

Supporting Information for the manuscript:

Transferable Mixing Of Atomistic And Coarse-Grain Water Models

Humberto Carlos Gonzalez[†], Leonardo Darré^{†,‡} and Sergio Pantano^{†*}

[†]Institut Pasteur de Montevideo, Uruguay

[‡]Department of Chemistry, King's College London, London, United Kingdom.

* To whom correspondence should be addressed:

Sergio Pantano,

Tel:+598-2522 0910, Fax:+598-2522 0910,

e-mail: spantano@pasteur.edu.uy

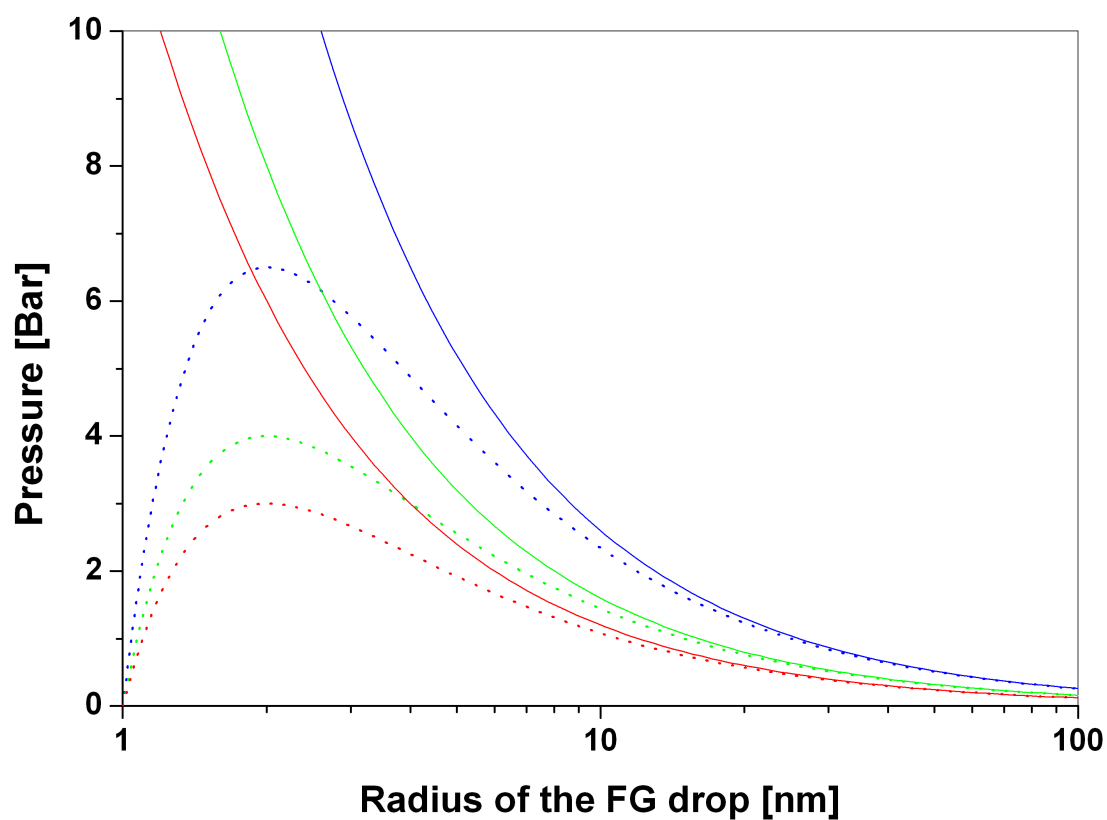


Figure SI 1. Variation of the pressure within the FG drop induced by the hybrid interface. Dotted lines correspond to the pressure calculated taking into account a variation of the interface tension as function of the radius of the FG droplet taking a Tolman length of 1 nm. The continuous line corresponds to the standard Young-Laplace equation (see main text). Red, Green and Blue colors indicate the TIP3P, SPC and SPC/E, respectively.

