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- (CE, SSAP, MODELER, Predator, , …)

    docking
- (PDB, SCOP, CATH,FSSP,DSSP , SWISSPROT, …)

    StEQ

    SSDB
- 3D

The structure bioinformatics core is available from

http://bioinfo.life.nctu.edu.tw/index.php. The snapshot of the webpage is shown
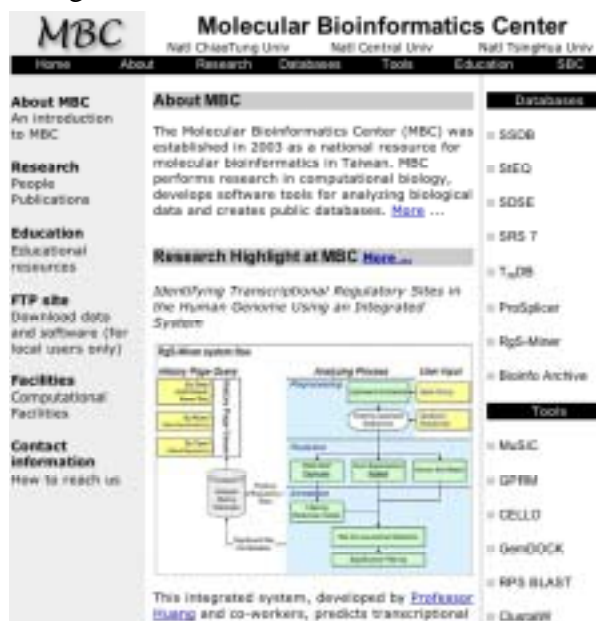
in Fig. 1.

Fig. 1 the snapshot of the structure bioinformatics core

The currently available bioinformatics services:

CELLO: subcellular localization prediction server (Fig.2)

Website: http://cello.life.nctu.edu.tw

Usage: CELLO presently handles protein sequences from Gram-negative bacteria and Eukarytic proteins only for version 2.1. We provide other prediction servies for other organism later.

Reference: Yu CS, Lin CJ, Hwang JK, Predicting Subcellular Localization of Proteins For Gram-Negative Bacteria by Support Vector Machines Based on n-Peptide Compositions. Protein Science (2004), 13, 1402-1406
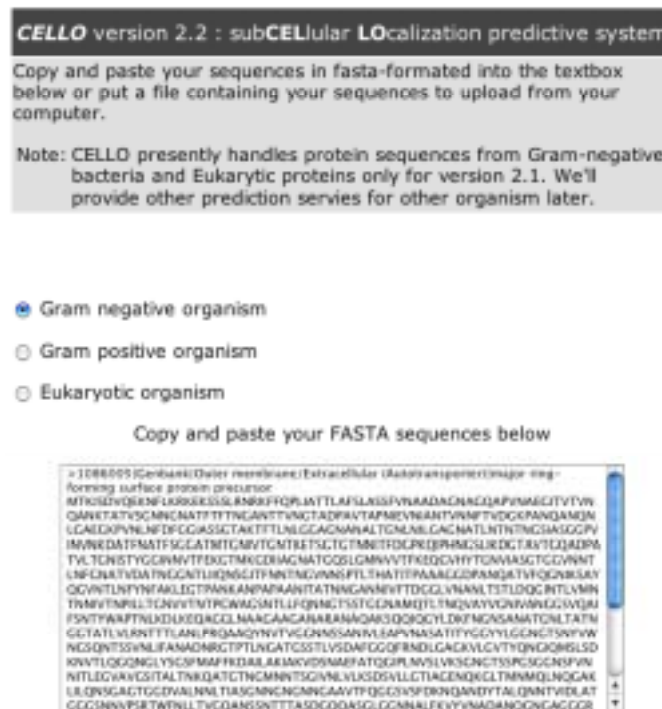

Fig. 2 The snapshot of the homepage of CELLO

SSDB: Database of disulfide patterns (Fig.3)

Website: http://e106.life.nctu.edu.tw/~ssbond/

Usage: The disulfide bonding patterns can be used to discriminate structure similarity. Our method, based on the hierarchical clustering scheme, is applicable to proteins with two or more disulfide bonds and is able to detect the structural similarities of proteins of low sequence identities (<25%). Our results show the surprisingly close relationship between disulfide-bonding patterns and proteins structures.

