Supplementary Table 1. Non-bonded interactions (hydrogen bonds and salt bridges) involved in the stabilization of the dimer interface as observed in the FomA·MgAMPPNP·fosfomycin complex. The second part of the dimer (amino acid residues marked with the asterisk) is generated by the symmetry operation y,x,-z.

Non-bonded interactions		**Distance (Å)**
Arg^{91} (NH1)	Glu^{77*} (OE2)	2.93
Arg^{91} (NH2)	Glu^{77*} (OE1)	2.78
Gln^{101} (N)	Gln^{101*} (OE1)	2.81
Gln^{101} (NE2)	Pro^{99*} (O)	2.96
Arg^{116} (NH1)	Glu^{118*} (OE1)	2.83
Arg^{116} (NH2)	Asp^{122*} (OD2)	2.24
Ser^{117} (OG)	Ala^{104*} (O)	2.73
Ser^{117} (OG)	Arg^{116*} (O)	3.70
Glu^{118} (N)	Arg^{116*} (O)	3.09
Glu^{77} (OE2)	Arg^{91*} (NH1)	2.93
Glu^{77} (OE1)	Arg^{91*} (NH2)	2.78
Gln^{101} (OE1)	Gln^{101*} (N)	2.81
Pro^{99} (O)	Gln^{101*} (NE2)	2.96
Glu^{118} (OE1)	Arg^{116*} (NH1)	2.83
Asp^{122} (OD2)	Arg^{116*} (NH2)	2.24
Ala^{104} (O)	Ser^{117*} (OG)	2.73
Arg^{116} (O)	Ser^{117*} (OG)	3.70
Arg^{116} (O)	Glu^{118*} (N)	3.09
Arg^{91} (NH1)	Glu^{77*} (OE1)	3.68
Arg^{91} (NH2)	Glu^{77*} (OE2)	3.56
Arg^{116} (NE)	Glu^{118*} (OE1)	3.73
Arg^{116} (NH1)	Asp^{122*} (OD2)	3.92
Arg^{116} (NH2)	Asp^{122*} (OD1)	3.55
Glu^{77} (OE1)	Arg^{91*} (NH1)	3.68
Glu^{77} (OE2)	Arg^{91*} (NH2)	3.56
Glu^{118} (OE1)	Arg^{116*} (NE)	3.73
Asp^{122} (OD2)	Arg^{116*} (NH1)	3.92
Asp^{122} (OD1)	Arg^{116*} (NH2)	3.55