

P3-101 - “Efficient algorithms for protein structure prediction and applications in RTB binding occupancy determination”

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Abstract:

This project will develop efficient computational approaches for protein structure prediction and validate the implemented approaches on a model protein, RTB. RTB, the lectin subunit of ricin, is being developed as a carrier for vaccine proteins within the P3 Center protein bioproduction cluster. The research involves interdisciplinary collaborations of computational science and biological sciences that will yield new “biological-user friendly” protein prediction software, as well as rapid chemical conjugation/mass spectrometry-based systems for directly probing structure-function relationships.