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**Promising Themes for Structural Bioinformatics and Computer Aided-Drug Design**

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There remain many promising themes for structural bioinformatics and computer aided-drug design. The prediction of protein-backbone conformation has dramatically been improved during 1995 to 2010. The patterns of backbone structure for domain are known to be only 1,000-2,000. However, the reason of that number has not been interpreted. If we can find that theory, we can categorize the proteins present now, and will be able to make new proteins. The promising theme is the prediction of side chain conformation. This will lead to the discovery of new function of unknown protein. Protein function has also many themes for structural bioinformatics and computer aided-drug design. Those themes include transition state of enzyme, binding and releasing steps of enzyme reaction, hydrophobic substrate recognition, bi-functional activity, and other curious enzyme mechanisms.

The final theme will be the whole-body prediction of organisms, including human.

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