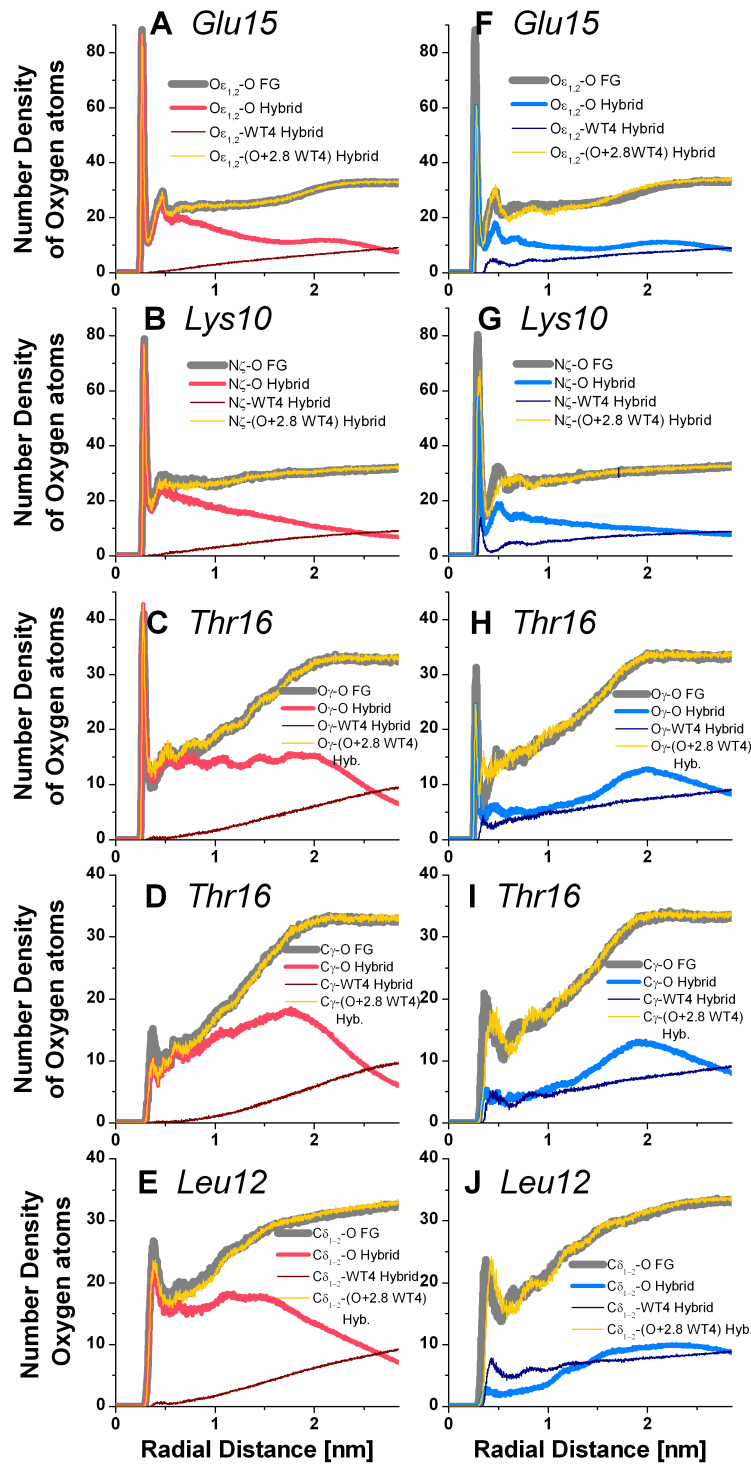


Figure SI 2. Solvation structure around FG amino acids calculated along the trajectories of systems 22 to 25 (using the v-rescale thermostat and Parrinello-Rahman barostat, see main text). A to F) Number densities of Oxygen atoms around representative residues using AMBER-TIP3P. G to K) Same as B to F using GROMOS-SPC/E.