Reference: C-C. Chuang, C-Y Chen, J.-M. Yang, P.-C. Lyu, J.-K. Hwang, Relationship between protein structures and disulfide-bonding patterns. Proteins: Structure, Function and Genetics (2003), 53, 1-5.
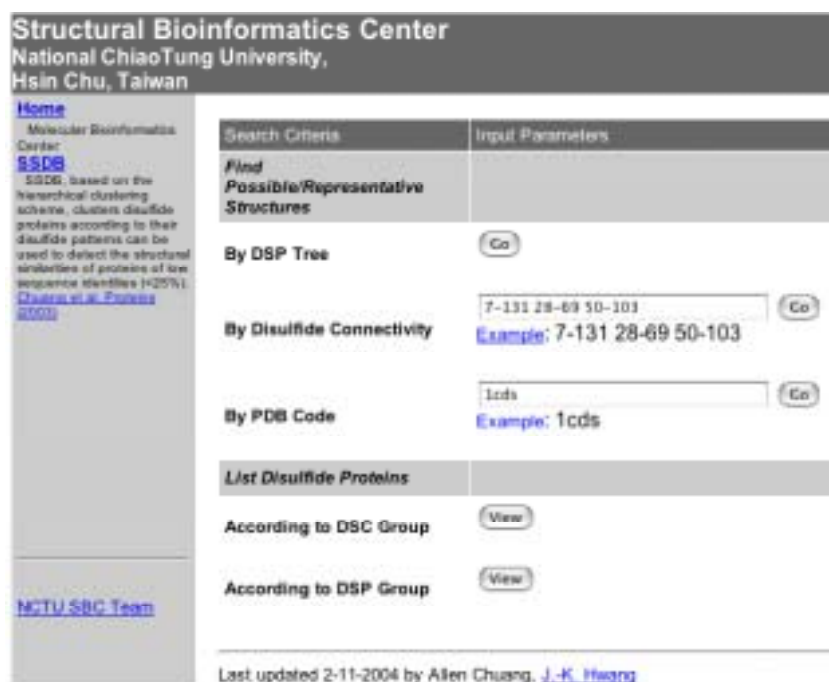
Fig. 3 The snapshot of the homepage of SSDB

SDSE: Sequence derived structural entropy (Fig.4)

Website: http://sdse.life.nctu.edu.tw/

Usage: To compute the structural entropy directly from protein sequences. The structural entropy is useful in identifying locally stable sequence fragment and in assisting protein structure design.

Reference: (1) Chan CC, Liang HK, Hsiao NW, Ko MT, Lyu PC, Hwang JK. The relationship between local structural entropy and protein thermostability. Proteins: Structure, Function and Bioinformatics (2004) 57, 684-691. (2) Liang HK, Huang CM, Ko MT, Hwang JK. The Amino Acid-Coupling Patterns in Thermophilic Proteins. Proteins: Structure, Function and Bioinformatics (2005), forthcoming.
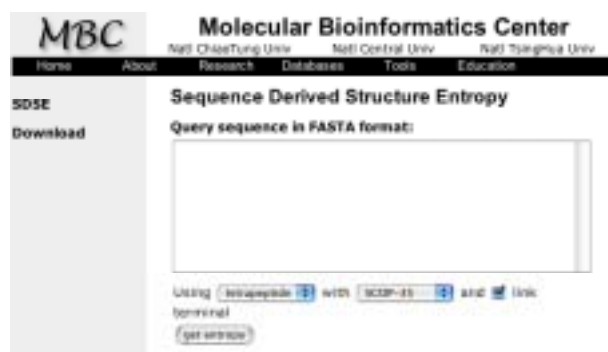

Fig. 4 The snapshot of the homepage of SDSE

PS²: Protein Structure Prediction Server (Fig.5)

Website: http://ps2.life.nctu.edu.tw/

Usage: Automated comparative protein structure prediction server using consensus sequence-profile alignment.

Reference: Chen *et al.* submittted.

Fig. 5 The snapshot of the homepage of PS2

The mirror sies

We have also provided the mirror site services: PDB mirror site: http://pdb.life.nthu.edu.tw/, SCOP mirror site: http://scop.life.nthu.edu.tw/ ; The PredictProtein server: http://biobug.life.nthu.edu.tw/predictprotein/index2.html

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