

June 22nd 7:00 – 8:00pm

JC Smith

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Drug Discovery for COVID-19 and Beyond

Abstract: We have established a supercomputer-driven pipeline for in-silico structure-based drug discovery using enhanced sampling molecular dynamics (MD) and ensemble docking. Ensemble docking makes use of MD results by docking compound databases into representative protein binding-site conformations, thus taking into account the dynamic properties of the binding sites. Using the nation's most powerful computer it is possible to perform the exhaustive docking of one billion compounds in under 24 hours. We have discovered experimentally-validated chemical probes for a number of therapeutic indications including antibiotic resistance, diabetes and Covid-19. Structure-based approaches for the design of vaccines against Group A Streptococcus and cancers are also described. Ending on a fundamental note, we describe the ageing of internal motions in single protein molecules and how this might influence ligand binding.

Bio Sketch: Prof. Jeremy C. Smith has led research groups in France, Germany and the United States. After postdoctoral work at Harvard with Nobel Laureate Martin Karplus, in 1989 he established a Biomolecular Simulation group at the Commissariat à l'Énergie Atomique in Saclay, near Paris. In 1998 he became the first chair in computational biology in Germany, at the University of Heidelberg, and in 2006 became the first University of Tennessee/Oak Ridge National Laboratory Governor's Chair and also Founding Director of the UT/ORNL Center for Molecular Biophysics. Smith's interests include the high-performance computer simulation of biological macromolecules in protein physics, drug discovery, vaccine design and energy, neutron and environmental sciences. He has supervised over 150 staff, students and postdoctoral fellows. As of 2021 Smith has published 470 peer-reviewed scientific articles that have been cited over 45,000 times.