

De novo biopharmaceuticals for challenging targets

Joseph Matthew Rogers

Center for Biopharmaceuticals, Department of Drug Design and Pharmacology (ILF), University of Copenhagen

** joseph.rogers@sund.ku.dk*

Thousands of human proteins are implicated in disease, but only a small fraction have a molecule capable of modulating their function. Such molecules are highly valuable as research tools and can be the basis of new therapeutics. However, there is a barrier to new molecule discovery: most proteins cannot be bound with high affinity and selectivity by conventional, small organic molecules. I will describe a technology that can quickly discover exceptional protein-binding molecules, in the form of *de novo* cyclic peptides. *De novo* meaning not a derivative of a known molecule. *De novo* meaning the scientist has the freedom to pre-select specific proteins to target. RaPID can synthesize trillions of unique cyclic peptide sequences and efficiently screen for *de novo* binding candidates. I will describe our use of RaPID to discover cyclic peptides able to modulate i) protein folding, and ii) protein interactions with RNA, opening up numerous disease-associated proteins for new molecule discovery.