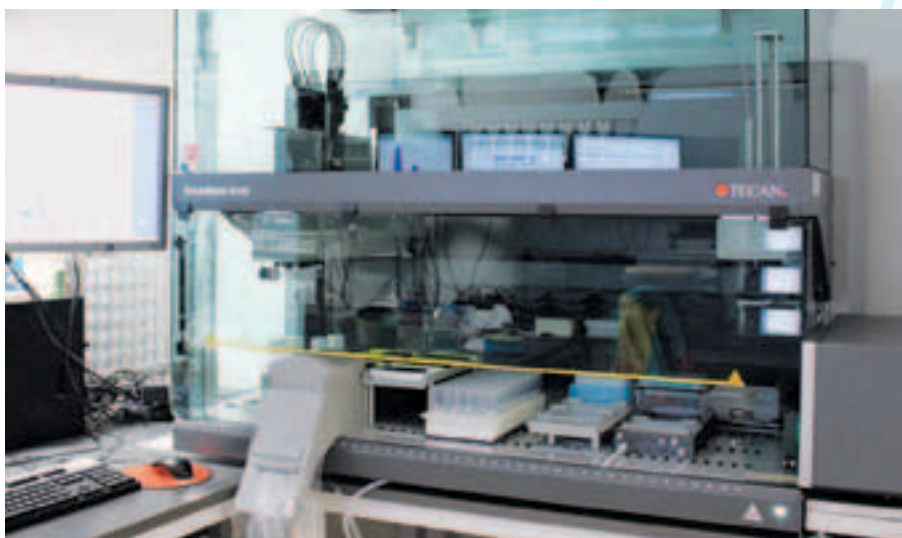


# Crystal clear results

The Protein Expression Purification Crystallization Core at Case Western Reserve University is designed to perform high throughput crystallization trials, taking advantage of the automation capabilities of Tecan's CrysScreen™ software and Freedom EVO® liquid handling platform to optimize crystallization parameters.



Dr Harry Gill, Director of the PECC laboratory



PECC Freedom EVO workstation

The Protein Expression Purification Crystallization Core (PECC) at Case Western Reserve University, Ohio, is a state-of-the-art automated facility designed to help researchers optimize protein crystallization for X-ray crystallography analysis. High throughput technologies are vital for rapid determination of optimal crystal growth conditions, allowing fast formulation of precisely controlled precipitation conditions and minimizing the quantity of protein and reagents required. Dr Harry Gill, Assistant Professor and Director of the PECC, explained: "Protein crystallization is an empirical science, requiring thousands of solution compositions to be tested for each protein to establish the optimal conditions for generation of protein crystals with well formed lattices that diffract X-rays. The advent of rapid genetic sequencing technologies means that many structural genomics laboratories and consortia are now looking at the three dimensional structures of

proteins on a genome-wide scale. The high throughput offered by laboratory automation is essential for these large scale studies, precisely controlling not just the concentrations and ratios of the target protein, buffers and precipitants, but also the liquid handling characteristics which can significantly influence crystal formation. Automation minimizes the variation inherent in manual techniques, and helps us to rapidly identify the conditions needed to crystallize a particular protein."

"The PECC was established to provide a highly efficient system for elucidating crystallization conditions for a variety of soluble and membrane proteins, and we use a three step robotic workflow to perform large scale protein crystallization trials. The first step is drop-setting nanoliter amounts of protein onto 96-well plates using a mosquito® Crystal automated drop-setter (TTP LABTech). The plates are then incubated

in a Rock Imager (Formulatrix), a fully automated incubation and imaging system which has been specially designed for protein crystallization. Once a hit – evidence of crystallization – has been identified by this system, data is exported to our Freedom EVO workstation, and we use its CrysScreen software to design and prepare an experiment in which crystallization parameters – such as pH, salt and precipitant concentration – are adjusted to optimize crystal formation. This new set of parameters is then tested using the drop-setter and incubation system, and the cycle is repeated until a high quality crystal structure is achieved.”

