Biofluidics involves the study from macromolecules to cells, in motion and confined in a physiological environment, where several forces of hydrodynamic, electrostatic and fluctuating origins act in multiple ways. To tackle such formidable problems, we have developed a multiscale approach based on representing macromolecules and cells in suspension via a hybrid Lagrangian / Eulerian framework. In general, the framework still involves a huge number of particles but one is mainly interested in the dynamics of a relatively small set of degrees of freedom. Therefore, a specific coarse-graining approach is needed to achieve biological realism and close the equations. In this talk, I will discuss how we constructed a multi-purpose computational tool that leverages high-end hardware and unfolds the potential of multiscale computing.