CTSI Seminar Series: Nobel laureate who pioneered computational biology is guest speaker

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The University at Buffalo Clinical and Translational Science Institute (CTSI) Science Seminar Series is pleased to present renowned biophysicist and professor of structural biology Michael Levitt for the 2017 O.P. Jones Lecture entitled, “The Birth and Future of Multiscale Modeling of Macromolecules.” The lecture, co-sponsored by the Department of Biomedical Informatics in the Jacobs School of Medicine and Biomedical Sciences, is scheduled for Tuesday, May 2, at 3:30 p.m. in Butler Auditorium, 150 Farber Hall, on UB’s South Campus.

Michael Levitt, PhD, Robert W. and Vivian K. Cahill Endowed Professor in Cancer Research, Department of Structural Biology, Stanford University School of Medicine

Levitt, along with Martin Karplus and Arieh Warshel, was awarded the 2013 Nobel Prize in Chemistry for the development of multiscale models for complex chemical systems. Levitt says the work leading to the prize began in 1967. “The simplifications used then at the dawn of the age of computational structural biology were mandated by computers that were almost a billion times less cost-effective than those we use today,” he said. “These same multiscale models have become increasingly popular in applications that range from simulation of atomic protein motion to protein folding and explanation of enzyme catalysis. In this talk, I describe the origins of computational structural biology and then go on to show some of the most exciting current and future applications.”

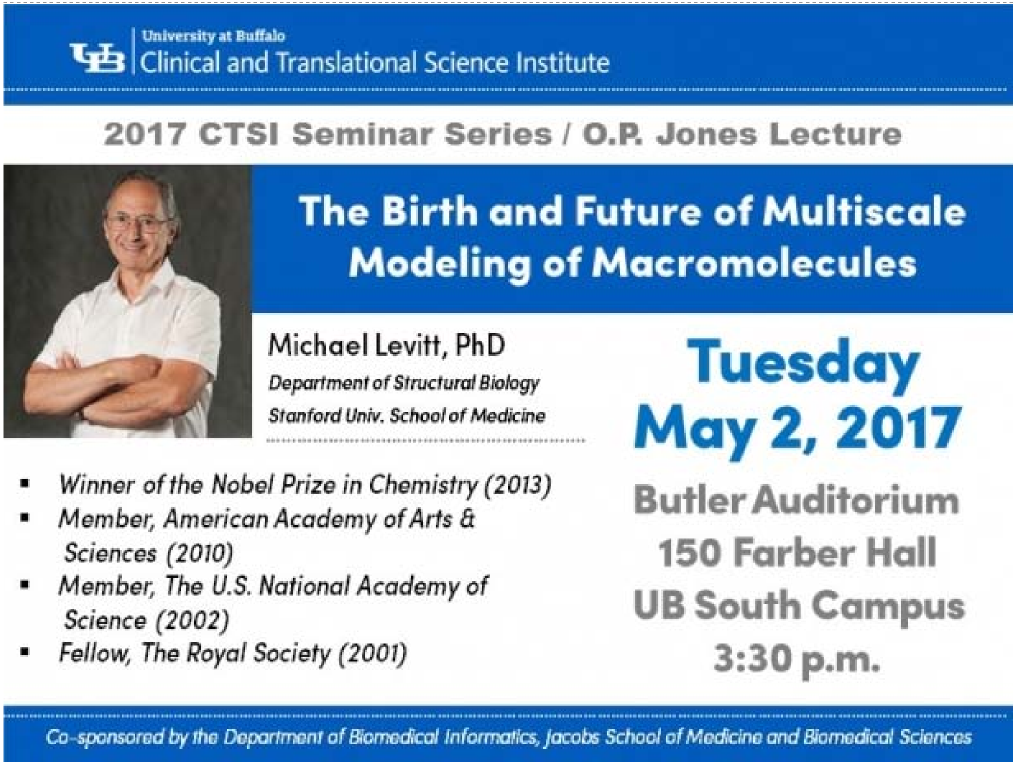
Born in South Africa in 1947, Levitt visited London at age 16 where he was “profoundly influenced” by John Kendrew's 1964 BBC TV series “The Thread of Life,” a program produced by the Royal College of Surgeons to explain the emerging field of molecular biology. After receiving a BSc in physics at King’s College London in 1967 and studying for a year with Prof. Shneior Lifson and his PhD student Arieh Warshel at the Weizmann Institute in Israel, Levitt joined the Laboratory of Molecular Biology (LMB), Cambridge, in 1968. His PhD thesis on Protein Conformation Analysis described the use of classical force-fields and introduced energy refinement. Levitt worked with Francis Crick as a visiting scientist at the Salk Institute in La Jolla, CA for two years in the late 1970s. Following appointments in the Weizmann Institute in Israel and the MRC Laboratory of Molecular Biology in Cambridge in the 1980s, he joined the faculty of the Department of Structural Biology at Stanford University in 1987, where he remains to this day an active programmer -- “a craft skill of which I am particularly proud,” he says.

Levitt’s “diverse interests” have included: RNA and DNA modeling, protein folding simulation, classification of protein folds and protein geometry, antibody modeling, x-ray refinement, antibody humanization, side-chain geometry, torsional normal mode, molecular dynamics in solution, secondary structure prediction, aromatic hydrogen bonds, structure databases and mass spectrometry.

A Fellow of the Royal Society since 2001 and a member of the National Academy of Sciences since 2002, Levitt continues to pursue his dual ambitions: “to work as single-mindedly as I did in the mid-1970s on hard problems and to help today’s young scientists gain the recognition and independence that my generation enjoyed.”

Please join the CTSI and the Department of Biomedical Informatics in welcoming him to UB this

May.



University at Buffalo
Clinical and Translational Science Institute

2017 CTSI Seminar Series / O.P. Jones Lecture

The Birth and Future of Multiscale Modeling of Macromolecules

Michael Levitt, PhD
Department of Structural Biology
Stanford Univ. School of Medicine

- *Winner of the Nobel Prize in Chemistry (2013)*
- *Member, American Academy of Arts & Sciences (2010)*
- *Member, The U.S. National Academy of Science (2002)*
- *Fellow, The Royal Society (2001)*

Tuesday
May 2, 2017

Butler Auditorium
150 Farber Hall
UB South Campus
3:30 p.m.

Co-sponsored by the Department of Biomedical Informatics, Jacobs School of Medicine and Biomedical Sciences

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