Supporting Information for "Upgraded AMBER Force Field for Zinc-binding Residues and Ligands for Predicting Structural Properties and Binding Affinities in Zinc Proteins"

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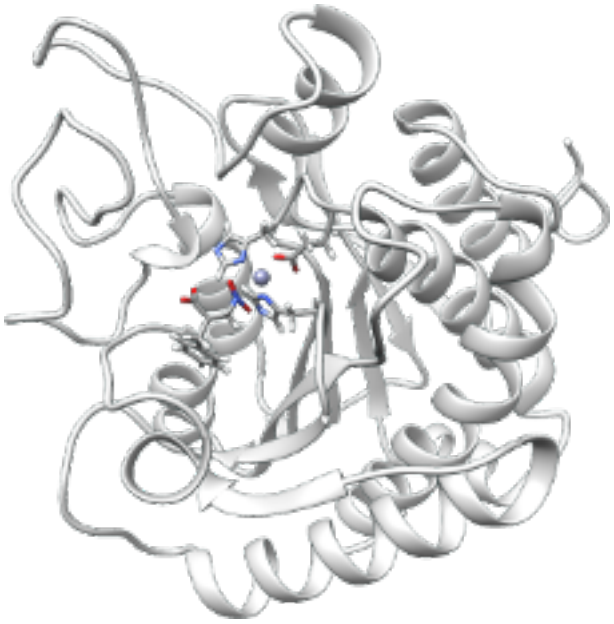


Figure S1: Structure of 2RFH.

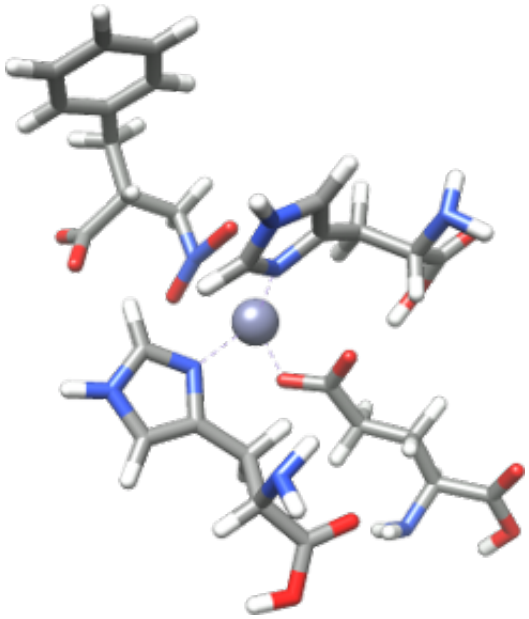


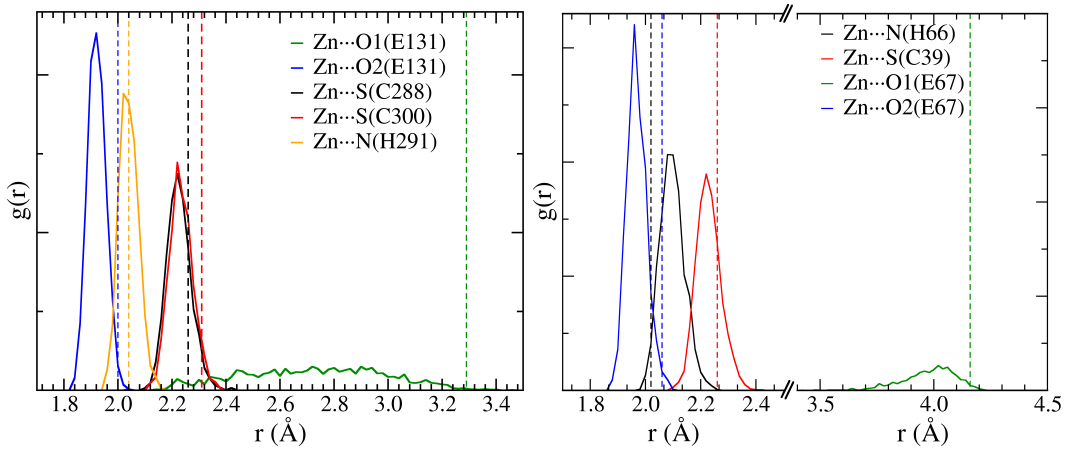
Figure S2: Complex used to reparametrize the inhibitor atomic charges.

