Biochemists devise new technique for blueprinting cell membrane proteins

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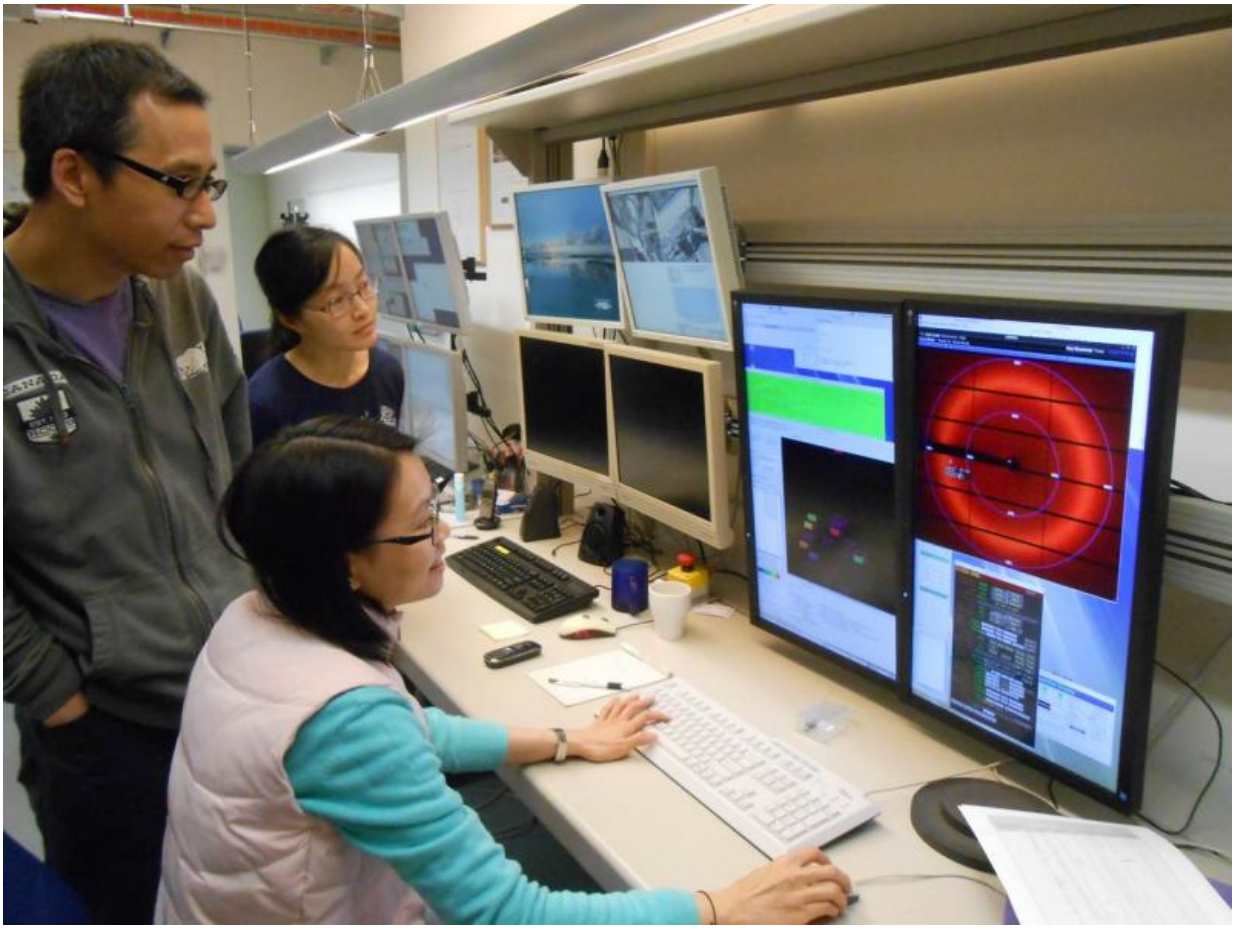

Biochemists from Trinity College Dublin have devised a new technique

that will make the difficult but critical job of blueprinting certain proteins considerably faster, easier and cheaper.

The breakthrough will make a big splash in the field of drug discovery and development, where precise protein structure blueprints can help researchers understand how individual proteins work. Critically, these blueprints can show weaknesses that allow drug developers to draw up specific battle plans in the fight against diseases and infections.

Professor of Membrane Structural and Functional Biology at Trinity, Martin Caffrey, is the senior author of the research, which has just been published in the international peer-reviewed journal *Acta Crystallographica D*.

He said: "This is a truly exciting development. We have demonstrated the method on a variety of cell membrane proteins, some of which act as transporters. It will work with existing equipment at a host of facilities worldwide, and it is very simple to implement."

Over 50% of drugs on the market target cell membrane proteins, which are vital for the everyday functioning of complex cellular processes. They act as transporters to ensure that specific molecules enter and leave our cells, as signal interpreters important in decoding messages and initiating responses, and as agents that speed up appropriate responses.

The major challenge facing researchers is the production of large membrane protein crystals, which are used to determine the precise 3-D structural blueprints. That challenge has now been lessened thanks to the Trinity biochemists' advent - the in meso in situ serial crystallography (IMISX) method.

Beforehand, researchers needed to harvest protein crystals and cool them at inhospitable temperatures in a complex set of events that was

damaging, inefficient and prone to error. The IMISX method allows researchers to determine structural blueprints as and where the crystals grow.

Professor Caffrey added: "The best part of this is that these proteins are as close to being 'live' and yet packaged in the crystals we need to determine their structure as they could ever be. As a result, this breakthrough is likely to supplant existing protocols and will make the early stages of drug development considerably more efficient."

More information: journals.iucr.org/d/issues/201 … /06/00/issconts.html

Provided by Trinity College Dublin