# X-ray crystallography resolves the marine carbon cycle at atomic resolution


Structural biology explores the structure of macromolecules such as proteins or nucleic acids like DNA. This research field requires the combination of molecular biology, biochemistry and biophysics in order to enhance our understanding of the function and interaction of such molecules. At present, X-ray crystallography is one of the most favorable methods to determine the 3D structure of macromolecules. For this approach, a soluble macromolecule needs to be crystallized to obtain a crystal, which is then exposed to X-ray beams at a synchrotron (a cyclic particle accelerator). In my PhD project, I use this technique at the German Electron Synchrotron (DESY) in Hamburg to reveal detailed insights into the function of bacterial enzymes which degrade algal polysaccharides that are relevant in the carbon cycle. Polysaccharides are one of the main components in many algae species. Due to the recycling of algal polysaccharides by marine bacteria, organic material becomes accessible to the marine food web and important biogeochemical processes like the global carbon cycle affecting all life on Earth.

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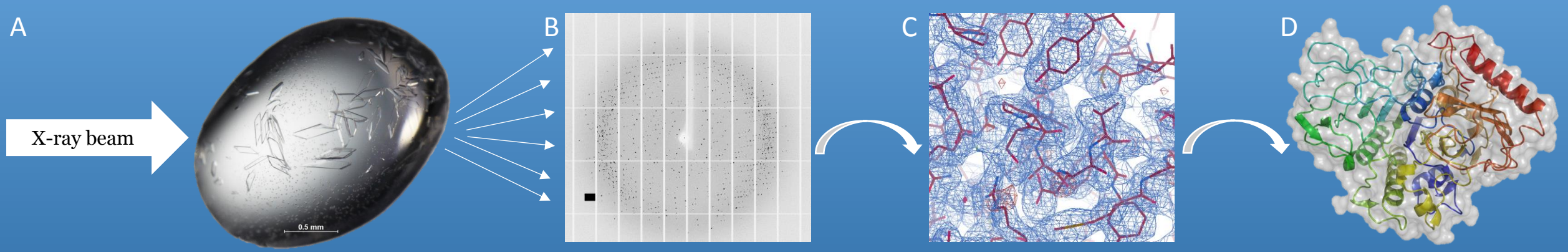


Protein crystals shot with a X-ray beam (A) leave a specific diffraction pattern in form of dark spots on a detector (B). Analysing hundreds of those images from different angles of the crystal results in a density map of the electrons (C), which is used to build the 3D protein structure (D) by incorporating each single amino acid into the electron density map.