

Job Description

Are you ready to embark on an exhilarating career journey that combines innovation, collaboration, and impactful scientific discovery? At Merck, a global leader in pharmaceuticals, renowned for our commitment to excellence and groundbreaking research, we are committed to improving lives through innovative medicines, vaccines, and animal health products.

Protein and Structural Chemistry (PSC), a global team in Discovery Chemistry (DC), supports protein structural determination from Discovery to Development, agnostic to the modalities (small molecule, peptide, and macromolecules). Furthermore, we elucidate the structural basis of mechanisms of action and perform analyses to develop formulations. PSC is a diverse and inclusive team of approximately 40 structural biologists that collaborate closely with medicinal and computational chemists, informaticians, mass spectrometrists, biophysicists, protein scientists, and pharmacologists who employ state-of-the-art capabilities to drive drug design and development.

We are seeking a creative, self-motivated structural biologist with exceptional interpersonal and problem-solving skills to join our growing PSC group. The successful candidate must have expertise in X-ray crystallography and Cryo-EM and will be responsible for all aspects of the experimental process from sample preparation and data collection through data processing, structure determination and the effective communication of structural analyses with key stakeholders. The position requires active interaction with the external scientific community, including presentations at external meetings. The successful candidate is expected to foster and contribute to a diverse workforce where colleagues and partners feel comfortable bringing their unique perspectives to work.

This position will be located in our newly renovated labs and office spaces within our vibrant research campus in Rahway, New Jersey, our company's headquarters. Our new labs are equipped with three state-of-the-art Cryo-EM microscopes including a FIB-SEM for cryo-electron tomography, instrumentation for Cryo-EM grid preparation, access to multiple synchrotrons around the world and frequent, regular access to the IMCA-CAT beamline, and crystallization equipment and automation.

Productive and collaborative interactions with other members of our global, cross-functional department are required in this role. Inclusive and collaborative use of internal expertise and resources will be essential to success.

There is an expectation for periodic travel.

Required Experience and Skills:

- Ph.D. in structural biology, biochemistry, or related field.
- Demonstrated experience in a broad range of activities for atomic resolution single particle Cryo-EM, including sample preparation, data collection, image processing and structure determination.
- Demonstrated experience in a broad range of activities for X-ray crystallography, including crystallization screening and optimization, crystal harvesting, data collection, and structure determination.

- Excellent written and oral communication skills to facilitate team progress and ensure clarity on program status for therapeutic team and management is required.
- Demonstrated strong organizational abilities with a proven track record of managing timeline effectively.
- Ability to prepare and publish peer-reviewed research.

Optional Experience and Skills:

- Experience with structure determination of small molecule-protein complexes and multi-subunit protein complexes.
- Experience with micro-electron diffraction.
- Characterization of drug formulations (e.g. VLPs/liposomes/LNPs) by electron microscopy.
- Knowledge of current biophysical and functional characterization methods (e.g. SPR, thermal shift, ligand-binding, and calorimetric assays) to guide construct design and optimization.
- Experience using computational tools for protein engineering and design.
- Experience with scientific programming (e.g. Python) and interest in the application of computational tools to answer structural biology questions.