NEWS RELEASE

New York Medical College and Interprotein Announce Research Partnership Agreement on Drug Discovery Research for small molecule PPI Inhibitors

September 20th, 2016 – New York Medical College (NYMC) and Interprotein Corporation (Interprotein) today announced that the both parties entered into a research partnership agreement. The partnership will focus on the research and development of C2 domain-interactive therapeutics, which are classified into protein-protein interaction (PPI*) inhibitors, against a variety of diseases such as cancer (including metastasis), fibrosis, pulmonary hypertension, and so on.

Under the agreement, NYMC and Interprotein will collaborate to identify small molecules that inhibit C2 domain-mediated interactions, combining NYMC's core expertise in C2 domain biology and Interprotein's platform technology INTENDD® for molecular design of small molecule PPI inhibitors.

NYMC and Interprotein are aiming at license of C2 domain-interactive therapeutics-related intellectual properties to the third parties (pharmaceutical companies) in collaboration.

***About PPI:**
Protein-protein interaction (PPI) is the general term of biological responses that are produced by binding of two or more protein molecules. For instance, it indicates a binding of cytokine to its receptor followed by intracellular signal transduction from the receptor. Thus, PPI plays an important role in the pathophysiology of many diseases.

About Interprotein:
Interprotein is focusing on drug discovery researches for PPI targets using two platform technologies, INTENDD® (INTerprotein's Engine for New Drug Design) and helix-loop-helix peptide (HLHP). INTENDD® is a strategy for structure-based drug discovery (SBDD) and consists of identification of small molecule binding site with real space 3D molecular models and *in silico* screening by SBSG® (Structure-Based Scaffold Generation) method, a unique computer algorithm for each binding site. HLHP is one of conformationally-constrained peptides and can be efficiently identified by dual approaches, rational design and random screening form phage-displayed peptide libraries.

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