Evaluating the dynamics and electrostatic interactions of folded proteins in implicit solvents

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Supplementary Materials

References

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(2) Karplus M, McCammon JA (1983) Dynamics of proteins: Elements and function. *Annu Rev Biochem* 52(1):263–300.

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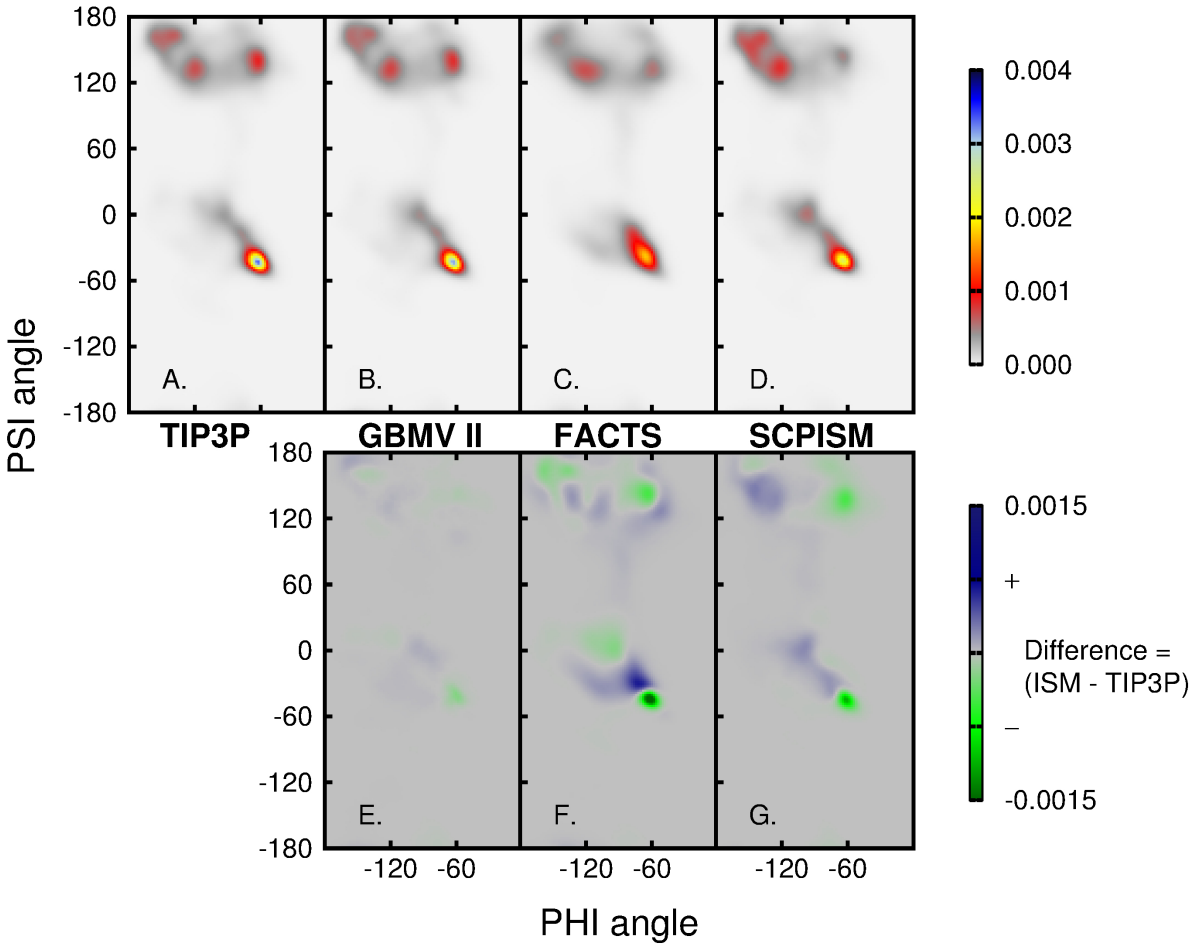

Figure S1:
Panel A to D: Distributions of torsion angles (ϕ angle ranging from -180° to 0° and ψ angle ranging from -180° to 180°) obtained from forty 10-ns simulations of unbound Src SH2 domain in TIP3P, GBMVII, FACTS and SCPISM solvent models. **Panel E to G:** Distributions of differences in torsion angles obtained from forty 10-ns simulations of unbound Src SH2 domain in GBMVII, FACTS and SCPISM solvent models with respect to those from TIP3P explicit solvent. Regions of torsion angles that are more populated in GBMVII, FACTS and SCPISM are colored in blue; regions of torsion angles that are less populated in GBMVII, FACTS and SCPISM are colored in green; regions of gray color indicate negligible difference in population between simulations in ISMs and TIP3P.

