

<i>Shigella</i>	<i>Salmonella</i>	Domain	% Matched residues	RMSD (Å)
MxiG <sub>152-200</sub>	PrgH <sub>171-223</sub>	D2	98	1.26
MxiG <sub>201-272</sub>	PrgH <sub>224-294</sub>	D3	99	1.49
MxiG <sub>273-340</sub>	PrgH <sub>295-362</sub>	D4	100	1.33
MxiJ <sub>21-77</sub>	PrgK <sub>20-76</sub>	D1	100	0.82
MxiJ <sub>97-191</sub>	PrgK <sub>96-196</sub>	D2	95	1.25
MxiD <sub>34-109</sub>	InvG <sub>34-106</sub>	N0	93	1.62, 1.63*
MxiD <sub>110-171</sub>	InvG <sub>108-172</sub>	N1	94	2.45, 2.60*

**S18 Fig. Ca RMSDs calculated from superposed orthologous protein domains in *Shigella* and *Salmonella*.**

The structure of the *Salmonella* domains has been obtained from the models with PDB ID 5TCP (PrgH, PrgK) or 6DV3 (InvG). Fraction of matched residues are relative to the *Shigella* domains.

\* Two RMSD values for the MxiD domains are reported because they have been refined with C8 symmetry.