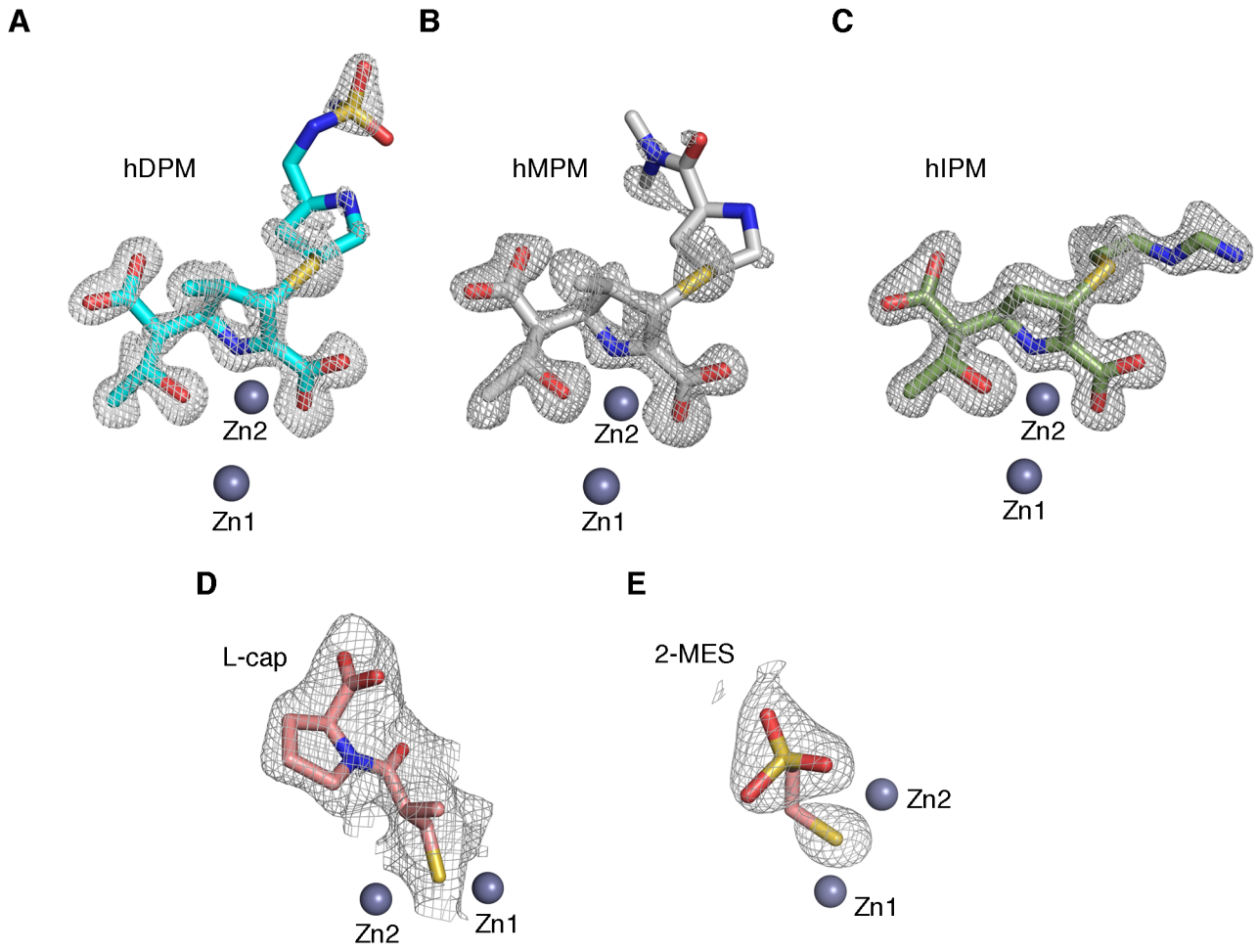

FIG S1

FIG S1 |*Fo*|–|*Fc*| electron density maps contoured at 2.0 σ (gray mesh). Zinc ions are shown as gray spheres. (A) hydrolyzed doripenem (hDPM) (B) hydrolyzed meropenem (hMPM) (C) hydrolyzed imipenem (hIPM) (D) L-captopril (L-cap) (E) 2-mercaptoethanesulfonate (2-MES)

