 Structures of many complex biological assemblies are increasingly determined using integrative approaches, in which data from multiple experimental methods are combined. Based on recommendations from the worldwide Protein Data Bank (wwPDB) integrative/hybrid methods task force, a standalone prototype system, called PDB-Dev, has been built for archiving integrative structures and making them publicly available [1]. Data standards and software tools have been developed for collecting, curating, validating, visualizing, archiving, and disseminating integrative structures that span diverse spatiotemporal scales and conformational states. Mechanisms have been created to validate integrative structures based on the experimental data underpinning the structure. Building upon the foundational framework, PDB-Dev has been further expanded to handle large dynamic macromolecular ensembles and integrative structures that combine experimental restraints with initial structural models computed by deep learning algorithms. Data standards and supporting tools have been extended to capture information regarding conformational dynamics and related kinetic data derived from biophysical methods. Following the FAIR (Findable, Accessible, Interoperable and Reusable) principles, PDB-Dev ensures that the results of integrative structure determination are freely accessible to everyone. Work is in progress to merge the PDB-Dev structures and supporting software tools with the PDB archive so that integrative structures can be disseminated widely through the PDB.


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