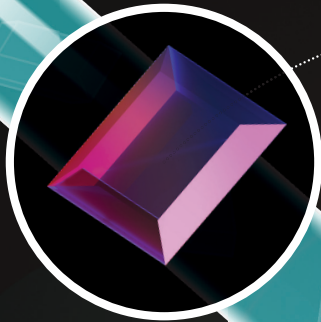
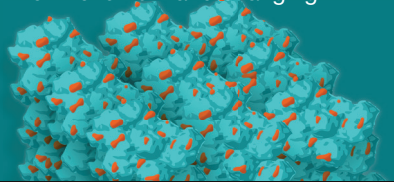


Viewing proteins in motion with time-resolved crystallography

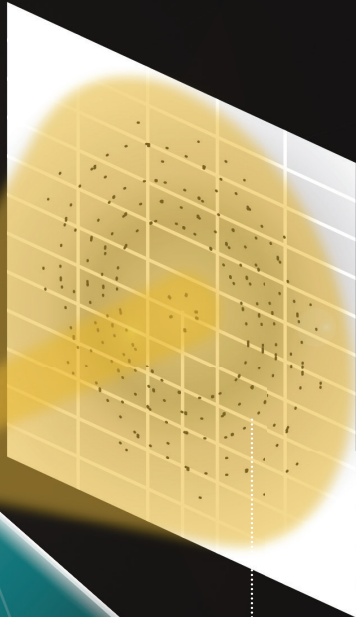
Time-resolved crystallography allows scientists to study how a protein's shape changes during a reaction. Scientists use a laser to trigger the reaction, and then an X-ray beam to capture a series of snapshots of the protein as the reaction unfolds. They can then put those snapshots together to create a movie of the molecule in action.

Protein crystal
A protein crystal consists of regularly arranged protein molecules. It also contains a lot of solvent, which gives the molecules space for a small amount of movement and changing shape.



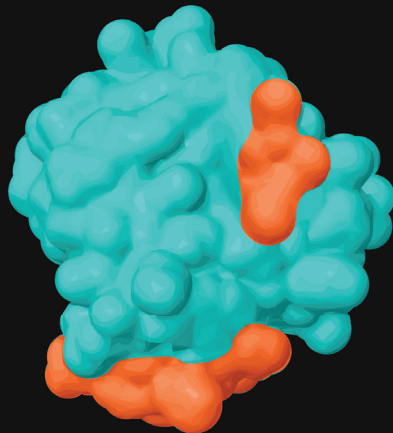
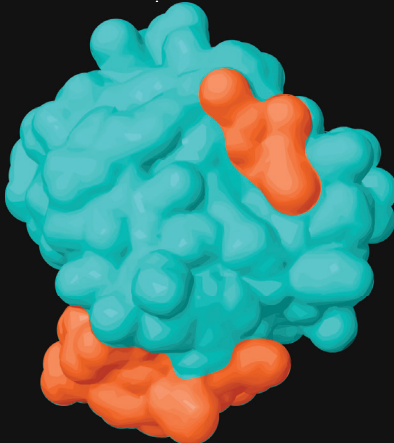
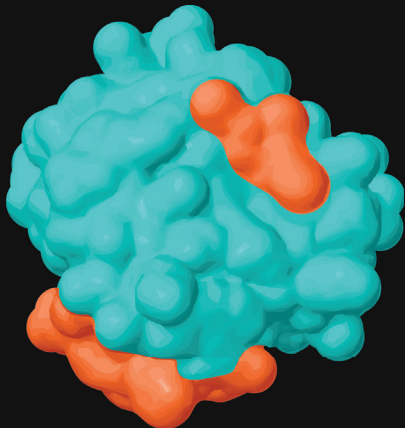
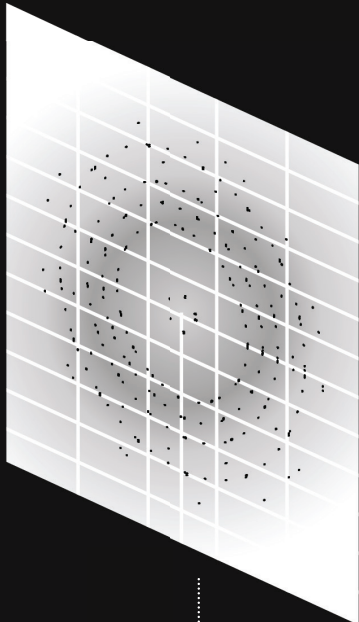
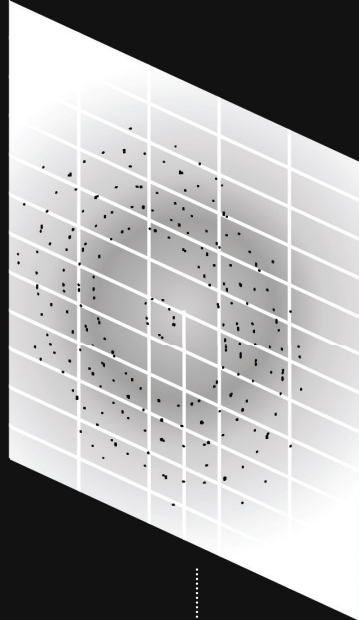
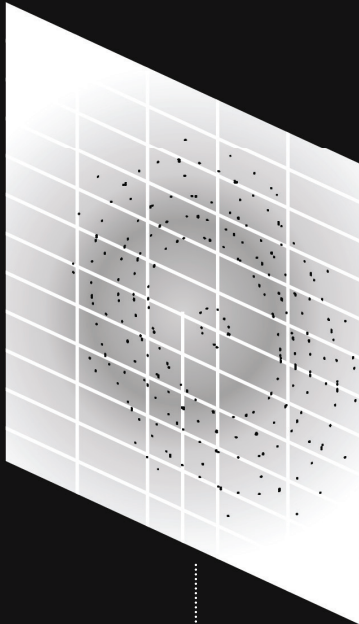
Laser
A trigger, such as a laser, is used to prompt the protein to change shape.

Crystal microjet



Diffraction pattern

X-ray
At one or more time slots after the initial trigger, the X-ray beam is used to analyse the structure of the protein.



Protein Structure Model

Snapshots
When the X-ray beam passes through the protein crystal it is deflected off course by the atoms in the protein. This produces a distinct pattern which can be used to build a model of the protein structure. In time-resolved crystallography, a different pattern is produced at each time slot. This series of snapshots can be put together to show a movie of the protein in motion.