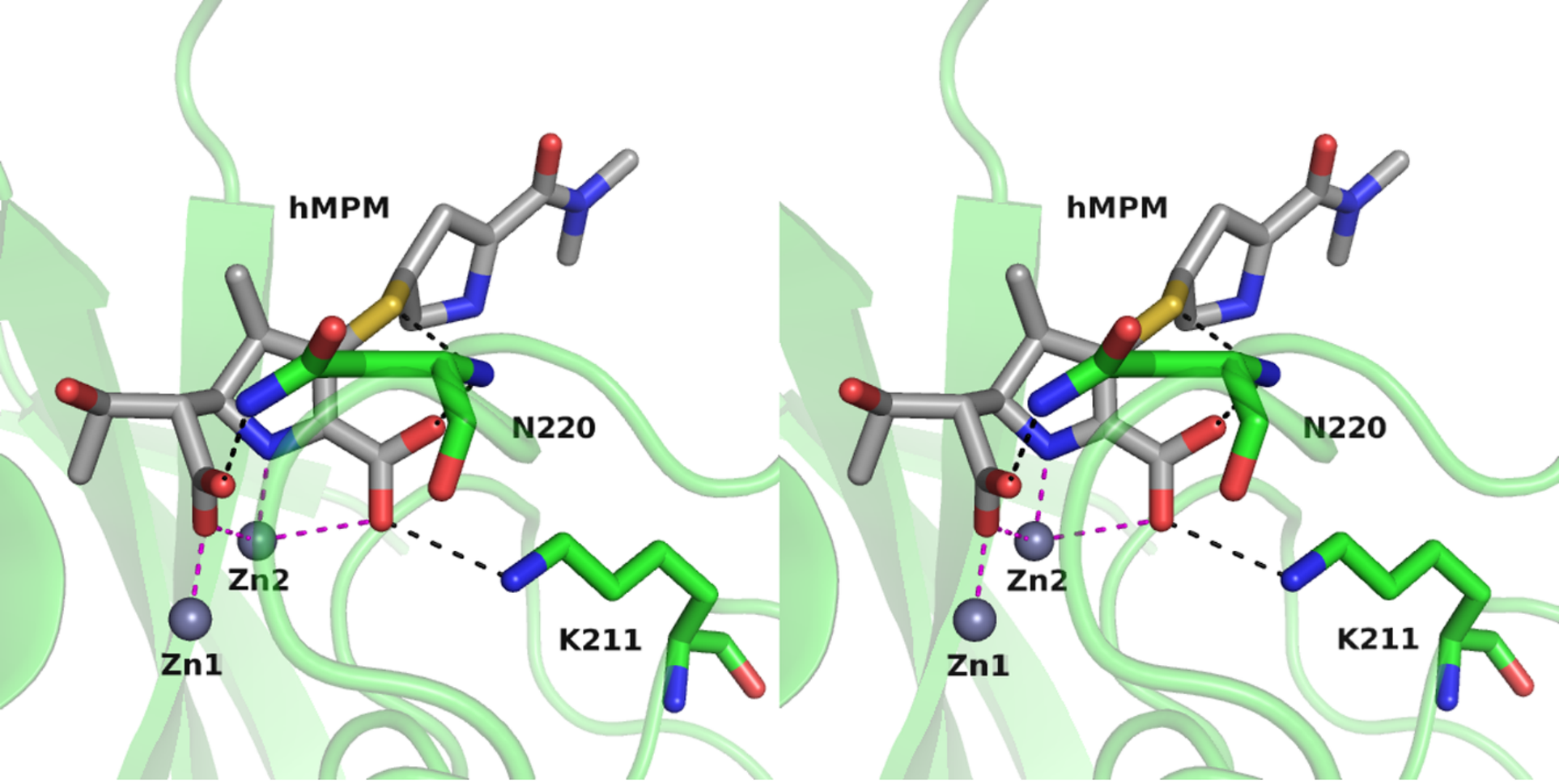

FIG S2

FIG S2 Stereo view of the binding mode between hydrolyzed meropenem (hMPM) and the B1 MBL NDM-1. Zinc ions are depicted as gray spheres, while amino acids coordinating Zn are illustrated in green sticks. Coordination and hydrogen bonds are drawn as magenta and black dashed lines, respectively. hMPM is illustrated in silver (carbon), ocher (sulfur), red (oxygen), and blue (nitrogen) sticks. The figure was adapted from PDB structure 4EYL.

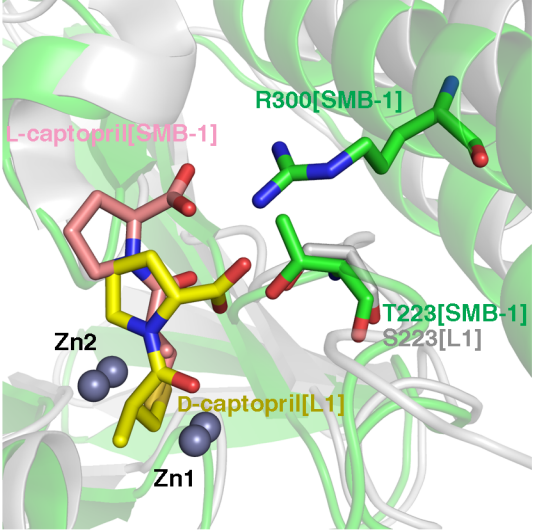

FIG S3

FIG S3 Inhibition of SMB-1 (green) and L1 (silver) by L- (pink) and D-captoprils (yellow), respectively. Captopril-bound L1 was adapted from PDB structure 2FU9.

Table S1. Results of susceptibility testing

Agents	MIC (μg/ml)	
	E. coli DH5α (pCL-SMB)	*E. coli* DH5α (pCL1920)
Meropenem	8	0.03
+L-captopril 8 μg/mL	8	0.03
+L-captopril 32 μg/mL	4	0.03
+L-captopril 128 μg/mL	2	0.03
+2-MES 8 μg/mL	8	0.03
+2-MES 32 μg/mL	4	0.03
+2-MES 128 μg/mL	2	0.03

MICs of L-captopril and 2-MES for *E. coli* DH5α were > 256 μg/ml, respectively