## **Electronic supplementary information**

## Topological frustration leading to backtracking in a coupled foldingbinding process

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Figure S1 Intermolecular native contacts between E3 and Im3 in the native bound state. The N-terminal segment (residues 1-15) and the central segment (residues 25-41) of E3 form 32 and 35 native contacts with Im3, respectively.



Figure S2. Average fraction of intramolecular native contacts within E3 ( $\langle Q_f \rangle$ ) and radius of gyration of E3 ( $\langle R_g \rangle$ ) at various fraction of intermolecular native contacts between E3 and Im3 ( $Q_b$ ) for simulation at 0.10 M salt. Errors are standard deviations of five independent simulations.



Figure S3. Representative conformations of  $I_P$ ,  $I_B$ , and  $I_F$  intermediate states for simulation at 0.10 M salt. E3 is shown in rainbow color and Im3 is shown in gray.



Figure S4 Two dimensional free energy landscapes using the fraction of intermolecular native contacts between  $E3^{1-15}$  and Im3 ( $Q_{inter}^{1-15}$ ), fraction of intermolecular native contacts between  $E3^{25-41}$  and Im3 ( $Q_{inter}^{25-41}$ ), and fraction of intermolecular native contacts between E3 and Im3 ( $Q_b$ ) as reaction coordinates for simulations at various salt concentrations.



Figure S5 Formation of intramolecular native contacts within E3<sup>25–41</sup> along the binding process at various salt concentrations. Errors are standard deviations of five independent simulations.



Figure S6 Energetic analysis for the native bound E3/Im3 complex at various salt concentrations. (A) Intermolecular native contact interactions between the two E3 segments and Im3. (B) Intermolecular electrostatic interactions between the two E3 segments and Im3. E3<sup>1-15</sup> and E3<sup>25-41</sup> are shown in red and blue, respectively.