

5.5. THE USE OF mmCIF ARCHITECTURE FOR PDB DATA MANAGEMENT

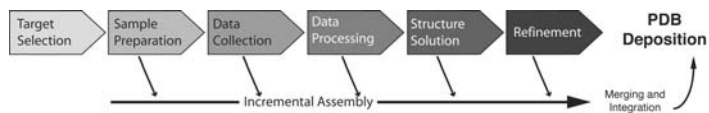


Fig. 5.5.3.5. Schematic diagram of a structure-determination data pipeline.

data file ready for deposition. The *PDB_EXTRACT* program also carries out this merging operation.

Some steps in the structure-determination pipeline may not be driven by software. For instance, the details of protein production may be held in laboratory databases or within laboratory notebooks. A version of *ADIT* with a data view including all of the structural genomics data extensions has been created for entering these data. This *ADIT* tool can also be used to validate and check the completeness of the final data file.

5.5.4. Access

All of the software tools and libraries described in this chapter are distributed with full source under an open-source licence. Applications are also distributed in binary form for Intel/Linux, Sun/Solaris, SGI/IRIX and Dec Alpha platforms.

The RCSB/PDB is operated by Rutgers, The State University of New Jersey; the San Diego Supercomputer Center at the University of California, San Diego; and the Center for Advanced Research in Biotechnology of the National Institute of Standards and Technology. RCSB/PDB is supported by funds from the National Science Foundation (NSF), the National Institute of General Medical Sciences (NIGMS), the Department of Energy (DOE), the National Library of Medicine (NLM), the National Cancer Institute (NCI), the National Center for Research Resources (NCRR), the National Institute of Biomedical Imaging and Bioengineering

(NIBIB), and the National Institute of Neurological Disorders and Stroke (NINDS).

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