CHAPTER OVERVIEW

9: Chemical Bonding II - Advanced Bonding Models

In 1912, Max von Laue, at the University of Munich in Germany, postulated that atoms in a crystal lattice had a regular, periodic structure with interatomic distances on the order of 1 A. Without having any evidence to support his claim on the periodic arrangements of atoms in a lattice, he further postulated that the crystalline structure can be used to diffract x-rays, much like a gradient in an infrared spectrometer can diffract infrared light. His postulate was based on the following assumptions: the atomic lattice of a crystal is periodic, x- rays are electromagnetic radiation, and the interatomic distance of a crystal are on the same order of magnitude as x- ray light. Laue's predictions were confirmed when two researchers: Friedrich and Knipping, successfully photographed the diffraction pattern associated with the x-ray radiation of crystalline copper (II) sulfate pentahydrate - and the science of x-ray crystallography was born. X-ray crystallography remains to this day the primary tool used by researchers in characterizing the structure and bonding of various compounds. In this Chapter, we will discuss the more advanced bonding models that predict molecular structures in three dimensions.

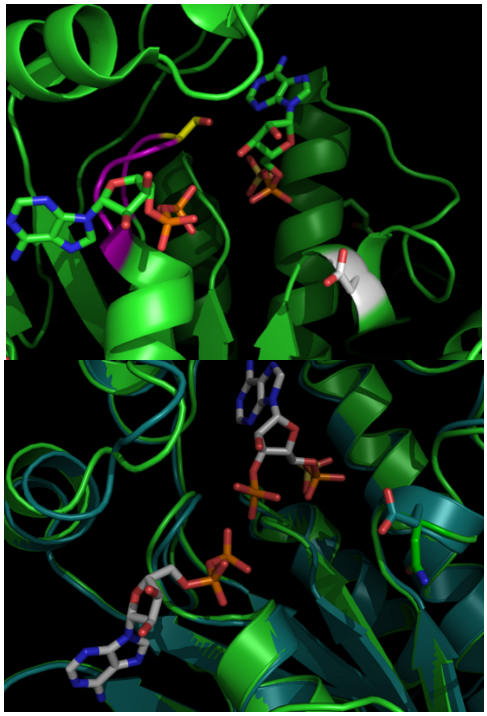

Figure 1: This is the structure of APS Kinase co-crystallized with ligands ADP and APS created via pymol by an undergrad working in the Structural Biology lab at UC Davis; Bottom right) This is the mutant overlay of APS kinase. The teal is the wild - type and the lime green is the mutant. D63 (from the wild-type) is mutated to asparagine. Images created by pymol by an undergrad working in the Structural Biology lab at UC Davis.

Chapter Sections

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