“We have also taken advantage of the Freedom EVO’s flexibility to increase our productivity in other areas. It is one of the most versatile systems on the market, and our workstation is configured to perform high throughput plasmid preparation in addition to optimization of crystallography. We also have an Infinite® M1000 multimode plate reader incorporated onto the Freedom EVO platform, enabling us to rapidly screen large libraries of DNA clones and to perform a broad range of spectrophotometric assays. The ability to fully integrate this reader into the Freedom EVO is a real bonus, as the Infinite M1000 is probably the most sensitive multimode instrument on the market for measurements in the deep UV spectrum. These measurements would normally have to be performed in a fluorometer to achieve the necessary sensitivity, requiring tedious manual reading of individual cuvettes. The Infinite reader is able to offer the same performance in an automation-friendly 96-well format, thanks to its premium Quad4 Monochromators™.

This instrument really is at the cutting edge of reader design, and is an indispensable tool in my research.”

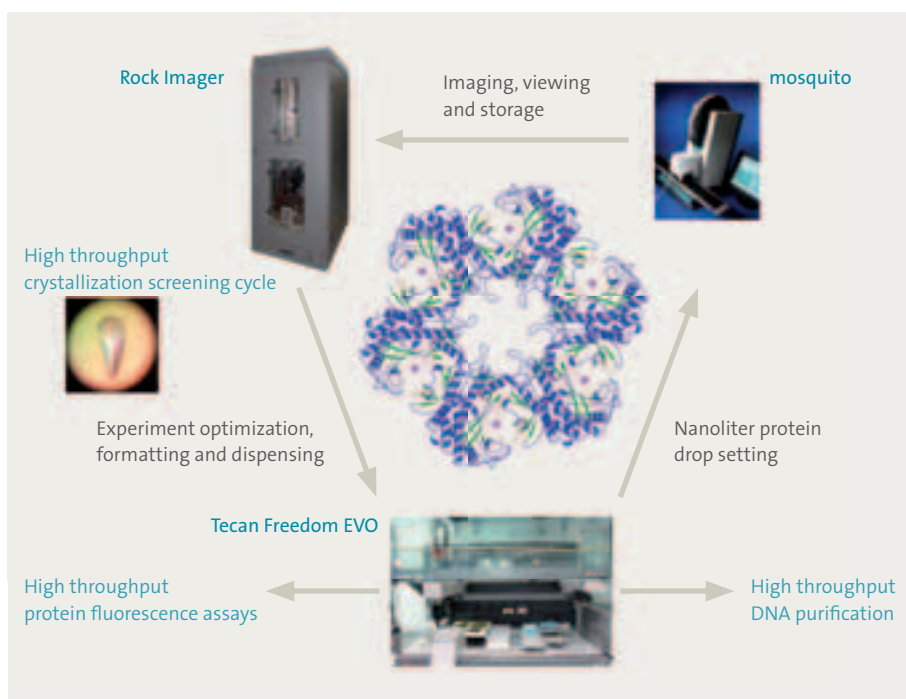
Harry concluded: “Automation of high throughput crystallization trials is crucial, ensuring accurate pipetting while minimizing the amount of protein required for each experiment. When we originally set up the PEPC, we evaluated a variety of liquid handling systems for this role. The availability of the specialized CrysScreen software, together with the flexibility of the Freedom EVO platform, made the Tecan system an obvious choice for this role. Thanks to CrysScreen, we are able to set up crystallization trials very quickly, achieving in minutes what would have taken almost a week to perform manually.”

Dr Gill would like to thank LCDR Matthew Swiergosz for his assistance with the Defense University Research Instrumentation Program (DURIP) awards and Char Rogge for her assistance with Action and Investment Funds created by the Ohio Board of Regents.

To find out more about Tecan’s Freedom EVO workstations, go to [www.tecan.com/freedomevo](http://www.tecan.com/freedomevo)

To learn more about the PEPC, visit [www.pepcc.case.edu](http://www.pepcc.case.edu)

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PEPC protein crystallization workflow