

SPECIAL PHYSICAL CHEMISTRY SEMINAR



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via Zoom

“CL-FEP: An Accurate End-State Free Energy Perturbation Approach”



Abstract: The accurate evaluation of free energy changes is essential for the study of chemical and biological systems. However, such evaluation is a computationally demanding task, commonly affected by convergence challenges. To address this issue, we implemented the Central Limit Free Energy Perturbation approach (CL-FEP) (1). CL-FEP, which is freely accessible at the CLFEP-GUI web server, allows evaluating the FEP identity directly from the energy samples of the end states of a system transformation without fitted parameters or stratification. The CL-FEP approach delivers excellent accuracy estimating the binding free energy of molecular and biomolecular complexes. The deviation between CL-FEP estimations and experimental values in dissimilar benchmark systems was below 1 kcal/mol. For large test sets, the mean absolute error of the free energy changes calculated with CL-FEP is between 1.1 and 1.4 kcal/mol, which is in the range of accuracy of the most reliable and computationally demanding free energy approaches applied to these systems.

We also employed CL-FEP to evaluate the interaction of Alpha-1 antitrypsin with the TMPRSS2 protease which results in the inhibition of SARS-CoV-2 infection (2). CL-FEP also found applications in the study of the antimicrobial activity of supramolecular ligands (3). Our work demonstrates that CL-FEP provides an attractive alternative to current end-state estimators of free energy changes. Delivering accurate free energy estimations at a reduced computational cost makes these calculations accessible even to large protein-protein complexes. Finally, since multiscale approaches are also in the focus of our research, we applied a rational prioritization strategy combining free energy and QM/MM calculations to address the problem of antibiotic resistance (4).

- (1) JCTC 2020, 16, 1396.
- (2) Nature Communications 2021, 12, 1726.
- (3) Cell Chemical Biology 2021, 28, 1310.
- (4) PNAS 2021, 118, e2113632118.