

Postdoctoral Fellowships at D. E. Shaw Research

D. E. Shaw Research is seeking postdoctoral fellows of exceptional ability to join our New York-based team. This is a unique opportunity to develop and work with transformative technology in a dynamic, interdisciplinary environment. Candidates should have expertise in computational chemistry, biology, or physics, or in a relevant area of computer science or applied mathematics.

Relevant areas of experience might include the study of allosteric interactions or other functionally important conformational changes in biological molecules, structure prediction or design for proteins or RNA, the study of protein-protein or protein-nucleic acid interactions, force field improvement through detailed comparisons of simulation data with NMR measurements or other experimental data, or development and implementation of new methodology (e.g., integrators, methods for enhanced sampling or free-energy calculations, or tools to efficiently analyze large simulation datasets). Specific knowledge of any of these areas is less critical, however, than outstanding intellectual ability, unusually strong research skills, and a history of innovation and accomplishment. We are committed to fostering a stimulating, rewarding, and flexible work environment, and we are prepared to offer above-market compensation to candidates of truly exceptional ability.

To submit an application, please use the link provided below:

<http://www.deshawresearch.com/recruit/jobs/Oncampus/UCSF/PF>

D. E. Shaw Research is an independent research group that is pursuing an ambitious, long-term strategy aimed at fundamentally transforming the process of drug discovery. We have developed a special-purpose supercomputer capable of executing molecular dynamics (MD) simulations orders of magnitude faster than was previously possible. Our current projects include investigations of proteins and other biomedically relevant macromolecules as well as the development of computational chemistry methods to enable more accurate and effective MD simulations.