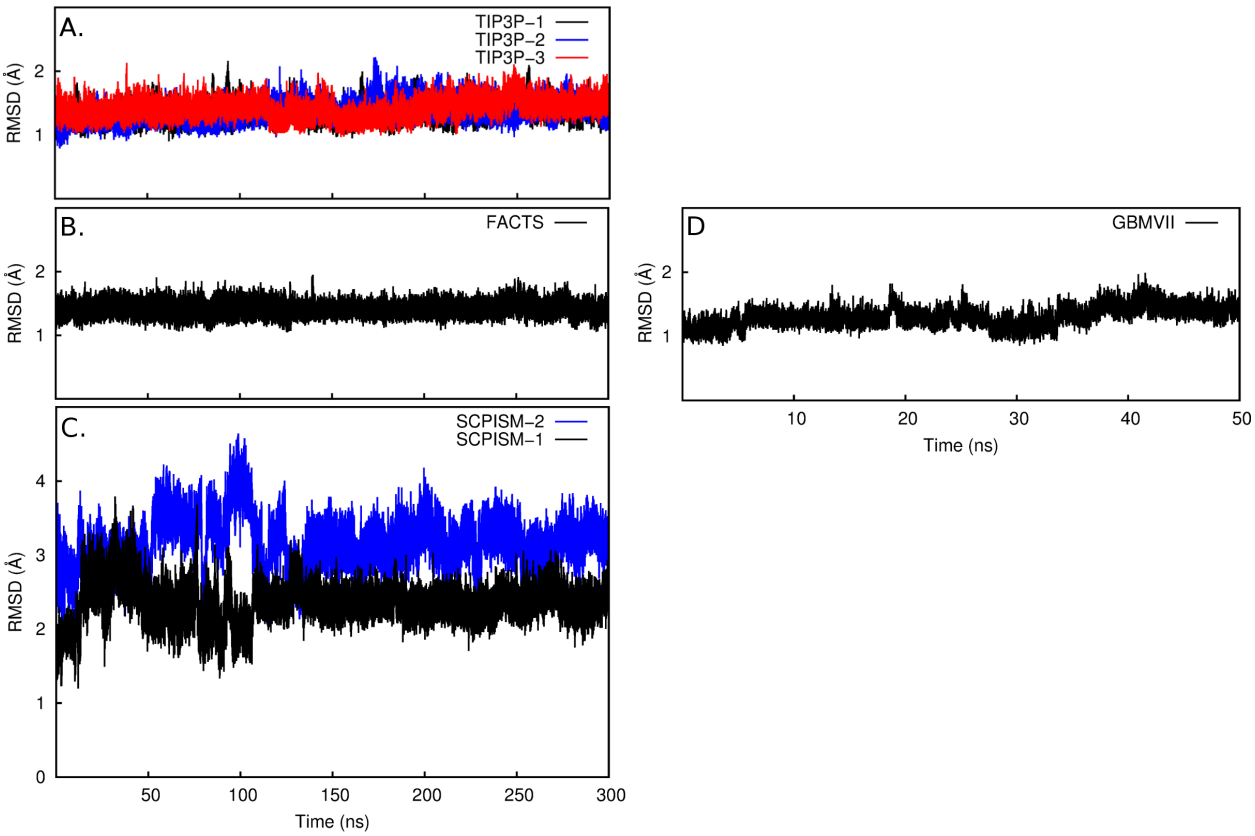

Figure S2: The rms differences in backbone (N, C, C_α atoms) coordinates between the energy-minimized structure of the unbound Src SH2 domain and the snapshots of trajectories calculated with TIP3P (panel A, three 300-ns trajectories), FACTS (panel B, one 300-ns trajectory), SCPISM (panel C, two 300-ns trajectories) and GBMV II (panel D, one 50-ns trajectory) solvents. The rmsd between the snapshots from trajectories calculated with FACTS or GBMVII solvation and the energy-minimized structure of the Src SH2 domain are similar to those obtained for TIP3P, with values that fluctuate around an average of 1.4 Å and remain stable over the course of the trajectories (panel A,B,D). The conformations sampled with TIP3P, GBMVII and FACTS solvation models, therefore, do not differ substantially from the energy-minimized structure. With SCPISM, the rmsd values vary considerably during the first 150 ns before reaching plateaus with average rmsd values greater than 2 Å. While the protein remained folded after 300-ns simulations with SCPISM, the conformations sampled are more dissimilar to the energy-minimized structure (panel C).
Long trajectories of the unbound Src SH2 domain solvated with ISMs were calculated using the same conditions and parameters as those used for forty 10-ns trajectories (see subsection "Simulations of Src SH2 Domain" in the main text).