Table S1: Reparameterized atomic charges for inhibitor (R)-2-benzyl-3-nitropropanoic acid. The atom name are taken from pdb file.

Atoms	Atomic Charges (e)
c01	-0.139928
h01	0.123791
c02	-0.148442
h02	0.110557
c03	-0.153123
h03	0.109600
c04	-0.139475
h04	0.120572
c05	-0.120288
h05	0.200177
c06	-0.122948
h06	0.020808
h07	0.017059
c07	0.043506
h08	0.159763
c08	1.099336
h09	-0.197668
h10	-0.287478
c09	-0.060979
c10	0.669963
o11	-0.669678
o12	-0.659541
n13	-0.369745
o14	-0.044830
o15	-0.561009

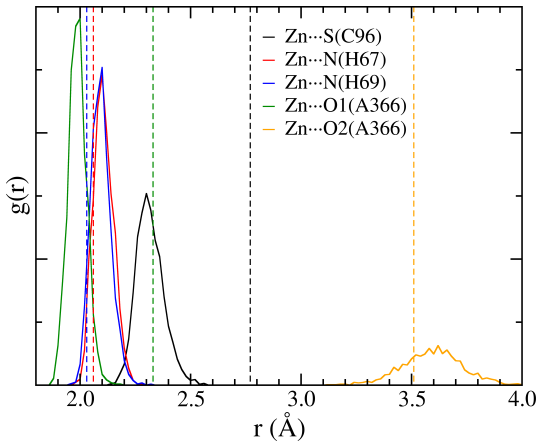
Table S2: X-Zn-Y angle mean value and standard deviation calculated for 4YBG, 2CDB, 1V4Y, 1KOL and 4Z1D proteins; with X and Y are indicated the interacting atoms.

Angle	Mean (°)	Standard deviation (°)
4YBG		
N(H291)-Zn-S(C288)	103.41	4.37
S(C288)-Zn-S(C300)	105.76	4.50
S(C300)-Zn-O2(E131)	88.11	5.11
O2(E131)-Zn-N(H291)	91.96	4.58
2CDB		
N(H66)-Zn-S(C39)	117.67	7.43
S(C39)-Zn-O2(E67)	112.88	8.82
1V4Y		
S(C96)-Zn-N(H67)	91.77	3.16
N(H67)-Zn-N(H69)	112.33	6.03
N(H69)-Zn-O1(A366)	99.05	5.04
O1(A366)-Zn-S(C96)	157.35	6.71
1KOL		
N(H67)-Zn-O1(D169)	97.03	5.46
S(C97)-Zn-O1(D169)	163.02	8.83
N(H67)-Zn-S(C97)	98.67	5.66
4Z1D		
S(C18)-Zn-N(H204)	164.57	6.58
N(H204)-Zn-O2(D252)	98.15	4.70
O2(D252)-Zn-O1(E241)	100.18	5.43
O1(E241)-Zn-S(C18)	96.83	4.64

