

Seminar Announcement

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<https://meet.google.com/zvt-isrg-aei>

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From Quarks to Drugs: A Cross-Disciplinary Application of Theoretical Physics to Drug Discovery

Computer simulations are playing an increasingly important role in several cross-disciplinary fields of Life Science. In particular, microscopic or multi-scale physics-based modeling can in principle be used to investigate the dynamics of biomolecules, thus providing insight into the fundamental mechanisms that drive both their functional and pathological structural changes. Unfortunately, in practice, the applicability of these approaches has been limited, because structural changes in general extremely rare events and because biomolecules are very complex many-body systems.

By exploiting some advanced mathematical methods, originally conceived within the framework of subatomic theoretical physics, my group has developed cross-disciplinary approaches to overcome this rare-event problem, enabling the direct simulation of fundamental protein structural changes. In particular, these methods have made it possible for the first time to reconstruct the entire folding process of biologically relevant proteins, with an atomic level of resolution.

Based on this technological advancement, an entirely new paradigm in rational drug discovery named Pharmacological Protein Inactivation by Folding Intermediate Targeting (PPI-FIT) was recently conceived. This scheme is based on the rationale of blocking the protein folding process, rather than inhibiting the biological function of native proteins.

Using the PPI-FIT paradigm we have discovered molecules that can selectively and dose-dependently modulate the cellular expression of the human prion protein, that is involved in severe neurodegenerative diseases. In addition, the PPI-FIT approach has been successfully applied for drug repurposing, leading to the discovery of molecules capable of repressing the propagation of COVID-19 virus in cellular colonies.