## IMPACT OF 3<sup>RD</sup> GENERATION SYNCHROTRON SOURCES ON STRUCTURAL BIOLOGY

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The three-dimensional structures determined by crystallography play a central role understanding protein-small molecule and proteinprotein interactions at the molecular level. Accurate details of such interactions have direct implications for drug design and development of other biomedical treatments. Consequently, during the past 15 years the protein structure determination by X-ray crystallography has increased about 8-fold. The use of synchrotron radiation was critical for this growth, as the fraction of macromolecular structures reporting the use of synchrotron radiation increased from 30% in 1990 to 88% in 2009. The superiority of the results obtained with the use of synchrotron radiation increases the pressure to build more stations dedicated for protein crystallography. Thus, the number of proteincrystallography-dedicated synchrotron stations has risen from 8 in 1985 to more than 120 worldwide, and there

are more than 20 stations either under construction or planned to be built in the near future. While this increase the number of stations was important, other advancements in technology and procedures were even more critical for the rapid growth of protein crystallography. These advancements include increases of beam intensity and improvements of beam tunability, better detectors, increased computational capacity and better software, and most importantly, improved data collection/processing protocols. An experimental protocol is a result of a compromise between the ideal experiment possible and the various practical limitations encountered at the beamline. The difficulty implementing the best experimental protocols can be illustrated by the sharp differences in productivity of technologically similar synchrotron beamlines. In this talk I will discuss factors influencing synchrotron beamline productivity.