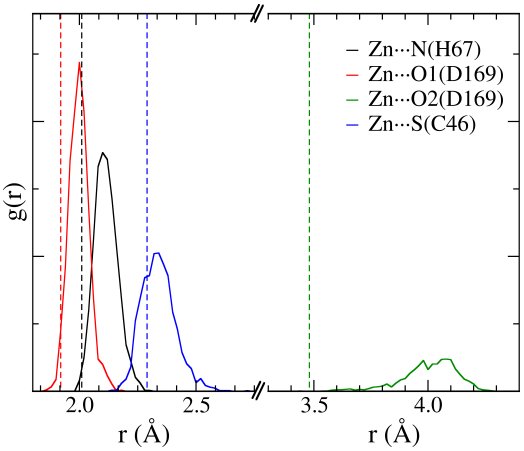


(a) **4YBG**

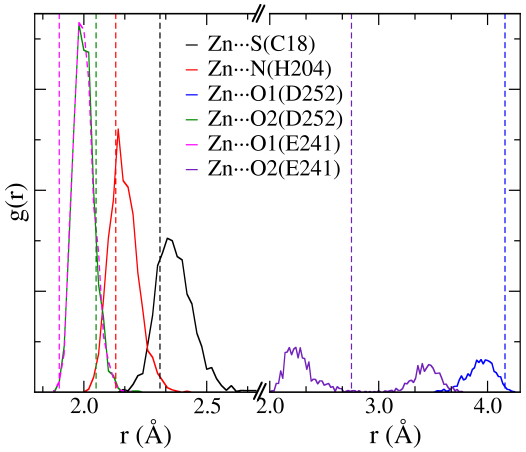
(b) **2CDB**



(c) **1V4Y**

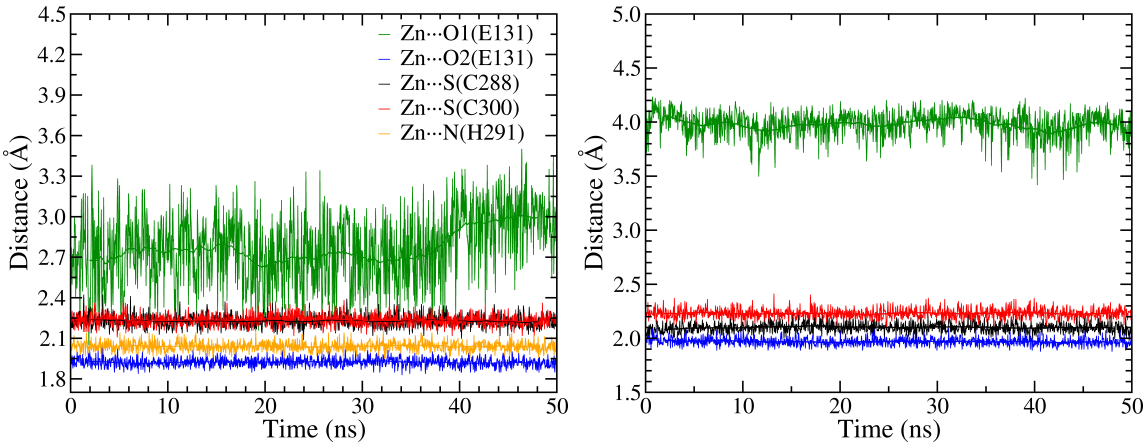


(d) **1KOL**



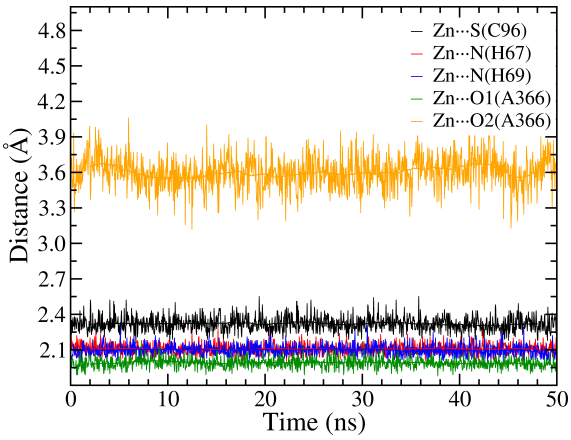
(e) **4Z1D**

Figure S3: Radial distribution function (full line) between Zn(II) and interacting oxygen or nitrogen or sulfur atom of glutamate, aspartate, histidine or cysteinate, respectively. The corresponding reference values extracted from X-ray structures are depicted with dashed line. The comparison was performed for 4YBG (a), 2CDB (b), 1V4Y (c), 1KOL (d) and 4Z1D (e).

