

Accelerating QM/MM Free Energy Computations via Int

Journal of Chemical Theory and Computation

14, 6327-6335

DOI: 10.1021/acs.jctc.8b00517

Citation Report

#	ARTICLE	IF	CITATIONS
1	Force matching as a stepping stone to QM/MM CB[8] host/guest binding free energies: a SAMPL6 cautionary tale. <i>Journal of Computer-Aided Molecular Design</i> , 2018, 32, 983-999.	2.9	21
2	Prediction of CB[8] host-guest binding free energies in SAMPL6 using the double-decoupling method. <i>Journal of Computer-Aided Molecular Design</i> , 2018, 32, 1059-1073.	2.9	13
3	Development of a Robust Indirect Approach for MM \rightarrow QM Free Energy Calculations That Combines Force-Matched Reference Potential and Bennett's Acceptance Ratio Methods. <i>Journal of Chemical Theory and Computation</i> , 2019, 15, 5543-5562.	5.3	54
4	Use of Interaction Energies in QM/MM Free Energy Simulations. <i>Journal of Chemical Theory and Computation</i> , 2019, 15, 4632-4645.	5.3	21
5	The Good, the Bad, and the Ugly: $\Delta G_{\text{bind}}^{\text{QM}}$, a New Dataset for Validating (S)QM/MM Free Energy Simulations. <i>Molecules</i> , 2019, 24, 681.	3.8	9
6	Accelerated Computation of Free Energy Profile at <i>Ab Initio</i> Quantum Mechanical/Molecular Mechanics Accuracy via a Semiempirical Reference Potential. 3. Gaussian Smoothing on Density-of-States. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 6814-6822.	5.3	11
7	Free energy level correction by Monte Carlo resampling with weighted histogram analysis method. <i>Chinese Journal of Chemical Physics</i> , 2020, 33, 183-195.	1.3	2
8	What Does the Brønsted Slope Measure in the Phosphoryl Transfer Transition State?. <i>ACS Catalysis</i> , 2020, 10, 13932-13945.	11.2	3
9	On the faithfulness of molecular mechanics representations of proteins towards quantum-mechanical energy surfaces. <i>Interface Focus</i> , 2020, 10, 20190121.	3.0	13
10	Alchemical Binding Free Energy Calculations in AMBER20: Advances and Best Practices for Drug Discovery. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 5595-5623.	5.4	177
11	Multi-level free energy simulation with a staged transformation approach. <i>Journal of Chemical Physics</i> , 2020, 153, 044115.	3.0	13
12	Repulsive Soft-Core Potentials for Efficient Alchemical Free Energy Calculations. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 4776-4789.	5.3	12
13	Making free-energy calculations routine: Combining first principles with machine learning. <i>Physical Review B</i> , 2020, 101, .	3.2	35
14	Multi-phase Boltzmann weighting: accounting for local inhomogeneity in molecular simulations of water-octanol partition coefficients in the SAMPL6 challenge. <i>Journal of Computer-Aided Molecular Design</i> , 2020, 34, 471-483.	2.9	7
15	Alchemical Hydration Free-Energy Calculations Using Molecular Dynamics with Explicit Polarization and Induced Polarity Decoupling: An On-the-Fly Polarization Approach. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 1146-1161.	5.3	14
16	Self-Parametrizing System-Focused Atomistic Models. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 1646-1665.	5.3	22
17	Biomolecular QM/MM Simulations: What Are Some of the Burning Issues?. <i>Journal of Physical Chemistry B</i> , 2021, 125, 689-702.	2.6	68
18	Accelerated Computation of Free Energy Profile at <i>Ab Initio</i> Quantum Mechanical/Molecular Mechanics Accuracy via a Semiempirical Reference Potential. 4. Adaptive QM/MM. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 1318-1325.	5.3	13

