Further development of profile–profile alignment methods for protein structure prediction

We had developed our own profile-profile comparison method, FORTE1 to make use of known structural information for protein structure prediction. The FORTE1 system utilizes the correlated coefficient as a similarity measurement between two profile columns to be compared. Our team employed several descendants of our unique profile-profile comparison method (FORTE Method; Patent Pending) – and won the third place, and was invited to give a presentation of our achievements in CASP6, the 2004 Olympic games of protein structure prediction. The techniques developed by us are expected to be applied to infer protein structures and functions for genes whose information will become more available through the genome projects.

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Fig. An example of the prediction result (PDB ID:1WGB) using the FORTE method in CASP6.
A thick line shows our prediction model and a thin line shows the native structure.