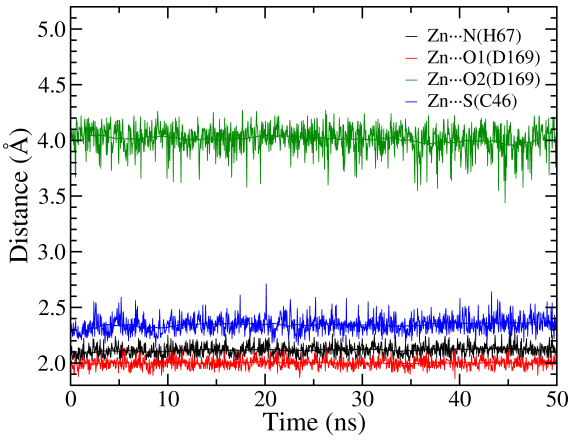


(a) **4YBG**

(b) **2CDB**

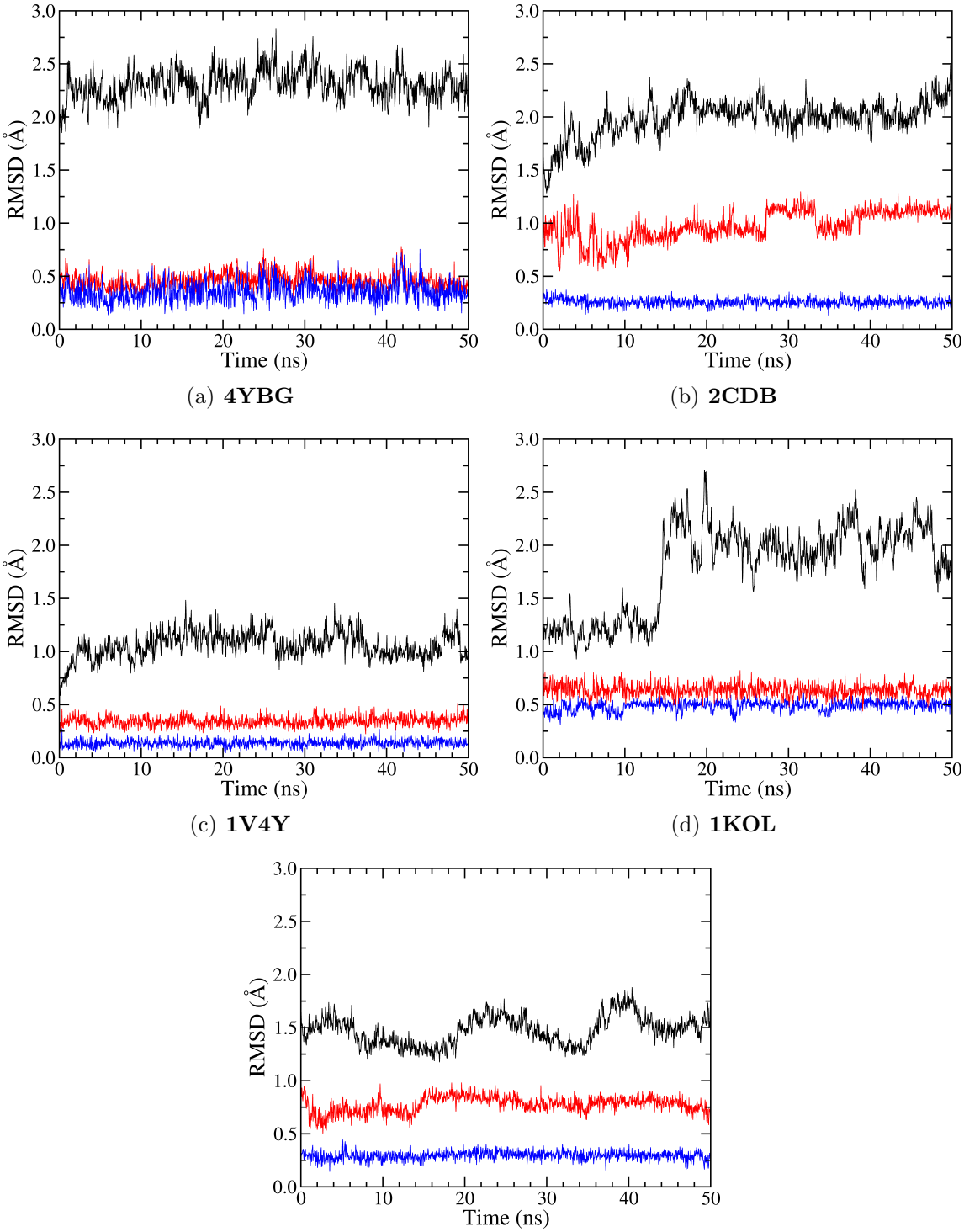


(c) **1V4Y**



(d) **1KOL**

Figure S4: Pair distribution function between Zn(II) and interacting oxygen, nitrogen or sulfur atom of glutamate, aspartate, histidine or cysteine, respectively. The comparison was performed for 4YBG (a), 2CDB (b), 1V4Y (c) and 1KOL (d).



(a) **4YBG** (b) **2CDB**

(c) **1V4Y** (d) **1KOL**

(e) **4Z1D**

Figure S5: RMSD values of the protein backbone, metal binding site, and binding atoms monitored along the 50 ns MD trajectories. In the plots, the black, red, and blue curves represent backbone, metal binding site, and binding atoms, respectively. The comparison was performed for 4YBG (a), 2CDB (b), 1V4Y (c), 1KOL (d) and 4Z1D (e).