#	ARTICLE	IF	CITATIONS
19	ParaMol: A Package for Automatic Parameterization of Molecular Mechanics Force Fields. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 2026-2047.	5.4	22
20	A replica exchange umbrella sampling (REUS) approach to predict host-guest binding free energies in SAMPL8 challenge. <i>Journal of Computer-Aided Molecular Design</i> , 2021, 35, 667-677.	2.9	5
21	Performing Molecular Dynamics Simulations and Computing Hydration Free Energies on the B3LYP-D3(BJ) Potential Energy Surface with Adaptive Force Matching: A Benchmark Study with Seven Alcohols and One Amine. <i>ACS Physical Chemistry Au</i> , 2021, 1, 14-24.	4.0	9
22	Reaction Path-Force Matching in Collective Variables: Determining Ab Initio QM/MM Free Energy Profiles by Fitting Mean Force. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 4961-4980.	5.3	14
23	A comparison of three DFT exchange-correlation functionals and two basis sets for the prediction of the conformation distribution of hydrated polyglycine. <i>Journal of Chemical Physics</i> , 2021, 155, 094104.	3.0	6
24	Comparison between ab initio and polarizable molecular dynamics simulations of 1-butyl-3-methylimidazolium tetrafluoroborate and chloride in water. <i>Journal of Molecular Liquids</i> , 2021, 337, 116521.	4.9	14
25	BAR-Based Multi-Dimensional Nonequilibrium Pulling for Indirect Construction of QM/MM Free Energy Landscapes: Varying the QM Region. <i>Advanced Theory and Simulations</i> , 2021, 4, 2100185.	2.8	14
26	Accurate MP2-based force fields predict hydration free energies for simple alkanes and alcohols in good agreement with experiments. <i>Journal of Chemical Physics</i> , 2020, 153, 244505.	3.0	5
28	Generation of Quantum Configurational Ensembles Using Approximate Potentials. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 7021-7042.	5.3	2
29	Testing and Optimizing the Drude Polarizable Force Field for Blocked Amino Acids Based on High-Level Quantum-Mechanical Energy Surfaces. <i>Journal of Computational Biophysics and Chemistry</i> , 0, , 1-9.	1.7	3
30	Seeding the multi-dimensional nonequilibrium pulling for Hamiltonian variation: indirect nonequilibrium free energy simulations at QM levels. <i>Physical Chemistry Chemical Physics</i> , 2022, 24, 8800-8819.	2.8	11
31	Affordable Ab Initio Path Integral for Thermodynamic Properties via Molecular Dynamics Simulations Using Semiempirical Reference Potential. <i>Journal of Physical Chemistry A</i> , 2021, 125, 10677-10685.	2.5	6
32	Optimizing the Calculation of Free Energy Differences in Nonequilibrium Work SQM/MM Switching Simulations. <i>Journal of Physical Chemistry B</i> , 2022, 126, 2798-2811.	2.6	5
33	Obtaining QM/MM binding free energies in the SAMPL8 drugs of abuse challenge: indirect approaches. <i>Journal of Computer-Aided Molecular Design</i> , 2022, 36, 263-277.	2.9	4
34	Polarizable molecular dynamics simulations on the conductivity of pure 1-methylimidazolium acetate systems. <i>Physical Chemistry Chemical Physics</i> , 2022, 24, 15245-15254.	2.8	5
35	Parametrization of Force Field Bonded Terms under Structural Inconsistency. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 4771-4782.	5.4	0
36	Universal QM/MM approaches for general nanoscale applications. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2023, 13, .	14.6	10
37	Exploring Routes to Enhance the Calculation of Free Energy Differences via Non-Equilibrium Work SQM/MM Switching Simulations Using Hybrid Charge Intermediates between MM and SQM Levels of Theory or Non-Linear Switching Schemes. <i>Molecules</i> , 2023, 28, 4006.	3.8	1

#	ARTICLE	IF	CITATIONS
38	Force field refinement for reproducing experimental infrared spectra of ionic liquids. <i>Physical Chemistry Chemical Physics</i> , 2023, 25, 19882-19890.	2.8	0
39	Accurate and Efficient Multilevel Free Energy Simulations with Neural Network-Assisted Enhanced Sampling. <i>Journal of Chemical Theory and Computation</i> , 2023, 19, 5394-5406.	5.3	2
40	Bridging semiempirical and <i>ab initio</i> QM/MM potentials by Gaussian process regression and its sparse variants for free energy simulation. <i>Journal of Chemical Physics</i> , 2023, 159, .	3.0	6