

Structural and Functional Classification of RNA Structures: Efforts and Applications

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One of the important goals of biological investigation is to classify and organize the experimental findings so that they are readily useful for deriving generalized rules.

Although there is a huge amount of information on RNA structures in PDB, there are redundant files, ambiguous synthetic sequences etc. Moreover, a systematic hierarchical

organization, reflecting RNA classification, is missing in PDB. The previous attempts were partially successful as regular updating the huge information was difficult for any small project. In this investigation, we have classified all the available RNA crystal structures from PDB through a programmatic approach. Hence, it would be now a trivial assignment to regularly update the classification as and when new structures are released. The classification can further determine (i) a non-redundant set of RNA structures and (ii) if available, a set of structures of identical sequence and function, which can highlight structural polymorphism, ligand-induced conformational

alterations etc. Presently, we have classified the available structures (1084 PDB entries having RNA chain longer than 9 nucleotides solved by X-ray crystallography at 3.5Å or better resolution) into nine functional classes and found 386 nonredundant files. The structures of same function and same source are mostly seen to be similar with subtle differences depending on their functional complexation. The web-server is available online at <http://www.saha.ac.in/biop/www/HD-RNAS.html> and is updated monthly. We could also predict possible function of some RNA structures through comparison of base pairing patterns with the set of non-redundant structures.