A prototyp – based evolutionary tree for zinc finger domains

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Zinc finger domains are protein structures first identified in the Xenopus transcription factor TFIIIA. A zinc finger is composed of 20 to 30 amino – acid residues. There are two residues at both extremities of the domain which are involved in the tetrahedral coordination of a zinc atom. It has been proposed that such a domain interacts with the DNA. Many classes of zinc fingers are characterized according to the number and positions of the histidine and cysteine involved in the zinc atom coordination [1],[2].
All biological disciplines are united by the idea that species share a common history. The use of evolutionary trees is a valued means in many biological problems, such as sequence alignments, protein structure and function prediction etc.
We construct an algorithm to firstly isolate the zinc finger domains from proteins. Using Case – Based Reasoning we generate an evolutionary tree. The architecture of the tree is based on the context – specific definition of different levels of prototyps (zinc finger families).

References

[1] **A. Klug, J. W. R. Schwabe**
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[2] **http://expasy.hcuge.ch/**