Research discovery: Near-complete set of templates for protein complexes exists today

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(Phys.org) -- Visualize trying to finish a jigsaw puzzle where each individual piece keeps changing shape. If that sounds like an impossible task, imagine the vexing job scientists have faced in computer modeling of interactions between tens of thousands of proteins that are fundamental to biology.

“Proteins are not rigid bodies — they change shape, and they’re flexible — so often you’d want to match two structures that do not match,” said Ilya Vakser, professor of bioinformatics and molecular biosciences and director of the Center for Bioinformatics at the University of Kansas. “A reliable solution to this problem has been a holy grail of computational structural biology.”

For years, scientists have depended on computer modeling to characterize proteins as physical objects. Such accurate computer modeling is based on “template” structures of proteins determined by X-ray crystallography and nuclear magnetic resonance.

Until now, it was believed that many years of work were required before a practically useful set of templates is available to model protein-protein complexes. But Vakser and his colleague Petras Kundrotas at KU, along with their collaborators at Université Paris-Sud, France, and University of California San Diego have discovered that an almost-whole set exists already, a breakthrough that has far-reaching implications for structural biology, and could pave the way for new drugs and therapies to treat a host of diseases.

Their paper, “Templates are available to model nearly all complexes of structurally characterized proteins,” is published in the Early Edition issue of *Proceedings of the National Academies of Sciences*.

An improved grasp of protein interactions would be key to developing drugs and therapies that change protein behavior to benefit human health, according to Vakser.

“You can think of the world of proteins as a crowded environment where a lot of individual molecules float around and bump into each other,” he said. “If it’s a random interaction, nothing happens — they walk away. But if it has physiological importance, then they might stick to each other and change shape or transfer an electron.”

The ability to influence these protein-protein interactions could mean new treatments for common killers like cancer and coronary heart disease, as well as a host of other ailments.

“This gives us a greater ability to model these interactions and to find ways to cure diseases,” Vakser said. “Lots of diseases are caused by abnormalities of protein-protein interactions, or interactions that are undesirable. But to modulate them through drugs, we need to know how it all happens.”

Best of all, the KU researcher said that new approaches to affect protein-protein interactions could be developed quickly.

“It wouldn’t be decades,” said Vakser. “As opposed to studies that would have importance many years from now, to drug design this has immediate application.”

Provided by University of Kansas