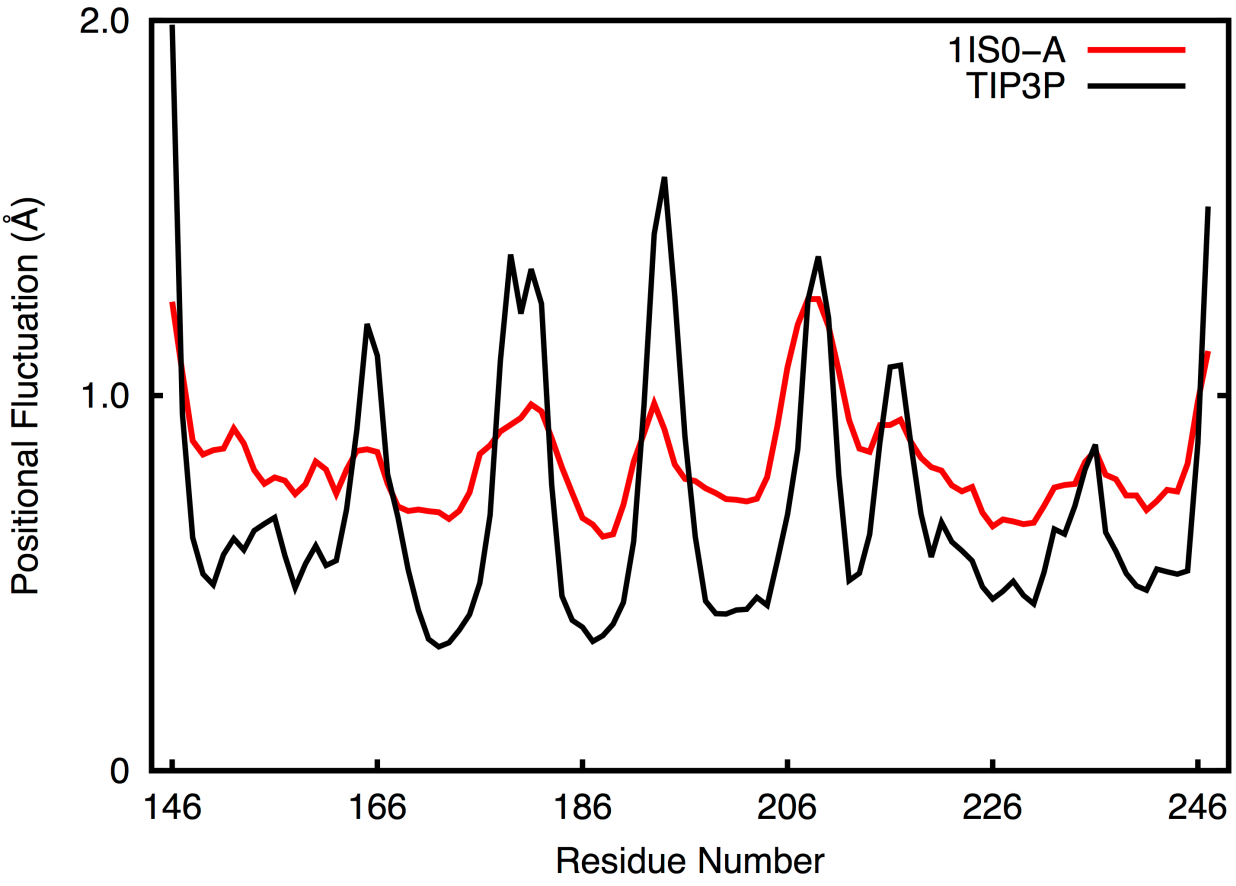

Figure S3:
Residue averages of the backbone (N, C, C_α) positional fluctuation atoms calculated from forty 10-ns trajectories of the unbound Src SH2 domain in TIP3P (black) and from the crystallographic temperature factors (red) of the 1.9-Å crystal structure for one of the two bound Src SH2 domains in the asymmetric unit (PDB ID: 1IS0, chain A). Positional fluctuations were calculated from the crystallographic temperature factors using the expression[2,3] $B = \frac{8\pi^2\langle\Delta R_i^2\rangle}{3}$, where B is the crystallographic temperature factor for atom i and $\langle\Delta R_i^2\rangle$ represents the squared positional fluctuation of atom i.