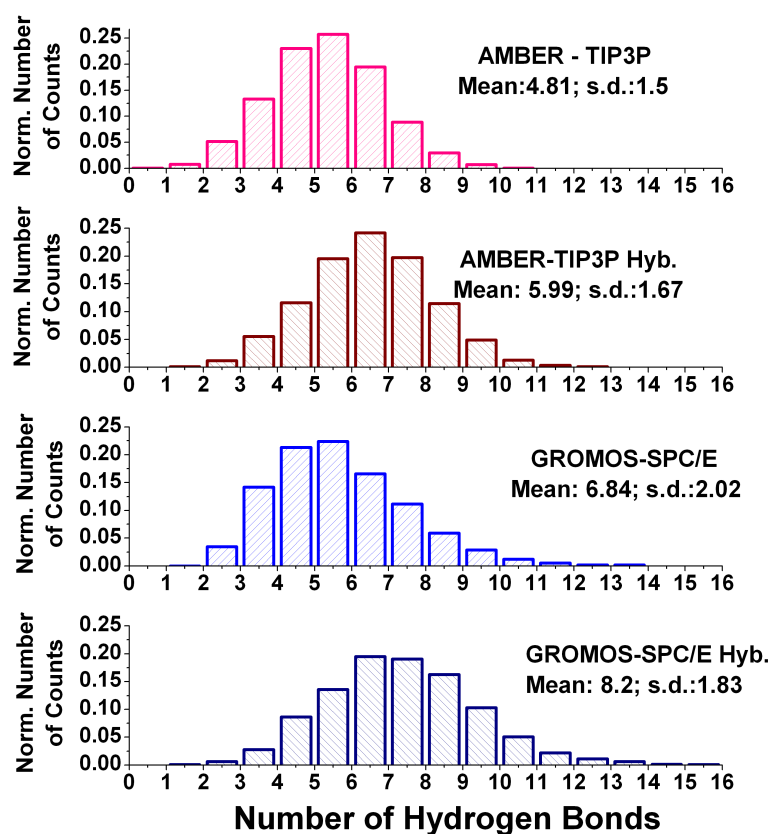


Figure SI 3. Inter side chain Hydrogen bonds calculated along the trajectories of systems 22 to 25 (using the v-rescale thermostat and Parrinello-Rahman barostat, see main text). Distribution of the normalized number of Hydrogen bonds for FG (light red or blue) and hybrid (dark red or blue) simulations for AMBER-TIP3P (top) and GROMOS-SPC/E (bottom). Mean values and standard deviation of each distribution are reported on the corresponding panels.

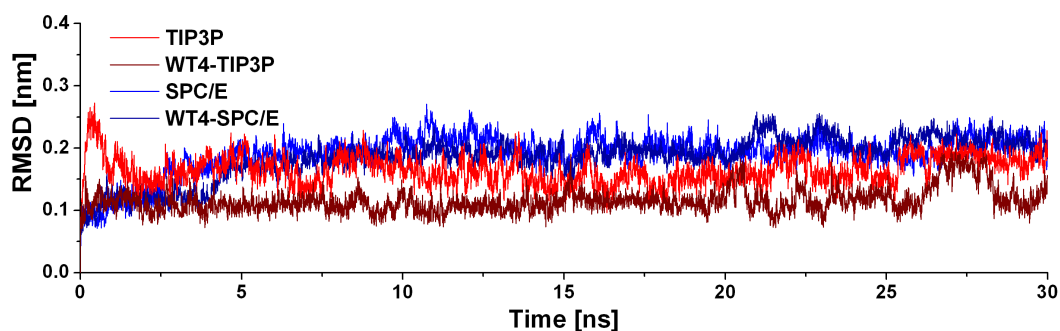


Figure SI 4. Structural comparison of simulations with different force fields and solvation approaches, using the V-rescale thermostat and Parrinello-Rahman barostat (systems 22 to 25 in Table 1, main text). The instantaneous RMSD are calculated on the C_{α} carbons. Light and dark colors indicate FG and hybrid solvation schemes, respectively.

