NMR Identification of the Binding Surfaces Involved in the *Salmonella* and *Shigella* Type III Secretion Tip-Translocon Protein-Protein Interactions

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Figure S1. Comparison of ¹H-¹⁵N TROSY spectra of (A) IpaD and (B) IpaD^{C322S}.



Figure S2. SipB⁸²⁻³¹² interacts with SipD^{C244S}. (A) Overlay of four ¹H-¹⁵N TROSY spectra of ¹⁵N/ILV SipD^{C244S} with increasing concentrations of unlabeled SipB⁸²⁻³¹². (B) Plot of peak intensity ratio ($I_{1:1}/I_{1:0}$) at SipD^{C244S}.SipB⁸²⁻³¹² molar ratio of 1:1.1 (C) Residues with peak intensity ratio ($I_{1:1}/I_{1:0}$) lower than 1 standard deviation below average (1 σ) are mapped onto the crystal structure of SipD^{C244S}.



Figure S3. Complete stereospecific ILV assignments of SipD^{C244S}.



Figure S4. Ile to Leu mutations used in assigning the isoleucine ${}^{13}C\delta1$ methyl peaks of SipD^{C244S}. Representative examples of ${}^{1}H{}^{-13}C$ HSQC spectra of ${}^{15}N/ILV$ SipD^{C244S} with point mutations in (A) I46L (B) I170L (C) I268L (D) I208L overlayed with the ${}^{1}H{}^{-13}C$ HSQC spectrum of wild type SipD^{C244S} used in assignment of isoleucine ${}^{13}C\delta1$ peak.



Figure S5. Representative strips from 3D ¹H-¹³C-¹³C HMQC-NOESY-HMQC used in assigning the ILV resonances of SipD^{C244S}. (A) Strips from a 3D ¹H-¹³C-¹³C HMQC-NOESY-HMQC dataset of perdeuterated ¹⁵N/ILV-labeled SipD^{C244S}. Asterisks mark the cross peak for each residue; NOEs with other residues are shown in blue lines. (B) Example of distance information from the crystal structure of SipD^{C244S} used in assigning the ILV resonances of SipD^{C244S}, with ILV methyls shown in spheres (Ile, red; Leu, blue & light blue; Val, pink & light pink). An expanded region showing the ILV methyls close to I208 shown with distances that correlated with the NOE peak intensities.



Figure S6. IpaB⁷⁴⁻²²⁴ interacts with IpaD. (A) Overlay of four ¹H-¹⁵N TROSY spectra of ¹⁵N/ILV IpaD with increasing concentrations of unlabeled IpaB⁷⁴⁻²²⁴. (B) Plot of peak intensity ratio ($I_{1:1}/I_{1:0}$) at IpaD:IpaB⁷⁴⁻²²⁴ molar ratio of 1:1.1. (C) Residues with peak intensity ratio ($I_{1:1}/I_{1:0}$) lower than 1 standard deviation below average (1 σ) are mapped onto the crystal structure of IpaD.



Figure S7. Deoxycholate (DOC) did not alter the surfaces of IpaD involved in binding IpaB. (A) Overlay of three ¹H-¹⁵N TROSY spectra of ¹⁵N/ILV IpaD^{C322S} in the presence of 0.4 mM DOC with increasing concentrations of unlabeled IpaB⁹⁻²²⁶. (B) Plot of peak intensity ratio ($I_{1:1}/I_{1:0}$) at IpaD^{C322S}:IpaB⁹⁻²²⁶ molar ratio of 1:1.1. (C) Residues with peak intensity ratio ($I_{1:1}/I_{1:0}$) lower than 1 standard deviation below average (1 σ) are mapped onto the crystal structure of IpaD. The presence (C) or absence of DOC (Fig. 3C) resulted in the same surfaces of IpaD perturbed upon titration with IpaB.



Figure S8. Immunobloting using SipD antibodies of (A) cultured supernatants and (B) whole-cell lysates of *Salmonella typhimurium* strains containing *sipD* gene knockout (Δ SipD), exogenous sipD introduced by a plasmid (+SipD), and exogeneous SipD with site directed mutants. Recombinant GB1-SipD^{C244S} was used as a positive control.