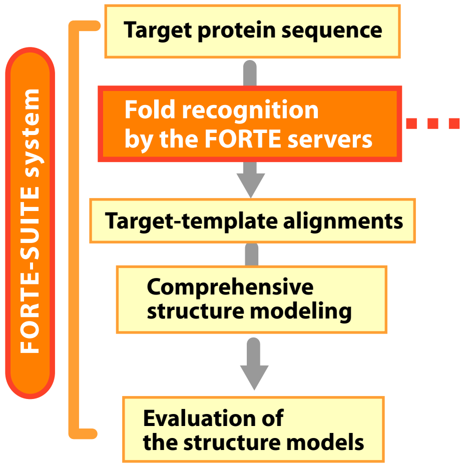
CASP6
- Critical Assessment of Techniques for Protein Structure Prediction

The CBRC-3D team (Kentaro Tomii, Takatsugu Hirokawa, Chie Motono) from CBRC took 3rd place in the "Fold Recognition" division of CASP6 and was invited to give a talk at the conference in Italy (4th to 8th Dec. 2004). This is a splendid achievement given over 200 participants and because international competition became increasingly more intense. This achievement comes after a six-year absence of any Japanese institutes winning this honor.
Another team from the CBRC, CBRC-DR (Tamotsu Noguchi, Shuichi Hirose, Kana Shimizu, Kentaro Tomii) were awarded 4th place in the "Domain Prediction" division.

【The system CBRC-3D team has applied】

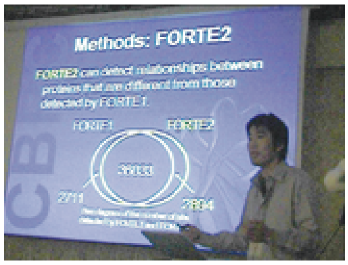


The *FORTE* method is...

An algorithm used to accurately align a target protein profile against a protein profile of known structure using a correlation coefficient to measure similarities.

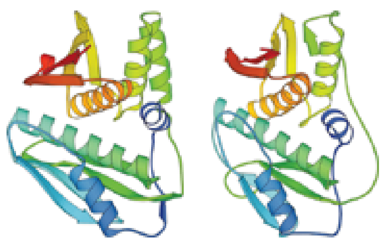
Good points

The need for increased predictive capacity and alignment accuracy became apparent after analyzing a vast amount of sequence data derived from the genome project.
It has been refined in designing the similarity measure, and also powered up by large number of complete and partial protein profiles, updated frequently by parallel computing technology.



Tomii, giving a lecture at the CASP6 conference in Italy

CBRC-3D (from left Hirokawa, Motono and Tomii)



Left) Predicted structure of one of the targets (T0223)
Right) Native protein structure

In the "Fold Recognition" division, the task was to predict the tertiary structure of a target protein from its amino acid sequence by finding the best match fold to its native structure from the Protein Data Bank using advanced sequence searches and fold-recognition techniques.
CBRC-3D used **FORTE** (described above) - a novel fold-recognition technique - and achieved the result of this time. This technology, used to predict 3D protein structure, holds considerable promise for predicting the structure and function of the ever-increasing number of genes being discovered in the genome project.

[Refereneces]
＊1) JP-AN 2002-377704, "System for Predicting Three-dimensional Structure of Protein", Kentato Tomii (26th Dec.2002)
＊2) Tomii, K., Akiyama, Y.: "FORTE: a profile-profile comparison tool for protein fold recognition", *Bioinformatics*, **20** (4), pp.594-595 (2004).
＊3) http://www.cbrc.jp/forte

What's CASP・・・?

CASP is an international experiment held every two years to evaluate the accuracy of methods used to predict protein structure by blind testing. Protein sequences just before X-ray or NMR analysis were posted on the Internet and participants sent in their 3D structure predictions for the given sequence. A total of 87 target sequences were set for questions in CASP6 from June to September and 224 teams and 65 servers from all over the world participated in it.

Moving to the new building

The recently completed "AIST Tokyo Waterfront Bio-IT Research Building", which now stands next to the AIST Tokyo Waterfront Main Building, houses researchers and projects directed at furthering our bio-IT research in Bioinformatics as well as collaborative efforts between industry, academia and government.
We have moved into the 1st, 8th, 9th and 10th floors of the building on the 14th February. Some of the teams will continue to use the 1st floor of the main building.
Please note our new address below.

2-42 Aomi, Koto-ku, Tokyo, 135-0064, Japan
(The telephone and fax numbers were not changed.)