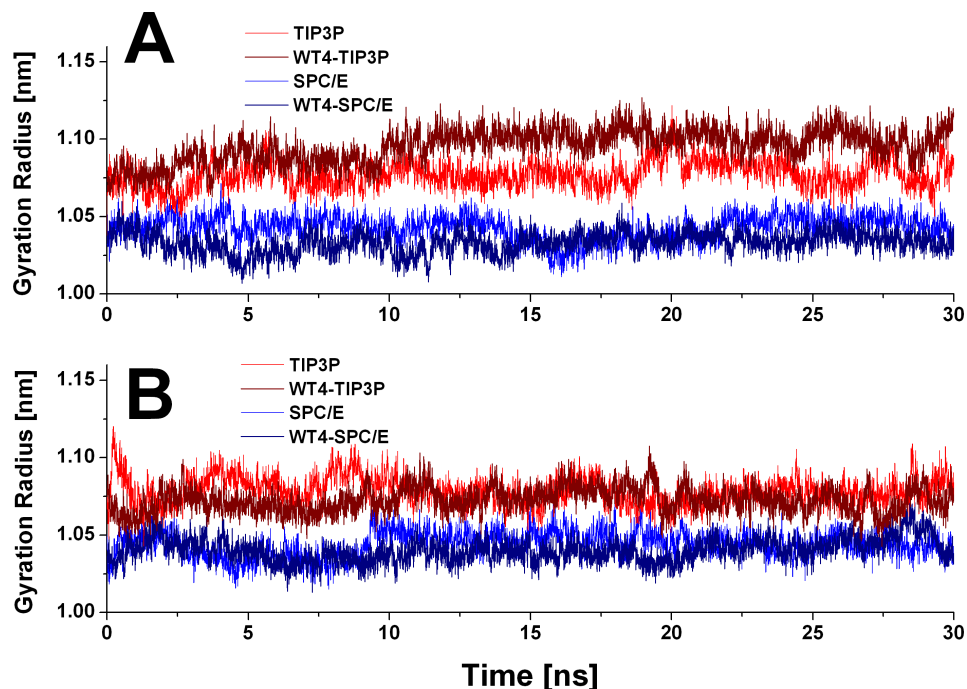


Figure SI 5. Gyration radii along MD trajectories of $\beta 1$ domain of the streptococcal protein G (PDB id: 1FCL). A) Simulations performed using the Berendsen's thermostat and barostats (systems 16 to 19 in Table 1, main text). B) Idem to A for simulations performed using the V-rescale and Parrinello-Rahman thermostat and barostats, respectively (systems 22 to 25 in Table 1, main text).

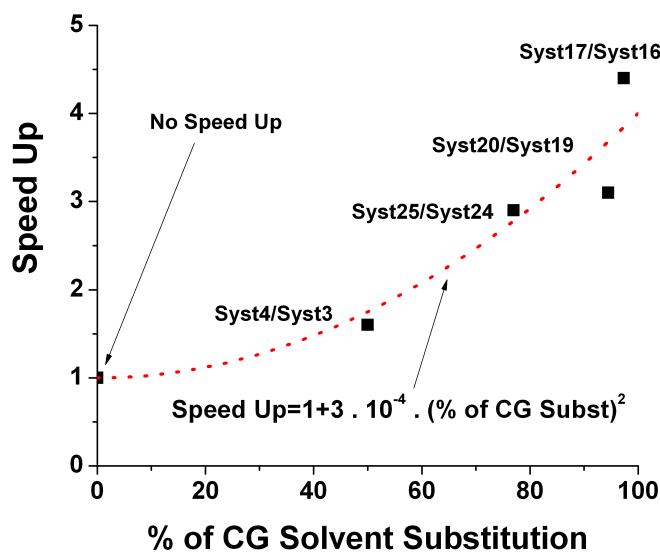


Figure SI 6. Speed up as a function of the percent of substitution of FG water by CG molecules. The speed up is calculated as the ratio between the wall-time needed to perform the simulations of the systems indicated. The quadratic function shown in the figure fits the data with a R value of 0.95.