

New protein structure model to inhibit cancer

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Researchers at the University of Hertfordshire have developed a new structural model of a protein, which makes it possible to develop more effective drugs to target diseases such as cancer, heart disease and influenza.

In a paper which will be published in the *Journal of [Structural Biology](#)* online later this month, a research team lead by Dr. Andreas Kukol at the University's School of Life Sciences, describes how they have developed a new 3D model of a [protein](#) which unleashes the inhibition of the growth of cells which, unless stunted, could lead to the spread of cancer or support infections such as [influenza](#).

“Our bodies are made up of proteins and therefore they are important for the proper functioning of the body,” said Dr. Kukol. “Malfunction of the protein can lead to cancer. This happens when it becomes over active, so our task has been to identify inhibitors.”

A research team led by Dr. Kukol developed a 3D model of the kinase IKK- β enzyme which is a protein that regulates other proteins.

“This enzyme controls proteins like policeman controls traffic,” said Dr. Kukol. “If the policeman or the enzyme gets out of control, then there will be chaos.”

The new 3D model can be used to find new inhibitors, such as organic molecules like aspirin that attach to the active site of the enzyme and make it less active thus stopping the spread of cancer or influenza.

The model is now ready for pharmaceutical companies to adopt so that they can develop more effective drugs to target these conditions. Dr. Kukol explained that the comparative modeling and computer simulation methods they used for this protein may be taken up by other research groups. In that way protein structure modelling could lead to more accurate models in the future.

Provided by University of Herfordshire

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