

# Polarization Models for Treating Electrostatics Interactions of Protein in Aqueous Solutions

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## **Abstract**

The polarization effect is important in simulations of the folding/unfolding process of solvated proteins. The fragment-based polarizable model was developed to simulate the solution conformations of  $\alpha$ -conotoxin GI and its single-disulfide analogues.<sup>1,2</sup> The polarizability is explicitly described by allowing the partial charges and fragment dipole moments to be variables, with values coming from the energy-based molecular fragmentation calculations. The employment of fragment-centered dipole moments in calculations of dipole-dipole interactions can save computational time in comparison with those polarization models using atom-centered dipole moments without much loss of accuracy. To further reduce the computational costs, the fragment-based polarization model is extended into a multi-layer coarsened-grained style.<sup>3</sup> According to the sensitivity to the electrostatics environment, a hybrid set of electrostatics parameters, such as secondary-structure- and residue-based dipoles, and atom-centered partial charges, are adopted. For the polarization 'inert' secondary-structures and residues, the coarsened-grained fragment dipole moments are parameterized to reproduce the electrostatics features of molecular fragments. In the case of electrostatics 'sensitive' atoms, the environment-dependent fluctuating charges are updated in each calculation. The electrostatics interaction of the whole chemical system is hence partitioned into several sub-terms coming from the fragment dipole-dipole, (fragment) dipole - (atom) charge, and atom charge-charge interactions. Our test calculations demonstrate that the fragment-based polarization model is capable of describing the structural properties (such as the relative conformational

energies, intramolecular hydrogen bonds, and disulfide bonds) with accuracy comparable to some other polarizable force fields (ABEEM/MM and OPLS-PFF) and the quantum mechanics/molecular mechanics (QM/MM) hybrid model.

**References:**

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