AMPLIFY: Advancing Membrane Protein Learning for Improved Factorial Yield

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Hello, my name is Phil Stansfeld. I'm a Professor in Life Sciences and also the Department of Chemistry here at the University of Warwick, and I'm here to introduce our PhD programme called Amplify, which is a HetSys PhD project in collaboration with Alex Darlington in the School of Engineering. This project is focusing on a series of proteins that are known as membrane proteins.

These membrane proteins are found in 25% of ourselves, so they're one of the most widely found protein across life, and because of that reason, they're also the target for about 50% of pharmaceutical drugs. Now, for the purpose of this PhD project, what we want to do is optimise these membrane proteins using computational tools that you'll develop as over the course of your PhD, and this is the current research group. We're based up on Gibbett Hill, which is one of the campuses of the University of Warwick, and we're based in a brand new building called the Interdisciplinary Biosciences Research Building.

My research group is made up of about six postdoctoral researchers and currently about six PhD students. What we want to do is use molecular dynamics simulations to study membrane protein structures, and these membrane protein structures will either come from experimental measurements or alternatively using machine learning-based approaches to develop these protein structures, and what we want to do is to take these frozen snapshots of these proteins to then breathe life into them using molecular simulations to show how drug molecules bind and also how these membrane proteins interact with the lipid bilayer.

Our overall goal is to optimise these proteins, suggest changes that could be made to the protein structures to increase their overall stability, but also to increase their overall yield, and so we ultimately want to develop a computational tool that will do this, and we can then collaborate with experimental colleagues who will use our tool to then propose and get either structures of these proteins or otherwise develop functional assays to understand, for example, how drugs bind to these proteins.

If you have any questions about this overall project, do please email either myself or otherwise Alex Darlington to discuss more. Thank you for your time.