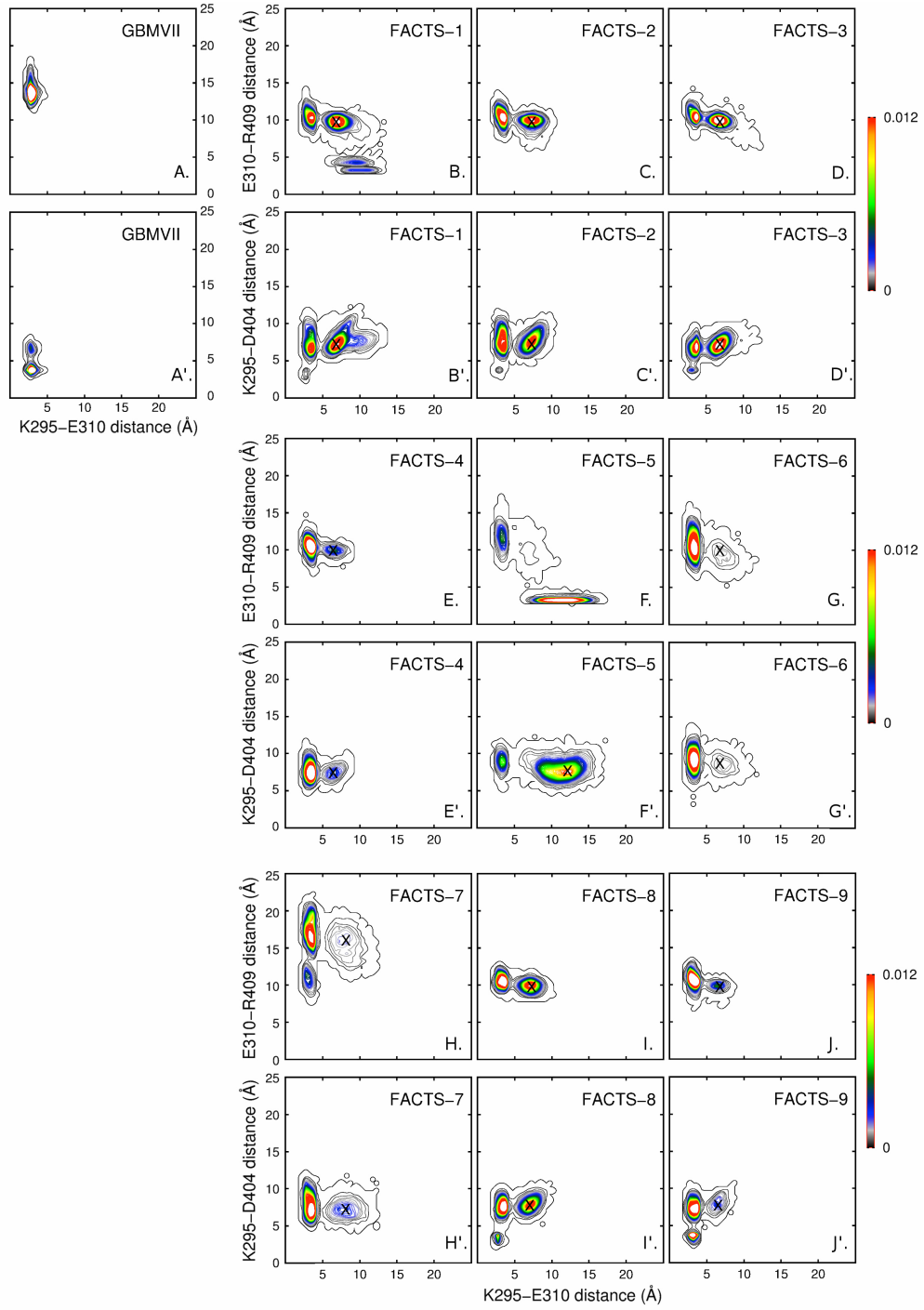

Figure S4:
Maps showing the distance distributions of the two sets of ion pairs in the Src Kinase switch electrostatic network: K295E310-E310R409 (panel A-J) and K295E310-K2950D404 (panel A'-J'). The distances were calculated from a 25-ns trajectory of the Lyn kinase domain in GBMVII (panel A and A') and nine 25-ns trajectories in FACTS (panel B-J and B'-J'). The highly populated intermediate states seen with FACTS (black X marks) may not exist with GBMVII. Residues are numbered according to the convention for the Src kinase domain. With GBMVII solvent, the simulation conditions and parameters were the same as those described in the subsection "Simulations of Lyn Kinase Domain" in the main text. The distance between two charged residues was calculated as described for Fig. 2 in the main text.