ± 0.25Å)
PDB ID	4NQ2

[a] Values in parentheses are for the highest resolution shell.

[b] The merging *R* factor is defined as $R_{merge} = \frac{\sum_{hkl}\sum_{i}\left|I_i(hkl) - \overline{I(hkl)}\right|}{\sum_{hkl}\sum_{i} I_i(hkl)}$.