Supplementary Table 1. Effect of metals on ZinT thermal denaturation profiles tested by differential scanning fluorimetry.

Metal	Counter-ion	[Metal] (μM)	Δ*T*m (°C)	
			1ºC/min	1ºC/10 sec
Ba^{2+}	Cl^-	10		+0.2±0.6
		500		0.0±0.2
Ca^{2+}	Cl^-	10		+0.4±0.7
		500		+0.5±0.1
Cd^{2+}	Cl^-	10		+4.5±0.2
		500		+7.0±0.3
Co^{2+}	Cl^-	10		+4.2±0.0
		500		+8.3±0.1
Cr^{3+}	Cl^-	10		+0.1±0.3
		500		+0.7±0.3
Cu^{2+}	Cl^-	10	+9.6±0.4	+5.2±0.2
		100	+5.7±0.1	
		500	+4.2±0.5	+3.6±0.3
Fe^{3+}	Cl^-	10		+0.6±0.3
		500		+0.5±0.2
Hg^{2+}	Cl^-	10	+6.1±0.3	
		100	+9.7±0.1	
		500	+7.4±0.1	
Mg^{2+}	Cl^-	10		+0.7±0.5
		500		+0.6±0.1
Mn^{2+}	Cl^-	10	+2.7±0.0	+0.5±0.0
		100	+2.8±0.1	
		500	+2.6±0.1	+0.9±0.0
Ni^{2+}	SO_4^{2-}	10	+8.5±0.3	+4.7±0.3
		100	+11.3±0.1	
		500	+10.6±0.1	+8.7±0.0
Pr^{3+}	CH_3COO^-	10		+0.5±0.7
		500		+0.6±0.1
Sr^{2+}	Cl^-	10		+0.6±0.0
		500		+8.7±0.0
Y^{3+}	Cl^-	10		+0.5±0.3
		500		-0.1±0.1
Zn^{2+}	SO_4^{2-}	10	+13.2±0.2	+10.8±0.3
		100	+13.7±0.1	
		500	+2.4±0.4	+11.8±0.3
			+12.4±0.2	

Supplementary Table 2 - Metal concentrations supplemented into growth medium of Δ*zinT* and Δ*galT Escherichia coli* strains.

Metal	Concentration (μM)
Cobalt (Co^{2+})	100
	250*
	400
	500*
	1000
Mercury (Hg^{2+})	1
	2.5
	10
	15*
	20*
	25
	40
	50
Cadmium (Cd^{2+})	25
	100
	250
	300*
	500*
Copper (Cu^{2+})	100
	500
	1000
	2000
	3000*
	5000
Nickel (Ni^{2+})	100
	500
	1000*
	1250
	2000
Zinc (Zn^{2+})	100
	200
	400
	500
	600*
	800*
	1000

* - metal concentrations presented in metal sensitivity assays (Figures 2-4 and Supplementary Figures S2-S4).

Supplementary Table 3. Data collection and processing statistics.

Beamline	ESRF ID 29
Detector	PILATUS 6M
Wavelength (Å)	1.0000
Data Processing	XDS
Space Group	$P\ 4_1\ 2_1\ 2$
Unit cell parameters (Å)	a=62.01, c=149.72
Resolution (Å)	45.8 - 1.79 (1.85 - 1.79)
Nr. Observations	191493 (11611)
Unique reflections	28379 (2634)
Completeness (%)	99.6 (97.0)
Multiplicity	6.7 (4.4)
R-merge (%) [a]	7.4 (57.6)
R-pim (%) [b]	3.0 (27.3)
R-meas (%) [c]	8.0 (64.3)
<I/σ(I)>	15.6 (1.7)
$CC^{½}$ [d]	0.999 (0.824)
Wilson Plot B	24.6
Z [e]	2
V_m	2.3
Estimated Solvent Content (%)	46

[a] R-merge = merging R-factor, $(\Sigma_{hkl} \Sigma_i |I_i(hkl) - <I(hkl)>|) / (\Sigma_{hkl} \Sigma_i I(hkl)) \times 100\%$.

[b] R-pim = precision independent R-factor, $\Sigma_{hkl} [1/(N_{hkl} -1)]^{1/2} \Sigma_i |I_i(hkl) - <I(hkl) >|/\Sigma_{hkl} \Sigma_i I_i (hkl)$, where I is the observed intensity, $<I>$ is the average intensity of multiple observations from symmetry-related reflections, and N_{hkl} is their redundancy. (Diederichs and Karplus, 1997);

[c] R-meas = redundancy independent R-factor, $\Sigma_h [N_{hkl}/(N_{hkl}-1)]^{1/2} \Sigma_i |I_i(hkl) - <I(hkl) >| / \Sigma_{hkl} \Sigma_i I_i(hkl) \times 100\%$. (Diederichs and Karplus, 1997);

[d] $CC^{1/2}$ is the correlation coefficient between two randomly calculated half-sets (Karplus et al, 2012)

[e] Nr. monomers in the asymmetric unit according to Matthews coefficient (Matthews, 1968)

References

(Diederichs and Karplus, 1997) - Diederichs, Kay, and P. Andrew Karplus. "Improved R-factors for diffraction data analysis in macromolecular crystallography." *Nature structural biology* 1997, 4(4): 269-275.

(Karplus et al, 2012) - Karplus, P. Andrew, and Kay Diederichs. "Linking crystallographic model and data quality." *Science* 2012, 336(6084): 1030-1033.

(Matthews, 1968) - Matthews, Brian W. "Solvent content of protein crystals." *Journal of molecular biology* 1968, 33(2): 491-497.

Supplementary Table 4. **Final refinement statistics**.

Resolution limits (Å)	47.75 - 1.79 (1.85 - 1.79)
R-factor (%) [a]	17.4 (26.7)
nr.reflections	28294 (2536)
Free R-factor (%) [b]	20.8 (32.6)
nr. reflections	1433 (141)
Overall coordinate error estimate (Å) [c]	0.17
Model composition	
non-hydrogen protein atoms	1775
Nº mol in asymmetric unit	1
Zinc atoms	8
Solvent molecules	181
Model r.m.s. deviations from ideality	
Bond lengths (Å)	0.012
Bond angles (º)	1.318
Chiral centers ($Å^3$)	0.051
Planar groups (Å)	0.006
Ramachandran plot statistics. Residues in:	
most favored regions (%)	97.4
allowed regions (%)	2.6
disallowed regions (%)	0
Rotamers ouliers (%)	2.23
C^{β} outliers	0
Clash score	1.3
Mean B values ($Å^2$) [d]	*Chain A*
protein main-chain	31.92
protein side-chain	40.34
Zinc (acetate)	43.03 (38.17)
solvent	38.36

[a] R-factor = $\Sigma_{hkl} ||F_o|-|F_c|| / \Sigma_{hkl} |F_o|$, where $|F_o|$ and $|F_c|$ are the observed and calculated structure factor amplitudes, respectively; [b] Free R-factor is the cross-validation R-factor computed from a randomly chosen subset of 5% of the total number of reflections, which were not used during the refinement.; [c] Maximum-likelihood estimate with PHENIX; [d] Calculated from equivalent isotropic B values, including the TLS contribution for the protein atoms.